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(54) Primers for synthesising full-length cDNA and their use

(57) Primers for synthesizing full-length cDNAs and their use are provided.

5602 cDNA encoding a human protein has been isolated and nucleotide sequences of 5'-, and 3' -ends of the cDNA have been determined. Furthermore, primers for synthesizing the full-length cDNA have been provided to clarify the function of the protein encoded by the cDNA. The full-length cDNA of the present invention containing the translation start site provides information useful for analyzing the functions of the protein.

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Description

FIELD OF THE INVENTION

[0001] The present invention relates to a polynucleotide encoding a novel protein, a protein encoded by the polynucleotide, and new uses of these.

BACKGROUND OF THE INVENTION

[0002] Currently, the sequencing projects, the determination and analysis of the genomic DNA of various living organisms have been in progress all over the world. The whole genomic sequences of more than 10 species of prokaryotes, a lower eukaryote, yeast, and a multicellular eukaryote, C. elegans are already determined. As to human genome, which is supposed to be composed of three thousand million base pairs, the world wide cooperative projects have been under way to analyze it, and the whole structure is predicted to be determined by the years 2002-2003. The aim of the determination of genomic sequence is to reveal the functions of all genes and their regulation and to understand living organisms as a network of interactions between genes, proteins, cells or individuals through deducing the information in a genome, which is a blueprint of the highly complicated living organisms. To understand living organisms by utilizing the genomic information from various species is not only important as an academie subject, but also socially significant from the viewpoint of industrial application.

[0003] However, determination of genomic sequences itself cannot identify the functions of all genes. For example, as for yeast, only the function of approximately half of the 6000 genes, which is predicted based on the genomic sequence, was able to be deduced. As for human, the number of the genes is predicted to be approximately one hundred thousand. Therefore, it is desirable to establish "a high throughput analysis system of the gene functions" which allows us to identify rapidly and efficiently the functions of vast amounts of the genes obtained by the genomic sequencing.

[0004] Many genes in the eukaryotic genome are split by introns into multiple exons. Thus, it is difficult to predict correctly the structure of encoded protein solely based on genomic information. In contrast, cDNA, which is produced from mRNA that lacks introns, encodes a protein as a single continuous amino acid sequence and allows us to identify the primary structure of the protein easily. In human cDNA research, to date, more than one million ESTs (Expression Sequence Tags) are publicly available, and the ESTs presumably cover not less than 80% of all human genes.

[0005] The information of ESTs is utilized for analyzing the structure of human genome, or for predicting the exon-regions of genomic sequences or their expression profile. However, many human ESTs have been derived from proximal regions to the 3'-end of cDNA, and information around the 5'-end of mRNA is extremely little. Among these human cDNAs, the number of the corresponding mRNAs whose encoding protein sequences are deduced is approximately 7000, and further, the number of full-length therein is only 5500. Thus, even including cDNA registered as EST, the percentage of human cDNA obtained so far is estimated to be 10-15% of all the genes.

[0006] It is possible to identify the transcription start site of mRNA on the genomic sequence based on the 5'-end sequence of a full-length cDNA, and to analyze factors involved in the stability of mRNA that is contained in the cDNA, or in its regulation of expression at the translation stage. Also, since a full-length cDNA contains ATG, the translation start site, in the 5'-region, it can be translated into a protein in a correct frame. Therefore, it is possible to produce a large amount of the protein encoded by the cDNA or to analyze biological activity of the expressed protein by utilizing an appropriate expression system. Thus, analysis of a full-length cDNA provides valuable information which complements the information from genome sequencing. Also, full-length cDNA clones that can be expressed are extremely valuable in empirical analysis of gene function and in industrial application.

[0007] Therefore, if a novel human full-length cDNA is isolated, it can be used for developing medicines for diseases in which the gene is involved. The protein encoded by the gene can be used as a drug by itself. Thus, it has great significance to obtain a full-length cDNA encoding a novel human protein.

[0008] In particular, human secretory proteins or membrane proteins would be useful by itself as a medicine like tissue plasminogen activator (TPA), or as a target of medicines like membrane receptors. In addition, genes for signal transduction-associated proteins (protein kinases, etc.), glycoprotein-associated proteins, transcription-associated proteins, etc. are genes whose relationships to human diseases have been elucidated. Moreover, genes for disease-associated proteins form a gene group rich in genes whose relationships to human diseases have been elucidated.

[0009] Therefore, it has great significance to isolate novel full-length cDNA clones of human, only few of which has been isolated. Especially, isolation of a novel cDNA clone encoding a secretory protein or membrane protein is desired since the protein itself would be useful as a medicine, and also the clones potentially include a gene associated with diseases. In addition, genes encoding proteins that are associated with signal transduction, glycoprotein, transcription, or diseases are expected to be useful as target molecules for therapy, or as medicines themselves. These genes form a gene group predicted to be strongly associated with diseases. Thus, identification of the full-length cDNA clones

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encoding those proteins has great significance.

SUMMARY OF THE INVENTION

[0010] An objective of the present invention is to provide a polynucleotide encoding a novel protein, a protein encoded by said polynucleotide, and novel usages of these.

[0011] The inventors have developed a method for efficiently cloning a human full-length cDNA that is predicted by the ATGpr etc. to be a full-length cDNA clone, from a full-length-enriched cDNA library that is synthesized by the oligo-capping method. Then, the inventors determined the nucleotide sequence of the obtained cDNA clones from both 5'- and 3'- ends.

[0012] Furthermore, the inventors analyzed the obtained clones by the BLAST search of the databases, SwissProt (http://www.ebi.ac.uk/ebi_docsSwissProt_db/swisshome.html), GenBank (http://www.ncbi.nlm.nih.gov/web/GenBank), and UniGene (Human) (http://www.ncbi.nlm.nih.gov/UniGene).

[0013] The full-length cDNA clones of the present invention have high fullness ratio since these were obtained by the combination of (1) construction of a full-length-enriched cDNA library that is synthesized by the oligo-capping method, and (2) a system in which the full-length ratio is evaluated from the nucleotide sequence of the 5'-end (selection based on the ATGpr, previously removed complete sequences to ESTs). However, the primer of the present invention enables to obtain full-length cDNA easily without any specialized methods as in the described method.

Homology analysis in which the analysis is carried out against a not-full-length cDNA fragment to postulate the function of a protein encoded by said fragment, is being commonly performed.

However, since such analysis is based on the information of the fragment, it is not clear as to whether this fragment corresponds to a part that is functionally important in the protein. In other words, the reliability of the homology analysis based on the information of a fragment is doubtful, as information related to the structure of the whole protein is not available. However, the homology analysis of the present invention is conducted based on the information of a full-length cDNA comprising the whole coding region of the cDNA, and therefore, the homology of various portions of the protein can be analyzed. Hence, the reliability of the homology analysis has been dramatically improved in the present invention.

[0014] The inventors completed the invention by finding that it is possible to synthesize a novel full-length cDNA by using the combination of a primer that is designed based on the nucleotide sequence of the 5'-ends of the selected full-length cDNA clones and any of an oligo-dT primer or a 3'-primer that is designed based on the nucleotide sequence of the 3'-ends of the selected clones.

[0015] Thus, the present invention relates to primers described below, a method for synthesizing a polynucleotide using the primers, and polynucleotides obtained by the method.

[0016] First, the present invention relates to

(1) use of an oligonucleotide as a primer for synthesizing the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-5547 and SEQ ID NOs: 16111-16164, or the complementary strand thereof, wherein said oligonucleotide is complementary to said polynucleotide or the complementary strand thereof and comprises at least 15 nucleotides;

(2) a primer set for synthesizing polynucleotides, the primer set comprising an oligo-dT primer and an oligonucleotide complementary to the complementary strand of the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-5547 and SEQ ID NOs: 16111-16164, wherein said oligonucleotide comprises at least 15 nucleotides; and

(3) a primer set for synthesizing polynucleotides, the primer set comprising a combination of an oligonucleotide comprising a nucleotide sequence complementary to the complementary strand of the polynucleotide comprising a 5'-end nucleotide sequence and an oligonucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising a 3'-end nucleotide sequence, wherein said oligonucleotides comprise at least 15 nucleotides and wherein said combination of 5'-end nucleotide sequence / 3'-end nucleotide sequence is selected from the combinations of 5'-end nucleotide sequence / 3'-end nucleotide sequence set forth in the SEQ ID NOs in Tables 1 and 2.

[0017] Tables 1 and 2 shows names of clones obtained in the examples described later, comprising the polynucleotide of the present invention (Table 1; 5547 clones, Table 2; 54 clones), names of nucleotide sequences at the 5'-end and 3'-end of the full-length cDNA, and their corresponding SEQ ID NOs. A blank indicates that the 3'-end sequence corresponding to the 5'-end sequence has not been determined for the same clone.

[0018] The SEQ ID NO of a 5'-end sequence is shown on the right side of the name of the 5'-end sequence, and the SEQ ID NO of a 3'-end sequence is shown on the right side of the name of the 3'-end sequence.

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Table 1

name of clone	name of 5'-end sequence	SEQ ID of 5'-end sequence	name of 3'-end sequence	SEQ ID of 3'-end sequence
HEMBA1000005	F-HEMBA1000005	1	R-HEMBA1000005	5548
HEMBA1000012	F-HEMBA1000012	2		
HEMBA1000020	F-HEMBA1000020	3		
HEMBA1000030	F-HEMBA1000030	4	R-HEMBA1000030	5549
HEMBA1000042	F-HEMBA1000042	5	R-HEMBA1000042	5550
HEMBA1000046	F-HEMBA1000046	6	R-HEMBA1000046	5551
HEMBA1000050	F-HEMBA1000050	7	R-HEMBA1000050	5552
HEMBA1000076	F-HEMBA1000076	8	R-HEMBA1000076	5553
HEMBA1000111	F-HEMBA1000111	9	R-HEMBA1000111	5554
HEMBA1000129	F-HEMBA1000129	10	R-HEMBA1000129	5555
HEMBA1000141	F-HEMBA1000141	11	R-HEMBA1000141	5556
HEMBA1000150	F-HEMBA1000150	12	R-HEMBA1000150	5557
HEMBA1000156	F-HEMBA1000156	13	R-nnnnnnnnnnnn	5558
HEMBA1000158	F-HEMBA1000158	14	R-HEMBA1000158	5559
HEMBA1000168	F-HEMBA1000168	15	R-nnnnnnnnnnnn	5560

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HEMBA1000180	F-HEMBA1000180	16	R-HEMBA1000180	5561	
HEMBA1000185	F-HEMBA1000185	17	R-HEMBA1000185	5562	
HEMBA1000193	F-HEMBA1000193	18	R-HEMBA1000193	5563	
HEMBA1000201	F-HEMBA1000201	19	R-HEMBA1000201	5564	
HEMBA1000213	F-HEMBA1000213	20	R-HEMBA1000213	5565	
HEMBA1000216	F-HEMBA1000216	21	R-HEMBA1000216	5566	
HEMBA1000227	F-HEMBA1000227	22	R-nnnnnnnnnnnn	5567	
HEMBA1000231	F-HEMBA1000231	23	R-HEMBA1000231	5568	
HEMBA1000243	F-HEMBA1000243	24	R-HEMBA1000243	5569	
HEMBA1000244	F-HEMBA1000244	25	R-HEMBA1000244	5570	
HEMBA1000251	F-HEMBA1000251	26	R-HEMBA1000251	5571	
HEMBA1000264	F-HEMBA1000264	27	R-HEMBA1000264	5572	
HEMBA1000280	F-HEMBA1000280	28	R-nnnnnnnnnnnn	5573	
HEMBA1000282	F-HEMBA1000282	29	R-HEMBA1000282	5574	
HEMBA1000288	F-HEMBA1000288	30	R-HEMBA1000288	5575	
HEMBA1000290	F-HEMBA1000290	31	R-HEMBA1000290	5576	
HEMBA1000302	F-HEMBA1000302	32	R-HEMBA1000302	5577	
HEMBA1000303	F-HEMBA1000303	33	R-nnnnnnnnnnnn	5578	
HEMBA1000304	F-HEMBA1000304	34	R-nnnnnnnnnnnn	5579	
HEMBA1000307	F-HEMBA1000307	35	R-HEMBA1000307	5580	
HEMBA1000327	F-HEMBA1000327	36			
HEMBA1000333	F-HEMBA1000333	37	R-nnnnnnnnnnnn	5581	
HEMBA1000338	F-HEMBA1000338	38	R-HEMBA1000338	5582	
HEMBA1000351	F-HEMBA1000351	39	R-HEMBA1000351	5583	
HEMBA1000355	F-HEMBA1000355	40	R-HEMBA1000355	5584	
HEMBA1000356	F-HEMBA1000356	41			
HEMBA1000357	F-HEMBA1000357	42	R-HEMBA1000357	5585	
HEMBA1000366	F-HEMBA1000366	43	R-HEMBA1000366	5586	
HEMBA1000369	F-HEMBA1000369	44	R-HEMBA1000369	5587	
HEMBA1000376	F-HEMBA1000376	45	R-HEMBA1000376	5588	
HEMBA1000387	F-HEMBA1000387	46	R-HEMBA1000387	5589	
HEMBA1000390	F-HEMBA1000390	47	R-HEMBA1000390	5590	
HEMBA1000392	F-HEMBA1000392	48	R-HEMBA1000392	5591	
HEMBA1000396	F-HEMBA1000396	49	R-HEMBA1000396	5592	
HEMBA1000411	F-HEMBA1000411	50	R-HEMBA1000411	5593	
HEMBA1000418	F-HEMBA1000418	51	R-HEMBA1000418	5594	
HEMBA1000422	F-HEMBA1000422	52	R-HEMBA1000422	5595	
HEMBA1000428	F-HEMBA1000428	53	R-HEMBA1000428	5596	
HEMBA1000434	F-HEMBA1000434	54	R-HEMBA1000434	5597	
HEMBA1000442	F-HEMBA1000442	55	R-HEMBA1000442	5598	
HEMBA1000456	F-HEMBA1000456	56	R-HEMBA1000456	5599	
HEMBA1000459	F-HEMBA1000459	57	R-HEMBA1000459	5600	
HEMBA1000460	F-HEMBA1000460	58	R-HEMBA1000460	5601	
HEMBA1000464	F-HEMBA1000464	59	R-HEMBA1000464	5602	
HEMBA1000469	F-HEMBA1000469	60	R-HEMBA1000469	5603	
HEMBA1000488	F-HEMBA1000488	61	R-HEMBA1000488	5604	

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HEMBA1000490	F-HEMBA1000490	62	R-HEMBA1000490	5605	
HEMBA1000491	F-HEMBA1000491	63	R-HEMBA1000491	5606	
HEMBA1000501	F-HEMBA1000501	64			
HEMBA1000504	F-HEMBA1000504	65	R-HEMBA1000504	5607	
HEMBA1000505	F-HEMBA1000505	66	R-HEMBA1000505	5608	
HEMBA1000508	F-HEMBA1000508	67	R-HEMBA1000508	5609	
HEMBA1000518	F-HEMBA1000518	68	R-HEMBA1000518	5610	
HEMBA1000519	F-HEMBA1000519	69	R-HEMBA1000519	5611	
HEMBA1000520	F-HEMBA1000520	70	R-HEMBA1000520	5612	
HEMBA1000523	F-HEMBA1000523	71	R-HEMBA1000523	5613	
HEMBA1000531	F-HEMBA1000531	72	R-HEMBA1000531	5614	
HEMBA1000534	F-HEMBA1000534	73			
HEMBA1000540	F-HEMBA1000540	74	R-HEMBA1000540	5615	
HEMBA1000542	F-HEMBA1000542	75			
HEMBA1000545	F-HEMBA1000545	76	R-HEMBA1000545	5616	
HEMBA1000555	F-HEMBA1000555	77	R-nnnnnnnnnnnn	5617	
HEMBA1000557	F-HEMBA1000557	78	R-HEMBA1000557	5618	
HEMBA1000561	F-HEMBA1000561	79	R-HEMBA1000561	5619	
HEMBA1000563	F-HEMBA1000563	80	R-HEMBA1000563	5620	
HEMBA1000568	F-HEMBA1000568	81	R-HEMBA1000568	5621	
HEMBA1000569	F-HEMBA1000569	82	R-nnnnnnnnnnnn	5622	
HEMBA1000575	F-HEMBA1000575	83	R-HEMBA1000575	5623	
HEMBA1000588	F-HEMBA1000588	84	R-HEMBA1000588	5624	
HEMBA1000591	F-HEMBA1000591	85	R-HEMBA1000591	5625	
HEMBA1000592	F-HEMBA1000592	86	R-HEMBA1000592	5626	
HEMBA1000594	F-HEMBA1000594	87	R-HEMBA1000594	5627	
HEMBA1000604	F-HEMBA1000604	88	R-HEMBA1000604	5628	
HEMBA1000608	F-HEMBA1000608	89	R-HEMBA1000608	5629	
HEMBA1000622	F-HEMBA1000622	90	R-HEMBA1000622	5630	
HEMBA1000636	F-HEMBA1000636	91	R-HEMBA1000636	5631	
HEMBA1000637	F-HEMBA1000637	92	R-HEMBA1000637	5632	
HEMBA1000655	F-HEMBA1000655	93	R-HEMBA1000655	5633	
HEMBA1000657	F-HEMBA1000657	94	R-HEMBA1000657	5634	
HEMBA1000662	F-HEMBA1000662	95	R-HEMBA1000662	5635	
HEMBA1000673	F-HEMBA1000673	96	R-HEMBA1000673	5636	
HEMBA1000682	F-HEMBA1000682	97	R-HEMBA1000682	5637	
HEMBA1000686	F-HEMBA1000686	98	R-HEMBA1000686	5638	
HEMBA1000702	F-HEMBA1000702	99	R-HEMBA1000702	5639	
HEMBA1000705	F-HEMBA1000705	100	R-HEMBA1000705	5640	
HEMBA1000719	F-HEMBA1000719	101	R-HEMBA1000719	5641	
HEMBA1000722	F-HEMBA1000722	102	R-HEMBA1000722	5642	
HEMBA1000726	F-HEMBA1000726	103	R-HEMBA1000726	5643	
HEMBA1000727	F-HEMBA1000727	104	R-HEMBA1000727	5644	
HEMBA1000747	F-HEMBA1000747	105	R-HEMBA1000747	5645	
HEMBA1000749	F-HEMBA1000749	106	R-HEMBA1000749	5646	
HEMBA1000752	F-HEMBA1000752	107	R-HEMBA1000752	5647	

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HEMBA1000774	F-HEMBA1000774	110	R-HEMBA1000774	5650
HEMBA1000791	F-HEMBA1000791	111	R-HEMBA1000791	5651
HEMBA1000817	F-HEMBA1000817	112	R-HEMBA1000817	5652
HEMBA1000822	F-HEMBA1000822	113	R-HEMBA1000822	5653
HEMBA1000827	F-HEMBA1000827	114	R-HEMBA1000827	5654
HEMBA1000843	F-HEMBA1000843	115	R-HEMBA1000843	5655
HEMBA1000851	F-HEMBA1000851	116	R-HEMBA1000851	5656
HEMBA1000852	F-HEMBA1000852	117	R-HEMBA1000852	5657
HEMBA1000867	F-HEMBA1000867	118	R-HEMBA1000867	5658
HEMBA1000869	F-HEMBA1000869	119	R-HEMBA1000869	5659
HEMBA1000870	F-HEMBA1000870	120	R-HEMBA1000870	5660
HEMBA1000872	F-HEMBA1000872	121	R-HEMBA1000872	5661
HEMBA1000876	F-HEMBA1000876	122	R-HEMBA1000876	5662
HEMBA1000908	F-HEMBA1000908	123	R-HEMBA1000908	5663
HEMBA1000910	F-HEMBA1000910	124	R-HEMBA1000910	5664
HEMBA1000918	F-HEMBA1000918	125	R-HEMBA1000918	5665
HEMBA1000919	F-HEMBA1000919	126	R-HEMBA1000919	5666
HEMBA1000934	F-HEMBA1000934	127	R-HEMBA1000934	5667
HEMBA1000942	F-HEMBA1000942	128	R-HEMBA1000942	5668
HEMBA1000943	F-HEMBA1000943	129	R-HEMBA1000943	5669
HEMBA1000946	F-HEMBA1000946	130	R-HEMBA1000946	5670
HEMBA1000960	F-HEMBA1000960	131	R-HEMBA1000960	5671
HEMBA1000968	F-HEMBA1000968	132	R-HEMBA1000968	5672
HEMBA1000971	F-HEMBA1000971	133	R-HEMBA1000971	5673
HEMBA1000972	F-HEMBA1000972	134	R-HEMBA1000972	5674
HEMBA1000974	F-HEMBA1000974	135	R-HEMBA1000974	5675
HEMBA1000975	F-HEMBA1000975	136	R-HEMBA1000975	5676
HEMBA1000985	F-HEMBA1000985	137	R-HEMBA1000985	5677
HEMBA1000986	F-HEMBA1000986	138	R-HEMBA1000986	5678
HEMBA1000991	F-HEMBA1000991	139	R-HEMBA1000991	5679
HEMBA1001007	F-HEMBA1001007	140	R-HEMBA1001007	5680
HEMBA1001008	F-HEMBA1001008	141	R-HEMBA1001008	5681
HEMBA1001009	F-HEMBA1001009	142	R-HEMBA1001009	5682
HEMBA1001017	F-HEMBA1001017	143	R-HEMBA1001017	5683
HEMBA1001019	F-HEMBA1001019	144	R-HEMBA1001019	5684
HEMBA1001020	F-HEMBA1001020	145	R-HEMBA1001020	5685
HEMBA1001022	F-HEMBA1001022	146	R-HEMBA1001022	5686
HEMBA1001024	F-HEMBA1001024	147	R-HEMBA1001024	5687
HEMBA1001026	F-HEMBA1001026	148	R-HEMBA1001026	5688
HEMBA1001043	F-HEMBA1001043	149	R-nnnnnnnnnnnn	5689
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HEMBA1001123	F-HEMBA1001123	164	R-HEMBA1001123	5703	
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HEMBA1001213	F-HEMBA1001213	172			
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HEMBA1003083	F-HEMBA1003083	444	R-HEMBA1003083	5975
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HEMBA1003129	F-HEMBA1003129	449	R-HEMBA1003129	5980
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HEMBA1003148	F-HEMBA1003148	453	R-HEMBA1003148	5984
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HEMBA1003175	F-HEMBA1003175	455	R-HEMBA1003175	5986
HEMBA1003179	F-HEMBA1003179	456		
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HEMBA1003403	F-HEMBA1003403	491		
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HEMBA1004816	F-HEMBA1004816	699	R-HEMBA1004816	6220
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HEMBA1004847	F-HEMBA1004847	701	R-HEMBA1004847	6222
HEMBA1004850	F-HEMBA1004850	702	R-HEMBA1004850	6223
HEMBA1004863	F-HEMBA1004863	703	R-HEMBA1004863	6224
HEMBA1004864	F-HEMBA1004864	704	R-HEMBA1004864	6225
HEMBA1004865	F-HEMBA1004865	705	R-HEMBA1004865	6226

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HEMBA1004880	F-HEMBA1004880	706	R-HEMBA1004880	6227
HEMBA1004889	F-HEMBA1004889	707	R-HEMBA1004889	6228
HEMBA1004900	F-HEMBA1004900	708	R-HEMBA1004900	6229
HEMBA1004909	F-HEMBA1004909	709	R-HEMBA1004909	6230
HEMBA1004918	F-HEMBA1004918	710	R-HEMBA1004918	6231
HEMBA1004923	F-HEMBA1004923	711	R-HEMBA1004923	6232
HEMBA1004929	F-HEMBA1004929	712	R-HEMBA1004929	6233
HEMBA1004930	F-HEMBA1004930	713	R-HEMBA1004930	6234
HEMBA1004933	F-HEMBA1004933	714	R-HEMBA1004933	6235
HEMBA1004934	F-HEMBA1004934	715	R-HEMBA1004934	6236
HEMBA1004944	F-HEMBA1004944	716	R-HEMBA1004944	6237
HEMBA1004954	F-HEMBA1004954	717	R-HEMBA1004954	6238
HEMBA1004956	F-HEMBA1004956	718	R-HEMBA1004956	6239
HEMBA1004960	F-HEMBA1004960	719	R-HEMBA1004960	6240
HEMBA1004972	F-HEMBA1004972	720	R-HEMBA1004972	6241
HEMBA1004973	F-HEMBA1004973	721	R-HEMBA1004973	6242
HEMBA1004977	F-HEMBA1004977	722	R-HEMBA1004977	6243
HEMBA1004978	F-HEMBA1004978	723	R-HEMBA1004978	6244
HEMBA1004980	F-HEMBA1004980	724	R-HEMBA1004980	6245
HEMBA1004983	F-HEMBA1004983	725	R-HEMBA1004983	6246
HEMBA1004995	F-HEMBA1004995	726	R-HEMBA1004995	6247
HEMBA1005008	F-HEMBA1005008	727	R-HEMBA1005008	6248
HEMBA1005009	F-HEMBA1005009	728	R-HEMBA1005009	6249
HEMBA1005019	F-HEMBA1005019	729	R-HEMBA1005019	6250
HEMBA1005029	F-HEMBA1005029	730	R-HEMBA1005029	6251
HEMBA1005035	F-HEMBA1005035	731	R-HEMBA1005035	6252
HEMBA1005039	F-HEMBA1005039	732	R-HEMBA1005039	6253
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HEMBA1005050	F-HEMBA1005050	734	R-HEMBA1005050	6255
HEMBA1005062	F-HEMBA1005062	735	R-HEMBA1005062	6256
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HEMBA1005079	F-HEMBA1005079	738	R-HEMBA1005079	6259
HEMBA1005083	F-HEMBA1005083	739	R-HEMBA1005083	6260
HEMBA1005101	F-HEMBA1005101	740	R-HEMBA1005101	6261
HEMBA1005113	F-HEMBA1005113	741	R-HEMBA1005113	6262
HEMBA1005123	F-HEMBA1005123	742	R-HEMBA1005123	6263
HEMBA1005133	F-HEMBA1005133	743	R-HEMBA1005133	6264
HEMBA1005149	F-HEMBA1005149	744	R-HEMBA1005149	6265
HEMBA1005152	F-HEMBA1005152	745	R-HEMBA1005152	6266
HEMBA1005159	F-HEMBA1005159	746	R-HEMBA1005159	6267
HEMBA1005185	F-HEMBA1005185	747	R-HEMBA1005185	6268
HEMBA1005201	F-HEMBA1005201	748	R-HEMBA1005201	6269
HEMBA1005202	F-HEMBA1005202	749	R-HEMBA1005202	6270
HEMBA1005206	F-HEMBA1005206	750		
HEMBA1005219	F-HEMBA1005219	751	R-HEMBA1005219	6271

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HEMBA1005232	F-HEMBA1005232	753	R-HEMBA1005232	6273
HEMBA1005241	F-HEMBA1005241	754	R-HEMBA1005241	6274
HEMBA1005244	F-HEMBA1005244	755	R-HEMBA1005244	6275
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HEMBA1005252	F-HEMBA1005252	757	R-HEMBA1005252	6277
HEMBA1005274	F-HEMBA1005274	758	R-HEMBA1005274	6278
HEMBA1005275	F-HEMBA1005275	759	R-HEMBA1005275	6279
HEMBA1005293	F-HEMBA1005293	760	R-HEMBA1005293	6280
HEMBA1005296	F-HEMBA1005296	761	R-HEMBA1005296	6281
HEMBA1005304	F-HEMBA1005304	762	R-HEMBA1005304	6282
HEMBA1005311	F-HEMBA1005311	763	R-HEMBA1005311	6283
HEMBA1005314	F-HEMBA1005314	764	R-HEMBA1005314	6284
HEMBA1005315	F-HEMBA1005315	765	R-HEMBA1005315	6285
HEMBA1005318	F-HEMBA1005318	766	R-HEMBA1005318	6286
HEMBA1005331	F-HEMBA1005331	767	R-HEMBA1005331	6287
HEMBA1005338	F-HEMBA1005338	768		
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HEMBA1005359	F-HEMBA1005359	770	R-HEMBA1005359	6289
HEMBA1005367	F-HEMBA1005367	771	R-HEMBA1005367	6290
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HEMBA1005374	F-HEMBA1005374	773	R-HEMBA1005374	6292
HEMBA1005382	F-HEMBA1005382	774		
HEMBA1005389	F-HEMBA1005389	775	R-HEMBA1005389	6293
HEMBA1005394	F-HEMBA1005394	776	R-HEMBA1005394	6294
HEMBA1005403	F-HEMBA1005403	777	R-HEMBA1005403	6295
HEMBA1005408	F-HEMBA1005408	778	R-HEMBA1005408	6296
HEMBA1005410	F-HEMBA1005410	779	R-HEMBA1005410	6297
HEMBA1005411	F-HEMBA1005411	780	R-HEMBA1005411	6298
HEMBA1005423	F-HEMBA1005423	781	R-HEMBA1005423	6299
HEMBA1005426	F-HEMBA1005426	782	R-HEMBA1005426	6300
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HEMBA1005468	F-HEMBA1005468	785	R-HEMBA1005468	6303
HEMBA1005469	F-HEMBA1005469	786	R-HEMBA1005469	6304
HEMBA1005472	F-HEMBA1005472	787	R-HEMBA1005472	6305
HEMBA1005474	F-HEMBA1005474	788		
HEMBA1005475	F-HEMBA1005475	789	R-HEMBA1005475	6306
HEMBA1005497	F-HEMBA1005497	790	R-HEMBA1005497	6307
HEMBA1005500	F-HEMBA1005500	791	R-HEMBA1005500	6308
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HEMBA1005511	F-HEMBA1005511	794	R-HEMBA1005511	6311
HEMBA1005513	F-HEMBA1005513	795		
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HEMBA1005528	F-HEMBA1005528	800	R-HEMBA1005528	6316
HEMBA1005530	F-HEMBA1005530	801	R-HEMBA1005530	6317
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HEMBA1005552	F-HEMBA1005552	803	R-HEMBA1005552	6319
HEMBA1005558	F-HEMBA1005558	804	R-HEMBA1005558	6320
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HEMBA1005576	F-HEMBA1005576	807	R-HEMBA1005576	6323
HEMBA1005577	F-HEMBA1005577	808	R-HEMBA1005577	6324
HEMBA1005581	F-HEMBA1005581	809	R-HEMBA1005581	6325
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HEMBA1005583	F-HEMBA1005583	811	R-HEMBA1005583	6327
HEMBA1005588	F-HEMBA1005588	812	R-HEMBA1005588	6328
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HEMBA1005621	F-HEMBA1005621	818	R-HEMBA1005621	6334
HEMBA1005627	F-HEMBA1005627	819	R-HEMBA1005627	6335
HEMBA1005631	F-HEMBA1005631	820	R-HEMBA1005631	6336
HEMBA1005632	F-HEMBA1005632	821	R-HEMBA1005632	6337
HEMBA1005634	F-HEMBA1005634	822	R-HEMBA1005634	6338
HEMBA1005666	F-HEMBA1005666	823	R-HEMBA1005666	6339
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HEMBA1005680	F-HEMBA1005680	826	R-HEMBA1005680	6342
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HEMBA1005717	F-HEMBA1005717	830	R-HEMBA1005717	6346
HEMBA1005732	F-HEMBA1005732	831	R-HEMBA1005732	6347
HEMBA1005737	F-HEMBA1005737	832	R-HEMBA1005737	6348
HEMBA1005746	F-HEMBA1005746	833	R-nnnnnnnnnnnn	6349
HEMBA1005755	F-HEMBA1005755	834	R-HEMBA1005755	6350
HEMBA1005765	F-HEMBA1005765	835	R-HEMBA1005765	6351
HEMBA1005780	F-HEMBA1005780	836	R-HEMBA1005780	6352
HEMBA1005813	F-HEMBA1005813	837	R-HEMBA1005813	6353
HEMBA1005815	F-HEMBA1005815	838	R-HEMBA1005815	6354
HEMBA1005822	F-HEMBA1005822	839	R-HEMBA1005822	6355
HEMBA1005829	F-HEMBA1005829	840	R-HEMBA1005829	6356
HEMBA1005834	F-HEMBA1005834	841	R-HEMBA1005834	6357
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HEMBA1005853	F-HEMBA1005853	843	R-HEMBA1005853	6359

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HEMBA1005909	F-HEMBA1005909	847	R-HEMBA1005909	6363
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HEMBA1005921	F-HEMBA1005921	849	R-HEMBA1005921	6365
HEMBA1005931	F-HEMBA1005931	850	R-HEMBA1005931	6366
HEMBA1005934	F-HEMBA1005934	851	R-HEMBA1005934	6367
HEMBA1005962	F-HEMBA1005962	852	R-HEMBA1005962	6368
HEMBA1005963	F-HEMBA1005963	853	R-HEMBA1005963	6369
HEMBA1005990	F-HEMBA1005990	854	R-HEMBA1005990	6370
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HEMBA1006036	F-HEMBA1006036	861	R-HEMBA1006036	6377
HEMBA1006042	F-HEMBA1006042	862	R-HEMBA1006042	6378
HEMBA1006067	F-HEMBA1006067	863	R-nnnnnnnnnnnn	6379
HEMBA1006081	F-HEMBA1006081	864	R-HEMBA1006081	6380
HEMBA1006090	F-HEMBA1006090	865	R-HEMBA1006090	6381
HEMBA1006091	F-HEMBA1006091	866	R-HEMBA1006091	6382
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HEMBA1006108	F-HEMBA1006108	868	R-HEMBA1006108	6384
HEMBA1006121	F-HEMBA1006121	869	R-HEMBA1006121	6385
HEMBA1006124	F-HEMBA1006124	870	R-HEMBA1006124	6386
HEMBA1006130	F-HEMBA1006130	871	R-HEMBA1006130	6387
HEMBA1006138	F-HEMBA1006138	872	R-nnnnnnnnnnnn	6388
HEMBA1006142	F-HEMBA1006142	873	R-HEMBA1006142	6389
HEMBA1006155	F-HEMBA1006155	874	R-HEMBA1006155	6390
HEMBA1006158	F-HEMBA1006158	875	R-HEMBA1006158	6391
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HEMBA1006248	F-HEMBA1006248	880	R-HEMBA1006248	6396
HEMBA1006252	F-HEMBA1006252	881	R-HEMBA1006252	6397
HEMBA1006253	F-HEMBA1006253	882	R-HEMBA1006253	6398
HEMBA1006259	F-HEMBA1006259	883	R-HEMBA1006259	6399
HEMBA1006268	F-HEMBA1006268	884	R-HEMBA1006268	6400
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HEMBA1006283	F-HEMBA1006283	887	R-HEMBA1006283	6403
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HEMBA1006291	F-HEMBA1006291	889	R-HEMBA1006291	6405

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HEMBA1006328	F-HEMBA1006328	893	R-HEMBA1006328	6409
HEMBA1006334	F-HEMBA1006334	894	R-HEMBA1006334	6410
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HEMBA1006347	F-HEMBA1006347	896	R-HEMBA1006347	6412
HEMBA1006349	F-HEMBA1006349	897	R-HEMBA1006349	6413
HEMBA1006359	F-HEMBA1006359	898	R-HEMBA1006359	6414
HEMBA1006364	F-HEMBA1006364	899	R-HEMBA1006364	6415
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HEMBA1006380	F-HEMBA1006380	901	R-HEMBA1006380	6417
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HEMBA1006421	F-HEMBA1006421	906	R-HEMBA1006421	6422
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HEMBA1006426	F-HEMBA1006426	908	R-HEMBA1006426	6424
HEMBA1006438	F-HEMBA1006438	909	R-HEMBA1006438	6425
HEMBA1006445	F-HEMBA1006445	910	R-HEMBA1006445	6426
HEMBA1006446	F-HEMBA1006446	911	R-HEMBA1006446	6427
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HEMBA1006474	F-HEMBA1006474	915	R-HEMBA1006474	6431
HEMBA1006483	F-HEMBA1006483	916	R-HEMBA1006483	6432
HEMBA1006485	F-HEMBA1006485	917	R-HEMBA1006485	6433
HEMBA1006486	F-HEMBA1006486	918	R-HEMBA1006486	6434
HEMBA1006489	F-HEMBA1006489	919	R-HEMBA1006489	6435
HEMBA1006492	F-HEMBA1006492	920	R-HEMBA1006492	6436
HEMBA1006494	F-HEMBA1006494	921	R-HEMBA1006494	6437
HEMBA1006497	F-HEMBA1006497	922	R-HEMBA1006497	6438
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HEMBA1006507	F-HEMBA1006507	924	R-HEMBA1006507	6440
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HEMBA1006530	F-HEMBA1006530	926	R-HEMBA1006530	6442
HEMBA1006535	F-HEMBA1006535	927	R-HEMBA1006535	6443
HEMBA1006540	F-HEMBA1006540	928	R-HEMBA1006540	6444
HEMBA1006546	F-HEMBA1006546	929	R-HEMBA1006546	6445
HEMBA1006559	F-HEMBA1006559	930	R-HEMBA1006559	6446
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HEMBA1006566	F-HEMBA1006566	932	R-HEMBA1006566	6448
HEMBA1006569	F-HEMBA1006569	933	R-HEMBA1006569	6449
HEMBA1006579	F-HEMBA1006579	934	R-HEMBA1006579	6450
HEMBA1006583	F-HEMBA1006583	935	R-HEMBA1006583	6451

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HEMBA1006612	F-HEMBA1006612	938	R-HEMBA1006612	6454
HEMBA1006617	F-HEMBA1006617	939	R-nnnnnnnnnnnn	6455
HEMBA1006624	F-HEMBA1006624	940	R-HEMBA1006624	6456
HEMBA1006631	F-HEMBA1006631	941	R-HEMBA1006631	6457
HEMBA1006635	F-HEMBA1006635	942	R-HEMBA1006635	6458
HEMBA1006639	F-HEMBA1006639	943	R-HEMBA1006639	6459
HEMBA1006643	F-HEMBA1006643	944	R-HEMBA1006643	6460
HEMBA1006648	F-HEMBA1006648	945	R-HEMBA1006648	6461
HEMBA1006652	F-HEMBA1006652	946	R-HEMBA1006652	6462
HEMBA1006653	F-HEMBA1006653	947	R-HEMBA1006653	6463
HEMBA1006659	F-HEMBA1006659	948		
HEMBA1006665	F-HEMBA1006665	949	R-HEMBA1006665	6464
HEMBA1006674	F-HEMBA1006674	950	R-HEMBA1006674	6465
HEMBA1006676	F-HEMBA1006676	951	R-HEMBA1006676	6466
HEMBA1006682	F-HEMBA1006682	952	R-HEMBA1006682	6467
HEMBA1006695	F-HEMBA1006695	953	R-HEMBA1006695	6468
HEMBA1006696	F-HEMBA1006696	954	R-HEMBA1006696	6469
HEMBA1006708	F-HEMBA1006708	955	R-HEMBA1006708	6470
HEMBA1006709	F-HEMBA1006709	956	R-HEMBA1006709	6471
HEMBA1006717	F-HEMBA1006717	957	R-HEMBA1006717	6472
HEMBA1006737	F-HEMBA1006737	958	R-HEMBA1006737	6473
HEMBA1006744	F-HEMBA1006744	959	R-HEMBA1006744	6474
HEMBA1006754	F-HEMBA1006754	960	R-HEMBA1006754	6475
HEMBA1006758	F-HEMBA1006758	961	R-HEMBA1006758	6476
HEMBA1006767	F-HEMBA1006767	962	R-HEMBA1006767	6477
HEMBA1006779	F-HEMBA1006779	963	R-HEMBA1006779	6478
HEMBA1006780	F-HEMBA1006780	964	R-HEMBA1006780	6479
HEMBA1006789	F-HEMBA1006789	965	R-HEMBA1006789	6480
HEMBA1006795	F-HEMBA1006795	966	R-HEMBA1006795	6481
HEMBA1006796	F-HEMBA1006796	967	R-HEMBA1006796	6482
HEMBA1006807	F-HEMBA1006807	968	R-HEMBA1006807	6483
HEMBA1006821	F-HEMBA1006821	969	R-HEMBA1006821	6484
HEMBA1006824	F-HEMBA1006824	970	R-HEMBA1006824	6485
HEMBA1006832	F-HEMBA1006832	971	R-HEMBA1006832	6486
HEMBA1006849	F-HEMBA1006849	972	R-HEMBA1006849	6487
HEMBA1006865	F-HEMBA1006865	973	R-HEMBA1006865	6488
HEMBA1006877	F-HEMBA1006877	974	R-nnnnnnnnnnnn	6489
HEMBA1006885	F-HEMBA1006885	975	R-HEMBA1006885	6490
HEMBA1006900	F-HEMBA1006900	976	R-HEMBA1006900	6491
HEMBA1006914	F-HEMBA1006914	977		
HEMBA1006921	F-HEMBA1006921	978	R-HEMBA1006921	6492
HEMBA1006926	F-HEMBA1006926	979	R-HEMBA1006926	6493
HEMBA1006929	F-HEMBA1006929	980	R-HEMBA1006929	6494
HEMBA1006936	F-HEMBA1006936	981	R-HEMBA1006936	6495

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HEMBA1006938	F-HEMBA1006938	982	R-HEMBA1006938	6496
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HEMBA1006949	F-HEMBA1006949	984	R-HEMBA1006949	6498
HEMBA1006973	F-HEMBA1006973	985	R-HEMBA1006973	6499
HEMBA1006976	F-HEMBA1006976	986	R-HEMBA1006976	6500
HEMBA1006993	F-HEMBA1006993	987	R-HEMBA1006993	6501
HEMBA1006996	F-HEMBA1006996	988	R-HEMBA1006996	6502
HEMBA1007002	F-HEMBA1007002	989	R-HEMBA1007002	6503
HEMBA1007017	F-HEMBA1007017	990	R-HEMBA1007017	6504
HEMBA1007018	F-HEMBA1007018	991	R-HEMBA1007018	6505
HEMBA1007045	F-HEMBA1007045	992	R-HEMBA1007045	6506
HEMBA1007051	F-HEMBA1007051	993	R-HEMBA1007051	6507
HEMBA1007052	F-HEMBA1007052	994	R-HEMBA1007052	6508
HEMBA1007062	F-HEMBA1007062	995	R-HEMBA1007062	6509
HEMBA1007066	F-HEMBA1007066	996	R-HEMBA1007066	6510
HEMBA1007073	F-HEMBA1007073	997	R-HEMBA1007073	6511
HEMBA1007078	F-HEMBA1007078	998	R-HEMBA1007078	6512
HEMBA1007080	F-HEMBA1007080	999		
HEMBA1007085	F-HEMBA1007085	1000	R-HEMBA1007085	6513
HEMBA1007087	F-HEMBA1007087	1001	R-HEMBA1007087	6514
HEMBA1007112	F-HEMBA1007112	1002	R-HEMBA1007112	6515
HEMBA1007113	F-HEMBA1007113	1003	R-HEMBA1007113	6516
HEMBA1007121	F-HEMBA1007121	1004		
HEMBA1007129	F-HEMBA1007129	1005	R-HEMBA1007129	6517
HEMBA1007147	F-HEMBA1007147	1006	R-HEMBA1007147	6518
HEMBA1007149	F-HEMBA1007149	1007	R-HEMBA1007149	6519
HEMBA1007151	F-HEMBA1007151	1008	R-HEMBA1007151	6520
HEMBA1007174	F-HEMBA1007174	1009	R-nnnnnnnnnnnn	6521
HEMBA1007178	F-HEMBA1007178	1010	R-HEMBA1007178	6522
HEMBA1007194	F-HEMBA1007194	1011	R-HEMBA1007194	6523
HEMBA1007203	F-HEMBA1007203	1012	R-HEMBA1007203	6524
HEMBA1007206	F-HEMBA1007206	1013	R-HEMBA1007206	6525
HEMBA1007224	F-HEMBA1007224	1014	R-HEMBA1007224	6526
HEMBA1007243	F-HEMBA1007243	1015		
HEMBA1007251	F-HEMBA1007251	1016	R-HEMBA1007251	6527
HEMBA1007256	F-HEMBA1007256	1017	R-HEMBA1007256	6528
HEMBA1007267	F-HEMBA1007267	1018	R-HEMBA1007267	6529
HEMBA1007273	F-HEMBA1007273	1019	R-HEMBA1007273	6530
HEMBA1007279	F-HEMBA1007279	1020	R-HEMBA1007279	6531
HEMBA1007281	F-HEMBA1007281	1021	R-HEMBA1007281	6532
HEMBA1007288	F-HEMBA1007288	1022	R-HEMBA1007288	6533
HEMBA1007300	F-HEMBA1007300	1023	R-HEMBA1007300	6534
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HEMBA1007319	F-HEMBA1007319	1025	R-HEMBA1007319	6536
HEMBA1007320	F-HEMBA1007320	1026	R-HEMBA1007320	6537
HEMBA1007322	F-HEMBA1007322	1027	R-HEMBA1007322	6538

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HEMBA1007341	F-HEMBA1007341	1029	R-HEMBA1007341	6540
HEMBA1007342	F-HEMBA1007342	1030	R-HEMBA1007342	6541
HEMBA1007347	F-HEMBA1007347	1031	R-HEMBA1007347	6542
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HEMBB1000008	F-HEMBB1000008	1033	R-HEMBB1000008	6544
HEMBB1000018	F-HEMBB1000018	1034	R-HEMBB1000018	6545
HEMBB1000024	F-HEMBB1000024	1035	R-HEMBB1000024	6546
HEMBB1000025	F-HEMBB1000025	1036	R-HEMBB1000025	6547
HEMBB1000030	F-HEMBB1000030	1037	R-HEMBB1000030	6548
HEMBB1000036	F-HEMBB1000036	1038	R-HEMBB1000036	6549
HEMBB1000037	F-HEMBB1000037	1039	R-HEMBB1000037	6550
HEMBB1000039	F-HEMBB1000039	1040	R-HEMBB1000039	6551
HEMBB1000044	F-HEMBB1000044	1041	R-HEMBB1000044	6552
HEMBB1000048	F-HEMBB1000048	1042	R-HEMBB1000048	6553
HEMBB1000050	F-HEMBB1000050	1043	R-HEMBB1000050	6554
HEMBB1000054	F-HEMBB1000054	1044	R-HEMBB1000054	6555
HEMBB1000055	F-HEMBB1000055	1045	R-HEMBB1000055	6556
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HEMBB1000083	F-HEMBB1000083	1047	R-HEMBB1000083	6558
HEMBB1000089	F-HEMBB1000089	1048	R-HEMBB1000089	6559
HEMBB1000099	F-HEMBB1000099	1049	R-HEMBB1000099	6560
HEMBB1000103	F-HEMBB1000103	1050	R-HEMBB1000103	6561
HEMBB1000113	F-HEMBB1000113	1051	R-HEMBB1000113	6562
HEMBB1000119	F-HEMBB1000119	1052	R-HEMBB1000119	6563
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HEMBB1000141	F-HEMBB1000141	1054	R-HEMBB1000141	6565
HEMBB1000144	F-HEMBB1000144	1055	R-HEMBB1000144	6566
HEMBB1000173	F-HEMBB1000173	1056	R-HEMBB1000173	6567
HEMBB1000175	F-HEMBB1000175	1057	R-HEMBB1000175	6568
HEMBB1000198	F-HEMBB1000198	1058	R-HEMBB1000198	6569
HEMBB1000215	F-HEMBB1000215	1059	R-HEMBB1000215	6570
HEMBB1000217	F-HEMBB1000217	1060	R-HEMBB1000217	6571
HEMBB1000218	F-HEMBB1000218	1061	R-HEMBB1000218	6572
HEMBB1000226	F-HEMBB1000226	1062	R-HEMBB1000226	6573
HEMBB1000240	F-HEMBB1000240	1063	R-HEMBB1000240	6574
HEMBB1000244	F-HEMBB1000244	1064	R-HEMBB1000244	6575
HEMBB1000250	F-HEMBB1000250	1065	R-HEMBB1000250	6576
HEMBB1000258	F-HEMBB1000258	1066	R-HEMBB1000258	6577
HEMBB1000264	F-HEMBB1000264	1067	R-HEMBB1000264	6578
HEMBB1000266	F-HEMBB1000266	1068	R-HEMBB1000266	6579
HEMBB1000272	F-HEMBB1000272	1069	R-HEMBB1000272	6580
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HEMBB1000284	F-HEMBB1000284	1071	R-HEMBB1000284	6582
HEMBB1000307	F-HEMBB1000307	1072	R-HEMBB1000307	6583
HEMBB1000312	F-HEMBB1000312	1073	R-HEMBB1000312	6584

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HEMBB1000318	F-HEMBB1000318	1075	R-HEMBB1000318	6586
HEMBB1000335	F-HEMBB1000335	1076	R-HEMBB1000335	6587
HEMBB1000336	F-HEMBB1000336	1077	R-HEMBB1000336	6588
HEMBB1000337	F-HEMBB1000337	1078	R-HEMBB1000337	6589
HEMBB1000338	F-HEMBB1000338	1079	R-HEMBB1000338	6590
HEMBB1000339	F-HEMBB1000339	1080	R-HEMBB1000339	6591
HEMBB1000341	F-HEMBB1000341	1081	R-HEMBB1000341	6592
HEMBB1000343	F-HEMBB1000343	1082	R-HEMBB1000343	6593
HEMBB1000354	F-HEMBB1000354	1083	R-HEMBB1000354	6594
HEMBB1000369	F-HEMBB1000369	1084	R-HEMBB1000369	6595
HEMBB1000374	F-HEMBB1000374	1085	R-HEMBB1000374	6596
HEMBB1000376	F-HEMBB1000376	1086	R-HEMBB1000376	6597
HEMBB1000391	F-HEMBB1000391	1087	R-HEMBB1000391	6598
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HEMBB1000420	F-HEMBB1000420	1091	R-HEMBB1000420	6602
HEMBB1000434	F-HEMBB1000434	1092	R-HEMBB1000434	6603
HEMBB1000438	F-HEMBB1000438	1093	R-HEMBB1000438	6604
HEMBB1000441	F-HEMBB1000441	1094	R-HEMBB1000441	6605
HEMBB1000449	F-HEMBB1000449	1095	R-HEMBB1000449	6606
HEMBB1000455	F-HEMBB1000455	1096	R-HEMBB1000455	6607
HEMBB1000472	F-HEMBB1000472	1097	R-HEMBB1000472	6608
HEMBB1000480	F-HEMBB1000480	1098	R-HEMBB1000480	6609
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HEMBB1000554	F-HEMBB1000554	1108	R-HEMBB1000554	6619
HEMBB1000556	F-HEMBB1000556	1109	R-HEMBB1000556	6620
HEMBB1000564	F-HEMBB1000564	1110	R-HEMBB1000564	6621
HEMBB1000573	F-HEMBB1000573	1111	R-HEMBB1000573	6622
HEMBB1000575	F-HEMBB1000575	1112	R-HEMBB1000575	6623
HEMBB1000586	F-HEMBB1000586	1113	R-HEMBB1000586	6624
HEMBB1000589	F-HEMBB1000589	1114	R-HEMBB1000589	6625
HEMBB1000591	F-HEMBB1000591	1115	R-HEMBB1000591	6626
HEMBB1000592	F-HEMBB1000592	1116	R-HEMBB1000592	6627
HEMBB1000593	F-HEMBB1000593	1117		
HEMBB1000598	F-HEMBB1000598	1118	R-HEMBB1000598	6628
HEMBB1000623	F-HEMBB1000623	1119	R-HEMBB1000623	6629

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HEMBB1000632	F-HEMBB1000632	1122	R-HEMBB1000632	6632	
HEMBB1000637	F-HEMBB1000637	1123	R-HEMBB1000637	6633	
HEMBB1000638	F-HEMBB1000638	1124	R-HEMBB1000638	6634	
HEMBB1000643	F-HEMBB1000643	1125	R-HEMBB1000643	6635	
HEMBB1000649	F-HEMBB1000649	1126	R-HEMBB1000649	6636	
HEMBB1000652	F-HEMBB1000652	1127	R-HEMBB1000652	6637	
HEMBB1000665	F-HEMBB1000665	1128	R-HEMBB1000665	6638	
HEMBB1000671	F-HEMBB1000671	1129	R-HEMBB1000671	6639	
HEMBB1000673	F-HEMBB1000673	1130	R-HEMBB1000673	6640	
HEMBB1000684	F-HEMBB1000684	1131	R-HEMBB1000684	6641	
HEMBB1000693	F-HEMBB1000693	1132	R-nnnnnnnnnnnn	6642	
HEMBB1000705	F-HEMBB1000705	1133	R-HEMBB1000705	6643	
HEMBB1000706	F-HEMBB1000706	1134	R-HEMBB1000706	6644	
HEMBB1000709	F-HEMBB1000709	1135	R-HEMBB1000709	6645	
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HEMBB1000726	F-HEMBB1000726	1137	R-HEMBB1000726	6647	
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HEMBB1000763	F-HEMBB1000763	1140	R-HEMBB1000763	6650	
HEMBB1000770	F-HEMBB1000770	1141	R-HEMBB1000770	6651	
HEMBB1000774	F-HEMBB1000774	1142			
HEMBB1000781	F-HEMBB1000781	1143	R-HEMBB1000781	6652	
HEMBB1000789	F-HEMBB1000789	1144	R-HEMBB1000789	6653	
HEMBB1000790	F-HEMBB1000790	1145	R-HEMBB1000790	6654	
HEMBB1000794	F-HEMBB1000794	1146	R-HEMBB1000794	6655	
HEMBB1000807	F-HEMBB1000807	1147	R-HEMBB1000807	6656	
HEMBB1000810	F-HEMBB1000810	1148	R-HEMBB1000810	6657	
HEMBB1000821	F-HEMBB1000821	1149	R-HEMBB1000821	6658	
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HEMBB1000826	F-HEMBB1000826	1151	R-HEMBB1000826	6660	
HEMBB1000827	F-HEMBB1000827	1152	R-HEMBB1000827	6661	
HEMBB1000831	F-HEMBB1000831	1153	R-HEMBB1000831	6662	
HEMBB1000835	F-HEMBB1000835	1154	R-HEMBB1000835	6663	
HEMBB1000840	F-HEMBB1000840	1155	R-HEMBB1000840	6664	
HEMBB1000848	F-HEMBB1000848	1156	R-HEMBB1000848	6665	
HEMBB1000852	F-HEMBB1000852	1157	R-HEMBB1000852	6666	
HEMBB1000870	F-HEMBB1000870	1158	R-HEMBB1000870	6667	
HEMBB1000876	F-HEMBB1000876	1159	R-HEMBB1000876	6668	
HEMBB1000883	F-HEMBB1000883	1160	R-HEMBB1000883	6669	
HEMBB1000887	F-HEMBB1000887	1161	R-HEMBB1000887	6670	
HEMBB1000888	F-HEMBB1000888	1162	R-HEMBB1000888	6671	
HEMBB1000890	F-HEMBB1000890	1163	R-HEMBB1000890	6672	
HEMBB1000893	F-HEMBB1000893	1164	R-HEMBB1000893	6673	
HEMBB1000908	F-HEMBB1000908	1165	R-HEMBB1000908	6674	

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HEMBB1000913	F-HEMBB1000913	1167	R-HEMBB1000913	6676
HEMBB1000915	F-HEMBB1000915	1168	R-HEMBB1000915	6677
HEMBB1000917	F-HEMBB1000917	1169	R-HEMBB1000917	6678
HEMBB1000927	F-HEMBB1000927	1170	R-HEMBB1000927	6679
HEMBB1000947	F-HEMBB1000947	1171	R-HEMBB1000947	6680
HEMBB1000959	F-HEMBB1000959	1172	R-HEMBB1000959	6681
HEMBB1000973	F-HEMBB1000973	1173	R-HEMBB1000973	6682
HEMBB1000975	F-HEMBB1000975	1174	R-HEMBB1000975	6683
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HEMBB1000991	F-HEMBB1000991	1177	R-HEMBB1000991	6686
HEMBB1000996	F-HEMBB1000996	1178	R-HEMBB1000996	6687
HEMBB1001004	F-HEMBB1001004	1179	R-HEMBB1001004	6688
HEMBB1001008	F-HEMBB1001008	1180	R-HEMBB1001008	6689
HEMBB1001011	F-HEMBB1001011	1181	R-HEMBB1001011	6690
HEMBB1001014	F-HEMBB1001014	1182	R-HEMBB1001014	6691
HEMBB1001020	F-HEMBB1001020	1183	R-HEMBB1001020	6692
HEMBB1001024	F-HEMBB1001024	1184	R-HEMBB1001024	6693
HEMBB1001037	F-HEMBB1001037	1185	R-HEMBB1001037	6694
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HEMBB1001056	F-HEMBB1001056	1188	R-HEMBB1001056	6697
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HEMBB1001096	F-HEMBB1001096	1193	R-HEMBB1001096	6702
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HEMBB1001105	F-HEMBB1001105	1195	R-HEMBB1001105	6704
HEMBB1001112	F-HEMBB1001112	1196		
HEMBB1001114	F-HEMBB1001114	1197	R-HEMBB1001114	6705
HEMBB1001117	F-HEMBB1001117	1198	R-HEMBB1001117	6706
HEMBB1001119	F-HEMBB1001119	1199	R-HEMBB1001119	6707
HEMBB1001126	F-HEMBB1001126	1200	R-HEMBB1001126	6708
HEMBB1001133	F-HEMBB1001133	1201	R-HEMBB1001133	6709
HEMBB1001137	F-HEMBB1001137	1202	R-HEMBB1001137	6710
HEMBB1001142	F-HEMBB1001142	1203	R-HEMBB1001142	6711
HEMBB1001151	F-HEMBB1001151	1204	R-HEMBB1001151	6712
HEMBB1001153	F-HEMBB1001153	1205	R-HEMBB1001153	6713
HEMBB1001169	F-HEMBB1001169	1206	R-HEMBB1001169	6714
HEMBB1001175	F-HEMBB1001175	1207	R-nnnnnnnnnnnn	6715
HEMBB1001177	F-HEMBB1001177	1208	R-HEMBB1001177	6716
HEMBB1001182	F-HEMBB1001182	1209	R-HEMBB1001182	6717
HEMBB1001199	F-HEMBB1001199	1210	R-HEMBB1001199	6718
HEMBB1001208	F-HEMBB1001208	1211	R-HEMBB1001208	6719

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HEMBB1001210	F-HEMBB1001210	1213	R-HEMBB1001210	6721
HEMBB1001218	F-HEMBB1001218	1214	R-HEMBB1001218	6722
HEMBB1001221	F-HEMBB1001221	1215	R-HEMBB1001221	6723
HEMBB1001234	F-HEMBB1001234	1216	R-HEMBB1001234	6724
HEMBB1001242	F-HEMBB1001242	1217	R-HEMBB1001242	6725
HEMBB1001249	F-HEMBB1001249	1218	R-HEMBB1001249	6726
HEMBB1001253	F-HEMBB1001253	1219	R-HEMBB1001253	6727
HEMBB1001254	F-HEMBB1001254	1220	R-HEMBB1001254	6728
HEMBB1001267	F-HEMBB1001267	1221	R-HEMBB1001267	6729
HEMBB1001271	F-HEMBB1001271	1222	R-HEMBB1001271	6730
HEMBB1001282	F-HEMBB1001282	1223	R-HEMBB1001282	6731
HEMBB1001288	F-HEMBB1001288	1224	R-HEMBB1001288	6732
HEMBB1001289	F-HEMBB1001289	1225	R-HEMBB1001289	6733
HEMBB1001294	F-HEMBB1001294	1226	R-HEMBB1001294	6734
HEMBB1001302	F-HEMBB1001302	1227	R-HEMBB1001302	6735
HEMBB1001304	F-HEMBB1001304	1228	R-HEMBB1001304	6736
HEMBB1001314	F-HEMBB1001314	1229	R-HEMBB1001314	6737
HEMBB1001315	F-HEMBB1001315	1230	R-HEMBB1001315	6738
HEMBB1001317	F-HEMBB1001317	1231	R-HEMBB1001317	6739
HEMBB1001326	F-HEMBB1001326	1232	R-HEMBB1001326	6740
HEMBB1001331	F-HEMBB1001331	1233	R-HEMBB1001331	6741
HEMBB1001335	F-HEMBB1001335	1234	R-HEMBB1001335	6742
HEMBB1001337	F-HEMBB1001337	1235	R-HEMBB1001337	6743
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HEMBB1001346	F-HEMBB1001346	1237	R-HEMBB1001346	6745
HEMBB1001348	F-HEMBB1001348	1238	R-HEMBB1001348	6746
HEMBB1001356	F-HEMBB1001356	1239	R-HEMBB1001356	6747
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HEMBB1001366	F-HEMBB1001366	1241	R-HEMBB1001366	6749
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HEMBB1001369	F-HEMBB1001369	1243	R-HEMBB1001369	6751
HEMBB1001380	F-HEMBB1001380	1244	R-HEMBB1001380	6752
HEMBB1001384	F-HEMBB1001384	1245	R-HEMBB1001384	6753
HEMBB1001387	F-HEMBB1001387	1246	R-HEMBB1001387	6754
HEMBB1001394	F-HEMBB1001394	1247	R-HEMBB1001394	6755
HEMBB1001410	F-HEMBB1001410	1248	R-HEMBB1001410	6756
HEMBB1001424	F-HEMBB1001424	1249	R-HEMBB1001424	6757
HEMBB1001426	F-HEMBB1001426	1250	R-HEMBB1001426	6758
HEMBB1001429	F-HEMBB1001429	1251	R-HEMBB1001429	6759
HEMBB1001436	F-HEMBB1001436	1252	R-HEMBB1001436	6760
HEMBB1001443	F-HEMBB1001443	1253	R-HEMBB1001443	6761
HEMBB1001449	F-HEMBB1001449	1254	R-HEMBB1001449	6762
HEMBB1001454	F-HEMBB1001454	1255	R-HEMBB1001454	6763
HEMBB1001458	F-HEMBB1001458	1256	R-HEMBB1001458	6764
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HEMBB1001500	F-HEMBB1001500	1260	R-HEMBB1001500	6768
HEMBB1001521	F-HEMBB1001521	1261	R-HEMBB1001521	6769
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HEMBB1001531	F-HEMBB1001531	1263	R-HEMBB1001531	6771
HEMBB1001535	F-HEMBB1001535	1264	R-HEMBB1001535	6772
HEMBB1001536	F-HEMBB1001536	1265	R-HEMBB1001536	6773
HEMBB1001537	F-HEMBB1001537	1266	R-HEMBB1001537	6774
HEMBB1001555	F-HEMBB1001555	1267	R-HEMBB1001555	6775
HEMBB1001562	F-HEMBB1001562	1268	R-HEMBB1001562	6776
HEMBB1001564	F-HEMBB1001564	1269	R-HEMBB1001564	6777
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HEMBB1001586	F-HEMBB1001586	1272	R-HEMBB1001586	6780
HEMBB1001588	F-HEMBB1001588	1273	R-HEMBB1001588	6781
HEMBB1001603	F-HEMBB1001603	1274	R-HEMBB1001603	6782
HEMBB1001618	F-HEMBB1001618	1275	R-HEMBB1001618	6783
HEMBB1001619	F-HEMBB1001619	1276	R-HEMBB1001619	6784
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HEMBB1001637	F-HEMBB1001637	1279	R-HEMBB1001637	6787
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HEMBB1001653	F-HEMBB1001653	1281	R-HEMBB1001653	6789
HEMBB1001665	F-HEMBB1001665	1282	R-HEMBB1001665	6790
HEMBB1001668	F-HEMBB1001668	1283	R-HEMBB1001668	6791
HEMBB1001673	F-HEMBB1001673	1284	R-HEMBB1001673	6792
HEMBB1001684	F-HEMBB1001684	1285	R-HEMBB1001684	6793
HEMBB1001685	F-HEMBB1001685	1286	R-HEMBB1001685	6794
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HEMBB1001704	F-HEMBB1001704	1288	R-HEMBB1001704	6796
HEMBB1001706	F-HEMBB1001706	1289	R-HEMBB1001706	6797
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HEMBB1001717	F-HEMBB1001717	1291	R-HEMBB1001717	6799
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HEMBB1001736	F-HEMBB1001736	1293	R-HEMBB1001736	6801
HEMBB1001747	F-HEMBB1001747	1294	R-HEMBB1001747	6802
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HEMBB1001756	F-HEMBB1001756	1297	R-HEMBB1001756	6805
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HEMBB1001762	F-HEMBB1001762	1299	R-HEMBB1001762	6807
HEMBB1001785	F-HEMBB1001785	1300	R-HEMBB1001785	6808
HEMBB1001797	F-HEMBB1001797	1301	R-HEMBB1001797	6809
HEMBB1001802	F-HEMBB1001802	1302	R-HEMBB1001802	6810
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HEMBB1001834	F-HEMBB1001834	1306		
HEMBB1001836	F-HEMBB1001836	1307	R-HEMBB1001836	6814
HEMBB1001839	F-HEMBB1001839	1308	R-HEMBB1001839	6815
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HEMBB1001868	F-HEMBB1001868	1312	R-HEMBB1001868	6819
HEMBB1001869	F-HEMBB1001869	1313	R-HEMBB1001869	6820
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HEMBB1001874	F-HEMBB1001874	1315	R-HEMBB1001874	6822
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HEMBB1001950	F-HEMBB1001950	1332	R-HEMBB1001950	6839
HEMBB1001952	F-HEMBB1001952	1333	R-HEMBB1001952	6840
HEMBB1001953	F-HEMBB1001953	1334	R-HEMBB1001953	6841
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HEMBB1002015	F-HEMBB1002015	1347	R-HEMBB1002015	6854
HEMBB1002042	F-HEMBB1002042	1348	R-HEMBB1002042	6855
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HEMBB1002049	F-HEMBB1002049	1352	R-HEMBB1002049	6859
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HEMBB1002069	F-HEMBB1002069	1355	R-HEMBB1002069	6862
HEMBB1002092	F-HEMBB1002092	1356	R-HEMBB1002092	6863
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HEMBB1002134	F-HEMBB1002134	1359		
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HEMBB1002152	F-HEMBB1002152	1362	R-HEMBB1002152	6868
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HEMBB1002193	F-HEMBB1002193	1365	R-HEMBB1002193	6871
HEMBB1002217	F-HEMBB1002217	1366	R-HEMBB1002217	6872
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HEMBB1002409	F-HEMBB1002409	1388		
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HEMBB1002425	F-HEMBB1002425	1390	R-HEMBB1002425	6895
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HEMBB1002453	F-HEMBB1002453	1392	R-HEMBB1002453	6897
HEMBB1002457	F-HEMBB1002457	1393	R-HEMBB1002457	6898
HEMBB1002458	F-HEMBB1002458	1394	R-HEMBB1002458	6899
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HEMBB1002495	F-HEMBB1002495	1398	R-HEMBB1002495	6903
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HEMBB1002510	F-HEMBB1002510	1401	R-HEMBB1002510	6906
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HEMBB1002582	F-HEMBB1002582	1410	R-HEMBB1002582	6915
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HEMBB1002596	F-HEMBB1002596	1412	R-HEMBB1002596	6917
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HEMBB1002610	F-HEMBB1002610	1417	R-HEMBB1002610	6922
HEMBB1002613	F-HEMBB1002613	1418	R-HEMBB1002613	6923
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HEMBB1002684	F-HEMBB1002684	1426	R-HEMBB1002684	6931
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HEMBB1002697	F-HEMBB1002697	1429	R-HEMBB1002697	6934
HEMBB1002699	F-HEMBB1002699	1430	R-HEMBB1002699	6935
HEMBB1002702	F-HEMBB1002702	1431	R-HEMBB1002702	6936
HEMBB1002705	F-HEMBB1002705	1432	R-HEMBB1002705	6937
HEMBB1002712	F-HEMBB1002712	1433	R-HEMBB1002712	6938
MAMMA1000009	F-MAMMA1000009	1434	R-MAMMA1000009	6939
MAMMA1000019	F-MAMMA1000019	1435	R-MAMMA1000019	6940
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MAMMA1000103	F-MAMMA1000103	1446	R-MAMMA1000103	6951
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MAMMA1000129	F-MAMMA1000129	1448	R-MAMMA1000129	6953
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MAMMA1000221	F-MAMMA1000221	1460	R-MAMMA1000221	6965
MAMMA1000227	F-MAMMA1000227	1461	R-MAMMA1000227	6966
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MAMMA1000264	F-MAMMA1000264	1466	R-MAMMA1000264	6971
MAMMA1000266	F-MAMMA1000266	1467	R-MAMMA1000266	6972
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MAMMA1000361	F-MAMMA1000361	1485	R-MAMMA1000361	6990
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MAMMA1000643	F-MAMMA1000643	1528	R-MAMMA1000643	7032
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MAMMA1000670	F-MAMMA1000670	1531	R-MAMMA1000670	7035
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MAMMA1000684	F-MAMMA1000684	1533	R-MAMMA1000684	7037

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MAMMA1000732	F-MAMMA1000732	1542	R-MAMMA1000732	7046	
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MAMMA1000897	F-MAMMA1000897	1577	R-MAMMA1000897	7079	
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MAMMA1003013	F-MAMMA1003013	1916		
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MAMMA1003019	F-MAMMA1003019	1918	R-MAMMA1003019	7414
MAMMA1003026	F-MAMMA1003026	1919	R-MAMMA1003026	7415
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MAMMA1003057	F-MAMMA1003057	1929	R-MAMMA1003057	7425
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MAMMA1003104	F-MAMMA1003104	1933	R-MAMMA1003104	7429
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NT2RM2001345	F-NT2RM2001345	2129
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NT2RM2001718	F-NT2RM2001718	2167
NT2RM2001723	F-NT2RM2001723	2168
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NT2RM2001743	F-NT2RM2001743	2171
NT2RM2001753	F-NT2RM2001753	2172
NT2RM2001760	F-NT2RM2001760	2173
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NT2RM2001771	F-NT2RM2001771	2175
NT2RM2001782	F-NT2RM2001782	2176
NT2RM2001784	F-NT2RM2001784	2177

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NT2RM4000024	F-NT2RM4000024	2216	R-NT2RM4000024	7438
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NT2RM4000061	F-NT2RM4000061	2220	R-NT2RM4000061	7442
NT2RM4000085	F-NT2RM4000085	2221	R-NT2RM4000085	7443
NT2RM4000086	F-NT2RM4000086	2222	R-NT2RM4000086	7444
NT2RM4000104	F-NT2RM4000104	2223	R-NT2RM4000104	7445

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NT2RM4000139	F-NT2RM4000139	2224	R-NT2RM4000139	7446
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NT2RM4000156	F-NT2RM4000156	2226	R-NT2RM4000156	7448
NT2RM4000167	F-NT2RM4000167	2227	R-nnnnnnnnnnnn	7449
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NT2RM4000202	F-NT2RM4000202	2233	R-NT2RM4000202	7455
NT2RM4000210	F-NT2RM4000210	2234	R-NT2RM4000210	7456
NT2RM4000215	F-NT2RM4000215	2235	R-NT2RM4000215	7457
NT2RM4000229	F-NT2RM4000229	2236	R-nnnnnnnnnnnn	7458
NT2RM4000233	F-NT2RM4000233	2237	R-NT2RM4000233	7459
NT2RM4000244	F-NT2RM4000244	2238	R-NT2RM4000244	7460
NT2RM4000251	F-NT2RM4000251	2239	R-NT2RM4000251	7461
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NT2RM4000290	F-NT2RM4000290	2241	R-NT2RM4000290	7463
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NT2RM4000344	F-NT2RM4000344	2244	R-NT2RM4000344	7466
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NT2RM4000366	F-NT2RM4000366	2248	R-NT2RM4000366	7470
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NT2RM4000603	F-NT2RM4000603	2270	R-NT2RM4000603	7492
NT2RM4000611	F-NT2RM4000611	2271	R-nnnnnnnnnnnn	7493
NT2RM4000616	F-NT2RM4000616	2272	R-NT2RM4000616	7494
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NT2RM4000689	F-NT2RM4000689	2274	R-NT2RM4000689	7496
NT2RM4000698	F-NT2RM4000698	2275	R-NT2RM4000698	7497
NT2RM4000700	F-NT2RM4000700	2276	R-nnnnnnnnnnnn	7498
NT2RM4000712	F-NT2RM4000712	2277	R-NT2RM4000712	7499
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NT2RM4000733	F-NT2RM4000733	2279	R-NT2RM4000733	7501
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NT2RM4000778	F-NT2RM4000778	2284	R-NT2RM4000778	7506
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NT2RM4000833	F-NT2RM4000833	2293	R-NT2RM4000833	7515
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NT2RM4000855	F-NT2RM4000855	2296	R-NT2RM4000855	7518
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NT2RM4001016	F-NT2RM4001016	2304	R-NT2RM4001016	7526
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NT2RM4001203	F-NT2RM4001203	2318	R-NT2RM4001203	7540
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NT2RM4001256	F-NT2RM4001256	2321	R-NT2RM4001256	7543
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NT2RM4001309	F-NT2RM4001309	2323	R-NT2RM4001309	7545
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NT2RM4001382	F-NT2RM4001382	2331	R-NT2RM4001382	7553
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NT2RM4001582	F-NT2RM4001582	2349	R-NT2RM4001582	7571
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NT2RM4001594	F-NT2RM4001594	2351	R-NT2RM4001594	7573
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NT2RM4001605	F-NT2RM4001605	2353	R-NT2RM4001605	7575
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NT2RM4001650	F-NT2RM4001650	2356	R-NT2RM4001650	7578
NT2RM4001662	F-NT2RM4001662	2357	R-NT2RM4001662	7579
NT2RM4001666	F-NT2RM4001666	2358	R-NT2RM4001666	7580
NT2RM4001682	F-NT2RM4001682	2359	R-NT2RM4001682	7581
NT2RM4001710	F-NT2RM4001710	2360	R-NT2RM4001710	7582
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NT2RM4001741	F-NT2RM4001741	2364	R-NT2RM4001741	7586
NT2RM4001746	F-NT2RM4001746	2365	R-NT2RM4001746	7587
NT2RM4001754	F-NT2RM4001754	2366	R-NT2RM4001754	7588
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NT2RP2001081	F-NT2RP2001081	2677		
NT2RP2001094	F-NT2RP2001094	2678	R-NT2RP2001094	7767
NT2RP2001119	F-NT2RP2001119	2679	R-NT2RP2001119	7768
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NT2RP2001149	F-NT2RP2001149	2682	R-NT2RP2001149	7771
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NT2RP2003228	F-NT2RP2003228	2864		
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NT2RP2003567	F-NT2RP2003567	2902		
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NT2RP2003604	F-NT2RP2003604	2905	R-NT2RP2003604	7976
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NT2RP2003687	F-NT2RP2003687	2909	R-NT2RP2003687	7980
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NT2RP2003704	F-NT2RP2003704	2912	R-NT2RP2003704	7983
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NT2RP3002861	F-NT2RP3002861	3463	R-NT2RP3002861	8506
NT2RP3002869	F-NT2RP3002869	3464	R-NT2RP3002869	8507
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NT2RP3003311	F-NT2RP3003311	3508	R-NT2RP3003311	8548
NT2RP3003313	F-NT2RP3003313	3509	R-NT2RP3003313	8549
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NT2RP3004669	F-NT2RP3004669	3621		
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NT2RP4000246	F-NT2RP4000246	3644	R-NT2RP4000246	8676
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NT2RP4000398	F-NT2RP4000398	3657		
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NT2RP4000713	F-NT2RP4000713	3684		
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NT2RP4000737	F-NT2RP4000737	3687		
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NT2RP4002018	F-NT2RP4002018	3816	R-NT2RP4002018	8835
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OVARC1000017	F-OVARC1000017	3844	R-OVARC1000017	8853
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OVARC1000335	F-OVARC1000335	3876	R-OVARC1000335	8883
OVARC1000347	F-OVARC1000347	3877	R-OVARC1000347	8884
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OVARC1000605	F-OVARC1000605	3907	R-OVARC1000605	8913
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OVARC1001129	F-OVARC1001129	3975	R-OVARC1001129	8974
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OVARC1001555	F-OVARC1001555	4027		
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OVARC1001600	F-OVARC1001600	4029	R-OVARC1001600	9023
OVARC1001610	F-OVARC1001610	4030	R-OVARC1001610	9024
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OVARC1002112	F-OVARC1002112	4076			
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PLACE1000292	F-PLACE1000292	4105	R-PLACE1000292	9096	
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PLACE1001054	F-PLACE1001054	4163		
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PLACE1001821	F-PLACE1001821	4232	R-PLACE1001821	9217
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PLACE1001989	F-PLACE1001989	4241	R-PLACE1001989	9225
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PLACE1002768	F-PLACE1002768	4292	R-PLACE1002768	9273
PLACE1002772	F-PLACE1002772	4293	R-PLACE1002772	9274

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PLACE1002811	F-PLACE1002811	4297	R-PLACE1002811	9277
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PLACE1002881	F-PLACE1002881	4304	R-PLACE1002881	9284
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PLACE1002991	F-PLACE1002991	4309	R-PLACE1002991	9289
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PLACE1002996	F-PLACE1002996	4311	R-PLACE1002996	9291
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PLACE1003044	F-PLACE1003044	4314	R-PLACE1003044	9294
PLACE1003045	F-PLACE1003045	4315		
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PLACE1003100	F-PLACE1003100	4317	R-PLACE1003100	9296
PLACE1003108	F-PLACE1003108	4318	R-PLACE1003108	9297
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PLACE1003420	F-PLACE1003420	4345	R-PLACE1003420	9323
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PLACE1003516	F-PLACE1003516	4349	R-PLACE1003516	9327
PLACE1003519	F-PLACE1003519	4350	R-PLACE1003519	9328
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PLACE1003592	F-PLACE1003592	4359	R-PLACE1003592	9337
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PLACE1003596	F-PLACE1003596	4361	R-PLACE1003596	9339
PLACE1003602	F-PLACE1003602	4362	R-PLACE1003602	9340
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PLACE1003892	F-PLACE1003892	4389		
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PLACE1003903	F-PLACE1003903	4391	R-PLACE1003903	9368
PLACE1003915	F-PLACE1003915	4392	R-PLACE1003915	9369
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PLACE1004103	F-PLACE1004103	4397		
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PLACE1004114	F-PLACE1004114	4399	R-PLACE1004114	9375
PLACE1004118	F-PLACE1004118	4400	R-PLACE1004118	9376
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PLACE1004156	F-PLACE1004156	4403	R-PLACE1004156	9379
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PLACE1004814	F-PLACE1004814	4463	R-PLACE1004814	9439
PLACE1004815	F-PLACE1004815	4464	R-PLACE1004815	9440
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PLACE1004885	F-PLACE1004885	4471	R-PLACE1004885	9447
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PLACE1004969	F-PLACE1004969	4479	R-PLACE1004969	9455
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PLACE1005101	F-PLACE1005101	4493	R-PLACE1005101	9468
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PLACE1005471	F-PLACE1005471	4521	R-PLACE1005471	9496
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PLACE1005480	F-PLACE1005480	4523	R-PLACE1005480	9498

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PLACE1005502	F-PLACE1005502	4526	R-PLACE1005502	9501
PLACE1005526	F-PLACE1005526	4527	R-PLACE1005526	9502
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PLACE1005656	F-PLACE1005656	4542	R-PLACE1005656	9517
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PLACE1005804	F-PLACE1005804	4553	R-PLACE1005804	9528
PLACE1005813	F-PLACE1005813	4554		
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PLACE1005834	F-PLACE1005834	4556	R-PLACE1005834	9530
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PLACE1005850	F-PLACE1005850	4558	R-PLACE1005850	9532
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PLACE1005884	F-PLACE1005884	4561	R-PLACE1005884	9535
PLACE1005890	F-PLACE1005890	4562		
PLACE1005898	F-PLACE1005898	4563	R-PLACE1005898	9536
PLACE1005921	F-PLACE1005921	4564	R-PLACE1005921	9537
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PLACE1005932	F-PLACE1005932	4567	R-PLACE1005932	9540
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PLACE1005936	F-PLACE1005936	4569	R-PLACE1005936	9542

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PLACE1006002	F-PLACE1006002	4576	R-PLACE1006002	9549
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PLACE1006011	F-PLACE1006011	4578	R-PLACE1006011	9551
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PLACE1006119	F-PLACE1006119	4583	R-PLACE1006119	9556
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PLACE1006157	F-PLACE1006157	4587	R-PLACE1006157	9560
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PLACE1006195	F-PLACE1006195	4593	R-PLACE1006195	9566
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PLACE1006288	F-PLACE1006288	4603	R-PLACE1006288	9576
PLACE1006318	F-PLACE1006318	4604	R-PLACE1006318	9577
PLACE1006325	F-PLACE1006325	4605	R-PLACE1006325	9578
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PLACE1006357	F-PLACE1006357	4607	R-PLACE1006357	9580
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PLACE1007053	F-PLACE1007053	4667	R-PLACE1007053	9638
PLACE1007068	F-PLACE1007068	4668		
PLACE1007097	F-PLACE1007097	4669	R-PLACE1007097	9639
PLACE1007105	F-PLACE1007105	4670	R-PLACE1007105	9640
PLACE1007111	F-PLACE1007111	4671	R-PLACE1007111	9641
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PLACE1007132	F-PLACE1007132	4673	R-PLACE1007132	9643
PLACE1007140	F-PLACE1007140	4674	R-PLACE1007140	9644
PLACE1007178	F-PLACE1007178	4675	R-PLACE1007178	9645
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PLACE1007238	F-PLACE1007238	4677	R-PLACE1007238	9647
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PLACE1007409	F-PLACE1007409	4694	R-PLACE1007409	9664
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PLACE1007452	F-PLACE1007452	4697	R-PLACE1007452	9667
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PLACE1009155	F-PLACE1009155	4839	R-PLACE1009155	9804
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PLACE1009246	F-PLACE1009246	4849	R-PLACE1009246	9814
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PLACE3000271	F-PLACE3000271	5158	R-PLACE3000271	10104
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PLACE3000400	F-PLACE3000400	5176	R-PLACE3000400	10122
PLACE3000401	F-PLACE3000401	5177	R-PLACE3000401	10123
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PLACE3000425	F-PLACE3000425	5183	R-PLACE3000425	10129
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PLACE4000156	F-PLACE4000156	5201	R-PLACE4000156	10146
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PLACE4000211	F-PLACE4000211	5203		
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THYRO1000017	F-THYRO1000017	5250			
THYRO1000026	F-THYRO1000026	5251	R-THYRO1000026	10175	
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THYRO1001671	F-THYRO1001671	5395	R-THYRO1001671	10317
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THYR01001745	F-THYR01001745	5401	R-THYR01001745	10323
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VESEN1000122	F-VESEN1000122	5410	R-VESEN1000122	10331
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Y79AA1000405	F-Y79AA1000405	5431	R-Y79AA1000405	10352
Y79AA1000410	F-Y79AA1000410	5432	R-Y79AA1000410	10353
Y79AA1000420	F-Y79AA1000420	5433	R-Y79AA1000420	10354
Y79AA1000469	F-Y79AA1000469	5434	R-Y79AA1000469	10355
Y79AA1000480	F-Y79AA1000480	5435	R-Y79AA1000480	10356
Y79AA1000538	F-Y79AA1000538	5436	R-Y79AA1000538	10357
Y79AA1000539	F-Y79AA1000539	5437	R-Y79AA1000539	10358
Y79AA1000540	F-Y79AA1000540	5438	R-Y79AA1000540	10359
Y79AA1000560	F-Y79AA1000560	5439	R-Y79AA1000560	10360
Y79AA1000574	F-Y79AA1000574	5440	R-Y79AA1000574	10361
Y79AA1000589	F-Y79AA1000589	5441		
Y79AA1000627	F-Y79AA1000627	5442	R-Y79AA1000627	10362
Y79AA1000705	F-Y79AA1000705	5443	R-Y79AA1000705	10363

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Y79AA1000734	F-Y79AA1000734	5444	R-Y79AA1000734	10364
Y79AA1000748	F-Y79AA1000748	5445	R-Y79AA1000748	10365
Y79AA1000752	F-Y79AA1000752	5446	R-Y79AA1000752	10366
Y79AA1000774	F-Y79AA1000774	5447	R-Y79AA1000774	10367
Y79AA1000782	F-Y79AA1000782	5448	R-Y79AA1000782	10368
Y79AA1000784	F-Y79AA1000784	5449	R-Y79AA1000784	10369
Y79AA1000794	F-Y79AA1000794	5450	R-Y79AA1000794	10370
Y79AA1000800	F-Y79AA1000800	5451	R-Y79AA1000800	10371
Y79AA1000802	F-Y79AA1000802	5452	R-nnnnnnnnnnnn	10372
Y79AA1000805	F-Y79AA1000805	5453	R-Y79AA1000805	10373
Y79AA1000824	F-Y79AA1000824	5454	R-Y79AA1000824	10374
Y79AA1000827	F-Y79AA1000827	5455	R-Y79AA1000827	10375
Y79AA1000833	F-Y79AA1000833	5456		
Y79AA1000850	F-Y79AA1000850	5457	R-Y79AA1000850	10376
Y79AA1000962	F-Y79AA1000962	5458	R-Y79AA1000962	10377
Y79AA1000966	F-Y79AA1000966	5459		
Y79AA1000968	F-Y79AA1000968	5460	R-Y79AA1000968	10378
Y79AA1000969	F-Y79AA1000969	5461	R-Y79AA1000969	10379
Y79AA1000976	F-Y79AA1000976	5462	R-Y79AA1000976	10380
Y79AA1000985	F-Y79AA1000985	5463	R-Y79AA1000985	10381
Y79AA1001023	F-Y79AA1001023	5464	R-Y79AA1001023	10382
Y79AA1001041	F-Y79AA1001041	5465	R-Y79AA1001041	10383
Y79AA1001048	F-Y79AA1001048	5466	R-Y79AA1001048	10384
Y79AA1001061	F-Y79AA1001061	5467	R-Y79AA1001061	10385
Y79AA1001068	F-Y79AA1001068	5468	R-Y79AA1001068	10386
Y79AA1001077	F-Y79AA1001077	5469	R-Y79AA1001077	10387
Y79AA1001078	F-Y79AA1001078	5470	R-Y79AA1001078	10388
Y79AA1001105	F-Y79AA1001105	5471	R-Y79AA1001105	10389
Y79AA1001145	F-Y79AA1001145	5472	R-Y79AA1001145	10390
Y79AA1001167	F-Y79AA1001167	5473	R-Y79AA1001167	10391
Y79AA1001177	F-Y79AA1001177	5474	R-Y79AA1001177	10392
Y79AA1001185	F-Y79AA1001185	5475	R-Y79AA1001185	10393
Y79AA1001211	F-Y79AA1001211	5476	R-Y79AA1001211	10394
Y79AA1001216	F-Y79AA1001216	5477	R-Y79AA1001216	10395
Y79AA1001228	F-Y79AA1001228	5478	R-Y79AA1001228	10396
Y79AA1001233	F-Y79AA1001233	5479	R-Y79AA1001233	10397
Y79AA1001236	F-Y79AA1001236	5480	R-Y79AA1001236	10398
Y79AA1001281	F-Y79AA1001281	5481	R-Y79AA1001281	10399
Y79AA1001299	F-Y79AA1001299	5482	R-Y79AA1001299	10400
Y79AA1001312	F-Y79AA1001312	5483	R-Y79AA1001312	10401
Y79AA1001323	F-Y79AA1001323	5484	R-Y79AA1001323	10402
Y79AA1001384	F-Y79AA1001384	5485	R-Y79AA1001384	10403
Y79AA1001391	F-Y79AA1001391	5486	R-Y79AA1001391	10404
Y79AA1001394	F-Y79AA1001394	5487	R-Y79AA1001394	10405
Y79AA1001402	F-Y79AA1001402	5488	R-Y79AA1001402	10406
Y79AA1001493	F-Y79AA1001493	5489	R-Y79AA1001493	10407

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Y79AA1001511	F-Y79AA1001511	5490	R-Y79AA1001511	10408	
Y79AA1001533	F-Y79AA1001533	5491	R-Y79AA1001533	10409	
Y79AA1001541	F-Y79AA1001541	5492	R-nnnnnnnnnnnn	10410	
Y79AA1001548	F-Y79AA1001548	5493	R-Y79AA1001548	10411	
Y79AA1001555	F-Y79AA1001555	5494	R-Y79AA1001555	10412	
Y79AA1001581	F-Y79AA1001581	5495			
Y79AA1001585	F-Y79AA1001585	5496	R-Y79AA1001585	10413	
Y79AA1001594	F-Y79AA1001594	5497	R-Y79AA1001594	10414	
Y79AA1001603	F-Y79AA1001603	5498	R-Y79AA1001603	10415	
Y79AA1001613	F-Y79AA1001613	5499	R-Y79AA1001613	10416	
Y79AA1001647	F-Y79AA1001647	5500	R-Y79AA1001647	10417	
Y79AA1001665	F-Y79AA1001665	5501	R-Y79AA1001665	10418	
Y79AA1001679	F-Y79AA1001679	5502	R-Y79AA1001679	10419	
Y79AA1001692	F-Y79AA1001692	5503	R-nnnnnnnnnnnn	10420	
Y79AA1001696	F-Y79AA1001696	5504	R-Y79AA1001696	10421	
Y79AA1001705	F-Y79AA1001705	5505	R-Y79AA1001705	10422	
Y79AA1001711	F-Y79AA1001711	5506	R-Y79AA1001711	10423	
Y79AA1001781	F-Y79AA1001781	5507	R-Y79AA1001781	10424	
Y79AA1001805	F-Y79AA1001805	5508	R-nnnnnnnnnnnn	10425	
Y79AA1001827	F-Y79AA1001827	5509	R-Y79AA1001827	10426	
Y79AA1001846	F-Y79AA1001846	5510	R-Y79AA1001846	10427	
Y79AA1001848	F-Y79AA1001848	5511	R-Y79AA1001848	10428	
Y79AA1001866	F-Y79AA1001866	5512	R-Y79AA1001866	10429	
Y79AA1001874	F-Y79AA1001874	5513	R-Y79AA1001874	10430	
Y79AA1001875	F-Y79AA1001875	5514	R-Y79AA1001875	10431	
Y79AA1001923	F-Y79AA1001923	5515	R-Y79AA1001923	10432	
Y79AA1001963	F-Y79AA1001963	5516			
Y79AA1002027	F-Y79AA1002027	5517	R-Y79AA1002027	10433	
Y79AA1002083	F-Y79AA1002083	5518	R-Y79AA1002083	10434	
Y79AA1002089	F-Y79AA1002089	5519	R-Y79AA1002089	10435	
Y79AA1002093	F-Y79AA1002093	5520	R-Y79AA1002093	10436	
Y79AA1002103	F-Y79AA1002103	5521	R-Y79AA1002103	10437	
Y79AA1002115	F-Y79AA1002115	5522	R-Y79AA1002115	10438	
Y79AA1002125	F-Y79AA1002125	5523	R-Y79AA1002125	10439	
Y79AA1002139	F-Y79AA1002139	5524	R-Y79AA1002139	10440	
Y79AA1002204	F-Y79AA1002204	5525	R-Y79AA1002204	10441	
Y79AA1002208	F-Y79AA1002208	5526	R-nnnnnnnnnnnn	10442	
Y79AA1002209	F-Y79AA1002209	5527	R-Y79AA1002209	10443	
Y79AA1002210	F-Y79AA1002210	5528	R-Y79AA1002210	10444	
Y79AA1002211	F-Y79AA1002211	5529	R-Y79AA1002211	10445	
Y79AA1002220	F-Y79AA1002220	5530	R-Y79AA1002220	10446	
Y79AA1002229	F-Y79AA1002229	5531	R-Y79AA1002229	10447	
Y79AA1002234	F-Y79AA1002234	5532	R-Y79AA1002234	10448	
Y79AA1002246	F-Y79AA1002246	5533	R-Y79AA1002246	10449	
Y79AA1002258	F-Y79AA1002258	5534	R-Y79AA1002258	10450	
Y79AA1002298	F-Y79AA1002298	5535	R-Y79AA1002298	10451	

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Y79AA1002307	F-Y79AA1002307	5536	R-Y79AA1002307	10452
Y79AA1002311	F-Y79AA1002311	5537	R-Y79AA1002311	10453
Y79AA1002351	F-Y79AA1002351	5538	R-Y79AA1002351	10454
Y79AA1002361	F-Y79AA1002361	5539	R-Y79AA1002361	10455
Y79AA1002399	F-Y79AA1002399	5540	R-Y79AA1002399	10456
Y79AA1002407	F-Y79AA1002407	5541	R-Y79AA1002407	10457
Y79AA1002416	F-Y79AA1002416	5542	R-Y79AA1002416	10458
Y79AA1002431	F-Y79AA1002431	5543	R-Y79AA1002431	10459
Y79AA1002433	F-Y79AA1002433	5544	R-nnnnnnnnnnnn	10460
Y79AA1002472	F-Y79AA1002472	5545	R-Y79AA1002472	10461
Y79AA1002482	F-Y79AA1002482	5546	R-Y79AA1002482	10462
Y79AA1002487	F-Y79AA1002487	5547	R-Y79AA1002487	10463

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Table 2

name of clone	name of 5'-end sequence	SEQ ID of 5'-end sequence	name of 3'-end sequence	SEQ ID of 3'-end sequence
HEMBA1000497	F-HEMBA1000497	16111	R-HEMBA1000497	16165
HEMBA1001750	F-HEMBA1001750	16112	R-HEMBA1001750	16166
HEMBA1003854	F-HEMBA1003854	16113	R-HEMBA1003854	16167
HEMBA1004193	F-HEMBA1004193	16114	R-HEMBA1004193	16168
HEMBA1004860	F-HEMBA1004860	16115	R-HEMBA1004860	16169
HEMBA1005572	F-HEMBA1005572	16116	R-HEMBA1005572	16170
HEMBA1006038	F-HEMBA1006038	16117	R-HEMBA1006038	16171
HEMBA1006092	F-HEMBA1006092	16118	R-HEMBA1006092	16172
HEMBA1006406	F-HEMBA1006406	16119	R-HEMBA1006406	16173
HEMBA1006650	F-HEMBA1006650	16120	R-HEMBA1006650	16174
HEMBA1006812	F-HEMBA1006812	16121	R-HEMBA1006812	16175
HEMBB1000672	F-HEMBB1000672	16122	R-HEMBB1000672	16176
HEMBB1001197	F-HEMBB1001197	16123	R-HEMBB1001197	16177
HEMBB1001871	F-HEMBB1001871	16124	R-HEMBB1001871	16178
MAMMA1001252	F-MAMMA1001252	16125	R-MAMMA1001252	16179
MAMMA1002094	F-MAMMA1002094	16126	R-MAMMA1002094	16180
NT2RM4000634	F-NT2RM4000634	16127	R-NT2RM4000634	16181
NT2RM4000657	F-NT2RM4000657	16128	R-NT2RM4000657	16182
NT2RM4000783	F-NT2RM4000783	16129	R-NT2RM4000783	16183
NT2RM4000857	F-NT2RM4000857	16130	R-NT2RM4000857	16184
NT2RM4001178	F-NT2RM4001178	16131	R-NT2RM4001178	16185
NT2RM4002420	F-NT2RM4002420	16132	R-NT2RM4002420	16186
NT2RP2000198	F-NT2RP2000198	16133	R-NT2RP2000198	16187
NT2RP2000551	F-NT2RP2000551	16134	R-NT2RP2000551	16188
NT2RP2000660	F-NT2RP2000660	16135	R-NT2RP2000660	16189

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NT2RP2001214	F-NT2RP2001214	16136	R-NT2RP2001214	16190
NT2RP2001460	F-NT2RP2001460	16137	R-NT2RP2001460	16191
NT2RP2001756	F-NT2RP2001756	16138	R-NT2RP2001756	16192
NT2RP2002056	F-NT2RP2002056	16139	R-NT2RP2002056	16193
NT2RP2002677	F-NT2RP2002677	16140	R-NT2RP2002677	16194
NT2RP2002755	F-NT2RP2002755	16141	R-NT2RP2002755	16195
NT2RP2002843	F-NT2RP2002843	16142	R-NT2RP2002843	16196
NT2RP2003101	F-NT2RP2003101	16143	R-NT2RP2003101	16197
NT2RP2003799	F-NT2RP2003799	16144	R-NT2RP2003799	16198
NT2RP2004095	F-NT2RP2004095	16145	R-NT2RP2004095	16199
NT2RP2004732	F-NT2RP2004732	16146	R-NT2RP2004732	16200
NT2RP2004920	F-NT2RP2004920	16147	R-NT2RP2004920	16201
NT2RP2005454	F-NT2RP2005454	16148	R-NT2RP2005454	16202
NT2RP2005776	F-NT2RP2005776	16149	R-NT2RP2005776	16203
NT2RP2005806	F-NT2RP2005806	16150	R-NT2RP2005806	16204
NT2RP2005882	F-NT2RP2005882	16151	R-NT2RP2005882	16205
NT2RP3001282	F-NT2RP3001282	16152	R-NT2RP3001282	16206
NT2RP3001723	F-NT2RP3001723	16153	R-NT2RP3001723	16207
NT2RP3002099	F-NT2RP3002099	16154	R-NT2RP3002099	16208
NT2RP3003155	F-NT2RP3003155	16155	R-NT2RP3003155	16209
NT2RP3004028	F-NT2RP3004028	16156	R-NT2RP3004028	16210
OVARC1000008	F-OVARC1000008	16157	R-OVARC1000008	16211
OVARC1000724	F-OVARC1000724	16158	R-OVARC1000724	16212
OVARC1000751	F-OVARC1000751	16159	R-OVARC1000751	16213
OVARC1001029	F-OVARC1001029	16160	R-OVARC1001029	16214
PLACE1000814	F-PLACE1000814	16161	R-PLACE1000814	16215
PLACE1003030	F-PLACE1003030	16162	R-PLACE1003030	16216
PLACE1005549	F-PLACE1005549	16163	R-PLACE1005549	16217
PLACE1007218	F-PLACE1007218	16164	R-PLACE1007218	16218

[0019] Furthermore, the present invention relates to the use of the above primers, as described below.

(4) A polynucleotide which can be synthesized with the primer set of (2) or (3).
(5) A polynucleotide comprising a coding region in the polynucleotide of (4).
(6) A substantially pure protein encoded by polynucleotide of (4).
(7) A partial peptide of the protein of (6).

[0020] In addition, the present invention comprises a polynucleotide described below and a protein encoded by the polynucleotide.

(8) An isolated polynucleotide selected from the group consisting of

(a) a polynucleotide comprising a coding region of the nucleotide sequence set forth in any one of the SEQ ID NOs in Tables 350 and 351;
(b) a polynucleotide comprising a nucleotide sequence encoding a protein comprising the amino acid sequence set forth in any one of the SEQ ID NOs in Tables 350 and 351;
(c) a polynucleotide comprising a nucleotide sequence encoding a protein comprising an amino acid sequence

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selected from the amino acid sequences set forth in the SEQ ID NOs in Tables 350 and 351, in which one or more amino acids are substituted, deleted, inserted, and/or added, wherein said protein is functionally equivalent to the protein comprising said amino acid sequence selected from the amino acid sequences set forth in the SEQ ID NOs in Tables 350 and 351;

(d) a polynucleotide that hybridizes with a polynucleotide comprising a nucleotide sequence selected from the nucleotide sequences set forth in the SEQ ID NOs in Tables 350 and 351, and that comprises a nucleotide sequence encoding a protein functionally equivalent to the protein encoded by the nucleotide sequence selected from the nucleotide sequences set forth in the SEQ ID NOs in Tables 350 and 351;

(e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a protein encoded by the polynucleotide of (a) to (d);

(f) a polynucleotide comprising a nucleotide sequence with at least 70% identity to the nucleotide sequence set forth in any one of the SEQ ID NOs in Tables 350 and 351.

(9). A substantially pure protein encoded by the polynucleotide of (8).

(10) An antibody against the protein or peptide of any one of (6), (7), and (9).

(11) A vector comprising the polynucleotide of (5) or (8).

(12) A transformant carrying the polynucleotide of (5) or (8), or the vector of (11).

(13) A transformant expressively carrying the polynucleotide of (5) or (8), or the vector of (11).

(14) A method for producing the protein or peptide of any one of (6), (7), and (9), comprising culturing the transformant of (13) and recovering the expression product.

(15) An oligonucleotide comprising the nucleotide sequence set forth in any one of the SEQ ID NOs in Tables 350 and 351 or the nucleotide sequence complementary to the complementary strand thereof, wherein said oligonucleotide comprises 15 nucleotides or more.

(16) Use of the oligonucleotide of (15) as a primer for synthesizing a polynucleotide.

(17) Use of the oligonucleotide of (15) as a probe for detecting a gene.

(18) An antisense polynucleotide against the polynucleotide of (8), or the portion thereof.

(19) A method for synthesizing a polynucleotide, the method comprising:

a) synthesizing a complementary strand using a cDNA library as a template, and using the primer set of (2) or (3), or the primer of (16); and

b) recovering the synthesized product.

(20) The method of (19), wherein the cDNA library is obtainable by oligo-capping method.

(21) The method of (19), wherein the complementary strand is obtainable by PCR.

(22) A method for detecting the polynucleotide of (8), the method comprising:

a) incubating a target polynucleotide with the oligonucleotide of (15) under the conditions where hybridization occurs, and

b) detecting the hybridization of the target polynucleotide with the oligonucleotide of (15).

(23) A database of polynucleotides and/or proteins, the database comprising information on at least one sequence selected from the nucleotide sequences set forth in the SEQ ID NOs in Tables 350 and 351 and/or the amino acid sequences set forth in the SEQ ID NOs in Tables 350 and 351, or a medium on which the database is stored.

[0021] Any patents, patent applications, and publications cited herein are incorporated by reference.

BRIEF DESCRIPTION OF THE DRAWINGS

[0022] Figure 1 shows the restriction maps of vectors pME18SFL3 and pUC19FL3.

[0023] Figure 2 shows the reproducibility of gene expression analysis. The respective intensities of gene expression observed in independent set of experiments are plotted in the vertical axis as well as in the horizontal axis.

[0024] Figure 3 shows the detection limit in gene expression analysis. The intensity of expression is shown in the vertical axis and the concentration (μg/ml) of probe used is shown in the horizontal axis.

DETAILED DESCRIPTION OF THE INVENTION

[0025] Herein, "polynucleotide" is defined as a molecule in which multiple nucleotides are polymerized. There are no limitations in the number of the polymerized nucleotides. In case that the polymer contains relatively low number

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of nucleotides, it is also described as an "oligonucleotide". The polynucleotide or the oligonucleotide of the present invention can be a natural or chemically synthesized product. Alternatively, it can be synthesized using a template DNA by an enzymatic reaction such as PCR.

[0026] All the cDNA provided by the invention are full-length cDNA. Herein, a "full-length cDNA" is defined as a cDNA which contains both ATG codon (the translation start site) and the stop codon. Accordingly, the untranslated regions, which are originally found in the upstream or downstream of the protein coding region in natural mRNA, may or may not be contained.

[0027] An "isolated polynucleotide" is a polynucleotide the structure of which is not identical to that of any naturally occurring nucleic acid or to that of any fragment of a naturally occurring genomic nucleic acid spanning more than three separate genes. The term therefore covers, for example,

(a) a DNA which has the sequence of part of a naturally occurring genomic DNA molecule but is not flanked by both of the coding sequences that flank that part of the molecule in the genome of the organism in which it naturally occurs;

(b) a nucleic acid incorporated into a vector or into the genomic DNA of a prokaryote or eukaryote in a manner such that the resulting molecule is not identical to any naturally occurring vector or genomic DNA;

(c) a separate molecule such as a cDNA, a genomic fragment, a fragment produced by polymerase chain reaction (PCR), or a restriction fragment; and

(d) a recombinant nucleotide sequence that is part of a hybrid gene, i.e., a gene encoding a fusion protein. Specifically excluded from this definition are nucleic acids present in mixtures of different (i) DNA molecules, (ii) transfected cells, or (iii) cell clones: e.g., as these occur in a DNA library such as a cDNA or genomic DNA library.

[0028] The term "substantially pure" as used herein in reference to a given polypeptide means that the protein or polypeptide is substantially free from other biological macromolecules. The substantially pure protein or polypeptide is at least 75% (e.g., at least 80, 85, 95, or 99%) pure by dry weight. Purity can be measured by any appropriate standard method, for example, by column chromatography, polyacrylamide gel electrophoresis, or HPLC analysis.

[0029] All the clones (5602 clones) of the present invention are novel and encode the full-length proteins. All the clones were prepared by oligo capping method, which can achieve cDNA cloning with high fullness ratio. The cDNA clones were selected by using ATGprI score as an index of the fullness ratio at the 5'-end, based on the sequence features of the 5'-end sequences. Selection was further carried out by searching GenBank database for EST sequences homologous to 5'-end sequence of each clone by BLAST [S.F. Altschul, W. Gish, W. Miller, E.W. Myers & D.L. Lipman J. Mol. Biol., 215:403-410 (1990); W. Gish, & D.J. States, Nature Genet., 3:266-272 (1993)] and by considering the number of matching (identical) EST sequences or the number of continuous amino acids in the 5'-end sequence initiated from the initiation codon.

[0030] Moreover, the clones were turn out to be not identical to any of the known human mRNA (namely novel) by homology search using the 5'-end sequence.

[0031] The primers of the present invention, which are used for synthesizing full-length cDNA, are selected from the group comprising SEQ ID NO: 1-5547 (5'-primer), or SEQ ID NO: 5548-10463 (3'-primer). Further, the primers of the present invention, which are used for synthesizing full-length cDNA, are selected from SEQ ID NO: 16111-16164 (5'-primer), or SEQ ID NO: 16165-16218 (3'-primer). Some of the nucleotides include a known EST as its part. However, the primers of the present invention are novel in terms that the primers enable to synthesize full-length cDNA. Because the known ESTs lack important information on what part of cDNA the ESTs correspond to, it is impossible to design primers on the basis of the ESTs.

[0032] All the full-length cDNA of the present invention can be synthesized using a primer set comprising the nucleotide sequences selected from both the 5'-and 3'-end sequences, or a set comprising a primer based on the 5'-end sequence and an oligo-dT primer, by a method such as PCR (Current protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 6.1-6.4).

[0033] Specifically, PCR can be performed using an oligonucleotide that has 15 nucleotides longer, and specifically hybridizes with the complementary strand of the polynucleotide that contains the nucleotide sequence selected from the 5'-end sequences shown in Table 1 and 2 (SEQ ID NO: 1-5547, or SEQ ID NO: 16111-16164), and an oligo-dT primer as a 5'-, and 3'-primer, respectively. The length of the primers is usually 15-100 bp, and favorably between 15-35 bp. In case of LA PCR, which is described below, the primer length of 25-35 bp may provide a good result.

[0034] A method to design a primer that enables a specific amplification based on the given nucleotide sequence is known to those skilled in the art (Current Protocols in Molecular Biology, Ausubel et al. edit, (1987) John Wiley & Sons, Section 6.1-6.4). In designing a primer based on the 5'-end sequence, the primer is designed so as that, in principle, the amplification products will include the translation start site. Accordingly, in case that a given 5'-end nucleotide sequence is the 5'- untranslated region (5'UTR), any part of the sequence can be used as a 5'-primer as far as the specificity toward the target cDNA is insured. The translation start site can be predicted using a known method such

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as the ATGpr as described below.

[0035] When synthesizing a polynucleotide, the target nucleotide sequence to be amplified can extend to several thousand bp in some cDNA. However, it is possible to amplify such a long nucleotides by using such as LA PCR (Long and Accurate PCR). It is advantageous to use LA PCR when synthesizing long DNA. In LA PCR, in which a special DNA polymerase having 3' →5' exonuclease activity is used, misincorporated nucleotides can be removed. Accordingly, accurate synthesis of the complementary strand can be achieved even with a long nucleotide sequence. By using LA PCR, it is reported that amplification of a nucleotide with 20 kb longer can be achieved under desirable condition (Takeshi Hayashi (1996) Jikken-Igaku Bessatsu, "Advanced Technologies in PCR" Youdo-sha).

[0036] A template DNA for synthesizing the cDNA of the present invention can be obtained by using cDNA libraries that are prepared by various methods. The full-length cDNA clones obtained here are those with high fullness ratio, which were obtained using a combination of (1) a method to prepare a full-length-enriched cDNA library using the oligo-capping method, and (2) an estimation system for fullness using the 5'-end sequence (selection based on the estimation by the ATGpr after removing clones that are not-full-length compared to the ESTs). However, it is possible to easily obtain a full-length cDNA by using the primers that are provided by the present invention, not by the above described specialized method.

The problem with the cDNA libraries prepared by the known methods or commercially available is that mRNA contained in the libraries has very low fullness ratio. Thus, it is difficult to screen full-length cDNA clone directly from the library using ordinary cloning methods. The present invention has revealed a primer that is capable of synthesizing a full-length cDNA. If provided with primers, it is possible to synthesize a target full-length cDNA by using enzymatic reactions such as PCR. In particular, a full-length-enriched cDNA library, synthesized by methods such as oligo-capping, is desirable to synthesize a full-length cDNA with more reliability.

[0037] The 5'-end sequence of the full-length cDNA clones of the invention can be used to isolate the regulatory element of transcription including the promoter on the genome. By the spring of the year 2000, a rough draft of the human genome (analysis of human genomic sequence with lower accuracy), which covers 90% of the genome, is planned to be accomplished, and by the year 2003, analysis of the entire human genomic sequence is going to be finished. However, it is hard to analyze with software the transcription start sites on the human genome, in which long introns exist. By contrast, it is easy to specify the transcription start site on the genomic sequence using the 5'-end sequence of the full-length cDNA clone, thus it is easy to obtain the genomic region involved in transcription regulation, which includes the promoter that is contained in the upstream of the transcription start site.

[0038] The full-length cDNAs cloned in the present invention are classified into 13 groups, based on the data such as ATGpr1 score, by which the fullness ratio can be evaluated. Specifically, the 13 groups consist of; the below-mentioned groups (1)-(3), containing 3690 clones (Table 9), and the group (12), containing 3 clones, wherein ATGpr1 (score defined in the ATGpr program) is higher than 0.3; and the below-mentioned groups (4)-(11), containing 1857 clones (Table 10), and the group (13), containing 52 clones, wherein, although ATGpr1 is 0.3 or less, the clones are judged to be full-length from various viewpoints. Names of the clones belonging to the groups (1)-(13) are as indicated in Examples or below.

(1) 1516 clones

Among the 3690 clones that have the maximal ATGpr1 score higher than 0.3, 1516 clones are novel full-length clones, in which at least either of the sequences of the 5'- and 3'-ends, or both are not identical to those of any human EST.

(2)377 clones

Among the 3690, 377 clones are novel full-length clones, in which the number of human EST having identical sequence at both 5'- and 3'-ends is 1 to 5.

(3) 1797 clones

Among the 3690, 1797 clones are novel full-length clones, in which the number of human EST having identical sequence at the 5'-end is not more than 20 (except the clones described above).

(4) 453 clones

Among the 1857 clones in which the maximal ATGpr1 score is 0.3 or less, the following 453 clones are estimated to be novel full-length clones since the clones have the maximal score 0.3 or more in the ATGpr2, and at least either of the sequences of their 5'- and 3'-ends, or both are not identical to those of any human EST. The ATGpr2 score is determined by using the ATGpr program with neglecting the information of the frequency of the six nucleotides contained within the sequence between the ATG codon and the stop codon (the maximal length is 300 nucleotides from the ATG codon) (Salamo A.A., Nishikawa T., and Swindells M.B. (1998) Bioinformatics, 14: 384-390; http://www.hri.co.jp/atgpr/). The ATGpr program for calculating the ATGpr2 score is described as the

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ATGpr2 program in the followings.

(5) 24 clones

Among the 1857 clones, 24 clones are estimated to be full-length since their maximal ATGpr2 scores are higher than 0.3, and also novel, though they have low scores in ATGpr1 program, in which the number of the human EST having identical sequence at both 5'- and 3'-ends is 1 to 5.

(6) 65 clones

Among the 1857 clones, 65 clones are estimated to be full-length since, though they have low scores in both programs, ATGpr1 and ATGpr2, the scores are the maximum in comparison to those of the other clones in the same cluster (at least two clones). The clones are also novel, if at least either of the sequences of the 5'- and 3'-ends, or both are not identical to those of any human EST.

(7) 32 clones

Among the 1857 clones, 32 clones are estimated to be full-length since, though they have low scores in both programs, ATGpr1 and ATGpr2, the scores are the maximum in comparison to those of the other clones in the same cluster (at least two clones). The clones are also novel, if the number of the human EST having identical sequence at both 5'- and 3'-ends is 1 to 5.

(8) 36 clones

Among the 1857 clones, 36 clones are full-length, which were selected by assembling the sequences of the other clones or human EST, although they have low scores in both programs, ATGpr1 and ATGpr2. The clones are also novel, if at least either of the sequences of the 5'- and 3'-ends, or both are not identical to those of any human EST.

(9) 81 clones

Among the 1857 clones, 81 clones are full-length, which were selected by assembling the sequences of the other clones or human EST, although they have low scores in both programs, ATGpr1 and ATGpr2. The clones are also novel, if the number of the human EST having identical sequence at the 5'-end is not more than 20 (other than the clones in which at least either of the sequences of the 5'- and 3'-ends, or both are not identical to those of any human EST).

(10) 938 clones

Among the 1857 clones, 938 clones are estimated to be full-length according to the fullness ratio shown in Table 4, although they have low scores in both programs, ATGpr1 and ATGpr2. The clones are also novel, if at least the sequence of the 5'-end is not identical to those of any human EST.

(11) 228 clones

Among the 1857 clones, 228 clones are estimated to be full-length according to the fullness ratio shown in Table 7, although they have low scores in both programs, ATGpr1 and ATGpr2. The clones are also novel, if at least the sequence of the 3'-end is not identical to those of any human EST.

(12) 3 clones

Three clones, HEMBA1006812, HEMBB1001871, and NT2RP3001282, whose maximal ATGpr1 values are higher than 0.3, are full-length and novel clones whose 5'-end sequences presumably contain a coding region which is initiated with ATG codon and which encodes 100 amino acids or more.

(13) 52 clones

The following 52 clones, which have maximal ATGpr1 values of 0.3 or less, are full-length with the fullness ratios shown in Table 4 although the fullness ratios are low:

HEMBA1000497, HEMBA1001750, HEMBA1003854, HEMBA1004193, HEMBA1004860, HEMBA1005572, HEMBA1006038, HEMBA1006092, HEMBA1006406, HEMBA1006650, HEMBB1000672, HEMBB1001197, MAMMA1001252, MAMMA1002094, NT2RM4000634, NT2RM4000657, NT2RM4000783, NT2RM4000857, NT2RM4001178, NT2RM4002420, NT2RP2000198, NT2RP2000551, NT2RP2000660, NT2RP2001214, NT2RP2001460, NT2RP2001756, NT2RP2002056, NT2RP2002677, NT2RP2002755, NT2RP2002843, NT2RP2003101, NT2RP2003799, NT2RP2004095, NT2RP2004732, NT2RP2004920, NT2RP2005454, NT2RP2005776, NT2RP2005806, NT2RP2005882, NT2RP3001723, NT2RP3002099, NT2RP3003155, NT2RP3004028, OVARC1000008, OVARC1000724, OVARC1000751, OVARC1001029, PLACE1000814,

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PLACE1003030, PLACE1005549, PLACE1007218, NT2RP4002298.

Moreover, the clones are novel clones whose 5' -end sequences presumably contain a coding region which is initiated with ATG codon and which encodes 50 amino acids or more. Among them, the following 20 clones is predicted to contain a coding region with 100 amino acids or more and should encode proteins:

HEMBA1000497, HEMBA1003854, HEMBA1004193, NT2RM4000657, NT2RM4001178, NT2RP2001756, NT2RP2002677, NT2RP2002755, NT2RP2002843, NT2RP2004095, NT2RP2004920, NT2RP2005806, NT2RP3002099, NT2RP3003155, OVARC1000724, OVARC1001029, PLACE1000814, PLACE1003030, PLACE1005549, PLACE1007218.

[0039] The protein encoded by the polynucleotide of the invention can be prepared as a recombinant protein or as a natural protein. For example, the recombinant protein can be prepared by inserting the polynucleotide encoding the protein of the invention into a vector, introducing the vector into an appropriate host cell and purifying the protein expressed within the transformed host cell, as described below. In contrast, the natural protein can be prepared, for example, by utilizing an affinity column to which an antibody against the protein of the invention (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wily & Sons, Section 16.1-16.19) is attached. The antibody used for affinity purification may be either a polyclonal antibody, or a monoclonal antibody. Alternatively, in vitro translation (See, for example, "On the fidelity of mRNA translation in the nuclease-treated rabbit reticulocyte lysate system." Dasso M.C., and Jackson R.J. (1989) Nucleic Acids Res. 17: 3129-3144) may be used for preparing the protein of the invention.

[0040] Proteins functionally equivalent to the proteins of the present invention can be prepared based on the activities, which were clarified in the above-mentioned manner, of the proteins of the present invention. Using the biological activity possessed by the protein of the invention as an index, it is possible to verify whether or not a particular protein is functionally equivalent to the protein of the invention by examining whether or not the protein has said activity.

[0041] Proteins functionally equivalent to the proteins of the present invention can be prepared by those skilled in the art, for example, by using a method for introducing mutations into an amino acid sequence of a protein (for example, site-directed mutagenesis (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 8.1-8.5). Besides, such proteins can be generated by spontaneous mutations. The present invention comprises the proteins having one or more amino acids substitutions, deletions, insertions and/or additions in the amino acid sequences of the proteins of the present invention (Tables 350 and 351), as far as the proteins have the equivalent functions to those of the proteins identified in the present Examples described later.

[0042] There are no limitations in the number and sites of amino acid mutations, as far as the proteins maintain the functions thereof. The number of mutations is typically 30% or less, or 20% or less, or 10% or less, preferably within 5% or less, or 3% or less of the total amino acids, more preferably within 2% or less or 1 % or less of the total amino acids. From the viewpoint of maintaining the protein function, it is preferable that a substituted amino has a similar property to that of the original amino acid. For example, Ala, Val, Leu, Ile, Pro, Met, Phe and Trp are assumed to have similar properties to one another because they are all classified into a group of non-polar amino acids. Similarly, substitution can be performed among non-charged amino acid such as Gly, Ser, Thr, Cys, Tyr, Asn, and Gln, acidic amino acids such as Asp and Glu, and basic amino acids such as Lys, Arg, and His.

[0043] In addition, proteins functionally equivalent to the proteins of the present invention can be isolated by using techniques of hybridization or gene amplification known to those skilled in the art. Specifically, using the hybridization technique (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 6.3-6.4)), those skilled in the art can usually isolate a DNA highly homologous to the DNA encoding the protein identified in the present Example based on the identified nucleotide sequence (Tables 350 and 351) or a portion thereof and obtain the functionally equivalent protein from the isolated DNA. The present invention include proteins encoded by the DNAs hybridizing with the DNAs encoding the proteins identified in the present Example, as far as the proteins are functionally equivalent to the proteins identified in the present Example. Organisms from which the functionally equivalent proteins are isolated are illustrated by vertebrates such as human, mouse, rat, rabbit, pig and bovine, but are not limited to these animals.

[0044] Washing conditions of hybridization for the isolation of DNAs encoding the functionally equivalent proteins are usually "1 × SSC, 0.1% SDS, 37°C"; more stringent conditions are "0.5 × SSC, 0.1% SDS, 42°C"; and still more stringent conditions are "0.1 × SSC, 0.1% SDS, 65°C". Alternatively, the following conditions can be given as hybridization conditions of the present invention. Namely, conditions in which the hybridization is done at "6 × SSC, 40% Formamide, 25°C", and the washing at "1 × SSC, 55°C" can be given. More preferable conditions are those in which the hybridization is done at "6 × SSC, 40% Formamide, 37°C", and the washing at "0.2 × SSC, 55°C". Even more preferable are those in which the hybridization is done at "6 × SSC, 50% Formamide, 37°C", and the washing at "0.1 × SSC, 62°C". The more stringent the conditions of hybridization are, the more frequently the DNAs highly homologous to the probe sequence are isolated. Therefore, it is preferable to conduct hybridization under stringent conditions. Examples of stringent conditions in the present invention are, washing conditions of "0.5 × SSC, 0.1% SDS, 42°C", or alternatively, hybridization conditions of "6 × SSC, 40% Formamide, 37°C", and the washing at "0.2 × SSC, 55°C". However, the above-mentioned combinations of SSC, SDS and temperature conditions are indicated just as examples.

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Those skilled in the art can select the hybridization conditions with similar stringency to those mentioned above by properly combining the above-mentioned or other factors (for example, probe concentration, probe length and duration of hybridization reaction) that determines the stringency of hybridization.

[0045] The amino acid sequences of proteins isolated by using the hybridization techniques usually exhibit high homology to those of the proteins of the present invention, which are shown in Tables 350 and 351. The present invention encompasses a polynucleotide comprising a nucleotide sequence that has a high identity to the nucleotide sequence of claim 8 (a).

Furthermore, the present invention encompasses a peptide, or protein comprising an amino acid sequence that has a high identity to the amino acid sequence encoded by the polynucleotide of claim 8 (b). The term "high identity" indicates sequence identity of at least 40% or more;

preferably 60% or more; and more preferably 70% or more. Alternatively, more preferable is identity of 90% or more, or 93% or more, or 95% or more, furthermore, 97% or more, or 99% or more. The identity can be determined by using the BLAST search algorithm.

[0046] With the gene amplification technique (PCR) (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 6.3-6.4)) using primers designed based on the nucleotide sequence (Tables 350 and 351) or a portion thereof identified in the present Example, it is possible to isolate a DNA fragment highly homologous to the polynucleotide sequence or a portion thereof and to obtain functionally equivalent protein to a particular protein identified in the present Example based on the isolated DNA fragment.

[0047] The "percent identity" of two amino acid sequences or of two nucleic acids is determined using the algorithm of Karlin and Altschul (Proc. Natl. Acad. Sei. USA 87:2264-2268, 1990), modified as in Karlin and Altschul (Proc. Natl. Acad. Sei. USA 90:5873-5877, 1993). Such an algorithm is incorporated into the BLASTN and BLASTX programs of Altschul et al. (J. Mol. Biol.215:403-410, 1990). BLAST nucleotide searches are performed with the BLASTN program, score = 100, wordlength = 12. BLAST protein searches are performed with the BLASTX program, score = 50, wordlength = 3. When gaps exist between two sequences, Gapped BLAST is utilized as described in Altschul et al. (Nucleic Acids Res.25:3389-3402,1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., BLASTX and BLASTN) are used. See http://www.ncbi.nlm.nih.gov.

[0048] The present invention also includes a partial peptide of the proteins of the invention. The partial peptide comprises a protein generated as a result that a signal peptide has been removed from a secretory protein. If the protein of the present invention has an activity as a receptor or a ligand, the partial peptide may function as a competitive inhibitor of the protein and may bind to the receptor (or ligand). In addition, the present invention comprises an antigen peptide for raising antibodies. For the peptides to be specific for the protein of the invention, the peptides comprise at least 7 amino acids, preferably 8 amino acids or more, more preferably 9 amino acids or more, and even more preferably 10 amino acids or more. The peptide can be used for preparing antibodies against the protein of the invention, or competitive inhibitors of them, and also screening for a receptor that binds to the protein of the invention. The partial peptides of the invention can be produced, for example, by genetic engineering methods, known methods for synthesizing peptides, or digesting the protein of the invention with an appropriate peptidase.

[0049] The present invention also relates to a vector into which the DNA of the invention is inserted. The vector of the invention is not limited as long as it contains the inserted DNA stably. For example, if *E. coli* is used as a host, vectors such as pBluescript vector (Stratagene) are preferable as a cloning vector. To produce the protein of the invention, expression vectors are especially useful. Any expression vector can be used as far as it is capable of expressing the protein *in vitro*, in *E. coli*, in cultured cells, or *in vivo*. For example, pBEST vector (Promega) is preferable for *in vitro* expression, pET vector (Invitrogen) for *E. coli*, pME18S-FL3 vector (GenBank Accession No. AB009864) for cultured cells, and pME18S vector (Mol. Cell. Biol. (1988) 8: 466-472) for *in vivo* expression. To insert the DNA of the invention, ligation utilizing restriction sites can be performed according to the standard method (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wily & Sons. Section 11.4-11.11).

[0050] The present invention also relates to a transformant carrying the vector of the invention. Any cell can be used as a host into which the vector of the invention is inserted, and various kinds of host cells can be used depending on the purposes. For strong expression of the protein in eukaryotic cells, COS cells or CHO cells can be used, for example.

[0051] Introduction of the vector into host cells can be performed, for example, by calcium phosphate precipitation method, electroporation method (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wily & Sons, Section 9.1-9.9), lipofectamine method (GIBCO-BRL), or microinjection method, etc.

[0052] The primer of the present invention can be used for synthesizing full-length cDNA, and also for the detection and/or diagnosis of the abnormality of the protein of the invention encoded by the full-length cDNA. For example, by utilizing polymerase chain reaction (genomic DNA-PCR, or RT-PCR) using the primer of the invention, DNA encoding the protein of the invention can be amplified. It is also possible to obtain the regulatory region of expression in the 5'-upstream by using PCR or hybridization since the transcription start site within the genomic sequence can be easily specified based on the 5'-end sequence of the full-length cDNA. The obtained genomic region can be used for detection and/or diagnosis of the abnormality of the sequence by RFLP analysis, SSCP, or direct sequencing.

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[0053] Furthermore, the "polynucleotide having a length of at least 15 nucleotides, comprising a nucleotide sequence that is complementary to a polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs in Tables 350 and 351, or its complementary strand" includes an antisense polynucleotide for suppressing the expression of the protein of the invention. To exert the antisense effect, the antisense polynucleotide has a length of at least 15 bp or more, for example, 50 bp or more, preferably 100 bp or more, and more preferably 500 bp or more, and has a length of usually 3000 bp or less and preferably 2000 bp or less. The antisense DNA can be used in the gene therapy of the diseases that are caused by the abnormality of the protein of the invention (abnormal function or abnormal expression). Said antisense DNA can be prepared, for example, by the phosphorothioate method ("Physicochemical properties of phosphorothioate oligodeoxynucleotides." Stein (1988) Nucleic Acids Res. 16: 3209-3221) based on the nucleotide sequence of the DNA encoding the protein (for example, the DNA set forth in any one of SEQ ID NOs in Tables 350 and 351).

[0054] The polynucleotide or antisense DNA of the present invention can be used in gene therapy, for example, by administrating it into a patient by the in vivo or ex vivo method with virus vectors such as retrovirus vectors, adenovirus vectors, and adeno-associated virus vectors, or non-virus vectors such as liposome.

[0055] The present invention also relates to antibodies that bind to the protein of the invention.
There are no limitations in the form of the antibodies of the invention. They include polyclonal antibodies, monoclonal antibodies, or their portions that can bind to the protein of the invention. They also include antibodies of all classes. Furthermore, special antibodies such as humanized antibodies are also included.

[0056] The polyclonal antibody of the invention can be obtained according to the standard method by synthesizing an oligopeptide corresponding to the amino acid sequence and immunizing rabbits with the peptides (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wily & Sons, Section 11.12-11.13). The monoclonal antibody of the invention can be obtained according to the standard method by purifying the protein expressed in *E. coli*, immunizing mice with the protein, and producing a hybridoma cell by fusing the spleen cells and myeloma cells (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wily & Sons, Section 11.4-11.11).

[0057] The antibody binding to the protein of the present invention can be used for purification of the protein of the invention, and also for detection and/or diagnosis of the abnormalities of the expression and structure of the protein. Specifically, proteins can be extracted, for example, from tissues, blood, or cells, and the protein of the invention is detected by Western blotting, immunoprecipitation, or ELISA, etc. for the above purpose.

[0058] Furthermore, the antibody binding to the protein of the present invention can be utilized for treating the diseases that associates with the protein of the invention. If the antibodies are used for treating patients, human antibodies or humanized antibodies are preferable in terms of their low antigenicity. The human antibodies can be prepared by immunizing a mouse whose immune system is replaced with that of human ("Functional transplant of megabase human immunoglobulin loci recapitulates human antibody response in mice" Mendez M.J. et al. (1997) Nat. Genet. 15: 146-156). The humanized antibodies can be prepared by recombination of the hypervariable region of a monoclonal antibody (Methods in Enzymology (1991) 203: 99-121).

[0059] The cDNA of the present invention encodes the amino acid sequence of a protein which is predicted to have the function(s) described below based on the homology search of the GenBank and SwissProt. Specifically, for instance, as shown in EXAMPLES, searching a known gene or protein that is homologous to the partial sequence of the full-length cDNA of the invention (5602 clone) and referring the function of the gene and of the protein encoded by the gene make it possible to predict the function of the protein encoded by the cDNA of the invention. In this way, each of 1437 clones out of the 5602 full-length cDNA clones of the invention was predicted to encode a protein that was classified into one or more of the following categories.

Secretory or membrane protein (261 clones)
Glycoprotein-associated protein (113 clones)
Signal transduction-associated protein (148 clones)
Transcription-associated protein (233 clones)
Disease-associated protein (437 clones)
Enzyme or metabolism-associated protein (301 clones)
Cell division- or cell proliferation-associated protein (74 clones)
Cytoskeleton-associated protein (92 clones)
RNA synthesis-associated protein (280 clones)
Nuclear protein (352 clones)
Protein synthesis- or transport-associated protein (112 clones)
Cellular defense-associated protein (23 clones)
Development- or growth-associated protein (23 clones)

[0060] It is also possible to predict the protein function by looking into the amino acid sequence for the motifs such

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as the signal sequence, transmembrane region, nuclear translocation signal, glycosylation signal, phosphorylation site, Zinc finger motif, and SH3 domain. The programs, PSORT (Nakai K., and Kanehisa M. (1992) Genomics 14: 897-911), SOSUI (Hirokawa T. et al. (1998) Bioinformatics 14: 378-379) (Mitsui Information Developing Inc.), and MEMSAT (Jones D.T., Taylor W.R., and Thornton J.M. (1994) Biochemistry 33: 3038-3049) can be used to predict the existence of the signal sequence or transmembrane region. Alternatively, a partial amino acid sequence of the protein is fused with another protein such as GFP, the fusion protein is transfected into cultured cells, and the localization is analyzed to predict the function of the original protein.

[0061] Based on the determined nucleotide sequences of the full-length cDNAs obtained in the present invention, it is possible to predict more detailed functions of the proteins encoded by the cDNA clones, for example, by searching the databases such as GenBank, Swiss-Prot and UniGene for homologies of the cDNAs; or by searching the amino acid sequences deduced from the full-length cDNAs for signal sequences by using software programs such as PSORT, for transmembrane regions by using software programs such as SOSUI or for motifs by using software programs such as Pfam (http://www.sanger.ac.uk/Software/Pfam/index.shtml) and PROSITE (http://www.expasy.ch/prosite/). As a matter of course, the functions are often predictable by using partial sequence information (preferably 300 nucleotides or more) instead of the full-length nucleotide sequences. However, the result of the prediction by using partial nucleotide sequence does not always agree with the result obtained by using full-length nucleotide sequence, and thus, it is needless to say that the prediction of function is preferably performed based on the full-length nucleotide sequences. GenBank, Swiss-Prot and UniGene databases were searched for homologies of the full-length nucleotide sequences of the 4997 clones (see Example 18). The amino acid sequences deduced from the full-length nucleotide sequences were searched for functional domains by PSORT, SOSUI and Pfam. Prediction of functions of proteins encoded by the clones and the categorization thereof were performed based on these results obtained.

The following 798 clones were categorized into secretory and/or membrane proteins.

HEMBA1000356, HEMBA1000518, HEMBA1000531, HEMBA1000637, HEMBA1000719, HEMBA1000817,
HEMBA1000822, HEMBA1000852, HEMBA1000870, HEMBA1000991, HEMBA1001052, HEMBA1001071,
HEMBA1001085, HEMBA1001286, HEMBA1001351, HEMBA1001407, HEMBA1001446, HEMBA1001515,
HEMBA1001557, HEMBA1001569, HEMBA1001661, HEMBA1001734, HEMBA1001746, HEMBA1001866,
HEMBA1002125, HEMBA1002150, HEMBA1002166, HEMBA1002417, HEMBA1002462, HEMBA1002475,
HEMBA1002477, HEMBA1002486, HEMBA1002609, HEMBA1002659, HEMBA1002661, HEMBA1002780,
HEMBA1002818, HEMBA1002876, HEMBA1002921, HEMBA1003071, HEMBA1003077, HEMBA1003079,
HEMBA1003086, HEMBA1003096, HEMBA1003281, HEMBA1003286, HEMBA1003538, HEMBA1003711,
HEMBA1003742, HEMBA1003803, HEMBA1004055, HEMBA1004143, HEMBA1004146, HEMBA1004207,
HEMBA1004341, HEMBA1004461, HEMBA1004577, HEMBA1004637, HEMBA1004752, HEMBA1004756,
HEMBA1004850, HEMBA1004889, HEMBA1004923, HEMBA1004930, HEMBA1005029, HEMBA1005035,
HEMBA1005050, HEMBA1005552, HEMBA1005576, HEMBA1005581, HEMBA1005588, HEMBA1005616,
HEMBA1005699, HEMBA1005991, HEMBA1006036, HEMBA1006038, HEMBA1006067, HEMBA1006173,
HEMBA1006198, HEMBA1006293, HEMBA1006310, HEMBA1006492, HEMBA1006502, HEMBA1006583,
HEMBA1006659, HEMBA1006758, HEMBA1006789, HEMBA1006921, HEMBA1006926, HEMBA1006976,
HEMBA1007203, HEMBA1007301, HEMBB1000037, HEMBB1000050, HEMBB1000054, HEMBB1000175,
HEMBB1000317, HEMBB1000556, HEMBB1000593, HEMBB1000631, HEMBB1000763, HEMBB1000827,
HEMBB1000915, HEMBB1000975, HEMBB1001112, HEMBB1001151, HEMBB1001177, HEMBB1001302,
HEMBB1001348, HEMBB1001564, HEMBB1001630, HEMBB1001871, HEMBB1001872, HEMBB1001925,
HEMBB1001962, HEMBB1002042, HEMBB1002044, HEMBB1002142, HEMBB1002190, HEMBB1002193,
HEMBB1002247, HEMBB1002383, HEMBB1002387, HEMBB1002550, HEMBB1002600, HEMBB1002692,
MAMMA1000045, MAMMA1000129, MAMMA1000133, MAMMA1000277, MAMMA1000278, MAMMA1000410,
MAMMA1000416, MAMMA1000472, MAMMA1000672, MAMMA1000684, MAMMA1000714, MAMMA1000734,
MAMMA1000778, MAMMA1000798, MAMMA1000842, MAMMA1000859, MAMMA1000897, MAMMA1000956,
MAMMA1001008, MAMMA1001030, MAMMA1001041, MAMMA1001073, MAMMA1001080, MAMMA1001139,
MAMMA1001154, MAMMA1001322, MAMMA1001388, MAMMA1001411, MAMMA1001487, MAMMA1001751,
MAMMA1001754, MAMMA1001771, MAMMA1002009, MAMMA1002427, MAMMA1002428, MAMMA1002461,
MAMMA1002524, MAMMA1002573, MAMMA1002598, MAMMA1002655, MAMMA1002684, MAMMA1002769,
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[0062] The following 142 clones were categorized into glycoprotein-associated proteins.

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[0063] The following 140 clones were categorized into signal transduction-associated proteins.

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[0064] The following 321 clones were categorized into transcription -associated proteins.

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[0065] The following 392 clones were categorized into disease-associated proteins.

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[0066] The following 427 clones presumably belong to enzymes and/or metabolism-associated proteins. HEMBA1000012, HEMBA1000129, HEMBA1000141, HEMBA1000150, HEMBA1000542, HEMBA1000852, HEMBA1001019, HEMBA1001257, HEMBA1001526, HEMBA1001620, HEMBA1001866, HEMBA1001896, HEMBA1002212, HEMBA1002513, HEMBA1002746, HEMBA1002973, HEMBA1003046, HEMBA1003136, HEMBA1003179, HEMBA1003250, HEMBA1003291, HEMBA1003408, HEMBA1003538, HEMBA1003679, HEMBA1003680, HEMBA1004199, HEMBA1004227, HEMBA1004408, HEMBA1004509, HEMBA1004734, HEMBA1004768, HEMBA1005394, HEMBA1005513, HEMBA1005737, HEMBA1005815, HEMBA1006031, HEMBA1006272, HEMBA1006278, HEMBA1006291, HEMBA1006309, HEMBA1006347, HEMBA1006485, HEMBA1006521, HEMBA1006624, HEMBA1006885, HEMBA1006976, HEMBA1007121, HEMBA1007224, HEMBA1007243, HEMBA1007300, HEMBB1000083, HEMBB1000217, HEMBB1000915, HEMBB1000947, HEMBB1001137, HEMBB1001346, HEMBB1001429, HEMBB1001443, HEMBB1001915, HEMBB1001950, HEMBB1002042, MAMMA1000020, MAMMA1000085, MAMMA1000672, MAMMA1000713, MAMMA1000841, MAMMA1000897, MAMMA1001008, MAMMA1001038, MAMMA1001059, MAMMA1001476, MAMMA1001501, MAMMA1002268, MAMMA1002470, MAMMA1002530, MAMMA1002573, MAMMA1002619, MAMMA1002655, MAMMA1002671, MAMMA1003013, MAMMA1003035, NT2RM1000039, NT2RM1000132, NT2RM1000153, NT2RM1000256, NT2RM1000280, NT2RM1000377, NT2RM1000553, NT2RM1000648, NT2RM1000702, NT2RM1000894, NT2RM1001072, NT2RM1001115, NT2RM2000013, NT2RM2000092, NT2RM2000322, NT2RM2000368, NT2RM2000371, NT2RM2000469, NT2RM2000504, NT2RM2000577, NT2RM2000594, NT2RM2000951, NT2RM2001238, NT2RM2001547, NT2RM2001632, NT2RM2001664, NT2RM2001698,

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[0067] The following 217 clones presumably belong to ATP- and/or GTP-binding proteins.

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[0068] The following 320 clones presumably belong to nuclear proteins.

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[0069] The following 296 clones presumably belong to DNA- and/or RNA-binding proteins. HEMBA1000158, HEMBA1000216, HEMBA1000561, HEMBA1000591, HEMBA1000851, HEMBA1001088, HEMBA1001137, HEMBA1001405, HEMBA1001510, HEMBA1001804, HEMBA1001809, HEMBA1001819, HEMBA1001847, HEMBA1001869, HEMBA1002177, HEMBA1002935, HEMBA1003408, HEMBA1003545, HEMBA1003568, HEMBA1003591, HEMBA1003662, HEMBA1003684, HEMBA1003760, HEMBA1003783, HEMBA1003805, HEMBA1003953, HEMBA1004321, HEMBA1004354, HEMBA1004389, HEMBA1004479, HEMBA1004669, HEMBA1004847, HEMBA1004973, HEMBA1005202, HEMBA1005359, HEMBA1005931, HEMBA1006248, HEMBA1006278, HEMBA1006283, HEMBA1006359, HEMBA1006652, HEMBA1007087, HEMBA1007194, HEMBB1000264, HEMBB1000789, HEMBB1001011, HEMBB1001482, HEMBB1001736, HEMBB1001749, HEMBB1001839, HEMBB1002217, MAMMA1000183, MAMMA1000284, MAMMA1000731, MAMMA1001105, MAMMA1001222, MAMMA1001260, MAMMA1001743, MAMMA1001837, MAMMA1002385, MAMMA1002617, MAMMA1002869, MAMMA1002937, MAMMA1003011, NT2RM1000086, NT2RM1000539, NT2RM1000555, NT2RM1000666, NT2RM1000691, NT2RM1000826, NT2RM1000885, NT2RM1001059, NT2RM1001092, NT2RM2000371, NT2RM2000624, NT2RM2000735, NT2RM2001105, NT2RM2001424, NT2RM2001575, NT2RM2001605, NT2RM2001670, NT2RM2001771, NT2RM2001823, NT2RM2001989, NT2RM2002004, NT2RM2002014, NT2RM2002088, NT2RM2002091, NT2RM4000046, NT2RM4000104, NT2RM4000167, NT2RM4000191, NT2RM4000202, NT2RM4000531, NT2RM4000595, NT2RM4000733, NT2RM4000751, NT2RM4000996, NT2RM4001092, NT2RM4001140, NT2RM4001178, NT2RM4001200, NT2RM4001483, NT2RM4001592, NT2RM4001783, NT2RM4001823, NT2RM4001828, NT2RM4001858, NT2RM4001880, NT2RM4001979, NT2RM4002093, NT2RM4002109, NT2RP1000470, NT2RP1000493, NT2RP1000574, NT2RP1000902, NT2RP1000966, NT2RP1001013, NT2RP1001073, NT2RP1001080, NT2RP2000008, NT2RP2000153, NT2RP2000258, NT2RP2000297, NT2RP2001127, NT2RP2001174, NT2RP2001233, NT2RP2001511, NT2RP2001756, NT2RP2001869, NT2RP2002079, NT2RP2002099, NT2RP2002503, NT2RP2002591, NT2RP2002939, NT2RP2003157, NT2RP2003329, NT2RP2003347, NT2RP2003480, NT2RP2003522, NT2RP2003564, NT2RP2003714, NT2RP2004187, NT2RP2004568, NT2RP2004920, NT2RP2005003, NT2RP2005139, NT2RP2005168, NT2RP2005436, NT2RP2005496, NT2RP2005701, NT2RP2005763, NT2RP2005776, NT2RP2005942,

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[0070] The following 66 clones presumably belong to the category of RNA synthesis-associated proteins.

HEMBA1000591, HEMBA1001579, HEMBA1003179, HEMBA1003591, HEMBA1006278, HEMBB1000226, NT2RM1000187, NT2RM1000852, NT2RM2000624, NT2RM2001989, NT2RM2002100, NT2RM4000191, NT2RM4001178, NT2RM4002093, NT2RP1000035, NT2RP1000272, NT2RP1000470, NT2RP1001080, NT2RP2000153, NT2RP2002928, NT2RP2003157, NT2RP2004568, NT2RP2005126, NT2RP2005436, NT2RP2005539, NT2RP2005605, NT2RP2005776, NT2RP2005942, NT2RP2006043, NT2RP2006238, NT2RP3000361, NT2RP3000397, NT2RP3001671, NT2RP3004504, NT2RP4000078, NT2RP4000111, NT2RP4000481, NT2RP4000518, NT2RP4000614, NT2RP4000929, NT2RP4001696, NT2RP4002058, OVARC1001232, OVARC1001577, PLACE1000406, PLACE1000596, PLACE1000755, PLACE1001739, PLACE1003704, PLACE1003885, PLACE1004564, PLACE1004814, PLACE1004902, PLACE1005373, PLACE1005646, PLACE1005876, PLACE1006196, PLACE1006626, PLACE1006878, PLACE1006917, PLACE1009476, PLACE1009925, PLACE1010194, PLACE1011114, THYRO1000121, Y79AA1001963,

[0071] The following 184 clones presumably belong to protein synthesis- and/or protein transport-associated proteins.

HEMBA1000012, HEMBA1000141, HEMBA1000592, HEMBA1003617, HEMBA1003773, HEMBA1004202, HEMBA1004276, HEMBA1004734, HEMBA1004847, HEMBA1004929, HEMBA1004930, HEMBA1005047, HEMBA1005202, HEMBA1006031, HEMBA1006272, HEMBA1006474, HEMBA1006652, HEMBA1006914, HEMBA1006973, HEMBA1007224, HEMBB1000915, HEMBB1001112, HEMBB1001137, HEMBB1001736, HEMBB1001831, HEMBB1001915, MAMMA1000085, MAMMA1000734, MAMMA1001008, MAMMA1002170, MAMMA1002219, MAMMA1002236, MAMMA1002619, NT2RM1000661, NT2RM1000833, NT2RM2000092, NT2RM2000504, NT2RM2000577, NT2RM2000821, NT2RM2001201, NT2RM2001592, NT2RM2001613, NT2RM2001648, NT2RM2001730, NT2RM2001760, NT2RM2002055, NT2RM4000155, NT2RM4000169, NT2RM4000344, NT2RM4000356, NT2RM4000421, NT2RM4000712, NT2RM4001054, NT2RM4001203, NT2RM4001382, NT2RM4001444, NT2RM4002062, NT2RM4002205, NT2RM4002623, NT2RP1000326, NT2RP1000522, NT2RP1000547, NT2RP1000746, NT2RP1000947, NT2RP1001569, NT2RP2000147, NT2RP2000710, NT2RP2000880, NT2RP2000943, NT2RP2001290, NT2RP2001392, NT2RP2001601, NT2RP2001613, NT2RP2001660, NT2RP2001740, NT2RP2002124, NT2RP2002606, NT2RP2002862, NT2RP2002959, NT2RP2002980, NT2RP2003137, NT2RP2003158, NT2RP2003391, NT2RP2003394, NT2RP2003401, NT2RP2003433, NT2RP2003704, NT2RP2003713, NT2RP2003737, NT2RP2003760, NT2RP2003981, NT2RP2004366, NT2RP2004389, NT2RP2004791, NT2RP2005012, NT2RP2005116, NT2RP2005360, NT2RP2005763, NT2RP2005784, NT2RP3000366, NT2RP3000759, NT2RP3000968, NT2RP3001113, NT2RP3001690, NT2RP3002045, NT2RP3002151, NT2RP3002529, NT2RP3002671, NT2RP3003301, NT2RP3003846, NT2RP3003876, NT2RP3004209, NT2RP4000370, NT2RP4000457, NT2RP4000879, NT2RP4000927, NT2RP4001041, NT2RP4001117,

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[0072] The following 130 clones presumably belong to cytoskeleton-associated proteins.

HEMBA1000156, HEMBA1000168, HEMBA1000411, HEMBA1000588, HEMBA1001043, HEMBA1001651, HEMBA1001661, HEMBA1002102, HEMBA1002161, HEMBA1002939, HEMBA1003235, HEMBA1003581, HEMBA1004499, HEMBA1004534, HEMBA1004697, HEMBA1004929, HEMBA1004972, HEMBA1005582, HEMBA1005595, HEMBA1006344, HEMBA1006737, HEMBB1001175, HEMBB1001282, HEMBB1001562, HEMBB1001802, MAMMA1000824, MAMMA1001041, MAMMA1001576, MAMMA1001679, MAMMA1001735, MAMMA1002297, MAMMA1002351, MAMMA1002622, MAMMA1002637, MAMMA1003127, NT2RM1000850, NT2RM1000898, NT2RM2000030, NT2RM2000260, NT2RM2000691, NT2RM2001324, NT2RM4000169, NT2RM4000229, NT2RM4000515, NT2RM4001217, NT2RP1000202, NT2RP1000348, NT2RP1000460, NT2RP1000478, NT2RP1001033, NT2RP1001294, NT2RP1001302, NT2RP2000070, NT2RP2000812, NT2RP2000814, NT2RP2001168, NT2RP2001245, NT2RP2001634, NT2RP2001900, NT2RP2003307, NT2RP2003394, NT2RP2004041, NT2RP2004242, NT2RP2004538, NT2RP2004587, NT2RP2004681, NT2RP2004732, NT2RP2004978, NT2RP2005491, NT2RP2005531, NT2RP2005712, NT2RP2006275, NT2RP3000753, NT2RP3001113, NT2RP3001216, NT2RP3001239, NT2RP3001272, NT2RP3001554, NT2RP3001690, NT2RP3001799, NT2RP3002688, NT2RP3003061, NT2RP3003185, NT2RP3003230, NT2RP3004569, NT2RP3004578, NT2RP4001004, NT2RP4001086, NT2RP4001256, NT2RP4001567, NT2RP4001927, OVARC1000001, OVARC1000106, OVARC1000437, OVARC1000520, OVARC1000679, OVARC1001731, OVARC1002050, PLACE1001104, PLACE1002571, PLACE1002591, PLACE1002655, PLACE1002714, PLACE1003625, PLACE1005287, PLACE1006552, PLACE1007946, PLACE1008426, PLACE1010148, PLACE1010547, PLACE1010743, PLACE1010896, PLACE1010960, PLACE1011310, PLACE1011922, PLACE2000216, PLACE2000274, PLACE2000371, PLACE2000458, PLACE3000145, PLACE3000416, PLACE4000009, THYRO1000132, THYRO1001405, THYRO1001458, Y79AA1000368, Y79AA1000794, Y79AA1000833, Y79AA1000962, Y79AA1002208.

[0073] The following 54 clones presumably belong to cell division-associated and/or cell proliferation-associated proteins.

HEMBA1001019, HEMBA1001595, HEMBA1002363, HEMBA1002997, HEMBA1003136, HEMBA1003369, HEMBA1004131, HEMBA1004354, HEMBA1005621, HEMBB1000037, HEMBB1000264, MAMMA1001768, MAMMA1002769, NT2RM1000354, NT2RM1000430, NT2RM1000874, NT2RM2001256, NT2RM2001743, NT2RM2001896, NT2RM2002145, NT2RM4000215, NT2RM4001714, NT2RP1000163, NT2RP1000333, NT2RP1000439, NT2RP2000346, NT2RP2001397, NT2RP2002595, NT2RP2003177, NT2RP2003596, NT2RP2003912, NT2RP2004396, NT2RP2005037, NT2RP2005520, NT2RP2005669, NT2RP2005835, NT2RP3001730, NT2RP3002081, NT2RP4000210, NT2RP4000415, NT2RP4001414, NT2RP4001634, OVARC1000013, OVARC1000937, PLACE1001383, PLACE1002433, PLACE1004316, PLACE1005287, PLACE1008808, PLACE1010720, PLACE1010833, Y79AA1000748, Y79AA1001236, Y79AA1001394

[0074] The following 36 clones presumably belong to the category of embryogenesis- and/or development-associated proteins:

HEMBA1000518, HEMBA1001847, HEMBA1001869, HEMBA1003545, HEMBA1004973, HEMBB1002442, MAMMA1001837, NT2RM2001670, NT2RM4000046, NT2RM4000531, NT2RM4001140, NT2RM4001858, NT2RP2002078, NT2RP2004187, NT2RP2006436, NT2RP3000603, NT2RP3000994, NT2RP3001580, NT2RP3001708, NT2RP3003071, NT2RP3004472, NT2RP3004617, NT2RP4000246, NT2RP4001567, OVARC1000304, OVARC1000746, PLACE1000793, PLACE1002532, PLACE1003258, PLACE1003625, PLACE1004460, PLACE1009622, PLACE4000558, THYRO1000085, Y79AA1001391, Y79AA1001692

[0075] The following 30 clones presumably belong to cellular defense-associated proteins.

HEMBA1000005, HEMBA1000531, HEMBA1003417, HEMBA1006253, NT2RM4000354, NT2RM4001880, NT2RP1000333, NT2RP1000493, NT2RP2000006, NT2RP2000045, NT2RP2000809, NT2RP2001536, NT2RP2002464, NT2RP2004920, NT2RP2005037, NT2RP3000590, NT2RP3001426, NT2RP3002062, NT2RP3002785, NT2RP3004262, NT2RP4001555, NT2RP4001638, PLACE1006958, PLACE1008275,

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PLACE1009113, PLACE1011858, PLACE4000014, THYRO1000684, Y79AA1002139, Y79AA1002229

[0076] Although it is unclear whether or not 261 clones out of clones other than the above-mentioned clones belong to any of the above-described categories, these clones are predicted to have some functions, based on the homology search using their full-length sequences.

HEMBA1000030, HEMBA1000307, HEMBA1000333, HEMBA1000488, HEMBA1000523, HEMBA1001197, HEMBA1001302, HEMBA1001455, HEMBA1001675, HEMBA1001714, HEMBA1001744, HEMBA1001967, HEMBA1002151, HEMBA1002215, HEMBA1002458, HEMBA1002777, HEMBA1003098, HEMBA1003199, HEMBA1003615, HEMBA1003836, HEMBA1004295, HEMBA1004573, HEMBA1004604, HEMBA1004795, HEMBA1005101, HEMBA1005201, HEMBA1005206, HEMBA1005530, HEMBA1005666, HEMBA1005990, HEMBA1006268, HEMBA1006398, HEMBA1006445, HEMBA1007174, HEMBA1007251, HEMBB1000036, HEMBB1000144, HEMBB1000973, HEMBB1001058, HEMBB1001234, HEMBB1001288, HEMBB1001331, HEMBB1001384, HEMBB1002266, HEMBB1002510, HEMBB1002705, MAMMA1000055, MAMMA1000625, MAMMA1001075, MAMMA1001181, MAMMA1001259, MAMMA1001730, MAMMA1002143, MAMMA1002699, MAMMA1002972, MAMMA1003113, NT2RM1000118, NT2RM1000186, NT2RM1000244, NT2RM1000421, NT2RM1000499, NT2RM1000623, NT2RM1000883, NT2RM2000502, NT2RM2000599, NT2RM2000718, NT2RM2001065, NT2RM2001196, NT2RM2001983, NT2RM2002109, NT2RM2002142, NT2RM4000030, NT2RM4000139, NT2RM4000156, NT2RM4000386, NT2RM4000590, NT2RM4001047, NT2RM4001155, NT2RM4001256, NT2RM4001320, NT2RM4001340, NT2RM4001347, NT2RM4001371, NT2RM4001582, NT2RM4001611, NT2RM4001731, NT2RM4001969, NT2RM4002034, NT2RM4002075, NT2RM4002226, NT2RP1000040, NT2RP1000363, NT2RP1000481, NT2RP1000513, NT2RP1000733, NT2RP1000860, NT2RP1000954, NT2RP1001011, NT2RP1001395, NT2RP1001457, NT2RP1001494, NT2RP2000054, NT2RP2000067, NT2RP2000133, NT2RP2000157, NT2RP2000764, NT2RP2000965, NT2RP2001839, NT2RP2001883, NT2RP2001976, NT2RP2001985, NT2RP2002185, NT2RP2002442, NT2RP2002727, NT2RP2002741, NT2RP2002986, NT2RP2003121, NT2RP2003265, NT2RP2003272, NT2RP2003857, NT2RP2003871, NT2RP2004425, NT2RP2004476, NT2RP2004710, NT2RP2004816, NT2RP2005441, NT2RP2005490, NT2RP2005620, NT2RP2005654, NT2RP2005675, NT2RP2005753, NT2RP2005841, NT2RP2006598, NT2RP3000047, NT2RP3000233, NT2RP3000868, NT2RP3000869, NT2RP3001399, NT2RP3001407, NT2RP3001457, NT2RP3001587, NT2RP3001712, NT2RP3001819, NT2RP3001854, NT2RP3001931, NT2RP3002273, NT2RP3002631, NT2RP3002682, NT2RP3002770, NT2RP3002818, NT2RP3002948, NT2RP3002972, NT2RP3003032, NT2RP3003290, NT2RP3003411, NT2RP3003491, NT2RP3003500, NT2RP3003726, NT2RP3004348, NT2RP3004507, NT2RP4000129, NT2RP4000498, NT2RP4000528, NT2RP4000737, NT2RP4000979, NT2RP4001010, NT2RP4001207, NT2RP4001228, NT2RP4001260, NT2RP4001339, NT2RP4001351, NT2RP4001474, NT2RP4001966, NT2RP4002018, OVARC1000209, OVARC1000876, OVARC1001065, OVARC1001092, OVARC1001419, OVARC1001555, OVARC1001711, OVARC1001943, PLACE1000004, PLACE1000066, PLACE1000610, PLACE1000636, PLACE1000769, PLACE1000987, PLACE1001036, PLACE1001845, PLACE1001920, PLACE1002665, PLACE1003602, PLACE1003611, PLACE1004256, PLACE1004550, PLACE1004868, PLACE1004930, PLACE1005052, PLACE1005102, PLACE1005176, PLACE1005187, PLACE1005331, PLACE1005727, PLACE1006003, PLACE1006335, PLACE1006385, PLACE1006506, PLACE1007105, PLACE1007537, PLACE1007705, PLACE1007791, PLACE1007897, PLACE1008080, PLACE1008368, PLACE1008398, PLACE1008465, PLACE1008627, PLACE1009020, PLACE1009060, PLACE1009186, PLACE1009443, PLACE1009571, PLACE1009670, PLACE1010105, PLACE1010261, PLACE1010310, PLACE1010522, PLACE1010579, PLACE1010628, PLACE1010661, PLACE1010761, PLACE1011185, PLACE1011340, PLACE1011586, PLACE2000246, PLACE2000411, PLACE3000477, THYRO1000173, THYRO1000401, THYRO1000666, THYRO1001033, THYRO1001347, THYRO1001656, THYRO1001703, THYRO1001721, Y79AA1000059, Y79AA1000181, Y79AA1000268, Y79AA1000313, Y79AA1000540, Y79AA1000966, Y79AA1000985, Y79AA1001323, Y79AA1001402, Y79AA1001679, Y79AA1001923, Y79AA1002083, Y79AA1002307, Y79AA1002311, Y79AA1002487,

[0077] In some cases, the predicted functions based on the partial sequences are different from those based on the full-length sequences. The reason is that a protein does not always belong solely to a single category of the above-described functional categories, and therefore, a protein may belong to two or more of the predicted functional categories. Besides, additional functions can be found for the clones classified into these functional categories by further analyses.

[0078] Since the protein encoded by clones of the invention contains full-length amino acid sequence, it is possible to analyze its biological activity, and its effect on cellular conditions such as cell proliferation and differentiation by expressing the protein as a recombinant protein using an appropriate expression system, injecting the recombinant into the cell, or raising a specific antibody against the protein.

[0079] If the protein is a secretory protein, membrane protein, or protein associated with glycoprotein, signal trans-

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duction, or transcription, its biological activity can be analyzed by the methods in "Gene Transcription" (Hames B.D., and Higgins S.J. edit. (1993)), "Glycobiology" (Fukuda M., and Kobata A. edit. (1993)), "Growth Factors" (McKay I., and Leigh I. edit. (1993)), "Extracellular Matrix" (Haralson M.A., and Hassell J.R. edit. (1995), "Transcription Factors" (Latchman D.S. edit. (1993)), "Signal Transduction" (Milligans G. edit. (1992)), "Protein Phosphorylation" (Hardies G. D. edit. (1993). and "Ion Channels" (Ashley R.H. edit. (1995) featured in "The Practical Approach Series" (IRL PRESS), or "Signal Transduction Protocols" (Kendall D.A., and Hill S.J. edit. (1995). "Glycoprotein Analysis in Biomedicine" (Hounsell E.F. edit. (1993)), featured in "Method in Molecular Biology" (Humana Press).

[0080] As to a protein associated with a disease, it is possible to perform a functional analysis as described above, but also possible to analyze correlation between the expression or the activity of the protein and a certain disease by using a specific antibody that is obtained by using expressed protein. Alternatively, it is possible to utilize the database Online Mendelian Inheritance in Man (OMIM) (http://www.ncbi.nlm.nih.gov/Omim/), which is a database of human genes and diseases, to analyze the protein.

New information is constantly being deposited in the OMIM database. Therefore, it is possible for one skilled in the art to find a new relationship between a particular disease and a gene of the present invention in the most up-to-date database.

[0081] Also, as for a secretory protein, membrane protein, signal transduction-associated protein, glycoprotein-associated protein, or transcription-associated protein, etc., search of the OMIM with the following keywords resulted in the finding that the proteins are associated with many diseases (the result of the OMIM search for secrete and membrane proteins is shown below). Also, association between proteins associated to signal transduction or transcription and diseases is reported in "Transcription Factor Research-1999" (Fujii, Tamura, Kageyama, and Satake edit. (1999) Jikken-Igaku Zoukan, Vol.17, No.3), and "Gene Medicine" ((1999) Vol.3, No.2). For example, in tumors, many proteins have been shown to play a role, including secretory proteins, membrane proteins, and proteins associated with signal transduction, glycoprotein, and transcription, and also proteins associated with metabolism, cytoskeleton, and cell cycle, as described in "Tumor Biology" (Matsubara S. (1992) Syoukabou Life Science series). Thus, besides the proteins associated with diseases, many proteins described above are also potentially associated with diseases, and thus useful as a target in the medicinal industry.

[0082] The result of the OMIM search for secretory and membrane proteins is shown below, in which the keywords,

(1) secretion protein,
(2) membrane protein,
(3) channel, and
(4) extracellular matrix were used.

[0083] Shown in the search result are only the accession numbers in the OMIM. Using the number, data showing the relationship between a disease and a gene or protein can be seen. The OMIM data has been renewed everyday.

1) Secretion protein
268 entries found, searching for "secretion protein"
104760, 176860, 160900, 107400, 118910, 139320, 603850, 147572,176880, 600946, 603215, 157147, 600174, 151675, 170280, 179512, 179513,138120, 179509, 246700, 179510, 600626, 179511, 600998, 109270, 601489, 154545, 179490, 185860, 603216, 122559, 601746,147290, 602672, 146770, 603062, 179508, 131230, 601591, 602421, 139250, 167805, 167770, 600041, 600564, 118825, 601146, 300090, 600753, 601652, 600759, 600768, 602434, 182590, 603166, 308230, 602534, 603489, 107470, 150390, 104610, 173120, 158106, 143890, 306900, 308700, 134797, 137350, 227500, 176300, 107730, 600760, 138079, 120180, 120160, 120150, 124092, 138160, 101000, 227600, 600509, 601199, 142410, 104311, 193400, 201910, 107300, 122560, 272800, 217000, 590050, 147670, 133170, 176730, 300300, 134370, 274600, 120140,162151, 158070, 152790, 120120, 106100, 300200, 192340, 190160, 138040, 147470, 147620, 173350, 147380, 152200, 152760, 157145, 153450, 264080, 113811, 600937, 600840, 188545, 202110, 600514, 186590, 603372, 136435, 137241, 252800, 214500, 207750, 138850, 139191, 142640, 138130, 189907, 603692, 600633, 603355, 107270, 600377, 147892, 232200, 600281, 232800, 602358, 137035, 601771, 601769, 253200, 601933, 118444, 600270, 120700, 600945, 603732, 147660, 600761, 172400, 600823, 600877, 130080, 171060, 107740, 307800, 602843, 130660, 152780, 124020, 601124, 601340, 601604, 601610, 171050, 312060, 232700, 300159, 142703, 600734, 125255, 168450, 123812, 188540, 147940, 188450, 600839, 182452, 188400, 182280, 176760, 263200, 600264, 188826, 252650, 601185, 162641, 137216, 601398, 601538, 118888, 118445, 601745, 190180, 601922, 182098, 602008, 147440, 602384, 600031, 109160, 602663, 151670, 602682, 602730, 602779, 146880, 603061, 142704, 603140, 106150, 600732, 153620, 603318, 139392, 600042, 102200, 603493, 182100, 264300, 603795, 184600
2) Membrane protein
1017 entries found, searching for "membrane protein"

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130500, 305360, 153330, 173610, 170995, 109270, 170993, 309060, 120920, 602333, 133740, 133710, 602690, 133730, 159430, 600897, 133090, 601178, 602413, 602003, 109280, 603237, 602173, 107776, 602334, 125305, 602335, 182879, 154045, 309845, 600594, 603718, 603241, 603214, 603657, 603177, 600182, 601476, 602879, 136950, 600723, 601114, 185880, 185881, 300096, 602257, 160900, 177070, 603062, 603344, 602977, 310200, 600959, 300100, 186945, 600039, 600267, 128240, 182900, 601097, 136430, 600946, 602534, 601047, 143450, 603141, 603700, 600579, 256540, 159440, 602414, 600403, 602048, 188860, 137290, 158343, 184756, 602910, 603179, 600279, 108733, 107770, 173335, 602625, 154050, 219800, 603850, 601028, 600447, 104225, 186946, 601767, 603143, 121015, 603215, 227400, 603735, 600179, 602421, 180721,

176801, 176860, 600753, 603142, 176790, 600266, 601239, 115501, 143890, 121014, 121011, 125950, 603534, 304040, 601134, 600754, 601510, 601595, 190315, 300172, 602216, 602261, 602262, 602461, 131560, 179514, 179512, 176981, 142461, 139310, 312080, 176640, 128239, 185470, 310300, 601403, 601757, 273800, 151460, 176943, 104311, 168468, 120130, 602887, 600164, 601531, 601832,104775, 600040, 603583, 176894, 602631, 166945, 182180, 120620, 141180, 601014, 139150, 182860, 177061, 600174, 180069, 191275, 104760, 601693, 300017, 603518, 601009, 134651, 601107, 603868, 600168, 136425, 603531, 603291, 600917, 603216, 102720, 300118, 179590, 135630, 602285, 107450, 602296, 303630, 176878, 120090, 600322, 138160, 601212, 603293, 131230, 112205, 600763, 600718, 300187, 170715, 601966, 300051, 602474,

120070, 600691, 600855, 182309, 602101, 602857, 194355, 162230, 600874, 113730, 155550, 602701, 306400, 601789, 231200, 107271, 175100, 182870, 305100, 301000, 601313, 157147, 147670, 139200, 603593,157655, 600934, 155970, 602049, 155960, 155760, 118990, 135620, 308230, 602694, 162060, 300023, 160993, 153619, 153432, 120131, 603823, 603167, 601023, 600816, 165040, 601681,166490, 300112, 120190, 300145, 163970, 600772, 602926, 602933, 602202, 400015, 151510, 600759, 602672, 602654, 603821, 116952, 151430, 602632, 155975, 602217, 150370, 600752, 601179, 600932, 603048, 603234, 601805, 603822, 603869, 601717, 601181, 313440, 139130, 107777, 109190, 603452, 191163, 191164, 602370, 176877, 103195, 600523, 191328, 601275, 204200, 602426, 603820, 600551, 600695, 600552, 600553, 602306, 601523,

602507, 602299, 600583, 114070, 600632, 603498, 185430, 600587, 235200, 173470, 603199, 601633, 602500, 208900, 180297, 156225, 516020, 190195, 141900, 102680, 193300, 101000, 193400, 300011, 107400, 257220,107741, 180380, 203200, 111700, 600024, 304800, 600065, 110750, 179605, 113705, 601638, 222900, 120120, 602509, 602469, 600930, 601383, 176261, 602574, 602997, 311770, 131550, 603616, 308700, 603372, 256100, 224100, 276903, 305900, 516000, 131195, 314555, 601567, 603866, 306900, 103390, 186720, 173850, 601050, 602505, 186590, 246530, 602689, 194380, 300041, 162643, 152790,120150, 600682, 600106, 272750, 188040, 602382, 601497, 113811, 182138, 212138, 601309, 109690, 114760, 176805, 601253, 123900, 602581, 189980,191190,110700, 600163, 137167, 600580, 601610, 190000, 123825, 603491,

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146880, 312610, 120940, 142871, 142790, 600937, 142600,134390,111250, 600979, 600997, 142460, 186845, 134635, 601017, 139191, 139090, 138850, 601040, 138720, 122561, 131100, 123610, 217070, 100500, 603377, 602354, 603302, 603207, 603086, 602188, 602095, 603867, 603842, 603798, 602602, 601194, 602607, 603713, 603681, 601252, 603648, 603646, 603644, 601282, 601284, 603667, 603712, 603594, 601872, 603425, 601843, 603263, 603208, 601411, 603201, 603189, 601463, 603164, 603152, 603087, 602874, 601492, 602893, 602057, 602859, 602746, 603879, 603510, 602458, 603380, 601581, 603765, 603283, 601599, 601733, 601852, 602316, 601615, 601617, 602184, 602894, 603005, 603030, 603861, 602835, 602136, 600153, 600074, 600046, 600023, 601625, 516006, 600018, 600016, 516002, 601590, 313475, 313470, 600244,

600528, 601611, 600282, 600327, 601568, 600368, 601730, 601535, 601745, 601929, 300169, 300150, 300132, 601533, 600385, 600464, 600424, 600429, 601756, 601488, 516005, 251100, 516004, 600918, 516003, 602192,

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516001, 240500, 600465, 602241, 602243, 230200, 601485, 601478, 601416, 602297, 601459, 601839, 602314, 193065, 193001, 191306, 600504, 601020, 191191, 602372, 190181, 600534, 188380, 186854, 186360, 600530, 185250, 182331, 600535, 182305, 601296, 600582, 600732, 600734, 600742, 600782, 176802, 176266, 600769, 601883, 600864, 601901, 176260, 173490, 600910, 601905, 171890, 600916, 601987, 602679, 162651, 161555, 160994, 602714, 602715, 602724, 602736, 300007, 602783, 275630, 602836, 270200, 602871, 159460, 602876, 154540, 153900, 602890, 601153, 602190, 602905, 153634, 153337, 602914,
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3) Channel (member of membrane protein)

272 entries found, searching for "channel"

176266, 600724, 170500, 182390, 123825, 114208, 114205, 601784, 114206, 600937, 114204, 603415, 600053, 114209, 114207, 600760, 118425, 601011, 192500, 176261, 600761, 176260, 600359, 600228, 600877, 602235, 300008, 182389, 182391, 601328, 601534, 600504, 602323, 601958, 602780, 602781, 601327, 601012, 600734, 603208, 182392, 603220, 603219, 603888, 600054, 602232, 601745, 603537, 602604, 603796, 302910, 602866, 601013, 602905, 602906, 600163, 152427, 180901, 600702, 600308, 602754, 107776, 602024, 314555, 601949, 600235, 602023, 176263, 600681, 176265, 193245, 603305, 176258, 602983, 601219, 601141, 176267, 602343, 602726, 138253, 176262, 600003, 600397, 602872, 138249, 600843, 600935, 600580, 600845, 602158, 602106, 176264, 300110, 176257, 602717, 603493, 176268, 600932, 602727, 138254,
603652, 300138, 602420, 600570, 600150, 603583, 602345, 603749, 601142, 176256, 600846, 138252, 602982, 603787, 602836, 603788, 602566, 603651, 602421, 100690, 107777, 100725, 100710, 600509, 603061, 154275, 304040, 154276, 180902, 121014, 602368, 139311, 601383, 108745, 601313, 601042, 600131, 186360, 600109, 600229, 600170, 603319, 601485, 118503, 180903, 602076, 124030, 601059, 601212, 601218, 147450, 600855, 600919, 601154, 601157, 171060, 600968, 182139, 131230, 121015, 600421, 113730, 249210, 310500, 600637, 125950, 118800, 156490, 602974, 104610, 121011, 602522, 118504, 300041, 160900, 601382, 602103, 600465, 602014, 600442, 601109, 602481, 277900, 254210, 138247, 164920, 170280, 171050, 128100, 173910, 600884, 123885, 602887, 600232, 180297, 137192, 600304, 138251, 603053, 300103,
603152, 603199, 118511, 118508, 138079, 600983, 182307, 603324, 305990, 603418, 114080, 232200, 600046, 600040, 602403, 603750, 603785, 104210, 600019, 600300, 182860, 603852, 603853, 603855, 516060

4) Extracellular matrix

167 entries found, searching for "extracellular matrix"

603479, 602201, 601418, 601548, 154870, 115437, 602285, 602262, 602261,134797, 600754, 120361, 116935, 602263, 603320, 601807, 603321, 185250, 185261, 253700, 128239, 120324, 193300, 276901, 308700, 600514, 600261, 602109, 120140, 120150, 147557, 193400, 600536, 188826, 120180, 118661, 120320, 152200, 135821, 112260, 230740, 602090, 155760, 192975, 190182, 602108, 601463, 186745, 600900, 600985, 600758, 602369,179590, 601211, 600065, 602178, 600262, 182888, 182889, 151510, 182120, 150325, 190181, 150370, 186355, 193065, 165070, 154705, 147559, 146650, 146640, 153619, 175100, 187380, 231050, 188060, 135820, 156790, 130660, 301870, 128240, 600076, 600119, 193210, 600215, 600245, 121010, 150240, 600309, 600491, 222600, 120328, 600564, 600596, 600616, 600700, 600742, 120325, 138297, 600930,
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[0084] There are several methods for analyzing the expression levels of genes associated with diseases. Differences in gene expression levels between diseased and normal tissues are studied by the analytical methods, for example, Northern hybridization and differential display. Other examples include a method with high-density cDNA filter, a method with DNA microarray and methods with PCR amplification (Experimental Medicine, Vol.17, No. 8, 980-1056 (1999); Cell Engineering (additional volume) DNA Microarray and Advanced PCR Methods, Muramatsu & Naba (eds.), Shujunsya). The varying levels of gene expression between diseased tussues and normal tissues can be studied by any of these analytical methods. When explicit difference in the expression level is observed for a gene, it can be conclude that the gene is closely associated with a disease or disorder. Instead of diseased tissues, cultured cells can be used

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for the assessment. Similarly, when gene expression is explicitly different between normal cells and cells reproducing disease-associated specific features, it can be concluded that the gene is closely associated with a disease or disorder. When the expression levels of genes are evidently varied during major cellular events (such as differentiation and apoptosis), the genes are involved in the cellular events and accordingly are candidates for disease- and/or disorder-associated genes. Further, genes exhibiting tissue-specific expression are genes playing important parts in the tissue functions and, therefore, can be candidates for genes associated with diseases and/or disorders affecting the tissues.

[0085] For example, non-enzymic protein glycation reaction is believed to be a cause for a variety of chronic diabetic complications. Accordingly, genes of which expression levels are elevated or decreased in a glycated protein-dependent manner in the endothelial cells, are associated with diabetic complications caused by glycated proteins (Diabetes 1996, 45 (Suppl. 3), S67-S72; Diabetes, 1997, 46 (Suppl. 2), S19-S25).

The onset of rheumatoid arthritis is thought to be involved in the proliferation of synovial cells covering inner surfaces of joint cavity and in inflammatory reaction resulted from the action of cytokines produced by leukocytes infiltrating into the joint synovial tissues (Rheumatism Information Center, http://www.rheuma-net.or.jp/). Recent studies have also revealed that tissue necrosis factor (TNF)-α participates in the onset (Current opinion in immunology 1999, 11, 657-662). When the expression of a gene exhibits responsiveness to the action of TNF on synovial cells, the gene is considered to be involved in rheumatoid arthritis. Many genes acting at the downstream of TNF-α and IL-1β among inflammation-associated cytokines have been previously identified. The respective stimulations are transduced through independent pathways of signaling cascade. There exists another signaling cascade for both stimulations, wherein NF-κ B is a common transducing molecule shared by the two stimulations (J. Leukoc. Biol., 1994, 56(5): 542-547). It has also been revealed that many inflammation-associated genes, including IL-2, IL-6 and G-CSF, are varied in the expression levels thereof in response to the signal through the common pathway (Trend Genet. 1999, 15(6): 229-235). It is assumed that genes of which expression levels are varied in response to the stimulation of TNF-α or IL-1β also participate in inflammation.

[0086] Ultraviolet radiation damage has been recognized as a risk factor for skin cancers, etc. (United States Environmental Protection Agency: Ozone Depletion Home Page, http://www.epa.gov/ozone/). Genes of which expression levels are varied in skin epidermal cells exposed to ultraviolet rays are considered to be associated with ultraviolet radiation damage of skin. In addition, genes associated with neural differentiation can be candidates for genes responsible for neurological diseases as well as candidates for genes usable for treating the diseases.

[0087] Clones exhibiting differences in the expression levels thereof can be selected by using gene expression analysis. The selection comprises, for example; analyzing cDNA clones by using high-density cDNA filter; and statistically treating the multiple signal values (signal values of radioisotope in the labeled probes or values obtained by measuring fluorescence intensities emitted from the fluorescent labels) for the respective clones by two-sample t-test, where the signal values are determined by multiple experiments of hybridization. The clones of interest are selectable based on the statistically significant differences in the signal distribution at $p<0.05$. However, selectable clones with significant difference in the expression levels thereof may be changed depending on the partial modification of statistical treatment. For example, the clones may be selected by conducting statistical treatment with two-sample t-test at $p<0.01$; or genes exhibiting more explicit differences in the expression levels thereof can be selected by performing statistical treatment with a pre-determined cut-off value for the significant signal difference. An alternative method is that the expression levels are simply compared with each other, and then, the clones of interest are selected based on the ratio of the expression levels thereof.

[0088] Clones that vary in their expression levels can also be selected by comparing the expression levels by PCR analysis, for example, by using the method of determining the band intensities representing the amounts of PCR products with ethidium bromide staining; the method of determining the values of radioisotope signals or fluorescence intensities of the PCR products when radiolabeled or fluorescent dye-labeled primers, respectively, are used in PCR amplification; or the method of determining the values of radioisotope signals or fluorescence intensities of the probes hybridized to the PCR products when radiolabeled or fluorescent dye-labeled probes, respectively, are used in the hybridization. If the expression level ratios obtained in multiple PCR experiments are constantly at least 2-fold, such a clone can be judged to vary in its expression level. When the ratios are several-fold or not less than 10-fold, the clone can be selected as a gene exhibiting the explicit difference in its expression level.

[0089] A survey of genes of which expression levels are varied specifically to the glycated protein in the endothelial cells has revealed genes with elevated expression levels, HEMBA1003958, HEMBA1004850, MAMMA1001256, MAMMA1002132, PLACE2000411 and PLACE3000119. On the other hand, a gene of which expression level is decreased specifically to the glycated protein is MAMMA1001783. These clones are genes associated with diabetes.

[0090] A survey of genes of which expression levels are varied in response to TNF-α (Tumor Necrosis Factor-alpha) in the primary cell culture of synovial tissue has revealed the following clones with elevated expression levels in the presence of TNF-α:

HEMBA1000005, HEMBA1000012, HEMBA1000020, HEMBA1000046, HEMBA1000076, HEMBA1000111, HEMBA1000168, HEMBA1000185, HEMBA1000201, HEMBA1000231, HEMBA1000243, HEMBA1000280,

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HEMBA1000282, HEMBA1000304, HEMBA1000307, HEMBA1000327, HEMBA1000356, HEMBA1000376,
HEMBA1000387, HEMBA1000390, HEMBA1000418, HEMBA1000460, HEMBA1000491, HEMBA1000501,
HEMBA1000518, HEMBA1000519, HEMBA1000520, HEMBA1000531, HEMBA1000534, HEMBA1000542,
HEMBA1000545, HEMBA1000591, HEMBA1000592, HEMBA1000594, HEMBA1000636, HEMBA1000655,
HEMBA1000657, HEMBA1000673, HEMBA1000682, HEMBA1000686, HEMBA1000722, HEMBA1000726,
HEMBA1000827, HEMBA1000870, HEMBA1000918, HEMBA1000971, HEMBA1000974, HEMBA1000986,
HEMBA1001019, HEMBA1001043, HEMBA1001051, HEMBA1001059, HEMBA1001060, HEMBA1001071,
HEMBA1001080, HEMBA1001109, HEMBA1001140, HEMBA1001172, HEMBA1001196, HEMBA1001213,
HEMBA1001226, HEMBA1001281, HEMBA1001299, HEMBA1001302, HEMBA1001303, HEMBA1001323,
HEMBA1001326, HEMBA1001327, HEMBA1001330, HEMBA1001351, HEMBA1001407, HEMBA1001411,
HEMBA1001446, HEMBA1001454, HEMBA1001569, HEMBA1001647, HEMBA1001714, HEMBA1001800,
HEMBA1001804, HEMBA1001809, HEMBA1001888, HEMBA1001912, HEMBA1001921, HEMBA1001967,
HEMBA1002084, HEMBA1002161, HEMBA1002166, HEMBA1002241, HEMBA1002337, HEMBA1002363,
HEMBA1002389, HEMBA1002458, HEMBA1002460, HEMBA1002469, HEMBA1002538, HEMBA1002542,
HEMBA1002547, HEMBA1002609, HEMBA1002624,
HEMBA1002659, HEMBA1002750, HEMBA1002770, HEMBA1002779, HEMBA1002810, HEMBA1002816,
HEMBA1002818, HEMBA1002850, HEMBA1002863, HEMBA1003021, HEMBA1003033, HEMBA1003078,
HEMBA1003166, HEMBA1003202, HEMBA1003204, HEMBA1003229, HEMBA1003235, HEMBA1003276,
HEMBA1003286, HEMBA1003296, HEMBA1003370, HEMBA1003376, HEMBA1003403, HEMBA1003418,
HEMBA1003433, HEMBA1003447, HEMBA1003560, HEMBA1003569, HEMBA1003571, HEMBA1003591,
HEMBA1003597, HEMBA1003598, HEMBA1003621, HEMBA1003656, HEMBA1003662, HEMBA1003680,
HEMBA1003715, HEMBA1003725, HEMBA1003729, HEMBA1003733, HEMBA1003742, HEMBA1003773,
HEMBA1003783, HEMBA1003950, HEMBA1004012, HEMBA1004015, HEMBA1004048, HEMBA1004074,
HEMBA1004086, HEMBA1004111, HEMBA1004131, HEMBA1004202, HEMBA1004203, HEMBA1004207,
HEMBA1004248, HEMBA1004274, HEMBA1004321, HEMBA1004330, HEMBA1004356, HEMBA1004366,
HEMBA1004405, HEMBA1004408, HEMBA1004429, HEMBA1004499, HEMBA1004507, HEMBA1004509,
HEMBA1004542, HEMBA1004596, HEMBA1004604, HEMBA1004776, HEMBA1004889, HEMBA1004934,
HEMBA1004978, HEMBA1005019, HEMBA1005047, HEMBA1005206, HEMBA1005219, HEMBA1005274,
HEMBA1005331, HEMBA1005338, HEMBA1005394, HEMBA1005423, HEMBA1005576, HEMBA1005732,
HEMBA1005746, HEMBA1006091, HEMBA1006142, HEMBA1006173, HEMBA1006198, HEMBA1006253,
HEMBA1006268, HEMBA1006309, HEMBA1006377, HEMBA1006474, HEMBA1006486, HEMBA1006492,
HEMBA1006502, HEMBA1006535, HEMBA1006579, HEMBA1006648, HEMBA1006659, HEMBA1006885,
HEMBA1006929, HEMBA1006941, HEMBA1007078, HEMBA1007080, HEMBA1007121, HEMBA1007194,
HEMBA1007300, HEMBA1007301, HEMBA1007322, HEMBB1000036, HEMBB1000044, HEMBB1000089,
HEMBB1000215, HEMBB1000217, HEMBB1000272, HEMBB1000420, HEMBB1000591, HEMBB1000593,
HEMBB1000631, HEMBB1000835, HEMBB1000887, HEMBB1000908, HEMBB1000975, HEMBB1000985,
HEMBB1001011, HEMBB1001014, HEMBB1001112, HEMBB1001133, HEMBB1001331, HEMBB1001337,
HEMBB1001366, HEMBB1001367, HEMBB1001384, HEMBB1001394, HEMBB1001429, HEMBB1001463,
HEMBB1001619, HEMBB1001684, HEMBB1001706, HEMBB1001753, HEMBB1001797, HEMBB1001802,
HEMBB1001812, HEMBB1001874, HEMBB1001910, HEMBB1001915, HEMBB1001973, HEMBB1001983,
HEMBB1001990, HEMBB1002190, HEMBB1002193, HEMBB1002249, HEMBB1002329, HEMBB1002342,
HEMBB1002371, HEMBB1002409, HEMBB1002442, HEMBB1002489, HEMBB1002492, HEMBB1002520,
HEMBB1002534, HEMBB1002596, HEMBB1002664, HEMBB1002692, HEMBB1002697, HEMBB1002705,
MAMMA1000092, MAMMA1000155, MAMMA1000163, MAMMA1000173, MAMMA1000175, MAMMA1000227,
MAMMA1000241, MAMMA1000257, MAMMA1000264, MAMMA1000266, MAMMA1000270, MAMMA1000307,
MAMMA1000410, MAMMA1000413, MAMMA1000416, MAMMA1000421, MAMMA1000472, MAMMA1000501,
MAMMA1000605, MAMMA1000643, MAMMA1000670, MAMMA1000684, MAMMA1000696, MAMMA1000732,
MAMMA1000752, MAMMA1000802, MAMMA1000824, MAMMA1000905, MAMMA1000921, MAMMA1000931,
MAMMA1000957, MAMMA1000962,
MAMMA1000998, MAMMA1001008, MAMMA1001050, MAMMA1001074, MAMMA1001078, MAMMA1001292,
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[0091] On the other hand, clones with decreased expression levels in the presence of TNFα are:

HEMBA1002150, HEMBB1000240, NT2RM2000469, NT2RM2000984, NT2RM2001688, NT2RM4000290, NT2RM4000496, NT2RM4000590, NT2RM4001047, NT2RM4001582, NT2RM4001611, NT2RM4001650, NT2RM4002075, NT2RM4002128, NT2RP1000174, NT2RP1000243, NT2RP1000581, NT2RP1000688, NT2RP1000767, NT2RP1000825, NT2RP1001185; NT2RP1001286, NT2RP1001432, NT2RP1001457, NT2RP2000001, NT2RP2000248, NT2RP2000841, NT2RP2001813, NT2RP2002137, NT2RP2002928, NT2RP2003517, NT2RP2003559, NT2RP2003564, NT2RP2004933, NT2RP2005038, NT2RP2006365, NT2RP3000072, NT2RP3000320, NT2RP3000484, NT2RP3000980, NT2RP3001111, NT2RP3001420, NT2RP3001495, NT2RP3002056, NT2RP3002057, NT2RP3002545, NT2RP3002713, NT2RP3002799, NT2RP3002869, NT2RP3002953, NT2RP3002955, NT2RP3003282, NT2RP3003290, NT2RP3003384, NT2RP3003385, NT2RP3003870, NT2RP3004207, NT2RP3004262, NT2RP3004527, NT2RP4000500, NT2RP4000524, NT2RP4000787, NT2RP4000927, NT2RP4000955, NT2RP4000989, NT2RP4001442, NT2RP4001638, NT2RP4001950, NT2RP4002888, NT2RP5003524, OVARC1001270, PLACE1000246, PLACE1002816.

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[0092] These are rheumatoid arthritis-associated clones.

[0093] A survey of genes of which expression levels are varied in primary cultured skin fibroblast cells exposed to ultraviolet light has revealed the following clones with elevated expression levels by ultraviolet radiation: HEMBA1000542, HEMBA1001808, HEMBA1002177, HEMBA1003314, MAMMA1001874, NT2RM2001100, NT2RP2005732, NT2RP3000592, NT2RP4000657, OVARC 1000004, OVARC1001092, OVARC1001342, PLACE1002816, NT2RM4001002, NT2RM4001813, NT2RM4002266, NT2RP2001174, NT2RP2001196, NT2RP2005358, NT2RP3000690, NT2RP3001216, NT2RP3003464, PLACE1006382, THYRO1000070, THYRO1001100, Y79AA1000342

[0094] On the other hand, the expression levels of the following clones were decreased by ultraviolet radiation: HEMBA1000005, HEMBA1000150, HEMBA1000156, HEMBA1000158, HEMBA1000168, HEMBA1000231, HEMBA1000304, HEMBA1000307, HEMBA1000333, HEMBA1000366, HEMBA1000369, HEMBA1000390, HEMBA1000396, HEMBA1000418, HEMBA1000434, HEMBA1000464, HEMBA1000469, HEMBA1000490, HEMBA1000504, HEMBA1000505, HEMBA1000557, HEMBA1000657, HEMBA1000673, HEMBA1000682, HEMBA1000686, HEMBA1000727, HEMBA1000752, HEMBA1000851, HEMBA1000852, HEMBA1000870, HEMBA1000872, HEMBA1001085, HEMBA1001121, HEMBA1001133, HEMBA1001235, HEMBA1001265, HEMBA1001281, HEMBA1001289, HEMBA1001299, HEMBA1001303, HEMBA1001310, HEMBA1001323, HEMBA1001595, HEMBA1001620, HEMBA1001640, HEMBA1001678, HEMBA1001712, HEMBA1001835, HEMBA1001950, HEMBA1001987, HEMBA1002253, HEMBA1002321, HEMBA1002341, HEMBA1002419, HEMBA1002679, HEMBA1002728, HEMBA1002818, HEMBA1002935, HEMBA1002999, HEMBA1003034, HEMBA1003071, HEMBA1003098, HEMBA1003142, HEMBA1003175, HEMBA1003202, HEMBA1003212, HEMBA1003220, HEMBA1003276, HEMBA1003373, HEMBA1003417, HEMBA1003447, HEMBA1003528, HEMBA1003684, HEMBA1003799, HEMBA1003885, HEMBA1003989, HEMBA1004011, HEMBA1004055, HEMBA1004133, HEMBA1004225, HEMBA1004272, HEMBA1004353, HEMBA1004631, HEMBA1004669, HEMBA1004705, HEMBA1004753, HEMBA1004776, HEMBA1004803, HEMBA1004816, HEMBA1004900, HEMBA1005047, HEMBA1005079, HEMBA1005101, HEMBA1005149, HEMBA1005152, HEMBA1005202, HEMBA1005314, HEMBA1005372, HEMBA1005511, HEMBA1005513, HEMBA1005518, HEMBA1005570, HEMBA1005577, HEMBA1005581, HEMBA1005588, HEMBA1005609, HEMBA1005632, HEMBA1005853, HEMBA1006031, HEMBA1006035, HEMBA1006485, HEMBA1006486, HEMBA1006502, HEMBA1006696, HEMBA1006789, HEMBA1006796, HEMBA1007085, HEMBA1007224, HEMBA1007301, HEMBA1007319, HEMBA1007341, HEMBA1007342, HEMBB1000036, HEMBB1000037, HEMBB1000217, HEMBB1000266, HEMBB1000317, HEMBB1000336, HEMBB1000354, HEMBB1000369, HEMBB1000399, HEMBB1000434, HEMBB1000438, HEMBB1000592, HEMBB1000673, HEMBB1000789, HEMBB1000810, HEMBB1000883, HEMBB1000887, HEMBB1001105, HEMBB1001182, HEMBB1001242, HEMBB1001267, HEMBB1001424, HEMBB1001464, HEMBB1001531, HEMBB1001618, HEMBB1001996, HEMBB1002092, HEMBB1002139, HEMBB1002142, HEMBB1002190, HEMBB1002453, HEMBB1002520, HEMBB1002550, HEMBB1002556, HEMBB1002600, HEMBB1002664, MAMMA1000009, MAMMA1000055, MAMMA1000069, MAMMA1000133, MAMMA1000171, MAMMA1000173, MAMMA1000287, MAMMA1000416, MAMMA1000585, MAMMA1000713, MAMMA1000760, MAMMA1000798, MAMMA1000831, MAMMA1000875, MAMMA1000876, MAMMA1000877, MAMMA1000906, MAMMA1000931, MAMMA1000962, MAMMA1001133, MAMMA1001139, MAMMA1001243, MAMMA1001271, MAMMA1001274, MAMMA1001298, MAMMA1001606, MAMMA1001630, MAMMA1001670, MAMMA1001743, MAMMA1001751, MAMMA1002140, MAMMA1002145, MAMMA1002158, MAMMA1002170, MAMMA1002236, MAMMA1002311, MAMMA1002498, MAMMA1002754, MAMMA1002780, MAMMA1002820, MAMMA1002843, MAMMA1002844, MAMMA1002871, MAMMA1003047, NT2RM1000037, NT2RM1000039, NT2RM1000080, NT2RM1000086, NT2RM1000341, NT2RM1000499, NT2RM1000669, NT2RM1000746, NT2RM1000781, NT2RM1000885, NT2RM1000905, NT2RM1000962, NT2RM2000239, NT2RM2000260, NT2RM2000371, NT2RM2000639, NT2RM2000649, NT2RM2000735, NT2RM2000821, NT2RM2000984, NT2RM2001035, NT2RM2001065, NT2RM2001105, NT2RM2001177, NT2RM2001194, NT2RM2001196, NT2RM2001243, NT2RM2001256, NT2RM2001424, NT2RM2001588, NT2RM2001635, NT2RM2001648, NT2RM2001652, NT2RM2001668, NT2RM2001706, NT2RM2001727, NT2RM2001730, NT2RM2001743, NT2RM2001753, NT2RM2001760, NT2RM2001771, NT2RM2001785, NT2RM2001800, NT2RM2001855, NT2RM2001896, NT2RM2001997, NT2RM2002030, NT2RM2002049, NT2RM2002091, NT2RM2002142, NT2RM2002145, NT2RM2002178, NT2RM2002580, NT2RM4000215, NT2RM4000344, NT2RM4000368, NT2RM4000421, NT2RM4000425, NT2RM4000457, NT2RM4000496, NT2RM4000515, NT2RM4000712, NT2RM4000787, NT2RM4000813, NT2RM4000820, NT2RM4000852, NT2RM4000950, NT2RM4000996, NT2RM4001016, NT2RM4001047, NT2RM4001054, NT2RM4001140, NT2RM4001151, NT2RM4001187, NT2RM4001204, NT2RM4001258, NT2RM4001437, NT2RM4001454, NT2RM4001489, NT2RM4001605, NT2RM4001611, NT2RM4001666, NT2RM4001710, NT2RM4001714, NT2RM4001715, NT2RM4001731, NT2RM4001741, NT2RM4001746, NT2RM4001856, NT2RM4001938, NT2RM4001940, NT2RM4001984,

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[0095] These clones are associated with ultraviolet radiation damage.

[0096] A survey of genes of which expression levels are varied in response to the stimulation for inducing cell differentiation (stimulation using retinoic acid (RA) or using RA/inhibitor (inhibitor for cell division)) in culture cells of neural strain, NT2, revealed the following clones with elevated expression levels in the presence of RA:

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[0097] On the other hand, clones of which expression levels decreased by RA are as follows:

HEMBA1000946, HEMBA1003569, HEMBA1005570, HEMBB1000915, NT2RM1000666, NT2RM2000092, NT2RM2000594, NT2RM2001256, NT2RM4001754, NT2RM4001905, NT2RP2001675, NT2RP2002047, NT2RP2005491, NT2RP3000980, NT2RP3002081, NT2RP3004594, NT2RP4001950, NT2RP4002408, OVARC1000431, OVARC1001942, OVARC1001943, PLACE1003190, PLACE1004868, PLACE1005923, PLACE1007257, PLACE1010624, Y79AA1000346

[0098] Clones of which expression levels increase by RA/inhibitor are as follows:

HEMBA1000046, HEMBA1000307, HEMBA1000434, HEMBA1000504, HEMBA1000588, HEMBA1000682, HEMBA1000726, HEMBA1000943, HEMBA1001071, HEMBA1001094, HEMBA1001122, HEMBA1001323, HEMBA1001361, HEMBA1001455, HEMBA1001709, HEMBA1001746, HEMBA1001869, HEMBA1002084, HEMBA1002583, HEMBA1002628, HEMBA1002801, HEMBA1002937, HEMBA1003096, HEMBA1003142, HEMBA1003229, HEMBA1003276, HEMBA1003309, HEMBA1003463, HEMBA1003597, HEMBA1003617, HEMBA1003725, HEMBA1003803, HEMBA1003879, HEMBA1003989, HEMBA1004000, HEMBA1004015, HEMBA1004024, HEMBA1004049, HEMBA1004056, HEMBA1004199, HEMBA1004248, HEMBA1004356, HEMBA1004554, HEMBA1004666, HEMBA1004725, HEMBA1004770, HEMBA1004803, HEMBA1004923, HEMBA1004934, HEMBA1004954, HEMBA1005039, HEMBA1005075, HEMBA1005113, HEMBA1005219, HEMBA1005232, HEMBA1005251, HEMBA1005304, HEMBA1005367, HEMBA1005372, HEMBA1005403, HEMBA1005410, HEMBA1005411, HEMBA1005548, HEMBA1005581, HEMBA1005631, HEMBA1005666, HEMBA1005755, HEMBA1005780, HEMBA1006067, HEMBA1006130, HEMBA1006364, HEMBA1006485, HEMBA1006559, HEMBA1006579, HEMBA1006754, HEMBB1000059, HEMBB1000575, HEMBB1000709, HEMBB1000822, HEMBB1000848, HEMBB1000852, HEMBB1000913, HEMBB1000985, HEMBB1001117, HEMBB1001210, HEMBB1001317, HEMBB1001394, HEMBB1001443, HEMBB1001668, HEMBB1001695,

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HEMBB1002049, HEMBB1002254, HEMBB1002266, HEMBB1002371, HEMBB1002502, HEMBB1002614, HEMBB1002617, HEMBB1002692, HEMBB1002697, MAMMA1000241, MAMMA1000424, MAMMA1000616, MAMMA1000731, MAMMA1000824, MAMMA1000908, MAMMA1000956, MAMMA1001038, MAMMA1001091, MAMMA1001243, MAMMA1001815; MAMMA1001820, MAMMA1002267, MAMMA1002769, MAMMA1002871, MAMMA1002941,
NT2RM1000355, NT2RM1000725, NT2RM1000829, NT2RM1000850, NT2RM1000898, NT2RM2000504, NT2RM2000635, NT2RM2000718, NT2RM2000821, NT2RM2001370, NT2RM2001582, NT2RM2001592, NT2RM2001613, NT2RM2001632, NT2RM2001635, NT2RM2001648, NT2RM2001659, NT2RM2001671, NT2RM2001695, NT2RM2001760, NT2RM2001782, NT2RM2001839, NT2RM2001879, NT2RM2001983, NT2RM4000104, NT2RM4000290, NT2RM4000425, NT2RM4000433, NT2RM4000471, NT2RM4000531, NT2RM4000852, NT2RM4001047, NT2RM4001347, NT2RM4001454, NT2RM4001557, NT2RM4001566, NT2RM4001582, NT2RM4001938, NT2RM4001953, NT2RM4002018, NT2RM4002409, NT2RM4002558, NT2RM4002594, NT2RP1000259, NT2RP1000418, NT2RP1000574, NT2RP1000629, NT2RP1000782, NT2RP1000856, NT2RP1000943, NT2RP1000988, NT2RP1001013, NT2RP1001173, NT2RP1001546, NT2RP2000091, NT2RP2000208, NT2RP2000274, NT2RP2000329, NT2RP2000369, NT2RP2000634, NT2RP2000842, NT2RP2000943, NT2RP2000987, NT2RP2001094, NT2RP2001277, NT2RP2001290, NT2RP2001366, NT2RP2001423, NT2RP2001436, NT2RP2001467, NT2RP2001506, NT2RP2001601, NT2RP2001663, NT2RP2001926, NT2RP2001985, NT2RP2002032, NT2RP2002041, NT2RP2002046, NT2RP2002078, NT2RP2002124, NT2RP2002185, NT2RP2002193, NT2RP2002312, NT2RP2002316, NT2RP2002426, NT2RP2002457, NT2RP2002475, NT2RP2002520, NT2RP2002595, NT2RP2002643, NT2RP2002672, NT2RP2002701, NT2RP2002710, NT2RP2002727, NT2RP2003099, NT2RP2003121, NT2RP2003137, NT2RP2003158, NT2RP2003206, NT2RP2003230, NT2RP2003272, NT2RP2003280, NT2RP2003347, NT2RP2003393, NT2RP2003401, NT2RP2003445, NT2RP2003456, NT2RP2003511, NT2RP2003517, NT2RP2003543, NT2RP2003596, NT2RP2003706, NT2RP2003871, NT2RP2004681, NT2RP2004743, NT2RP2004775, NT2RP2004933, NT2RP2004967, NT2RP2005003, NT2RP2005270, NT2RP2005289, NT2RP2005344, NT2RP2005453, NT2RP2005555, NT2RP2005767, NT2RP2005853, NT2RP2006043, NT2RP2006393, NT2RP2006436, NT2RP2006441, NT2RP2006467, NT2RP2006534, NT2RP2006565, NT2RP3000348, NT2RP3000359, NT2RP3000366, NT2RP3000403, NT2RP3000418, NT2RP3000441, NT2RP3000561, NT2RP3000759, NT2RP3000826, NT2RP3001007, NT2RP3001096, NT2RP3001126, NT2RP3001355, NT2RP3001396, NT2RP3001449, NT2RP3001490, NT2RP3001679, NT2RP3001727, NT2RP3001752, NT2RP3001777, NT2RP3001782, NT2RP3001799, NT2RP3001854, NT2RP3001989, NT2RP3002142, NT2RP3002248, NT2RP3002343, NT2RP3002484, NT2RP3002529, NT2RP3002549, NT2RP3002628, NT2RP3002687, NT2RP3002688, NT2RP3002810, NT2RP3003032, NT2RP3003139, NT2RP3003193, NT2RP3003203, NT2RP3003204, NT2RP3003210, NT2RP3003212, NT2RP3003264, NT2RP3003282, NT2RP3003500, NT2RP3004041, NT2RP3004215, NT2RP4000147, NT2RP4000259, NT2RP4000360, NT2RP4000448, NT2RP4000524, NT2RP4000588, NT2RP4000879, NT2RP4000907, NT2RP4000989, NT2RP4001079, NT2RP4001150, NT2RP4001219, NT2RP4001260, NT2RP4001274, NT2RP4001353, NT2RP4001547, NT2RP4001677, NT2RP4002052, OVARC1000006, OVARC1000092, OVARC1000321, OVARC1000384, OVARC1000408, OVARC1000414, OVARC1000520, OVARC1000526, OVARC1000588, OVARC1000679, OVARC1000682, OVARC1000769, OVARC1000850, OVARC1000862, OVARC1000886, OVARC1000984, OVARC1001000, OVARC1001004, OVARC1001154, OVARC1001170, OVARC1001173, OVARC1001200, OVARC1001268, OVARC1001376, OVARC1001419, OVARC1001425, OVARC1001476, OVARC1001480, OVARC1001542, OVARC1001873, OVARC1001928, OVARC1001987, OVARC1002066, OVARC1002082, OVARC1002112, OVARC1002127, PLACE1000014, PLACE1000048, PLACE1000184, PLACE1000185, PLACE1000246, PLACE1000292, PLACE1000332, PLACE1000347, PLACE1000564, PLACE1000656, PLACE1000712, PLACE1001000, PLACE1001168, PLACE1001185, PLACE1001241, PLACE1001294, PLACE1001311, PLACE1001395, PLACE1001570, PLACE1001608, PLACE1001610, PLACE1001716, PLACE1001746, PLACE1001817, PLACE1001821, PLACE1001844, PLACE1001897, PLACE1002066, PLACE1002119, PLACE1002157, PLACE1002205, PLACE1002256, PLACE1002259, PLACE1002399, PLACE1002438, PLACE1002474, PLACE1002477, PLACE1002500, PLACE1002514, PLACE1002578, PLACE1002815, PLACE1002851, PLACE1002968, PLACE1003108, PLACE1003174, PLACE1003200, PLACE1003238, PLACE1003256, PLACE1003334, PLACE1003342, PLACE1003516, PLACE1003521, PLACE1003537, PLACE1003592, PLACE1003596, PLACE1003723, PLACE1003760, PLACE1003771, PLACE1003783, PLACE1003795, PLACE1003892, PLACE1003968, PLACE1004103, PLACE1004256, PLACE1004405, PLACE1004460, PLACE1004506, PLACE1004629, PLACE1004674, PLACE1004813, PLACE1004979, PLACE1005066, PLACE1005101, PLACE1005102, PLACE1005128, PLACE1005181, PLACE1005287, PLACE1005305, PLACE1005327, PLACE1005477, PLACE1005595, PLACE1005603, PLACE1005666, PLACE1005804,

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PLACE1005884, PLACE1005934, PLACE1006076, PLACE1006119, PLACE1006159, PLACE1006164, PLACE1006170, PLACE1006382, PLACE1006492, PLACE1006629, PLACE1006704, PLACE1006731, PLACE1006760, PLACE1006779, PLACE1006795, PLACE1006805, PLACE1006962, PLACE1007045, PLACE1007111, PLACE1007282, PLACE1007386, PLACE1007416, PLACE1007484, PLACE1007544, PLACE1007645, PLACE1007743, PLACE1007746, PLACE1007807, PLACE1007858, PLACE1008002, PLACE1008181, PLACE1008273, PLACE1008368, PLACE1008405, PLACE1008532, PLACE1008568, PLACE1008625, PLACE1008696, PLACE1008867, PLACE1009027, PLACE1009039, PLACE1009045, PLACE1009110, PLACE1009298, PLACE1009328, PLACE1009581, PLACE1009621, PLACE1009622, PLACE1009637, PLACE1009925, PLACE1009935, PLACE1010089, PLACE1010106, PLACE1010152, PLACE1010274, PLACE1010491, PLACE1010629, PLACE1010630, PLACE1010714, PLACE1010739, PLACE1010891, PLACE1010896, PLACE1010925, PLACE1010965, PLACE1011026, PLACE1011046, PLACE1011214, PLACE1011399, PLACE1011433, PLACE1011492, PLACE1011641, PLACE1011649, PLACE1011719, PLACE1011762, PLACE1011858, PLACE1011923, PLACE2000014, PLACE2000039, PLACE2000216, PLACE2000302, PLACE2000317, PLACE2000342, PLACE2000347, PLACE2000379, PLACE3000121, PLACE3000124, PLACE3000160, PLACE3000242, PLACE3000271, PLACE3000353, PLACE3000362, PLACE3000365, PLACE3000400, PLACE3000401, PLACE4000034, PLACE4000089, PLACE4000522, PLACE4000558, SKNMC1000050, THYRO1000040, THYRO1000197, THYRO1000241, THYRO1000327, THYRO1000394, THYRO1000488, THYRO1000501, THYRO1000585, THYRO1000596, THYRO1000625, THYRO1000805, THYRO1000934, THYRO1001133, THYRO1001134, THYRO1001173, THYRO1001213, THYRO1001262, THYRO1001290, THYRO1001721, Y79AA1000037, Y79AA1000800, Y79AA1000976, Y79AA1001078, Y79AA1001228, Y79AA1001299, Y79AA1001402, Y79AA1001585, Y79AA1001696, Y79AA1001711, Y79AA1001827, Y79AA1001875, Y79AA1002027, Y79AA1002211, Y79AA1002234, Y79AA1002258

[0099] On the other hand, clones of which expression levels decrease by RA/inhibitor are as follows:

HEMBA1000012, HEMBA1000501, HEMBA1000946, HEMBA1003220, HEMBA1003403, HEMBA1003569, HEMBA1003591, HEMBA1003926, HEMBA1004168, HEMBA1004507, HEMBA1005009, HEMBA1005296, HEMBA1005528, HEMBA1005570, HEMBA1006467, HEMBA1006486, HEMBA1006492, HEMBA1007322, HEMBB1000055, HEMBB1000244, HEMBB1001665, MAMMA1000684, MAMMA1001139, MAMMA1001743, NT2RM1000257 NT2RM1000318, NT2RM1000539, NT2RM1000666, NT2RM2000092, NT2RM2000192, NT2RM2000371, NT2RM2000594, NT2RM4000511, NT2RM4001140, NT2RM4001754, NT2RM4001905, NT2RM4001940, NT2RM4002593, NT2RP1000086, NT2RP1000439, NT2RP1001073, NT2RP2000098, NT2RP2000965, NT2RP2001397, NT2RP2002047, NT2RP2004226, NT2RP2004396, NT2RP2004655, NT2RP2005126, NT2RP2005464, NT2RP2005712, NT2RP2005859, NT2RP2005890, NT2RP3000980, NT2RP3001383, NT2RP3001621, NT2RP3002081, NT2RP3002181, NT2RP3002244, NT2RP3002590, NT2RP3003059, NT2RP3004258, NT2RP3004378, NT2RP3004527, NT2RP3004594, NT2RP4001760, NT2RP4001950, NT2RP4002047, NT2RP4002408, NT2RP5003459, OVARC1000004, OVARC1000035, OVARC1000431, OVARC1001051, OVARC1001129, OVARC1001176, OVARC1001261, OVARC1001342, OVARC1001942, OVARC1001943, PLACE1002171, PLACE1002465, PLACE1003190, PLACE1003375, PLACE1004128, PLACE1005026, PLACE1005876, PLACE1005923, PLACE1007257, PLACE1007375, PLACE1007507, PLACE1008941, PLACE1010624, PLACE1011090, PLACE1011219, THYRO1000270, Y79AA1000346, Y79AA1001541

[0100] These clones are also associated with neural differentiation and, therefore, are candidates for genes associated with neurological diseases.

[0101] For example, if the protein encoded by the cDNA of the present invention is a regulatory factor of cellular conditions such as growth and differentiation, it can be used for developing medicines as follows. The protein or antibody provided by the invention is injected into a certain kind of cells by microinjection. Then, using the cells, it is possible to screen low molecular weight compounds by measuring the change in the cellular conditions, or the activation or inhibition of a particular gene. The screening can be performed as follows. First, the protein is expressed and purified as recombinant. The purified protein is microinjected into cells such as various cell lines, or primary culture cells, and the cellular change such as growth and differentiation can be examined. Alternatively, the induction of genes whose expression is known to be associated with a particular change of cellular conditions may be detected by the amount of mRNA or protein. Or, the amount of intracellular molecules (low molecular weight compounds, etc.) that is changed by the function of the gene product (protein) which is known to be associated with a particular change of cellular conditions may be detected. The compounds to be screened (both low and high molecular compounds are acceptable) can be added to the culture media and assessed for their activity by measuring the change of the cellular conditions. Instead of microinjection, cell lines introduced with the gene obtained in the invention can be used for the screening. If the gene product is turn out to be associated with a particular change in the cellular conditions, the change of the product can be used as a measurement for screening. Once a compound is screened out which can activate or inhibit

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the function of the protein of the invention, it can be applied for developing medicines.

[0102] If the protein encoded by the cDNA of the present invention is a secretory protein, membrane protein, or protein associated with signal transduction, glycoprotein, transcription, or diseases, it can be used in functional assays for developing medicines.

[0103] In case of a membrane protein, it is most likely to be a protein that functions as a receptor or ligand on the cell surface. Therefore, it is possible to reveal a new relationship between a ligand and receptor by screening the membrane protein of the invention based on the binding activity with the known ligand or receptor. Screening can be performed according to the known methods.

[0104] For example, a ligand against the protein of the invention can be screened in the following manner. Namely, a ligand that binds to a specific protein can be screened by a method comprising the steps of: (a) contacting a test sample with the protein of the invention or a partial peptide thereof, or cells expressing these, and (b) selecting a test sample that binds to said protein, said partial peptide, or said cells.

[0105] On the other hand, for example, screening using cells expressing the protein of the present invention that is a receptor protein can also be performed as follows. It is possible to screen receptors that is capable of binding to a specific protein by using procedures (a) attaching the sample cells to the protein of the invention or its partial peptide, and (b) selecting cells that can bind to the said protein or its partial peptide.

[0106] In a following screening as an example, first the protein of the invention is expressed, and the recombinant protein is purified. Next, the purified protein is labeled, binding assay is performed using a various cell lines or primary cultured cells, and cells that are expressing a receptor are selected (Growth and differentiation factors and their receptors, Shin-Seikagaku Jikken Kouza Vol.7 (1991) Honjyo, Arai, Taniguchi, and Muramatsu edit, p203-236, Tokyo-Kagaku-Doujin). A protein of the invention can be labeled with RI such as ^{125}I, and enzyme (alkaline phosphatase etc.). Alternatively, a protein of the invention may be used without labeling and then detected by using a labeled antibody against the protein. The cells that are selected by the above screening methods, which express a receptor of the protein of the invention, can be used for the further screening of an agonists or antagonists of the said receptor.

[0107] Once the ligand binding to the protein of the invention, the receptor of the protein of the invention or the cells expressing the receptor are obtained by screening, it is possible to screen a compound that binds to the ligand and receptor. Also it is possible to screen a compound that can inhibit both bindings (agonists or antagonists of the receptor, for example) by utilizing the binding activities.

[0108] When the protein of the invention is a receptor, the screening method comprises the steps of (a) contacting the protein of the invention or cells expressing the protein of the invention with the ligand, in the presence of a test sample, (b) detecting the binding activity between said protein or cells expressing said protein and the ligand, and (c) selecting a compound that reduces said binding activity when compared to the activity in the absence of the test sample. Furthermore, when the protein of the invention is a ligand, the screening method comprises the steps of (a) contacting the protein of the invention with its receptor or cells expressing the receptor in the presence of samples, (b) detecting the binding activity between the protein and its receptor or the cells expressing the receptor, and (c) selecting a compound that can potentially reduce the binding activity compared to the activity in the absence of the sample.

[0109] Samples to screen include cell extracts, expressed products from a gene library, synthesized low molecular compound, synthesized peptide, and natural compounds, for example, but are not construed to be listed here. A compound that is isolated by the above screening using a binding activity of the protein of the invention can also be used as a sample.

[0110] A compound isolated by the screening may be a candidate to be an agonist or an antagonist of the receptor of the protein. By utilizing an assay that monitors a change in the intracellular signaling such as phosphorylation which results from reduction of the binding between the protein and its receptor, it is possible to identify whether the obtained compound is an agonist or antagonist of the receptor. Also, the compound may be a candidate of a molecule that can inhibit the interaction between the protein and its associated proteins (including a receptor) in vivo. Such compounds can be used for developing drugs for precaution or cures of a disease with which the protein is associated.

[0111] Secretory proteins may regulate cellular conditions such as growth and differentiation. It is possible to find out a novel factor that regulates cellular conditions by adding the secretory protein of the invention to a certain kind of cell, and performing a screening by utilizing the cellular changes in growth or differentiation, or activation of a particular gene.

[0112] The screening can be performed, for example, as follows. First, the protein of the invention is expressed and purified in a recombinant form. Then, the purified protein is added to a various kind of cell lines or primary cultured cells, and the change in the cell growth and differentiation is monitored. The induction of a particular gene that is known to be involved in a certain cellular change is detected by the amounts of mRNA and protein. Alternatively, the amount of an intracellular molecule (low-molecular-weight compounds, etc.) that is changed by the function of a gene product (protein) that is known to function in a certain cellular change is used for the detection.

[0113] Once the screening reveals that the protein of the invention can regulate cellular conditions or the functions, it is possible to apply the protein as a pharmaceutical and diagnostic medicine for associated diseases by itself or by

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altering a part of it into an appropriate composition.

[0114] As is above described for membrane proteins, the secretory protein provided by the invention may be used to explore a novel ligand-receptor interaction using a screening based on the binding activity to a known ligand or receptor. A similar method can be used to identify an agonist or antagonist. The resulting compounds obtained by the methods can be a candidate of a compound that can inhibit the interaction between the protein of the invention and an interacting molecule (including a receptor). The compounds may be able to use as a preventive, therapeutic, and diagnostic medicine for the diseases, in which the protein may play a certain role.

[0115] Proteins associated with signal transduction or transcription may be a factor that affects a certain protein or gene in response to intracellular/extracellular stimuli. It is possible to find out a novel factor that can affect a protein or gene by expressing the protein provided by the invention in a certain types of cells, and performing a screening utilizing the activation of a certain intracellular protein or gene.

[0116] The screening may be performed as follows. First, a transformed cell line expressing the protein is obtained. Then, the transformed cell line and the untransformed original cell line are compared for the changes in the expression of a certain gene by detecting the amount of its mRNA or protein. Alternatively, the amount of an intracellular molecule (low molecular weight compounds) that is changed by the function of a certain gene product (protein) may be used for the detection. Furthermore, the change of the expression of a certain gene can be detected by introducing a fusion gene that comprises a regulatory region of the gene and a marker gene (luciferase, beta-galactosidase, etc.) into a cell, expressing the protein provided by the invention into the cell, and estimating the activity of a marker gene product (protein).

[0117] If the protein or gene of the invention is associated with diseases, it is possible to screen a gene or compound that can regulate its expression and/or activity either directly or indirectly by utilizing the protein of the present invention.

[0118] For example, the protein of the invention is expressed and purified as a recombinant protein. Then, the protein or gene that interacts with the protein of the invention is purified, and screened based on the binding. Alternatively, the screening can be performed by adding with a compound of a candidate of the inhibitor added in advance and monitoring the change of binding activity. In another method, a transcription regulatory region locating in the 5'-upstream of the gene encoding the protein of the invention that is capable of regulating the expression of other genes is obtained, and fused with a marker gene. The fusion is introduced into a cell, and the cell is added with compounds to explore a regulatory factor of the expression of the said gene.

[0119] The compound obtained by the screening can be used for developing pharmaceutical and diagnostic medicines for the diseases with which the protein of the present invention is associated. Similarly, if the regulatory factor obtained in the screening is turn out to be a protein, compounds that can newly affect the expression or activity of the protein may be used as a medicine for the diseases with which the protein of the invention is associated.

[0120] If the protein of the invention has an enzymatic activity, regardless as to whether it is a secretory protein, membrane protein, or proteins associated with signal transduction, glycoprotein, transcription, or diseases, a screening may be performed by adding a compound to the protein of the invention and monitoring the change of the compound. The enzymatic activity may also be utilized to screen a compound that can inhibit the activity of the protein.

[0121] In a screening given as an example, the protein of the invention is expressed and the recombinant protein is purified. Then, compounds are contacted with the purified protein, and the amount of the compound and the reaction products is examined. Alternatively, compounds that are candidates of an inhibitor are pretreated, then a compound (substrate) that can react with the purified protein is added, and the amount of the substrate and the reaction products is examined.

[0122] The compounds obtained in the screening may be used as a medicine for diseases with which the protein of the invention is associated. Also they can be applied for tests that examine whether the protein of the invention functions normally *in vivo*.

[0123] Whether the secretory protein, membrane protein, signal transduction-associated protein, glycoprotein-associated protein, or transcription-associated protein of the present invention is a novel protein associated with diseases or not is determined in another method than described above, by obtaining a specific antibody against the protein of the invention, and examining the relationship between the expression or activity of the protein and a certain disease. In an alternative way, it may be analyzed referred to the methods in "Molecular Diagnosis of Genetic Diseases" (Elles R. edit, (1996) in the series of "Method in Molecular Biology" (Humana Press).

[0124] Proteins associated with diseases are targets of screening as mentioned, and thus are very useful in developing drugs which regulate their expression and activity. Also, the proteins are useful in the medicinal industry as a diagnostic marker of the associated disease or a target of gene therapy.

[0125] Compounds isolated as mentioned above can be administered patients as it is, or after formulated into a pharmaceutical composition according to the known methods. For example, a pharmaceutically acceptable carrier or vehicle, specifically sterilized water, saline, plant oil, emulsifier, or suspending agent can be mixed with the compounds appropriately. The pharmaceutical compositions can be administered to patients by a method known to those skilled in the art, such as intraarterial, intravenous, or subcutaneous injections. The dosage may vary depending on the weight

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or age of a patient, or the method of administration, but those skilled in the art can choose an appropriate dosage properly. If the compound is encoded by DNA, the DNA can be cloned into a vector for gene therapy, and used for gene therapy. The dosage of the DNA and the method of its administration may vary depending on the weight or age of a patient, or the symptoms, but those skilled in the art can choose properly.

[0126] The present invention further relates to databases comprising at least a sequence of polynucleotide and/or protein, or a medium recorded in such databases, selected from the sequence data of the nucleotide and/or the amino acids indicated in Table 350 and Table 351.

The term "database" means a set of accumulated information as machine-searchable and readable information of nucleotide sequence. The databases of the present invention comprise at least one of the novel nucleotide sequences of polynucleotides provided by the present invention. The databases of the present invention can consist of only the sequence data of the novel polynucleotides provided by the present invention or can comprise other information on nucleotide sequences of known full-length cDNAs or ESTs. The databases of the present invention can be comprised of not only the information on the nucleotide sequences but also the information on the gene functions revealed by the present invention. Additional information such as names of DNA clones carrying the full-length cDNAs can be recorded or linked together with the sequence data in the databases.

[0127] The database of the present invention is useful for gaining complete gene sequence information from partial sequence information of a gene of interest. The database of the present invention comprises nucleotide sequence information of full-length cDNAs. Consequently, by comparing the information in this database with the nucleotide sequence of a partial gene fragment yielded by differential display method or subtraction method, the information on the full-length nucleotide sequence of interest can be gained from the sequence of the partial fragment as a starting clue.

[0128] The sequence information of the full-length cDNAs constituting the database of the present invention contains not only the information on the complete sequences but also extra information on expression frequency of the genes as well as homology of the genes to known genes and known proteins. Thus the extra information facilitates rapid functional analyses of partial gene fragments. Further, the information on human genes is accumulated in the database of the present invention, and therefore, the database is useful for isolating a human homologue of a gene originating from other species. The human homologue can be isolated based on the nucleotide sequence of the gene from the original species.

[0129] At present, information on a wide variety of gene fragments can be obtained by differential display method and subtraction method. In general, these gene fragments are utilized as tools for isolating the full-length sequences thereof. When the gene fragment corresponds to an already-known gene, the full-length sequence is easily obtained by comparing the partial sequence with the information in known databases. However, when there exists no information corresponding to the partial sequence of interest in the known databases, cDNA cloning should be carried out for the full-length cDNA. It is often difficult to obtain the full-length nucleotide sequence using the partial sequence information as an initial clue. If the full-length of the gene is not available, the amino acid sequence of the protein encoded by the gene remains unidentified. Thus the database of the present invention can contribute to the identification of full-length cDNAs corresponding to gene fragments, which cannot be revealed by using databases of known genes.

[0130] The present invention has provided 5602 novel full-length cDNA clones, and primers for synthesizing the cDNA. As has not yet proceeded the isolation of full-length cDNA within the human, the invention has great significance. The full-length cDNA clones contain the translation initiation site, and thus provide a useful information for analysis of protein functions.

[0131] The cDNA clones are assumed to encode proteins such as secretory proteins, membrane proteins, signal transduction-associated protein, glycoprotein-associated protein, or transcription-associated protein, etc., which have important functions in vivo, and also predicted to be associated with many diseases. The genes and proteins associated with diseases are useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as a target of gene therapy.

[0132] The invention is illustrated more specifically with reference to the following examples, but is not to be construed as being limited thereto.

EXAMPLE 1

Construction of a cDNA library by the oligo-capping method.

[0133] The NT-2 neuron progenitor cells (Stratagene), a teratocarcinoma cell line from human embryo testis, which can differentiate into neurons by the treatment with retinoic acid were used.

The NT-2 cells were cultured according to the manufacturer's instructions as follows.

(1) NT-2 cells were cultured without induction by retinoic acid treatment (NT2RM1, NT2RM2, NT2RM4).

(2) After cultured, NT-2 cells were induced by adding retinoic acid, and then were cultured for 48 hours (NT2RP1).

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(3) After cultured, NT-2 cells were induced by adding retinoic acid, and then were cultured for 2 weeks (NT2RP2, NT2RP3, NT2RP4, NT2RP5).

[0134] Also, the human neuroblastoma cell line SK-N-MC (ATCC HTB-10) (SKNMC1), and human retinoblastoma cell line Y79 (ATCC HTB-18) (Y79AA1) were cultured according to the culture conditions described in the ATCC catalogue (http://www.atcc.org/). The cells were harvested separately, and mRNA was extracted from each cell by the method described in the literature (Molecular Cloning 2nd edition. (1989) Sambrook J., Fritsch, E.F., and Maniatis T., Cold Spring Harbor Laboratory Press). Furthermore, poly(A)$^+$RNA was purified from the mRNA using oligo-dT cellulose.

[0135] Similarly, human placenta (PLACE1, PLACE2, PLACE3, PLACE4), human ovary cancer tissue (OVARC1), tissues from human embryo at 10 weeks, which is enriched with head (HEMBA1), or body (HEMBB1), human mammary gland (MAMMA1), human thyroid gland (THYRO1), and primary cultured cells of human blood vessel endothelium (VESEN1) were used to extract mRNA by the method described in the literature (Molecular Cloning 2nd edition. (1989) Sambrook J., Fritsch, E.F., and Maniatis T., Cold Spring Harbor Laboratory Press). Furthermore, poly(A)$^+$RNA was purified from the mRNA using oligo-dT cellulose.

[0136] Each poly(A)$^+$RNA was used to construct a cDNA library by the oligo-capping method (Maruyama M. and Sugano S. (1994) Gene, 138: 171-174). Using the Oligo-cap linker (SEQ ID NO: 10464) and the Oligo-dT primer (SEQ ID NO: 10465), bacterial alkaline phosphatase (BAP) treatment, tobacco acid phosphatase (TAP) treatment, RNA ligation, the first strand cDNA synthesis, and removal of RNA were performed as described in the reference (Suzuki and Kanno (1996) Protein Nucleic acid and Enzyme, 41: 197-201; Suzuki Y. et al. (1997) Gene, 200: 149-156). Next, 5'- and 3'-PCR primers (SEQ ID NO: 10466, and 10467, respectively) were used for performing PCR to convert the cDNA into double stranded cDNA, which was then digested with SfiI. Then, the DraIII-cleaved pUC19FL3 vector (Figure 1; for NT2RM1, and NT2RP1), or the DraIII-cleaved pME18SFL3 (Figure 1) (GenBank AB009864, expression vector; for NT2RM2, NT2RM4, NT2RP2, NT2RP3, NT2RP4, NT2RP5, SKNMC1, Y79AA1, PLACE1, PLACE2, PLACE3, PLACE4, OVARC1, HEMBA1, HEMBB1, MAMMA1, THYRO1, and VESEN1) was used for cloning the cDNA in a unidirectional manner, and cDNA libraries were obtained. The nucleotide sequence of the 5'- and 3'- ends of the cDNA clones was analyzed with a DNA sequencer (ABI PRISM 377, PE Biosystems) after sequencing reactions were performed with the DNA sequencing reagents (Dye Terminator Cycle Sequencing FS Ready Reaction Kit, dRhodamine Terminator Cycle Sequencing FS Ready Reaction Kit, or BigDye Terminator Cycle Sequencing FS Ready Reaction Kit, PE Biosystems), according to the instructions. The data were compiled into a database.

[0137] The full-length-enriched cDNA libraries except those for NT2RM1 and NT2RP1 were constructed using eukaryotic expression vector pME18SFL3. The vector contains SRα promoter and SV40 small t intron in the upstream of the cloning site, and SV40 polyA added signal sequence site in the downstream. As the cloning site of pME18SFL3 has asymmetrical DraIII sites, and the ends of cDNA fragments contain SfiI sites complementary to the DraIII sites, the cloned cDNA fragments can be inserted into the downstream of the SRα promoter unidirectionally. Therefore, clones containing full-length cDNA can be expressed transiently by introducing the obtained plasmid directly into COS cells. Thus, the clones can be analyzed very easily in terms of the proteins that are the gene products of the clones, or in terms of the biological activities of the proteins.

[0138] Herein, the cDNA libraries and the name of each clone are related as shown in Table 3. Therein, "xxxxxx" represents the clone number of six digits. Thus, the sequences are named by the library name, the clone number plus F- for the 5'-end, or R- for the 3'-end.

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Table 3

library: clone	5'-end sequence	3'-end sequence
NT2RM1:		
NT2RM1xxxxxx	F-NT2RM1xxxxxx	
NT2RP1:		
NT2RP1xxxxxx	F-NT2RP1xxxxxx	
NT2RM2:		
NT2RM2xxxxxx	F-NT2RM2xxxxxx	R-NT2RM2xxxxxx
NT2RM4:		
NT2RM4xxxxxx	F-NT2RM4xxxxxx	R-NT2RM4xxxxxx

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NT2RP2:		
NT2RP2xxxxxx	F-NT2RP2xxxxxx	R-NT2RP2xxxxxx
NT2RP3:		
NT2RP3xxxxxx	F-NT2RP3xxxxxx	R-NT2RP3xxxxxx
NT2RP4:		
NT2RP4xxxxxx	F-NT2RP4xxxxxx	R-NT2RP4xxxxxx
NT2RP5:		
NT2RP5xxxxxx	F-NT2RP5xxxxxx	R-NT2RP5xxxxxx
SKNMC1:		
SKNMC1xxxxxx	F-SKNMC1xxxxxx	R-SKNMC1xxxxxx
Y79AA1:		
Y79AA1xxxxxx	F-Y79AA1xxxxxx	R-Y79AA1xxxxxx
PLACE1:		
PLACE1xxxxxx	F-PLACE1xxxxxx	R-PLACE1xxxxxx
PLACE2:		
PLACE2xxxxxx	F-PLACE2xxxxxx	R-PLACE2xxxxxx
PLACE3:		
PLACE3xxxxxx	F-PLACE3xxxxxx	R-PLACE3xxxxxx
PLACE4:		
PLACE4xxxxxx	F-PLACE4xxxxxx	R-PLACE4xxxxxx
OVARC1:		
OVARC1xxxxxx	F-OVARC1xxxxxx	R-OVARC1xxxxxx
HEMBA1:		
HEMBA1xxxxxx	F-HEMBA1xxxxxx	R-HEMBA1xxxxxx
HEMBB1:		
HEMBB1xxxxxx	F-HEMBB1xxxxxx	R-HEMBB1xxxxxx
MAMMA1:		
MAMMA1xxxxxx	F-MAMMA1xxxxxx	R-MAMMA1xxxxxx
THYRO1:		
THYRO1xxxxxx	F-THYRO1xxxxxx	R-THYRO1xxxxxx
VESEN1:		
VESEN1xxxxxx	F-VESEN1xxxxxx	R-VESEN1xxxxxx

EXAMPLE 2

Estimation of the fullness ratio at the 5'-ends of the clones contained in the cDNA libraries constructed by the oligo-capping method.

[0139] The fullness ratio at the 5'-end sequence of the 59,823 clones in the human cDNA libraries constructed by the oligo-capping method was determined as follows. Of all the clones whose 5'-end sequences were found in those of known human mRNA in the public database, a clone was judged to be "full-length", if it had a longer 5'-end sequence than that of the known human mRNA, or, even though the 5'-end sequence was shorter, if it contained the translation initiation codon. A clone which did not contain the translation initiation codon was judged to be "not-full-length". The fullness ratio ((the number of full-length clones)/(the number of full-length and not-full-length clones)) at the 5'-end of the cDNA clones from each library was determined by comparing with the known human mRNA. As a result, the fullness

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ratio of the 5'-ends was 63.5%. The result indicates that the fullness ratio at the 5'-end sequence was extremely high.

EXAMPLE 3

Assessment of the fullness ratio of the 5'-end of the cDNA by the ATGpr and the ESTiMateFL.

[0140] The ATGpr, developed by Salamov A.A., Nishikawa T., and Swindells M.B. in the Helix Research Institute, is a program for prediction of the translation initiation codon based on the characteristics of the sequences in the vicinity of the ATG codon. The results are shown with expectations (also described as ATGpr1 below) that an ATG is a true initiation codon (0.05-0.94) (can be described as ATGpr1). When the program was applied to the 5'-end sequences of the clones from the cDNA library that was obtained by the oligo-capping method and that had 65% fullness ratio, the sensitivity and specificity of estimation of a full-length clone (clone containing the N-terminal end of ORF) were improved to 82-83% by selecting only clones having the ATGpr1 score 0.6 or higher.

[0141] Furthermore, the program was used to assess the fullness of 18,959 clones in the human libraries obtained here, which have 5'-ends matched to a known human mRNA.

[0142] Briefly, the maximal ATGpr1 score of the clones was determined, and then their 5'-end sequence was compared with the known human mRNA to estimate whether the clone is full-length or not. The result is shown in Table 4.

[0143] Based on the knowledge that known mRNAs, in general, are highly expressed in the cell, similar estimation was performed with genes having a low number in the EST hit, which represent relatively low abundant mRNAs, and the result is shown in Table 5.

[0144] In the table, the number of full-length clones indicate that of clones containing the N-terminal end of ORF, and so does the number of not-full-length clones that of clones without the N-terminal end of ORF. The fullness ratio represents (the number of full-length clones)/(the number of full-length clones plus the number of not-full-length clones).

Table 4

The maximal ATGpr1 score and the fullness ratio of the 5'-end sequences of clones obtained from human cDNA libraries constructed by the oligo-capping method; clones having a matched 5'-end with that of a known mRNA.

maximal ATGpr1 score	number of (full-length clones plus not-full-length clones)	number of full-length clones	fullness ratio
>=0.70	11,193	9,346	83.5%
>=0.50	13,369	10,549	78.9%
>=0.30	15,489	11,340	73.2%
>=0.15	17,394	11,811	67.9%
>=0.00	18,959	12,046	63.5%

Table 5

The maximal ATGpr1 score and the fullness ratio of the 5'-end sequences of the clones obtained from human cDNA libraries constructed by the oligo-capping method; clones having 5 EST hits or less among the clones having a matched 5'-end with that of a known mRNA.

maximal ATGpr1 score	number of (full-length clones plus not-full-length clones)	number of full-length clones	fullness ratio
>=0.70	2,801	1,934	69.0%
>=0.50	3,683	2,393	65.0%
>=0.30	4,683	2,707	57.8%
>=0.15	5,559	2,890	52.0%
>=0.00	6,113	3,013	49.8%

[0145] Next, the ESTiMateFL was used for the estimation. The ESTiMateFL, developed by Nishikawa and Ota in the Helix Research Institute, is a method for the selection of a clone with high fullness ratio by comparing with the 5'-end or 3'-end sequences of ESTs in the public database.

[0146] By the method, a cDNA clone is judged to be most likely not to be full-length if there exist any ESTs which

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have longer 5'-end or 3'-end sequences than the clone. The method is systematized for high throughput analysis. A clone is judged to be full-length if the clone has a longer 5'-end sequence than ESTs in the public database. Even if a clone has a shorter 5'-end, the clone is judged to be full-length if the difference in length is within 50 bases, and otherwise judged not to be full-length, for convenience.

[0147] In case of the clones whose 5'-end sequence is matching with the known mRNA, 80% of the clones judged to be full-length by comparing with ESTs was also judged to be full-length by comparing with the known mRNA. Also, 80% of the clones judged to be not full-length by comparing with ESTs was also judged to be not full-length by comparing with the known mRNA.

[0148] The precision of the estimation by comparing with ESTs is improved with increasing number of ESTs to be compared. However, in case that a limited number of ESTs are available, the reliability becomes low. Thus, the method is effective in excluding clones with high probability of being not-full-length, from the cDNA clones that is synthesized by the oligo-capping method and that have the 5'-end sequences with about 60 % fullness ratio. In particular, the ESTiMateFL is efficiently used to estimate the fullness ratio at the 3'-end sequence of cDNA of a human unknown mRNA which has a significant number of EST deposits in the public database.

[0149] The 18,959 clones isolated from human cDNA libraries constructed by the oligo-capping method, which have the 5'-end sequence matched with a known human mRNA, were estimated by using the ATGpr and ESTiMateFL. Briefly, the 5'-end sequence of the respective clone was analyzed to obtain the maximal ATGpr1 score, and compared with the ORF of the known human mRNA that matches with it to determine whether the clone is full-length or not. Then, the 5'-end sequence of the respective clone was analyzed by the ESTiMateFL to judge whether the clone is full-length or not. Specifically, the 5'-end sequences of the 18,959 clones were compared with those of ESTs by the ESTiMateFL and the clones other than those that are not full-length were selected. Then, the selected clones were used to analyze the relationship between the ATGpr and the fullness ratio. The result was summarized in Table 6. Also, among the selected, the clones in which the number of the EST hit is not more than 5 were selected and analyzed. The result was summarized in Table 7, which represents the result of the analysis of mRNA with relatively low abundance.

[0150] Therein, the number of being full-length, the number of being not full-length, and the fullness ratio indicate the number of the clones that contain the N-terminus of the ORF, the number of the clones that do not contain the N-terminus of the ORF, and (the number of being full-length)/(the number of being full-length) plus (the number of being not full-length), respectively.

Table 6

The maximal ATGpr1 score and the fullness ratio of the 5'-end sequence in the clones isolated from human cDNA libraries constructed by the oligo-capping method, which have the 5'-end sequence matched with a known human mRNA, and also other than those being not full-length according to the comparison with ESTs.

maximal ATGpr1 score	number of (full-length clones plus not-full-length clones)	number of full-length clones	fullness ratio
>=0.70	9,068	8,349	92.1%
>=0.50	10,345	9,318	90.1%
>=0.30	11,425	9,964	87.2%
>=0.15	12,254	10,335	84.3%
>=0.00	12,785	10,484	82.0%

Table 7

Maximal ATGpr1 score and fullness ratio of the 5'-end sequence of the clones, which were isolated from the human cDNA libraries constructed by the oligo-capping method, whose 5'-end sequence is identical to a known human mRNA, in which the number of the EST hit is not more than 5.

maximal ATGpr1 score	number of (full-length clones plus not-full-length clones)	number of full-length clones	fullness ratio
>=0.70	1,959	1,510	77.1%
>=0.50	2,469	1,821	73.8%
>=0.30	2,975	2,046	68.8%
>=0.15	3,368	2,164	64.3%

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Table 7 (continued)

Maximal ATGpr1 score and fullness ratio of the 5'-end sequence of the clones, which were isolated from the human cDNA libraries constructed by the oligo-capping method, whose 5'-end sequence is identical to a known human mRNA, in which the number of the EST hit is not more than 5.

maximal ATGpr1 score	number of (full-length clones plus not-full-length clones)	number of full-length clones	fullness ratio
>=0.00	3,661	2,226	60.8%

[0151] The 19,226 clones, isolated from the human cDNA libraries constructed by the oligo-capping method, whose 5'-end sequence is identical to that of a known human mRNA were estimated by the ATGpr2, and the correlation between the score and the fullness ratio was estimated. Specifically, the maximal ATGpr2 score of the clones identical to a known human mRNA was determined, and then their fullness ratio was estimated by comparing the 5'-ends with ORF of known human mRNA. The result was shown in Table 8.

Table 8

Maximal ATGpr2 score and fullness ratio of the 5'-end sequence of the clones, which are isolated from the human cDNA libraries constructed by the oligo-capping method, whose 5'-end sequence is identical to a known human mRNA.

maximal ATGpr2 score	number of (full-length clones plus not-full-length clones)	number of full-length clones	fullness ratio
>=0.30	10,748	8,031	74.7%
>=0.15	16,383	11,226	68.5%
>=0.00	19,226	12,285	63.9%

[0152] According to the above results, it was found that, in case of using clones isolated from human cDNA libraries constructed by the oligo-capping method, the fullness ratio of the clones that have low score in the ATGpr can be improved by estimating their 5'-end sequence using the combination of the ATGpr and the ESTiMateFL. Therefore, the method was applied to select a cDNA clone with high fullness ratio.

EXAMPLE 4

Clustering of the 5'-end and 3'-end sequences of cDNA clones.

[0153] The 5'-end and 3'-end sequences of cDNA clones were obtained, and clustered separately. The single pass data of the nucleotide sequence of the 5'-end and 3'-end was subject to the BLAST search between the sequence data of all the clones synthesized in example 1, and the clones considered to be originating from the same gene were put together into a group. If the 5'-end of a clone contains the consensus sequence of 300 bases or more with identity 95% or more, or the 3'-end contains the consensus sequence of 200 bases or more and having identity 90% or more, the clones were put in the same group.

[0154] The groups of the 5'-end sequence and the 3'-end sequence were further clustered so as that the groups from the same clone can be in the same group (cluster).

EXAMPLE 5

Characterization of the cloned sequence.

[0155] The data of the 5'-end sequence of the cloned sequence was characterized by the following way:

(1) examining whether it is identical to those of mRNA from human and other species (including authorized sequences) and human EST by the BLAST homology search of the GenBank,
(2) examining whether it has longer 5'-end than those of human mRNA and human EST,
(3) determining the scores in the ATGpr1 and ATGpr2 programs of all the initiation codons in the 5'-end sequence, and

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(4) determining the number of the human EST clone(s) that is judged to be identical by the BLAST homology search of the GenBank.

[0156] The data of the 3'-end sequence of the cloned sequence was characterized by the above (1) and (4).

[0157] These characterized data were used for the final selection of the clones.

EXAMPLE 6

Identity to the human mRNA and human EST, and comparison of the length of the 5'-end.

[0158] The 5'-end and 3'-end sequences of the cloned sequence was judged to be identical to those of mRNA from human or other species when the sequence to compare has the length of 200 bases or longer, and the obtained homology is 94% or more. The 5'-end and 3'-end sequences of the cloned sequence was judged to be identical to those of human EST when the sequence to compare has the length of 200 bases or longer, and the obtained homology is 90% or more.

[0159] The sequence of the clone was judged to be full-length in comparison with human mRNA when the sequence has longer 5'-end, or it contains the translation initiation site. The sequence of the clone was judged to be full-length in comparison with human EST in the database when the sequence has longer 5'-end, or while it has shorter end, the difference in length between the two sequences is 50 bases or less. The other clones were judged to be not full-length.

EXAMPLE 7

Prediction of the fullness ratio by the ATGpr.

[0160] The score in the ATGpr1 is the expectation to be full-length based on calculations, and the higher score reflects the higher probability to be full-length as shown in Example 3. The maximal ATGpr1 score and the maximal ATGpr2 score represent the score obtained with all the initiation codons contained in the 5'-end sequence of the cloned sequence, and were used for the characterization.

EXAMPLE 8

Prediction of the novelty using the number of the identical ESTs by the homology search.

[0161] For both the 5'-end and 3'-end sequences of the clones, the number of the identical ESTs was determined by the homology search on the GenBank. Human ESTs were judged to be identical when the EST has a sequence of 200 nucleotides or more with 90% or more matching with the 5'-end sequence. The number of the identical ESTs were used for characterization and as an index of novelty. The clone having not identical sequence at the 5'-end and 3'-end sequences to those of mRNA as well as those of ESTs is a gene encoding a novel protein. Similarly, a clone having either the 5'-end or the 3'-end sequences, which has low number of the identical ESTs, is judged to be a gene encoding a novel protein.

EXAMPLE 9

Characterization of clusters.

[0162] The clusters of the groups of the 5'-end and 3'-end sequences were characterized according to the following criteria.

(1) Whether it is identical to the mRNA sequences from human or other species (including authorized sequences), or human ESTs by the BLAST search of the GenBank.
A cluster containing at least one sequence of all the 5'-end and 3'-end sequences, which is identical to one of the mRNA sequences, was regarded to be the same cluster of the mRNA sequence.
(2) Whether it has longer 5'-end than human mRNA sequence and human ESTs.
When all the 5'-end sequences contained in a cluster are judged to be not full-length compared with the mRNA sequences and human ESTs, the cluster was regarded as being not full-length.
(3) The scores in the ATGpr1 and ATGpr2 using all the initiation codons contained in the 5'-end sequences.
The maximal ATGpr1 score among those of all the 5'-end sequences in a cluster was determined as the ATGpr1 score of the cluster. The ATGpr2 score of the cluster was also determined in the same way.

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(4) The number of the identical human ESTs determined by the BLAST search of the GenBank.

[0163] The maximum number was determined in the numbers of ESTs identical to each of 5'-end sequences contained in a cluster. The number of the ESTs identical to the 5'-end sequences in the cluster was defined as the maximum number. The number of the ESTs identical to the 3'-end sequences in a cluster was determined in the same way.

EXAMPLE 10

Methods for selection of the clusters by the characteristics.

[0164] Data obtained by the characterization described above was used to discard the clusters that are identical to any mRNA sequence from human and other species (including authorized sequences), or those clusters that are not full-length. From the rest of the clusters, the clusters that fulfill any of the following conditions were selected.

(a) A cluster in which the number of the identical ESTs for the 5'-end sequence is 20 or less, and the ATGpr1 score exceeds 0.3.
(b) A cluster having the ATGpr1 score not more than 0.3, in which the number of the identical ESTs for both the 5'-end sequence and the 3'-end sequence is 5 or less, and multiple clones are contained.
(c) A cluster having the ATGpr1 score not more than 0.3, in which the number of the identical ESTs for the 5'-end sequence is 0, and the number of the identical ESTs for the 3'-end sequence is not less than 1.
(d) A cluster having the ATGpr1 score not more than 0.3, in which the number of the identical ESTs for the 5'-end sequence is not less than 1 and not more than 5, and the number of the identical ESTs for the 3'-end sequence is 0.

[0165] The clusters selected by (a) contain at least one clone that is novel and having high fullness ratio. The clusters selected by (b), (c), and (d) contain at least one clone that is novel and having low fullness ratio, but is still full-length.

EXAMPLE 11

Methods for selection of clones from clusters.

[0166] In the clusters comprising a single clone, the clone was selected.
[0167] In the clusters comprising multiple clones, in which multiple clones have the ATGpr1 score higher than 0.3, a clone with the highest score was selected.
[0168] In the clusters comprising multiple clones, in which multiple clones have the ATGpr1 score not more than 0.3, a clone with the highest ATGpr2 score was selected, if the score was higher than 0.3.
[0169] In the clusters comprising multiple clones, in which the clones have the scores not more than 0.3 in both the ATGpr1 and the ATGpr2, a clone with the highest scores in both the ATGpr1 and ATGpr2 was selected.
[0170] In the clusters comprising multiple clones, in which the above selection by the ATGpr score was not applicable, selected was a clone having longer 5'-end by assembling the 5'-end sequence, 3'-end sequence, and human ESTs. For assembling, the Sequencher™ (Hitachi Soft Engineering) was used. When even the selection by assembling failed, all the clones were judged to be full-length.
[0171] As a result, 3690 clones were the clones that have the maximal ATGpr1 score higher than 0.3. On the other hand, 477 clones were the clones that have the maximal ATGpr1 score not more than 0.3, and the maximal ATGpr2 score higher than 0.3. The number of the clones having the highest scores in both the ATGpr1 and ATGpr2, while the scores were not more than 0.3, were 97. The number of the clones which were not selected by the ATGpr scores, but were selected by assembling the 5'-end sequence, 3'-end sequence, and human ESTs, were 117. The clones that have the score in both the ATGpr1 and ATGpr2 not more than 0.3, but were selected because the cluster comprises a single clone, were 1166. In the clones, at least either of the 5'-end or 3'-end sequence was not identical to any of human ESTs. Some clones were selected because the cluster comprises a single clone, or by assembling, in which there is no ATG codon (9 clones: HEMBA1001960, HEMBA106569, HEMBB1001454, NT2PR2002839, NT2RP2005325, NT2RP2006323, PLACE1004506, PLACE1005526, and THYRO1001177). The sequences that do not contain the ATG codon were considered to be corresponding to the 5'-UTR. Although the clones do not have the scores in the ATGpr1 and ATGpr2, the clones were yet judged to be full-length according to the fullness ratio, as shown in Table 4, 5, 6, 7, and 8. The above clones that were finally judged to be full-length were classified into 11 groups according to the following criteria.

Group (1): 1516 clones
Among the 3690 clones having the maximal ATGpr1 score higher than 0.3, the following 1516 clones were having

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high fullness ratio and a novel clone, in which at least either of the 5'-end or 3'-end sequence, or both of them were not identical to any of human ESTs.

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Group (2): 377 clones

Among the 3690 clones, the following 377 clones were full-length, and a novel clone, in which the number of the identical human ESTs for both the 5'-end and 3'-end sequences is 1 or higher and not more than 5.

HEMBA1000156, HEMBA1000231, HEMBA1000244, HEMBA1000302, HEMBA1000523, HEMBA1000531, HEMBA1000555, HEMBA1000568, HEMBA1000971, HEMBA1001009, HEMBA1001133, HEMBA100113 7, HEMBA1001257, HEMBA1001281, HEMBA1001289, HEMBA1001310, HEMBA1001377, HEMBA10013 88, HEMBA1001413, HEMBA1001455, HEMBA1001579, HEMBA1001702, HEMBA1001781, HEMBA1001 804, HEMBA1001819, HEMBA1001864, HEMBA1001869, HEMBA1001912, HEMBA1001915, HEMBA100 2084, HEMBA1002102, HEMBA1002212, HEMBA1002495, HEMBA1002513, HEMBA1002863, HEMBA10 02935, HEMBA1002970, HEMBA1002971, HEMBA1002997, HEMBA1002999, HEMBA1003035, HEMBA1 003041, HEMBA1003433, HEMBA1003568, HEMBA1003680, HEMBA1003692, HEMBA1003804, HEMBA 1003893, HEMBA1003953, HEMBA1004097, HEMBA1004207, HEMBA1004502, HEMBA1004560, HEMB A1004638, HEMBA1004693, HEMBA1004973, HEMBA1004977, HEMBA1005223, HEMBA1005244, HEM BA1005314, HEMBA1005680, HEMBA1005737, HEMBA1005746, HEMBA1005822, HEMBA1005891, HE MBA1006445, HEMBA1006535, HEMBA1006566, HEMBA1006877, HEMBA1006936, HEMBA1007178, H EMBA1007251, HEMBA1007267, HEMBB1000030, HEMBB1000215, HEMBB1000226, HEMBB1000449, HEMBB1000789, HEMBB1000975, HEMBB1001153, HEMBB1001175, HEMBB1001234, HEMBB1001387, HEMBB1001905, HEMBB100190 6, HEMBB1002300, HEMBB1002383, HEMBB1002489, HEMBB1002607, HEMBB1002705, MAMMA1000257, MAMMA1000416, MAMMA1000831, MAMMA1000841, MAMMA1001021, MAMMA1001041, MAMMA1001105, MAMMA1001139, MAMMA1001198, MAMMA1001730, MAMMA1001837, MAMMA100219 8, MAMMA1002209, MAMMA1002219, MAMMA1002292, MAMMA1002297, MAMMA1002637, MAMMA10026 50, MAMMA1002796, MAMMA1002987, MAMMA1003135, MAMMA1003150,

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THYRO1000368, THYRO1000662, THYRO1000712, THYRO1000783, THYRO1000952, THYRO1000988 THYRO1001661, THYRO1001854, Y79AA1000037, Y79AA1000059, Y79AA1000985, Y79AA100110, 5, Y79AA1001177, Y79AA1001211, Y79AA1001281, Y79AA1001533, Y79AA1001923, Y79AA10020 83, Y79AA1002204, Y79AA1002407,

Group (3): 1797 clones

Among the 3690 clones, the following 1797 clones were full-length, and novel clones, in which the number of the identical human ESTs for the 5'-end sequence is not more than 20 (except clones in which at least either of the 5'-end or 3'-end sequence, or both of them are not identical to any of human ESTs, and clones in which the number of the identical human ESTs for both the 5'-end and 3'-end sequences is 1 or higher and not more than 5).

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PLACE1000769, PLACE1000785, PLACE1000793, PLACE1000798, PLACE100 0856, PLACE1000863, PLACE1000977, PLACE1000987, PLACE1001054, PLACE1001092, PLACE10 01168, PLACE1001185, PLACE1001238, PLACE1001294, PLACE1001304, PLACE1001351, PLACE1 001383, PLACE1001399, PLACE1001412, PLACE1001608, PLACE1001692, PLACE1001761, PLACE 1001781, PLACE1001817, PLACE1001844, PLACE1001869, PLACE1001920, PLACE1002046, PLACE1002072, PLACE1002090, PLACE1002140, PLACE1002171, PLACE1002342, PLACE1002395, PLACE1002499, PLACE1002571, PLACE1002722, PLACE1002794, PLACE100281 1, PLACE1002815, PLACE1002816, PLACE1002834, PLACE1002908, PLACE1002996, PLACE10030 27, PLACE1003092, PLACE1003100, PLACE1003136, PLACE1003176, PLACE1003200, PLACE1003 296, PLACE1003302, PLACE1003353, PLACE1003394, PLACE1003454, PLACE1003537, PLACE100 3592, PLACE1003596, PLACE1003602, PLACE1003625, PLACE1003704, PLACE1003886, PLACE10 03892, PLACE1003903, PLACE1003915, PLACE1003923, PLACE1003968, PLACE1004103, PLACE1004183, PLACE1004258, PLACE1004316, PLACE1004358, PLACE1004376, PLACE1004405, PLACE1004437, PLACE1004550, PLACE1004629, PLACE1004674, PLACE100473 6, PLACE1004777, PLACE1004814, PLACE1004902, PLACE1004930, PLACE1004969, PLACE10049 82, PLACE1005027, PLACE1005055, PLACE1005066, PLACE1005101, PLACE1005102, PLACE1005 181, PLACE1005187, PLACE1005261, PLACE1005287, PLACE1005305, PLACE1005308, PLACE100 5327, PLACE1005335, PLACE1005373, PLACE1005550, PLACE1005557, PLACE1005595, PLACE10 05603, PLACE1005623, PLACE1005630, PLACE1005698, PLACE1005727, PLACE1005739, PLACE1 005803, PLACE1005813, PLACE1005851, PLACE1005955, PLACE1006040, PLACE1006119, PLACE1006139, PLACE1006159, PLACE1006167, PLACE1006196, PLACE1006236, PLACE1006246, PLACE1006325, PLACE1006335, PLACE1006469, PLACE100648 8, PLACE1006492, PLACE1006615, PLACE1006678, PLACE1006819, PLACE1006883, PLACE10069 17, PLACE1006989, PLACE1007021, PLACE1007053, PLACE1007105, PLACE1007178, PLACE1007 238, PLACE1007239, PLACE1007243, PLACE1007282, PLACE1007367, PLACE1007386, PLACE100 7402, PLACE1007409, PLACE1007416, PLACE1007454, PLACE1007507, PLACE1007511, PLACE10 07547, PLACE1007598, PLACE1007621, PLACE1007632, PLACE1007645, PLACE1007649, PLACE1 007688, PLACE1007690, PLACE1007697, PLACE1007705, PLACE1007706, PLACE1007725, PLACE 1007730, PLACE1007746, PLACE1007846, PLACE1007858, PLACE1007908, PLACE1007954, PLAC E1007955, PLACE1007958, PLACE1007969, PLACE1007990, PLACE1008044, PLACE1008122, PLACE1008132, PLACE1008198, PLACE1008209, PLACE1008356, PLACE1008368, PLACE1008398, PLACE1008429, PLACE1008524, PLACE1008531, PLACE100856 8, PLACE1008603, PLACE1008629, PLACE1008650, PLACE1009027, PLACE1009045, PLACE10090 60, PLACE1009091, PLACE1009186, PLACE1009298, PLACE1009319, PLACE1009338, PLACE1009 444, PLACE1009468, PLACE1009476, PLACE1009571, PLACE1009581, PLACE1009596, PLACE100 9622, PLACE1009670, PLACE1009721, PLACE1009731, PLACE1009763, PLACE1009845, PLACE10 09921, PLACE1009995, PLACE1010023, PLACE1010031, PLACE1010053, PLACE1010074, PLACE1010076, PLACE1010096, PLACE1010102, PLACE1010105, PLACE1010106, PLACE1010134, PLACE1010152, PLACE101019 4, PLACE1010274, PLACE1010362, PLACE1010364, PLACE1010383, PLACE1010491, PLACE10104 92, PLACE1010522, PLACE1010529, PLACE1010599, PLACE1010622, PLACE1010630, PLACE1010 720, PLACE1010761, PLACE1010771, PLACE1010786, PLACE1010800, PLACE1010833, PLACE101 0856, PLACE1010857, PLACE1010870, PLACE1010877, PLACE1010925, PLACE1010944, PLACE10 10960, PLACE1011041, PLACE1011090, PLACE1011160, PLACE1011214, PLACE1011219, PLACE1 011221, PLACE1011263, PLACE1011291, PLACE1011310, PLACE1011332, PLACE1011371, PLACE 1011433, PLACE1011477, PLACE1011586, PLACE1011646, PLACE1011675, PLACE1011858, PLAC E1011923, PLACE2000007, PLACE2000021, PLACE2000030, PLACE2000164, PLACE2000172, PLACE2000302, PLACE2000341, PLACE2000399, PLACE2000404, PLACE2000427, PLACE3000009, PLACE300012 1, PLACE3000148, PLACE3000156, PLACE3000160, PLACE3000197, PLACE3000226, PLACE30002 42, PLACE3000339, PLACE3000353, PLACE3000413, PLACE3000477, PLACE4000009, PLACE4000 034, PLACE4000089, PLACE4000106, PLACE4000259, PLACE4000269, PLACE4000326, PLACE400 0369, PLACE4000431, PLACE4000445, PLACE4000581, PLACE4000593, PLACE4000650, PLACE40 00670, SKNMC1000046, SKNMC1000050, SKNMC1000091, THYRO1000017, THYRO1000040, THYRO1000121, THYRO1000173, THYRO1000197, THYRO1000199, THYRO1000206, THYRO1000242, THYRO100027 0, THYRO1000288, THYRO1000320, THYRO1000327, THYRO1000358, THYRO1000394, THYRO10004 01, THYRO1000488, THYRO1000502, THYRO1000569, THYRO1000570, THYRO1000585, THYRO1000 605, THYRO1000715, THYRO1000756, THYRO1000777, THYRO1000829, THYRO1000855, THYRO100 0926, THYRO1000983, THYRO1000984, THYRO1001120, THYRO1001134, THYRO1001173, THYRO10 01204,

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THYRO1001271, THYRO1001287, THYRO1001313, THYRO1001347, THYRO1001363, THYRO1 001405, THYRO1001406, THYRO1001537, THYRO1001584, THYRO1001671, THYRO1001703, THYRO 1001721, THYRO1001793,
VESEN1000122, Y79AA1000013, Y79AA1000181, Y79AA1000202, Y79AA1000214, Y79AA1000230, Y79AA1000231, Y79AA1000258, Y79AA1000313, Y79AA1000328, Y79AA1000342, Y79AA100036 8, Y79AA1000420, Y79AA1000469, Y79AA1000480, Y79AA1000539, Y79AA1000540, Y79AA10005 60, Y79AA1000574, Y79AA1000589, Y79AA1000705, Y79AA1000734, Y79AA1000748, Y79AA1000 752, Y79AA1000774, Y79AA1000782, Y79AA1000784, Y79AA1000794, Y79AA1000800, Y79AA100 0833, Y79AA1000966, Y79AA1000968, Y79AA1001023, Y79AA1001041, Y79AA1001048, Y79AA10 01077, Y79AA1001078, Y79AA1001216, Y79AA1001228, Y79AA1001236, Y79AA1001312, Y79AA1 001323, Y79AA1001394, Y79AA1001402, Y79AA1001493, Y79AA1001511, Y79AA1001548, Y79AA 1001585, Y79AA1001603, Y79AA1001647, Y79AA1001665, Y79AA1001679, Y79AA1001696, Y79A A1001705, Y79AA1001711, Y79AA1001781, Y79AA1001805, Y79AA1001827, Y79AA1001963, Y79 AA1002027, Y79AA1002089, Y79AA1002093, Y79AA1002125, Y79AA1002208, Y79AA1002209, Y7 9AA1002210, Y79AA1002234, Y79AA1002258, Y79AA1002307, Y79AA1002311, Y79AA1002351, Y 79AA1002416, Y79AA1002487,

Group (4): 453 clones

Among the 1857 clones having the maximal ATGpr1 score not more than 0.3 (including the 9 clones whose 5'-end sequence does not contain the ATG codon), the following 453 clones were judged to be full-length since their ATGpr2 score was 0.3 or higher (Table 11). The clones were novel clones, in which at least either of the 5'-end or 3'-end sequence is not identical to any of human ESTs.

HEMBA1000180, HEMBA1000280, HEMBA1000282, HEMBA1000333, HEMBA1000351, HEMBA1000357, HEMBA1000376, HEMBA1000469, HEMBA1000504, HEMBA1000519, HEMBA1000545, HEMBA100055 7, HEMBA1000575, HEMBA1000726, HEMBA1000822, HEMBA1000934, HEMBA1000943, HEMBA10009 60, HEMBA1000972, HEMBA1001020, HEMBA1001051, HEMBA1001060, HEMBA1001071, HEMBA1001 208, HEMBA1001319, HEMBA1001383, HEMBA1001411, HEMBA1001433, HEMBA1001435, HEMBA100 1478, HEMBA1001522, HEMBA1001636, HEMBA1001651, HEMBA1001658, HEMBA1001709, HEMBA10 01745, HEMBA1001791, HEMBA1001835, HEMBA1001844, HEMBA1001888, HEMBA1001940, HEMBA1 001962, HEMBA1002022, HEMBA1002185, HEMBA1002348, HEMBA1002621, HEMBA1002645, HEMBA 1002661, HEMBA1002728, HEMBA1002921, HEMBA1002924, HEMBA1002934, HEMBA1002968, HEMBA1003037, HEMBA1003071, HEMBA1003166, HEMBA1003202, HEMBA1003204, HEMBA1003220, HEMBA1003229, HEMBA1003276, HEMBA1003296, HEMBA1003373, HEMBA1003531, HEMBA100364 0, HEMBA1003856, HEMBA1003926, HEMBA1003942, HEMBA1003987, HEMBA1004024, HEMBA10042 67, HEMBA1004323, HEMBA1004433, HEMBA1004577, HEMBA1004730, HEMBA1004778, HEMBA1004 803, HEMBA1004807, HEMBA1004880, HEMBA1004900, HEMBA1004983, HEMBA1005123, HEMBA100 5241, HEMBA1005311, HEMBA1005318, HEMBA1005353, HEMBA1005374, HEMBA1005447, HEMBA10 05588, HEMBA1005593, HEMBA1005606, HEMBA1005679, HEMBA1005894, HEMBA1005911, HEMBA1 006036, HEMBA1006124, HEMBA1006253, HEMBA1006259, HEMBA1006364, HEMBA1006380, HEMBA 1006426, HEMBA1006562, HEMBA1006597, HEMBA1006639, HEMBA1006653, HEMBA1006696, HEMB A1006744, HEMBA1006824, HEMBA1006949, HEMBA1007078, HEMBA1007129, HEMBA1007147, HEM BA1007206, HEMBA1007279, HEMBA1007327,
HEMBB1000005, HEMBB1000055, HEMBB1000144, HEMBB1000258, HEMBB1000318, HEMBB1000335, HEMBB1000354, HEMBB1000374, HEMBB1000402, HEMBB1000404, HEMBB1000480, HEMBB100049 3, HEMBB1000554, HEMBB1000573, HEMBB1000649, HEMBB1000652, HEMBB1000709, HEMBB10007 49, HEMBB1000790, HEMBB1000827, HEMBB1000831, HEMBB1000893, HEMBB1001004, HEMBB1001 008, HEMBB1001047, HEMBB1001315, HEMBB1001317, HEMBB1001326, HEMBB1001367, HEMBB100 1424, HEMBB1001436, HEMBB1001458, HEMBB1001535, HEMBB1001565, HEMBB1001747, HEMBB10 01749, HEMBB1001797, HEMBB1001836, HEMBB1001863, HEMBB1001875, HEMBB1001911, HEMBB1 001922, HEMBB1001925, HEMBB1001944, HEMBB1001983, HEMBB1001996, HEMBB1001997, HEMBB 1002092, HEMBB1002247, HEMBB1002266, HEMBB1002387, HEMBB1002425, HEMBB1002458, HEMB B1002522, HEMBB1002534, HEMBB1002582, HEMBB1002596, HEMBB1002617, HEMBB1002702, MAMMA1000043, MAMMA1000092, MAMMA1000129, MAMMA1000198, MAMMA1000221, MAMMA1000307, MAMMA1000331, MAMMA1000360, MAMMA1000402, MAMMA1000414, MAMMA1000500, MAMMA100052 2, MAMMA1000576, MAMMA1000594, MAMMA1000597, MAMMA1000720, MAMMA1000775, MAMMA10007 78, MAMMA1000798, MAMMA1000862, MAMMA1000876, MAMMA1000931, MAMMA1000940, MAMMA1000 941, MAMMA1000975, MAMMA1001038, MAMMA1001186, MAMMA1001220, MAMMA1001256, MAMMA100 1274, MAMMA1001341, MAMMA1001397, MAMMA1001420, MAMMA1001547, MAMMA1001670, MAMMA10 01679, MAMMA1001711,

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MAMMA1001745, MAMMA1001760, MAMMA1001769, MAMMA1001815, MAMMA1 001907, MAMMA1002056, MAMMA1002078, MAMMA1002093, MAMMA1002125, MAMMA1002132, MAMMA 1002145, MAMMA1002250, MAMMA1002311, MAMMA1002411, MAMMA1002498, MAMMA1002571, MAMM A1002701, MAMMA1002727, MAMMA1002728, MAMMA1002746, MAMMA1002764, MAMMA1002765, MAM MA1002820, MAMMA1002830, MAMMA1002909, MAMMA1002941, MAMMA1002973, MAMMA1003004, MA MMA1003007, MAMMA1003039, MAMMA1003089,

NT2RM4000086, NT2RM4000265, NT2RM4000414, NT2RM4000779, NT2RM4000855, NT2RM4001160, NT2RM4001313, NT2RM4001437, NT2RM4001754, NT2RM4001953, NT2RM4001984, NT2RP200007 7, NT2RP2000183, NT2RP2000420, NT2RP2000678, NT2RP2000715, NT2RP2000842, NT2RP20009 70, NT2RP2001149, NT2RP2001226, NT2RP2001295, NT2RP2001347, NT2RP2001569, NT2RP2001 663, NT2RP2001936, NT2RP2002041, NT2RP2002172, NT2RP2002219, NT2RP2002316, NT2RP200 2546, NT2RP2002591, NT2RP2002643, NT2RP2002741, NT2RP2002750, NT2RP2002778, NT2RP20 02857, NT2RP2003000, NT2RP2003073, NT2RP2003237, NT2RP2003394, NT2RP2003517, NT2RP2 003668, NT2RP2003988, NT2RP2004232, NT2RP2004523, NT2RP2004736, NT2RP2004767, NT2RP 2004775, NT2RP2004961, NT2RP2004962, NT2RP2004982, NT2RP2005407, NT2RP2005726, NT2R P2006258, NT2RP2006261, NT2RP2006454, NT2RP3000055, NT2RP3000233, NT2RP3000341, NT2 RP3000418, NT2RP3000451, NT2RP3000561, NT2RP3000582, NT2RP3001281, NT2RP3001339, NT 2RP3001340, NT2RP3001383, NT2RP3001432, NT2RP3001580, NT2RP3001589, NT2RP3002004, N T2RP3002173, NT2RP3003133, NT2RP3003346, NT2RP3003403, NT2RP3003576, NT2RP3003625, NT2RP3003665, NT2RP3003800, NT2RP3003828, NT2RP3004070, NT2RP3004470, NT2RP4000023, NT2RP4000035, NT2RP4000102, NT2RP4000167, NT2RP4000214, NT2RP4000218, NT2RP400042 4, NT2RP4000915, NT2RP4002075,

OVARC1000085, OVARC1000092, OVARC1000145, OVARC1000414, OVARC1000496, OVARC1000526, OVARC1000948, OVARC1001011, OVARC1001600, OVARC1001805, OVARC1001813, OVARC100184 6,

PLACE1000540, PLACE1000599, PLACE1001088, PLACE1001377, PLACE1001440, PLACE1001517, PLACE1001672, PLACE1001756, PLACE1002157, PLACE1002205, PLACE1002259, PLACE100239 9, PLACE1002477, PLACE1002583, PLACE1002968, PLACE1003238, PLACE1003566, PLACE10035 93, PLACE1003618, PLACE1004274, PLACE1004716, PLACE1004773, PLACE1004815, PLACE1004 979, PLACE1005052, PLACE1005086, PLACE1005128, PLACE1005176, PLACE1005467, PLACE100 5639, PLACE1005850, PLACE1006003, PLACE1006017, PLACE1006288, PLACE1006371, PLACE10 06629, PLACE1007478, PLACE1008330, PLACE1008584, PLACE1008851, PLACE1008941, PLACE1 009039, PLACE1009493, PLACE1009539, PLACE1009637, PLACE1009947, PLACE1010231, PLACE 1010562, PLACE1010579, PLACE1010739, PLACE1010802, PLACE1010896, PLACE1011032, PLAC E1011185, PLACE1011452, PLACE1011465, PLACE1011520, PLACE1011567, PLACE1011719, PLA CE2000011, PLACE2000017, PLACE2000061, PLACE2000187, PLACE2000216, PLACE2000335, PL ACE2000347, PLACE2000366, PLACE2000394, PLACE2000398, PLACE2000425, PLACE2000450, P LACE2000477, PLACE3000119, PLACE3000207, PLACE3000230, PLACE3000271, PLACE3000373, PLACE3000399, PLACE3000401, PLACE3000406, PLACE4000247, PLACE4000320, PLACE4000367, PLACE4000401,

THYRO1000111, THYRO1000187, THYRO1000484, THYRO1000596, THYRO1000625, THYRO1000815, THYRO1000865, THYRO1001003, THYRO1001031, THYRO1001133, THYRO1001401, THYRO100142 6, THYRO1001434, THYRO1001559, THYRO1001570, THYRO1001706, THYRO1001746, THYRO10017 72, THYRO1001907, Y79AA1000033, Y79AA1000346, Y79AA1000805, Y79AA1001692, Y79AA1002 220,

Group (5): 24 clones

The following 24 clones having low score in the ATGpr1 were judged to be full-length since their ATGpr2 score was 0.3 or higher (Table 11). The clones were novel clones, in which the number of the identical human ESTs for both the 5'-end and 3'-end sequences is 1 or higher and not more than 5.

HEMBA1000622, HEMBA1000749, HEMBA1000876, HEMBA1001226, HEMBA1001391, HEMBA1002742, HEMBA1003908, HEMBA1004000, HEMBB1000336, MAMMA1000356, MAMMA1000883, MAMMA100159 0, NT2RP2000289, NT2RP2001467, PLACE1002853, PLACE1003420, PLACE1004836, PLACE10049 13, PLACE1006795, PLACE1008181, PLACE1008715, PLACE4000344, THYRO1000129, THYRO1001 321,

Group (6): 65 clones

The following 65 clones having low scores in both the ATGpr1 and ATGpr2 (Table 11) were judged to be full-length, since both scores were still the maximum in a cluster compared with those of the other clones(at least 2 clones or more) in the same cluster. The clones were novel clones, in which at least either of the 5'-end or 3'-end sequence is not identical to any of human ESTs.

HEMBA1000604, HEMBA1000673, HEMBA1001024, HEMBA1001026, HEMBA1001734, HEMBA1001784,

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HEMBA1001808, HEMBA1003902, HEMBA1004164, HEMBA1004909, HEMBA1005232, HEMBA100557 7, HEMBA1006461, HEMBA1006695, HEMBB1001119, HEMBB1001337, HEMBB1001536, HEMBB10018 68, HEMBB1002045, HEMBB1002579, MAMMA1000444, MAMMA1000761, MAMMA1000943, MAMMA1001 820, MAMMA1002360,
NT2RM4000366, NT2RM4001856, NT2RM4002390, NT2RP2000108, NT2RP2000257, NT2RP2001506, NT2RP2002047, NT2RP2002066, NT2RP2002475, NT2RP2004400, NT2RP2004587, NT2RP200528 9, NT2RP2005694, NT2RP3001898, NT2RP3003264, NT2RP3003433, NT2RP3003842, OVARC10012 40, PLACE1001323, PLACE1002227, PLACE1002500, PLACE1002604, PLACE1002772, PLACE1003 478, PLACE1004681, PLACE1005108, PLACE1005932, PLACE1006318, PLACE1006368, PLACE100 6506, PLACE1006904, PLACE1007557, PLACE1007877, PLACE1009048, PLACE1011109, PLACE10 11643, PLACE4000548, THYRO1000279, Y79AA1000410, Y79AA1002103,

Group (7): 32 clones

The following 32 clones having low scores in both the ATGpr1 and ATGpr2 (Table 11) were judged to be full-length, since both scores were still the maximum in a cluster compared with those of the other clones(at least 2 clones or more) in the same cluster. The clones were novel clones, in which the number of the identical human ESTs for both the 5'-end and 3'-end sequences is 1 or higher and not more than 5.

HEMBA1000251, HEMBA1001803, HEMBA1001918, HEMBA1002257, HEMBA1003064, HEMBA1003714, HEMBA1004405, HEMBA1005508, HEMBB1000054, HEMBB1001142, MAMMA1000175, MAMMA100116 2, MAMMA1002972, NT2RM4000425, NT2RP2004512, NT2RP2005531, NT2RP2005942, NT2RP20065 54, NT2RP3001007, NT2RP3001318, OVARC1000017, OVARC1000068, OVARC1000486, PLACE1001 705, PLACE1002319, PLACE1007743, PLACE1007829, PLACE1008630, PLACE1009925, PLACE101 1492, PLACE1011749, THYRO1000793,

The following 117 clones, selected by assembling the sequence of the other clones in the same cluster and human ESTs, have high fullness ratio. The clones were classified into the following group (8) and (9).

HEMBA1001323, HEMBA1001330, HEMBA1001712, HEMBA1001820, HEMBA1002204, HEMBA1002349, HEMBA1002538, HEMBA1003309, HEMBA1003939, HEMBA1004015, HEMBA1004295, HEMBA100467 2, HEMBA1004865, HEMBA1005251, HEMBA1006158, HEMBA1006676, HEMBA1006779, HEMBA10072 88, HEMBB1000218, HEMBB1000272, HEMBB1000399, HEMBB1000491, HEMBB1000996, HEMBB1001 114, HEMBB1001850, HEMBB1002015, MAMMA1000287, MAMMA1001683, MAMMA1001686, MAMMA100 2612, NT2RM2000609, NT2RM4002438, NT2RM4002567, NT2RP2000270, NT2RP2000758, NT2RP2001290, NT2RP2001526, NT2RP2002124, NT2RP2002736, NT2RP2002753, NT2RP2003456, NT2RP200372 7, NT2RP2003871, NT2RP2003968, NT2RP2004321, NT2RP2004412, NT2RP2004580, NT2RP20052 93, NT2RP2005476, NT2RP2005753, NT2RP2005815, NT2RP2005841, NT2RP2005857, NT2RP2006 393, NT2RP2006467, NT2RP3000109, NT2RP3000449, NT2RP3001245, NT2RP3001634, NT2RP300 2056, NT2RP3002810, NT2RP3002955, NT2RP3003032, NT2RP3003138, NT2RP3003500, NT2RP30 03819, NT2RP4000078, NT2RP4000515, NT2RP4000517, NT2RP4001407, NT2RP4001889, NT2RP4 002905, OVARC1000071, OVARC1001883, PLACE1000292, PLACE1001007, PLACE1001395, PLACE1001691, PLACE1001746, PLACE1001748, PLACE1001845, PLACE1002066, PLACE1003373, PLACE100390 0, PLACE1004118, PLACE1004256, PLACE1004284, PLACE1004336, PLACE1004506, PLACE10049 34, PLACE1005077, PLACE1005111, PLACE1005409, PLACE1005730, PLACE1006076, PLACE1006 360, PLACE1006470, PLACE1006760, PLACE1006867, PLACE1007045, PLACE1007111, PLACE100 7807, PLACE1008080, PLACE1008244, PLACE1008369, PLACE1008405, PLACE1008426, PLACE10 08621, PLACE1009020, PLACE1009621, PLACE1010089, PLACE1010270, PLACE3000276, THYRO1 000805, THYRO1001365, THYRO1001673, Y79AA1001848,

Group (8): 36 clones

Among the 117 clones described above, the following 36 clones were novel clones, in which at least either of the 5'-end or 3'-end sequence, or both of them were not identical to any of human ESTs.

HEMBA1001330, HEMBA1001712, HEMBA1001820, HEMBA1002204, HEMBA1002349, HEMBA1003939, HEMBA1004295, HEMBA1004865, HEMBA1006779, HEMBB1000218, HEMBB1000491, HEMBB100099 6, HEMBB1001114, MAMMA1000287, MAMMA1001686, MAMMA1002612, NT2RP2002736, NT2RP20037 27, NT2RP2004580, NT2RP2005841, NT2RP2006393, PLACE1002066, PLACE1003373, PLACE1003 900, PLACE1004118, PLACE1004336, PLACE1004506, PLACE1004934, PLACE1005409, PLACE100 5730, PLACE1006470, PLACE1008080, PLACE3000276, THYRO1000805, THYRO1001365, THYRO10 01673,

Group (9): 81 clones

Among the 117 clones described above, the following 81 clones were the clones in which the number of the identical

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human ESTs for the 5'-end sequence is not more than 20 (except clones in which at least either of the 5'-end or 3'-end sequence, or both of them are not identical to any of human ESTs, and clones in which the number of the identical human ESTs for both the 5'-end and 3'-end sequences is 1 or higher and not more than 5).

HEMBA1001323, HEMBA1002538, HEMBA1003309, HEMBA1004015, HEMBA1004672, HEMBA1005251, HEMBA1006158, HEMBA1006676, HEMBA1007288, HEMBB1000272, HEMBB1000399, HEMBB100185 0, HEMBB1002015, MAMMA1001683, NT2RM2000609, NT2RM4002438, NT2RM4002567, NT2RP20002 70, NT2RP2000758, NT2RP2001290, NT2RP2001526, NT2RP2002124, NT2RP2002753, NT2RP2003 456, NT2RP2003871, NT2RP2003968, NT2RP2004321, NT2RP2004412, NT2RP2005293, NT2RP200 5476, NT2RP2005753, NT2RP2005815, NT2RP2005857, NT2RP2006467, NT2RP3000109, NT2RP30 00449, NT2RP3001245, NT2RP3001634, NT2RP3002056, NT2RP3002810, NT2RP3002955, NT2RP3 003032, NT2RP3003138, NT2RP3003500, NT2RP3003819, NT2RP4000078, NT2RP4000515, NT2RP 4000517, NT2RP4001407, NT2RP4001889, NT2RP4002905,

OVARC1000071, OVARC1001883, PLACE1000292, PLACE1001007, PLACE1001395, PLACE1001691, PLACE1001746, PLACE1001748, PLACE1001845, PLACE1004256, PLACE1004284, PLACE100507 7, PLACE1005111, PLACE1006076, PLACE1006360, PLACE1006760, PLACE1006867, PLACE10070 45, PLACE1007111, PLACE1007807, PLACE1008244, PLACE1008369, PLACE1008405, PLACE1008 426, PLACE1008621, PLACE1009020, PLACE1009621, PLACE1010089, PLACE1010270, Y79AA100 1848,

Group (10): 938 clones

The following 938 clones having low scores in both the ATGpr1 and ATGpr2 were judged to be full-length according to the fullness ratio shown in Table 4. The clones were novel clones, in which at least the 5'-end sequence was not identical to any of human ESTs.

HEMBA1000042, HEMBA1000213, HEMBA1000264, HEMBA1000355, HEMBA1000366, HEMBA1000411, HEMBA1000422, HEMBA1000428, HEMBA1000434, HEMBA1000442, HEMBA1000464, HEMBA100054 0, HEMBA1000563, HEMBA1000569, HEMBA1000655, HEMBA1000662, HEMBA1000702, HEMBA10007 05, HEMBA1000722, HEMBA1000747, HEMBA1000769, HEMBA1000773, HEMBA1000774, HEMBA1000 827, HEMBA1000843, HEMBA1000852, HEMBA1000870, HEMBA1000908, HEMBA1000985, HEMBA100 0991, HEMBA1001017, HEMBA1001019, HEMBA1001094, HEMBA1001121, HEMBA1001172, HEMBA10 01265, HEMBA1001327, HEMBA1001375, HEMBA1001432, HEMBA1001454, HEMBA1001463, HEMBA1 001515, HEMBA1001517, HEMBA1001557, HEMBA1001566, HEMBA1001585, HEMBA1001589, HEMBA 1001608, HEMBA1001675, HEMBA1001678, HEMBA1001681, HEMBA1001718, HEMBA1001761, HEMB A1001945, HEMBA1001960, HEMBA1001964, HEMBA1001991,

HEMBA1002003, HEMBA1002008, HEMBA1002039, HEMBA1002100, HEMBA1002113, HEMBA1002139, HEMBA1002144, HEMBA1002153, HEMBA1002226, HEMBA1002253, HEMBA1002270, HEMBA100232 1, HEMBA1002328, HEMBA1002337, HEMBA1002381, HEMBA1002486, HEMBA1002552, HEMBA10025 55, HEMBA1002558, HEMBA1002561, HEMBA1002590, HEMBA1002628, HEMBA1002629, HEMBA1002 651, HEMBA1002659, HEMBA1002666, HEMBA1002678, HEMBA1002712, HEMBA1002716, HEMBA100 2730, HEMBA1002748, HEMBA1002780, HEMBA1002801, HEMBA1002826, HEMBA1002833, HEMBA10 02886, HEMBA1002896, HEMBA1003083, HEMBA1003086, HEMBA1003098, HEMBA1003133, HEMBA1 003197, HEMBA1003212, HEMBA1003273, HEMBA1003278, HEMBA1003304, HEMBA1003314, HEMBA 1003328, HEMBA1003330, HEMBA1003348, HEMBA1003376, HEMBA1003384, HEMBA1003595, HEMB A1003597, HEMBA1003622, HEMBA1003637, HEMBA1003656, HEMBA1003715, HEMBA1003725, HEM BA1003733, HEMBA1003758, HEMBA1003773, HEMBA1003784, HEMBA1003885, HEMBA1003937, HE MBA1003950, HEMBA1003976,

HEMBA1004012, HEMBA1004045, HEMBA1004138, HEMBA1004241, HEMBA1004272, HEMBA1004306, HEMBA1004312, HEMBA1004334, HEMBA1004354, HEMBA1004356, HEMBA1004366, HEMBA100439 4, HEMBA1004396, HEMBA1004429, HEMBA1004460, HEMBA1004461, HEMBA1004482, HEMBA10045 06, HEMBA1004538, HEMBA1004586, HEMBA1004617, HEMBA1004629, HEMBA1004631, HEMBA1004 666, HEMBA1004670, HEMBA1004733, HEMBA1004816, HEMBA1004820, HEMBA1004918, HEMBA100 4956, HEMBA1004960, HEMBA1004978, HEMBA1004995, HEMBA1005008, HEMBA1005062, HEMBA10 05274, HEMBA1005275, HEMBA1005293, HEMBA1005304, HEMBA1005315, HEMBA1005372, HEMBA1 005389, HEMBA1005426, HEMBA1005500, HEMBA1005506, HEMBA1005511, HEMBA1005520, HEMBA 1005568, HEMBA1005570, HEMBA1005616, HEMBA1005627, HEMBA1005631, HEMBA1005632, HEMB A1005670, HEMBA1005699, HEMBA1005705, HEMBA1005765, HEMBA1005780, HEMBA1005853, HEM BA1005909, HEMBA1005931, HEMBA1005934, HEMBA1005962, HEMBA1005999,

HEMBA1006002, HEMBA1006005, HEMBA1006042, HEMBA1006067, HEMBA1006090, HEMBA1006142, HEMBA1006268, HEMBA1006334, HEMBA1006359, HEMBA1006416, HEMBA1006419, HEMBA100642 1, HEMBA1006446, HEMBA1006471, HEMBA1006486, HEMBA1006489, HEMBA1006546, HEMBA10065 69,

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HEMBA1006595, HEMBA1006617, HEMBA1006635, HEMBA1006648, HEMBA1006665, HEMBA1006 821, HEMBA1006849, HEMBA1006865, HEMBA1006929, HEMBA1007045, HEMBA1007051, HEMBA100 7073, HEMBA1007113, HEMBA1007256, HEMBA1007273, HEMBA1007322, HEMBA1007347, HEMBB1000039, HEMBB1000044, HEMBB1000059, HEMBB1000089, HEMBB1000099, HEMBB1000113, HEMBB1000141, HEMBB1000250, HEMBB1000264, HEMBB1000274, HEMBB1000284, HEMBB100030 7, HEMBB1000312, HEMBB1000317, HEMBB1000337, HEMBB1000341, HEMBB1000343, HEMBB10003 69, HEMBB1000376, HEMBB1000434, HEMBB1000441, HEMBB1000455, HEMBB1000472, HEMBB1000 518, HEMBB1000530, HEMBB1000564, HEMBB1000575, HEMBB1000586, HEMBB1000598, HEMBB100 0637, HEMBB1000638, HEMBB1000643, HEMBB1000665, HEMBB1000726, HEMBB1000738, HEMBB10 00770, HEMBB1000794, HEMBB1000821, HEMBB1000822, HEMBB1000883, HEMBB1000888, HEMBB1 000890, HEMBB1000910, HEMBB1000959, HEMBB1000981, HEMBB1001037, HEMBB1001051, HEMBB 1001060, HEMBB1001133, HEMBB1001208, HEMBB1001209, HEMBB1001218, HEMBB1001221, HEMB B1001249, HEMBB1001254, HEMBB1001267, HEMBB1001282, HEMBB1001302, HEMBB1001304, HEM BB1001335, HEMBB1001348, HEMBB1001356, HEMBB1001366, HEMBB1001380, HEMBB1001443, HE MBB1001463, HEMBB1001464, HEMBB1001521, HEMBB1001527, HEMBB1001537, HEMBB1001555, HEMBB1001586, HEMBB1001619, HEMBB1001630, HEMBB1001637, HEMBB1001641, HEMBB1001706, HEMBB1001735, HEMBB100175 3, HEMBB1001762, HEMBB1001802, HEMBB1001880, HEMBB1001899, HEMBB1001921, HEMBB10019 30, HEMBB1001952, HEMBB1001953, HEMBB1001973, HEMBB1001988, HEMBB1002002, HEMBB1002 005, HEMBB1002009, HEMBB1002042, HEMBB1002049, HEMBB1002069, HEMBB1002115, HEMBB100 2139, HEMBB1002189, HEMBB1002232, HEMBB1002254, HEMBB1002255, HEMBB1002280, HEMBB10 02306, HEMBB1002364, HEMBB1002371, HEMBB1002381, HEMBB1002453, HEMBB1002477, HEMBB1 002509, HEMBB1002531, HEMBB1002601, HEMBB1002603, HEMBB1002610, HEMBB1002613, HEMBB 1002623, HEMBB1002635, HEMBB1002664, HEMBB1002677, HEMBB1002683, HEMBB1002686, HEMB B1002699, HEMBB1002712,

MAMMA1000009, MAMMA1000045, MAMMA1000103, MAMMA1000133, MAMMA1000134, MAMMA1000155, MAMMA1000241, MAMMA1000254, MAMMA1000264, MAMMA1000266, MAMMA1000340, MAMMA100038 5, MAMMA1000423, MAMMA1000424, MAMMA1000446, MAMMA1000478, MAMMA1000501, MAMMA10005 16, MAMMA1000565, MAMMA1000585, MAMMA1000605, MAMMA1000616, MAMMA1000621, MAMMA1000 643, MAMMA1000669, MAMMA1000696, MAMMA1000707, MAMMA1000714, MAMMA1000718, MAMMA100 0732, MAMMA1000733, MAMMA1000839, MAMMA1000845, MAMMA1000855, MAMMA1000863, MAMMA10 00867, MAMMA1000880, MAMMA1000905, MAMMA1000942, MAMMA1000957, MAMMA1000987, MAMMA1 000998, MAMMA1001003, MAMMA1001024, MAMMA1001030, MAMMA1001035, MAMMA1001050, MAMMA 1001067, MAMMA1001082, MAMMA1001092, MAMMA1001145, MAMMA1001161, MAMMA1001203, MAMM A1001243, MAMMA1001268, MAMMA1001280, MAMMA1001298, MAMMA1001322, MAMMA1001324, MAM MA1001383, MAMMA1001408, MAMMA1001435, MAMMA1001442, MAMMA1001446, MAMMA1001501, MAMMA1001575, MAMMA1001606, MAMMA1001671, MAMMA1001715, MAMMA1001740, MAMMA1001788, MAMMA1001818, MAMMA1001854, MAMMA1001878, MAMMA1001931, MAMMA100199 2, MAMMA1002032, MAMMA1002082, MAMMA1002084, MAMMA1002108, MAMMA1002118, MAMMA10021 40, MAMMA1002215, MAMMA1002267, MAMMA1002298, MAMMA1002299, MAMMA1002310, MAMMA1002 322, MAMMA1002339, MAMMA1002347, MAMMA1002352, MAMMA1002361, MAMMA1002392, MAMMA100 2417, MAMMA1002428, MAMMA1002446, MAMMA1002475, MAMMA1002480, MAMMA1002545, MAMMA10 02556, MAMMA1002566, MAMMA1002597, MAMMA1002603, MAMMA1002623, MAMMA1002625, MAMMA1 002629, MAMMA1002636, MAMMA1002662, MAMMA1002698, MAMMA1002708, MAMMA1002721, MAMMA 1002744, MAMMA1002754, MAMMA1002758, MAMMA1002780, MAMMA1002833, MAMMA1002835, MAMM A1002838, MAMMA1002844, MAMMA1002858, MAMMA1002880, MAMMA1002887, MAMMA1002908, MAM MA1002930, MAMMA1002970, MAMMA1002982, MAMMA1003003, MAMMA1003019, MAMMA1003026, MA MMA1003031, MAMMA1003040, MAMMA1003055,

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OVARC1000133, OVARC1000198, OVARC1000240, OVARC1000427, OVARC1000431, OVARC1000533 , OVARC1000543, OVARC1000573, OVARC1000578, OVARC1000678, OVARC1000679, OVARC100070 0, OVARC1000769, OVARC1000802, OVARC1000891, OVARC1000897, OVARC1000936, OVARC10009 37, OVARC1000960, OVARC1000971, OVARC1001000, OVARC1001062, OVARC1001072, OVARC1001 085, OVARC1001118, OVARC1001129, OVARC1001169, OVARC1001261, OVARC1001268, OVARC100 1282, OVARC1001330, OVARC1001339, OVARC1001342, OVARC1001357, OVARC1001442, OVARC10 01480, OVARC1001542, OVARC1001547, OVARC1001615, OVARC1001726, OVARC1001795, OVARC1 001900, OVARC1001901, OVARC1001911, OVARC1001989, OVARC1002044, OVARC1002066, OVARC 1002143,

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PLACE1004242, PLACE1004257, PLACE1004425, PLACE1004467, PLACE1004471, PLACE1004518 , PLACE1004658, PLACE1004693, PLACE1004813, PLACE1004827, PLACE1004838, PLACE100484 0, PLACE1004900, PLACE1004972, PLACE1005146, PLACE1005162, PLACE1005453, PLACE10054 71, PLACE1005477, PLACE1005502, PLACE1005526, PLACE1005528, PLACE1005574, PLACE1005 584, PLACE1005611, PLACE1005802, PLACE1005884, PLACE1005898, PLACE1005968, PLACE100 6002, PLACE1006129, PLACE1006143, PLACE1006187, PLACE1006205, PLACE1006223, PLACE10 06382, PLACE1006521, PLACE1006534, PLACE1006540, PLACE1006617, PLACE1006640, PLACE1 006779, PLACE1006792, PLACE1006800, PLACE1006805, PLACE1006815, PLACE1006860, PLACE 1006878, PLACE1007097, PLACE1007132, PLACE1007140, PLACE1007276, PLACE1007286, PLAC E1007525, PLACE1007677, PLACE1007737, PLACE1007866,

PLACE1008045, PLACE1008111, PLACE1008201, PLACE1008231, PLACE1008392, PLACE1008424, PLACE1008437, PLACE1008455, PLACE1008625, PLACE1008748, PLACE1008757, PLACE100879 8, PLACE1008807, PLACE1008920, PLACE1008947, PLACE1009150, PLACE1009246, PLACE10093 08, PLACE1009410, PLACE1009477, PLACE1009613, PLACE1009639, PLACE1009879, PLACE1009 888, PLACE1009924, PLACE1009935, PLACE1010069, PLACE1010083, PLACE1010181, PLACE101 0341, PLACE1010624, PLACE1010628, PLACE1010631, PLACE1010662, PLACE1010916, PLACE10 10947, PLACE1011057, PLACE1011133, PLACE1011143, PLACE1011296, PLACE1011340, PLACE1 011419, PLACE1011503, PLACE1011641, PLACE1011649, PLACE1011650, PLACE1011729, PLACE 1011778, PLACE1011874, PLACE1011962, PLACE1011995,

PLACE2000003, PLACE2000103, PLACE2000115, PLACE2000132, PLACE2000140, PLACE2000176 , PLACE2000317, PLACE2000342, PLACE2000419, PLACE2000435, PLACE2000455, PLACE200046 5, PLACE3000004, PLACE3000124, PLACE3000136, PLACE3000158, PLACE3000169, PLACE30001 99,

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PLACE3000208, PLACE3000218, PLACE3000341, PLACE3000362, PLACE3000365, PLACE3000 388, PLACE3000400, PLACE3000402, PLACE3000475, PLACE4000093, PLACE4000100, PLACE400 0233, PLACE4000252, PLACE4000379, PLACE4000411, PLACE4000494,
THYRO1000026, THYRO1000035, THYRO1000085, THYRO1000132, THYRO1000156, THYRO1000186, THYRO1000190, THYRO1000221, THYRO1000241, THYRO1000438, THYRO1000452, THYRO100055 8, THYRO1000602, THYRO1000641, THYRO1000658, THYRO1000699, THYRO1000748, THYRO10007 96, THYRO1000843, THYRO1000895, THRO1000974, THYRO1000975, THYRO1001062, THYRO1001 093, THYRO1001121, THYRO1001177, THYRO1001262, THYRO1001290, THYRO1001322, THYRO100 1411, THYRO1001480, THYRO1001541, THYRO1001573, THYRO1001617, THYRO1001895, Y79AA10 00065, Y79AA1000405, Y79AA1000538, Y79AA1000802, Y79AA1000969, Y79AA1001061, Y79AA1 001167, Y79AA1001384, Y79AA1001594, Y79AA1001875, Y79AA1002211,

Group (11): 228 clones

The following 228 clones having low scores in both the ATGpr1 and ATGpr2 were judged to be full-length according to the fullness ratio shown in Table 7. The clones were a novel clone, in which at least the 3'-end sequence was not identical to any of human ESTs.

HEMBA1000111, HEMBA1000243, HEMBA1000338, HEMBA1000390, HEMBA1000418, HEMBA1000459, HEMBA1000518, HEMBA1000791, HEMBA1000974, HEMBA1001007, HEMBA1001077, HEMBA100109 9, HEMBA1001123, HEMBA1001294, HEMBA1001299, HEMBA1001442, HEMBA1001861, HEMBA10019 42, HEMBA1001979, HEMBA1002160, HEMBA1002162, HEMBA1002166, HEMBA1002389, HEMBA1002 498, HEMBA1002592, HEMBA1002679, HEMBA1002944, HEMBA1003034, HEMBA1003142, HEMBA100 3548, HEMBA1003571, HEMBA1003579, HEMBA1003598, HEMBA1003630, HEMBA1003958, HEMBA10 04038, HEMBA1004042, HEMBA1004049, HEMBA1004132, HEMBA1004225, HEMBA1004748, HEMBA1 004770, HEMBA1005039, HEMBA1005152, HEMBA1005159, HEMBA1005359, HEMBA1005408, HEMBA 1005410, HEMBA1005443, HEMBA1005497, HEMBA1005552, HEMBA1005634, HEMBA1005717, HEMB A1005829, HEMBA1005921, HEMBA1006328, HEMBA1006438, HEMBA1006540, HEMBA1006780, HEM BA1006921, HEMBA1006938, HEMBA1007017, HEMBA1007341,
HEMBB1000050, HEMBB1000420, HEMBB1000487, HEMBB1000490, HEMBB1000523, HEMBB1000684, HEMBB1000840, HEMBB1000876, HEMBB1000913, HEMBB1000915, HEMBB1000917, HEMBB100106 3, HEMBB1001102, HEMBB1001177, HEMBB1001253, HEMBB1001271, HEMBB1001454, HEMBB10015 00, HEMBB1001588, HEMBB1001618, HEMBB1001704, HEMBB1001717, HEMBB1001756, HEMBB1001 867, HEMBB1001967, HEMBB1002043, HEMBB1002094, HEMBB1002190, HEMBB1002520, HEMBB100 2556, HEMBB1002590,
MAMMA1000117, MAMMA1000227, MAMMA1000270, MAMMA1000302, MAMMA1000348, MAMMA1000413, MAMMA1000431, MAMMA1000483, MAMMA1000559, MAMMA1000723, MAMMA1000744, MAMMA100075 2, MAMMA1000782, MAMMA1000802, MAMMA1000851, MAMMA1000877, MAMMA1000962, MAMMA10010 74, MAMMA1001133, MAMMA1001191, MAMMA1001206, MAMMA1001249, MAMMA1001330, MAMMA1001 452, MAMMA1001502, MAMMA1001663, MAMMA1001806, MAMMA1001836, MAMMA1001880, MAMMA100 1890, MAMMA1001908, MAMMA1001963, MAMMA1002058, MAMMA1002155, MAMMA1002158, MAMMA10 02230, MAMMA1002282, MAMMA1002293, MAMMA1002332, MAMMA1002359, MAMMA1002494, MAMMA1 002573, MAMMA1002618, MAMMA1002622, MAMMA1002646, MAMMA1002748, MAMMA1002871, MAMMA 1002892, MAMMA1003140,
NT2RM4000327, NT2RM4000532, NT2RM4001414, NT2RM4001776, NT2RM4002499, NT2RP2000076, NT2RP2000523, NT2RP2000603, NT2RP2000644, NT2RP2000731, NT2RP2001196, NT2RP200167 8, NT2RP2001926, NT2RP2003206, NT2RP2003704, NT2RP2003912, NT2RP2004396, NT2RP20046 81, NT2RP3000512, NT2RP3000542, NT2RP3000736, NT2RP3000865, NT2RP3002057, NT2RP3003 384, NT2RP3004334, NT2RP3004349, NT2RP3004527, NT2RP4000049, OVARC1000058, OVARC100 0191, OVARC1000302, OVARC1001051, OVARC1001117, OVARC1001668, OVARC1001745, OVARC10 01812, OVARC1001928,
PLACE1000583, PLACE1001272, PLACE1001414, PLACE1002537, PLACE1003205, PLACE1003361, PLACE1003516, PLACE1003864, PLACE1004384, PLACE1004491, PLACE1004793, PLACE100498 5, PLACE1005085, PLACE1005666, PLACE1005845, PLACE1006164, PLACE1006262, PLACE10067 54, PLACE1007852, PLACE1008331, PLACE1008643, PLACE1009050, PLACE1009155, PLACE1009 172, PLACE1009183, PLACE1009200, PLACE1009398, PLACE1009595, PLACE1010702, PLACE101 0891, PLACE1011165, PLACE1011203, PLACE1011375, PLACE1011576, PLACE1011762, PLACE10 11964, PLACE2000136, PLACE2000264, PLACE2000305, PLACE2000379, PLACE3000220, PLACE4 000250, THYRO1000092,THYRO1000471, THYRO1000852, THYRO1001534, THYRO1001595, THYRO 1001745.

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EXAMPLE 12

Homology search using the 5'-end and 3'-end sequences of the selected clones.

[0172] The 5' -end sequences of the selected 5547 clones were used for the homology search of the SwissProt. and both the 5' -end 3' -end sequences were used for the search of the GenBank and UniGene (ref. the result of the search of the SwissProt, GenBank (except ESTs and STSs), and UniGene (Human) was attached).

[0173] Each search result is shown in the last part of this SPECIFICATION by arranging each item in the following format.

	5' -end sequence	3' -end sequence
Swiss-Prot	Homology search result 1	-----
GenBank	Homology search result 2	Homology search result 3
UniGene	Homology search result 4	Homology search result 5

[0174] According to the top hit data, at least 1430 clones were predicted to encode a protein belonging to any of the categories, secretory or membrane protein, glycoprotein, protein associated with signal transduction, protein associated with transcription, protein associated with diseases, enzyme or protein associated with metabolism, protein associated with cell division or cell proliferation, protein associated with cytoskeleton, protein associated with RNA synthesis, nuclear protein, protein associated with protein synthesis or transport, protein associated with cellular defense, or protein associated with development or growth. Among the clones predicted belonging to any of the categories, 1001 clones were estimated to have a relatively high homology with the known proteins or genes in the same category. In addition, 429 clones were estimated to have a relatively low homology with the known proteins in the same category.

[0175] Herein, the term "relatively high homology" is defined as having 60% or more identity and the P-value 10^{-10} or less in comparison with known sequences in the SwissProt database, or 64% or more identity and the P-value 10^{-15} or less in comparison with those in the GenBank and UniGene databases (see the attached list). Also, the term "relatively low homology" is defined as not fulfilling the requirements to be "relatively high homology", but still having the scores, 25% or more identity and the P-value 10^{-6} or less, using the sequence having 55 nucleotides or more, in comparison with known sequences in the SwissProt database (see the attached list). The P-value is a score obtained statistically by taking into account the probability of occurrence of the similarity between two sequences. In general, the smaller P-value reflects the higher similarity (Altschul S.F., Gish W., Miller W., Myers E.W., and Lipman D.J. (1990) "Basic local alignment search tool" J.Mol. Biol., 215: 403-410; Gish W., and States D.J. (1993) "Identification of protein coding regions by database similarity search" Nature Genet. 3: 266-272).

[0176] The clones predicted to encode a protein in the category of secretory protein or membrane protein have the keywords, "signal", "transmembrane", "membrane", "extracellular matrix", "receptor", "G-protein coupled receptor", "ionic channel", "voltage-gated channel", "calcium channel", "cell adhesion", "collagen", or "connective tissue", or descriptions from which the clone can be predicted to be a secretory or membrane protein, in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0177] The clones predicted to encode a protein in the category of glycoprotein have the keywords, "glycoprotein", or descriptions from which the clone can be predicted to be a glycoprotein, in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0178] The clones predicted to encode a protein in the category of proteins associated with signal transduction have the keywords, "serine/threonine-protein kinase", "tyrosine-protein kinase", "SH3 domain", or "WD repeat", or descriptions from which the clone can be predicted to be a protein associated with signal transduction (such as "ADP-ribosylation factor"), in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0179] The clones predicted to encode a protein in the category of proteins associated with transcription have the keywords, "transcription regulation", "zinc finger", or "homeobox", or descriptions from which the clone can be predicted to be a protein associated with transcription, in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0180] The clones predicted to encode a protein in the category of proteins associated with diseases are the clones in which the top hit data of the SwissProt using the 5'-end sequence, or the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence is a gene or protein that is deposited in the Online Mendelian Inheritance in Man (OMIM) database, which is a database of human genes and diseases, or the top hit data has descriptions from which the clone can be predicted to be a protein associated with diseases.

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[0181] The clones predicted to encode a protein in the category of enzyme or proteins associated with metabolism are the clones in which the top hit data of the SwissProt using the 5'-end sequence, or the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence is a gene or protein with E.C.No. (Enzyme commission number), or the top hit data has descriptions from which the clone can be predicted to be an enzyme or protein associated with metabolism (such as "metabolism", "oxidoreductase", or "lipid").

[0182] The clones predicted to encode a protein in the category of proteins associated with cell division or cell proliferation have the keywords, "cell division", "cell cycle", "mitosis", or "chromosomal protein", or descriptions from which the clone can be predicted to be a protein associated with cell division or cell proliferation (such as "histone", "cell growth", or "apoptosis"), in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0183] The clones predicted to encode a protein in the category of proteins associated with cytoskeleton have the keywords, "structural protein", "cytoskeleton", "actin-binding", or "microtubules", or descriptions from which the clone can be predicted to be a protein associated with cytoskeleton, in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0184] The clones predicted to encode a protein in the category of proteins associated with RNA synthesis include the above clones predicted to be a protein associated with transcription, and also the clones which have the keywords, "RNA splicing", or "RNA processing", or descriptions from which the clone can be predicted to be a protein associated with RNA synthesis (such as "RNA helicase", "polyadenylation", or "RNA transport"), in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0185] The clones predicted to encode a protein in the category of nuclear protein include the above clones predicted to be a protein associated with transcription, and also the clones which have the keyword, "nuclear protein", or descriptions from which the clone can be predicted to be a nuclear protein, in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0186] The clones predicted to encode a protein in the category of proteins associated with protein synthesis or transport have the keywords, "translation regulation", "protein biosynthesis", "amino-acid biosynthesis", "ribosomal protein", or "protein transport", or descriptions from which the clone can be predicted to be a protein associated with protein synthesis or transport (such as "signal recognition particle", "ubiquitin", "proteosome", or "protease"), in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0187] The clones predicted to encode a protein in the category of proteins associated with cellular defense have the keywords, "heat shock", "chaperone", "DNA repair", or "DNA damage", or descriptions from which the clone can be predicted to be a protein associated with cellular defense, in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0188] The clones predicted to encode a protein in the category of proteins associated with development or growth have the keyword, "developmental protein", or descriptions from which the clone can be predicted to be a protein associated with development or growth, in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0189] The following 1430 clones were predicted to encode a protein belonging to any of the categories, secretory or membrane protein, glycoprotein, protein associated with signal transduction, protein associated with transcription, protein associated with diseases, enzyme or protein associated with metabolism, protein associated with cell division or cell proliferation, protein associated with cytoskeleton, protein associated with RNA synthesis, nuclear protein, protein associated with protein synthesis or transport, protein associated with cellular defense, or protein associated with development or growth.

HEMBA1000005, HEMBA1000012, HEMBA1000020, HEMBA1000030, HEMBA1000158, HEMBA1000185, HEMBA1000201, HEMBA1000216, HEMBA1000303, HEMBA1000459, HEMBA1000488, HEMBA100049 1, HEMBA1000523, HEMBA1000531, HEMBA1000542, HEMBA1000561, HEMBA1000569, HEMBA10005 88, HEMBA1000591, HEMBA1000657, HEMBA1000673, HEMBA1000752, HEMBA1000827, HEMBA1000 851, HEMBA1000852, HEMBA1000972, HEMBA1000991, HEMBA1001017, HEMBA1001019, HEMBA100 1059, HEMBA1001071, HEMBA1001088, HEMBA1001123, HEMBA1001137, HEMBA1001174, HEMBA10 01257, HEMBA1001302, HEMBA1001351, HEMBA1001387, HEMBA1001407, HEMBA1001476, HEMBA1 001510, HEMBA1001569, HEMBA1001570, HEMBA1001579, HEMBA1001595, HEMBA1001620, HEMBA 1001672, HEMBA1001678, HEMBA1001714, HEMBA1001744, HEMBA1001800, HEMBA1001804, HEMB A1001809, HEMBA1001819, HEMBA1001822, HEMBA1001847, HEMBA1001896, HEMBA1001913, HEM BA1001921, HEMBA1002003, HEMBA1002035, HEMBA1002092, HEMBA1002102, HEMBA1002150, HE MBA1002160, HEMBA1002161, HEMBA1002162, HEMBA1002212, HEMBA1002229, HEMBA1002257, H EMBA1002341, HEMBA1002363, HEMBA1002417, HEMBA1002495, HEMBA1002513, HEMBA1002547, HEMBA1002555, HEMBA1002569, HEMBA1002609, HEMBA1002688, HEMBA1002716, HEMBA1002810, HEMBA1002896,

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[0190] Among the clones, 1001 clones were estimated to have a relatively high homology with the known proteins or genes in the same category.

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[0191] The following 429 clones were estimated to have a relatively low homology with the known proteins in the same category.

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NT2RP2004098, NT2RP2004187, NT2RP2004568, NT2RP2004791, NT2RP2005022, NT2RP2005037, NT2RP2005038, NT2RP2005204, NT2RP2005344, NT2RP2005465, NT2RP2005496, NT2RP2005531, NT2RP2005690, NT2RP2005763, NT2RP2005767, NT2RP2006275,

NT2RP3000046, NT2RP3000047, NT2RP3000361, NT2RP3000397, NT2RP3000418, NT2RP3000527, NT2RP3000590, NT2RP3000603, NT2RP3000759, NT2RP3000868, NT2RP3000994,

NT2RP3001216, NT2RP3001274, NT2RP3001355, NT2RP3001399, NT2RP3001407, NT2RP3001426, NT2RP3001427,

NT2RP3001587, NT2RP3001708, NT2RP3002056, NT2RP3002273, NT2RP3002377, NT2RP3002399, NT2RP3002663, NT2RP3002785, NT2RP3002909,

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NT2RP3004209, NT2RP3004253, NT2RP3004454, NT2RP3004472, NT2RP3004475, NT2RP3004507, NT2RP3004569, NT2RP3004578, NT2RP3004617, NT2RP3004669,

NT2RP4000210, NT2RP4000212, NT2RP4000259, NT2RP4000312, NT2RP4000370, NT2RP4000417, NT2RP4000449, NT2RP4000457, NT2RP4000498, NT2RP4000528, NT2RP4000879, NT2RP4000925,

NT2RP4001041, NT2RP4001095, NT2RP4001122, NT2RP4001126, NT2RP4001148, NT2RP4001149, NT2RP4001150, NT2RP4001174, NT2RP4001207, NT2RP4001219, NT2RP4001372, NT2RP4001375,

NT2RP4001551, NT2RP4001592, NT2RP4001638, NT2RP4001725, NT2RP4001790, NT2RP4001823, NT2RP4001838, NT2RP4001849, NT2RP4001893, NT2RP4001927, NT2RP4001946, NT2RP4002408,

NT2RP5003477, NT2RP5003522, NT2RP5003524,

OVARC1000004, OVARC1000087, OVARC1000139, OVARC1000309, OVARC1000543, OVARC1000746, OVARC1000846, OVARC1000876, OVARC1000885, OVARC1000912,

OVARC1001180, OVARC1001329, OVARC1001476, OVARC1001555, OVARC1001610, OVARC1001762, OVARC1001880, OVARC1001942, OVARC1002050, OVARC1002138,

PLACE1000066, PLACE1000142, PLACE1000420, PLACE1000547, PLACE1000583, PLACE1000863,

PLACE1001387, PLACE1001632, PLACE1001692, PLACE1001989,

PLACE1002450, PLACE1002571, PLACE1002722, PLACE1002775, PLACE1002811, PLACE1002991,

PLACE1003190, PLACE1003258, PLACE1003420, PLACE1003493, PLACE1003605, PLACE1003669, PLACE1003704, PLACE1003915,

PLACE1004197, PLACE1004428, PLACE1004471, PLACE1004629, PLACE1004751, PLACE1004902,

PLACE1005287, PLACE1005557, PLACE1005611, PLACE1005763, PLACE1005890,

PLACE1006157, PLACE1006469, PLACE1006731,

PLACE1007238, PLACE1007375, PLACE1007488, PLACE1007544, PLACE1007598, PLACE1007729, PLACE1008244, PLACE1008275, PLACE1008947,

PLACE1009094, PLACE1009319, PLACE1009622, PLACE1009721, PLACE1009845,

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PLACE1009861,

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PLACE2000034, PLACE2000164, PLACE2000274, PLACE2000399, PLACE2000411, PLACE2000458,

PLACE3000148, PLACE3000156, PLACE3000242, PLACE3000322, PLACE3000353, PLACE3000373,

PLACE4000009, PLACE4000014, PLACE4000259, PLACE4000431, PLACE4000522, PLACE4000558, PLACE4000581, PLACE4000590, PLACE4000612,

SKNMC1000011,

THYRO1000072, THYRO1000852, THYRO1000934, THYRO1000951,

Y79AA1000258, Y79AA1000368, Y79AA1000539, Y79AA1000589, Y79AA1000962; Y79AA1001048, Y79AA1001233, Y79AA1001394, Y79AA1001581, Y79AA1001613, Y79AA1001692, Y79AA1001848, Y79AA1001874, Y79AA1001963,

Y79AA1002027, Y79AA1002139, Y79AA1002208, Y79AA1002209, Y79AA1002472, Y79AA1002482,

(1) Among the 1430 clones, the following 259 clones were predicted to encode a protein in the category of secretory protein or membrane protein (including the clones belonging to plural categories).
HEMBA1000005, HEMBA1001017, HEMBA1001059, HEMBA1001071, HEMBA1001351, HEMBA1001407, HEMBA1001476, HEMBA1001569, HEMBA1001678, HEMBA1001804, HEMBA1002150, HEMBA100254 7, HEMBA1002555, HEMBA1002688, HEMBA1002716, HEMBA1002999, HEMBA1003071, HEMBA10030 77, HEMBA1003538, HEMBA1003598, HEMBA1003690, HEMBA1004207, HEMBA1004356, HEMBA1004 389, HEMBA1004756, HEMBA1005338, HEMBA1005367, HEMBA1005576, HEMBA1005699, HEMBA100 5963, HEMBA1005990, HEMBA1006310, HEMBA1006344, HEMBA1006562, HEMBA1006976, HEMBA10 07045, HEMBA1007301, HEMBB1000037, HEMBB1000119, HEMBB1000317, HEMBB1000530, HEMBB1 000915, HEMBB1001112, HEMBB1001119, HEMBB1001151, HEMBB1001282, HEMBB1001331, HEMBB 1002042, HEMBB1002092, HEMBB1002193, HEMBB1002600, MAMMA1000103, MAMMA1000424, MAMM A1000672, MAMMA1000734, MAMMA1000897, MAMMA1001008, MAMMA1001030, MAMMA1001041, MAM MA1001075, MAMMA1001080, MAMMA1001751, MAMMA1001754, MAMMA1002143, MAMMA1002219, MA MMA1002485, MAMMA1002636, MAMMA1002938, MAMMA1003104, NT2RM1000199, NT2RM1000355, N T2RM1000430, NT2RM1000648, NT2RM1000742, NT2RM1000770, NT2RM1000811, NT2RM1000833, NT2RM1000867, NT2RM1000882, NT2RM1000883, NT2RM1001139, NT2RM2000374, NT2RM2000402, NT2RM2000422, NT2RM2000566, NT2RM2000623, NT2RR2001324, NT2RM2001499, NT2RM200158 8, NT2RM2001592, NT2RM2001613, NT2RM2001635, NT2RM2001648, NT2RM2001760, NT2RM20021 09, NT2RM2002145, NT2RM4000156, NT2RM4000169, NT2RM4000386, NT2RM4000433, NT2RM4000795, NT2RM4001032, NT2RM4001054, NT2RM4001410, NT2RM4001605; NT2RM4001930, NT2RM4001987, NT2RM4002073, NT2RM4002145, NT2RM4002189, NT2RM4002558, NT2RM400256 5, NT2RM4002571, NT2RM4002594, NT2RP1000130, NT2RP1000326, NT2RP1000363, NT2RP10004 13, NT2RP1000547, NT2RP1000782, NT2RP1000856, NT2RP1001247, NT2RP1001313, NT2RP1001 546, NT2RP1001569, NT2RP2000056,

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NT2RP2000257, NT2RP2000842, NT2RP2001081, NT2RP200 1991, NT2RP2002025, NT2RP2002193, NT2RP2002256, NT2RP2002312, NT2RP2002479, NT2RP20 02504, NT2RP2003433, NT2RP2003706, NT2RP2003760, NT2RP2004194, NT2RP2004655, NT2RP2 005020, NT2RP2005344, NT2RP2005465, NT2RP2005752, NT2RP2005753, NT2RP2005835, NT2RP 2005933, NT2RP2006275, NT2RP2006565, NT2RP2006571, NT2RP3000324, NT2RP3000739, NT2R P3000919, NT2RP3001140, NT2RP3001355, NT2RP3001676, NT2RP3001708, NT2RP3001727, NT2 RP3002659, NT2RP3003059, NT2RP3003101, NT2RP3003203, NT2RP3003212, NT2RP3003242, NT 2RP3003672, NT2RP3003701, NT2RP3003716, NT2RP3003918, NT2RP3004207, NT2RP3004253, N T2RP4000008, NT2RP4000212, NT2RP4000243, NT2RP4000417, NT2RP4000878, NT2RP4000907, NT2RP4000925, NT2RP4000928, NT2RP4001079, NT2RP4001117, NT2RP4001150, NT2RP4001174 , NT2RP4001313, NT2RP4001315, NT2RP4001345, NT2RP4001372, NT2RP4001574, NT2RP400182 3, NT2RP4001966, NT2RP5003524, OVARC1000060, OVARC1000326, OVARC1000543, OVARC10006 82, OVARC1000722, OVARC1000912, OVARC1001055, OVARC1001154, OVARC1001261, OVARC1001329, OVARC1001419, OVARC1001506, OVARC1001542, OVARC1001610, OVARC1001713 , OVARC1001802, OVARC1001943, PLACE1000611, PLACE1001092, PLACE1001136, PLACE100129 4, PLACE1002437, PLACE1002500, PLACE1002722, PLACE1002782, PLACE1002816, PLACE10034 20, PLACE1003493, PLACE1003596, PLACE1004104, PLACE1004197, PLACE1004203, PLACE1004 277, PLACE1004629, PLACE1004751, PLACE1005494, PLACE1005804, PLACE1005890, PLACE100 6157, PLACE1007409, PLACE1007852, PLACE1008044, PLACE1008273, PLACE1008309, PLACE10 08603, PLACE1008643, PLACE1009659, PLACE1009670, PLACE1009845, PLACE1009861, PLACE1 011371, PLACE1011492, PLACE1011896, PLACE2000034, PLACE2000341, PLACE2000399, PLACE 2000458, PLACE3000020, PLACE3000322, PLACE3000353, PLACE4000052, PLACE4000269, PLAC E4000522, PLACE4000581, THYRO1000783, Y79AA1000258, Y79AA1000346, Y79AA1001874,

(2) The following 111 clones were predicted to encode a protein in the category of glycoprotein (including the clones belonging to plural categories).

HEMBA1000752, HEMBA1001017, HEMBA1001059, HEMBA1001071, HEMBA1001302, HEMBA1002150 , HEMBA1002547, HEMBA1002555, HEMBA1003077, HEMBA1003538, HEMBA1003598, HEMBA100386 6, HEMBA1004356, HEMBA1005338, HEMBA1005576, HEMBA1005699, HEMBA1006562, HEMBA10069 76, HEMBA1007301, HEMBB1000317, HEMBB1000530, HEMBB1001119, HEMBB1002092, HEMBB1002 193, MAMMA1000672, MAMMA1000897, MAMMA1001030, MAMMA1001388, MAMMA1001771, MAMMA100 2485, MAMMA1002636, MAMMA1002938, NT2RM1000648, NT2RM2000374, NT2RM2000407, NT2RM20 00422, NT2RM2000623, NT2RM2001499, NT2RM2001588, NT2RM2001839, NT2RM2001930, NT2RM4 000156, NT2RM4000233, NT2RM4001410, NT2RM4001987, NT2RM4002145, NT2RM4002189, NT2RM 4002194, NT2RM4002558, NT2RM4002571, NT2RP1000856, NT2RP1001247, NT2RP2000056, NT2R P2001991, NT2RP2002025, NT2RP2002325, NT2RP2002385, NT2RP2003706, NT2RP2005933, NT2 RP3001140, NT2RP3003242, NT2RP3003672, NT2RP3003701, NT2RP3003716, NT2RP3003914, NT 2RP3004253, NT2RP4000212, NT2RP4000417, NT2RP4000925, NT2RP4001149, NT2RP4001150, N T2RP4001219, NT2RP4001345, NT2RP4001372, NT2RP5003522, NT2RP5003524, OVARC1000543, OVARC1000682, OVARC1000722, OVARC1001055, OVARC1001154, OVARC1001506, OVARC1001713 PLACE1002437, PLACE1002722, PLACE1003258, PLACE1003493, PLACE1004197, PLACE100475 1, PLACE1005698, PLACE1005804, PLACE1006157, PLACE1006754, PLACE1008643, PLACE10090 94, PLACE1009861, PLACE1011371, PLACE2000034, PLACE2000062, PLACE2000399, PLACE2000458, PLACE3000009, PLACE3000020, PLACE3000353, PLACE3000373, PLACE4000052 , PLACE4000230, PLACE4000522, PLACE4000581, THYRO1000852, Y79AA1001874,

(3) The following 147 clones were predicted to encode a protein in the category of proteins associated with signal transduction (including the clones belonging to plural categories).

HEMBA1000030, HEMBA1000185, HEMBA1000303, HEMBA1000459, HEMBA1000491, HEMBA1000657, HEMBA1000991, HEMBA1001174, HEMBA1001387, HEMBA1001822, HEMBA1001921, HEMBA100221 2, HEMBA1002341, HEMBA1002417, HEMBA1002810, HEMBA1002896, HEMBA1003291, HEMBA10033 14, HEMBA1003560, HEMBA1003615, HEMBA1003621, HEMBA1003805, HEMBA1004286, HEMBA1004 604, HEMBA1006173, HEMBA1006540, HEMBA1006973, HEMBA1007174, HEMBB1000632, HEMBB100 0781, HEMBB1001051, HEMBB1001177, HEMBB1001234, HEMBB1001294, HEMBB1001384, HEMBB10 02193, HEMBB1002477, HEMBB1002635, MAMMA1001305, MAMMA1002699, MAMMA1002842, MAMMA1 003057, MAMMA1003113, NT2RM1000118, NT2RM1000186, NT2RM1000772, NT2RM1000850, NT2RM 1001072, NT2RM2000124, NT2RM2000612, NT2RM2001065, NT2RM2001221, NT2RM2001345, NT2R M2001652, NT2RM2001983, NT2RM2002109, NT2RM2002128, NT2RM4000327, NT2RM4000354, NT2 RM4000798,

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NT2RM4001203, NT2RM4001411, NT2RM4001412, NT2RM4001582, NT2RM4001629, NT 2RM4001758, NT2RM4002226, NT2RP1000018, NT2RP1000112, NT2RP1000701, NT2RP1000825, N T2RP1001395, NT2RP1001410, NT2RP1001457, NT2RP1001482, NT2RP2002058, NT2RP2002710, NT2RP2003702, NT2RP2003912, NT2RP2004232, NT2RP2004768, NT2RP2005022, NT2RP2005620, NT2RP2005890, NT2RP3000299, NT2RP3000403, NT2RP3000742, NT2RP3000845, NT2RP300176 4, NT2RP3002004, NT2RP3002785, NT2RP3002909, NT2RP3003230, NT2RP3003411, NT2RP30034 64, NT2RP3003800, NT2RP3004475, NT2RP3004534, NT2RP4000147, NT2RP4000376, NT2RP4001122, NT2RP4001375, NT2RP4001644, NT2RP4001725, NT2RP4001760, NT2RP4001849, NT2RP4001927, NT2RP4002408, NT2RP5003477, OVARC1000437, OVARC1000465, OVARC100064 9, OVARC1000945, OVARC1001476, OVARC1001861, PLACE1001377, PLACE1001384, PLACE10013 87, PLACE1002493, PLACE1002591, PLACE1002685, PLACE1003353, PLACE1004128, PLACE1004 918, PLACE1005502, PLACE1005739, PLACE1005968, PLACE1006385, PLACE1007238, PLACE100 7375, PLACE1007488, PLACE1008244, PLACE1008650, PLACE1009319, PLACE1009468, PLACE10 10083, PLACE1010942, PLACE1011041, PLACE1011046, PLACE1011923, PLACE2000164, PLACE3 000145, PLACE3000350, PLACE3000475, THYRO1001595, Y79AA1000059, Y79AA1000966,

(4) The following 230 clones were predicted to encode a protein in the category of proteins associated with transcription (including the clones belonging to plural categories).

HEMBA1000201, HEMBA1000216, HEMBA1000488, HEMBA1000561, HEMBA1000851, HEMBA1001137, HEMBA1001510, HEMBA1001579, HEMBA1001800, HEMBA1001809, HEMBA1001819, HEMBA100184 7, HEMBA1002035, HEMBA1002092, HEMBA1002569, HEMBA1002609, HEMBA1003545, HEMBA10035 68, HEMBA1003684, HEMBA1003760, HEMBA1003953, HEMBA1004097, HEMBA1004321, HEMBA1004 353, HEMBA1004479, HEMBA1004758, HEMBA1005359, HEMBA1005528, HEMBA1005548, HEMBA100 5931, HEMBA1006253, HEMBA1006278, HEMBA1006359, HEMBA1006559, HEMBB1000250, HEMBB10 00789, HEMBB1001011, HEMBB1001314, HEMBB1001482, HEMBB1001908, HEMBB1002134, HEMBB1 002217, MAMMA1000155, MAMMA1000183, MAMMA1000388, MAMMA1001633, MAMMA1001820, MAMMA 1001837, MAMMA1002650, MAMMA1002937, NT2RM1000055, NT2RM1000666, NT2RM1000691, NT2R M1000894, NT2RM1001092, NT2RM2000013, NT2RM2000735, NT2RM2001035, NT2RM2001575, NT2 RM2001605, NT2RM2001670, NT2RM2001771, NT2RM2001797, NT2RM2002580, NT2RM4000024, NT 2RM4000104, NT2RM4000191, NT2RM4000496, NT2RM4000531, NT2RM4000734, NT2RM4000751, N T2RM4000996, NT2RM4001140, NT2RM4001200, NT2RM4001483, NT2RM4001592, NT2RM4001746, NT2RM4001783, NT2RM4001823, NT2RM4001828, NT2RM4001858, NT2RM4001979, NT2RP1000111, NT2RP1000333, NT2RP1000574, NT2RP1000721, NT2RP1000860, NT2RP2000008, NT2RP200013 3, NT2RP2000297, NT2RP2000931, NT2RP2001174, NT2RP2001233, NT2RP2002252, NT2RP20025 03, NT2RP2002591, NT2RP2003125, NT2RP2003228, NT2RP2003293, NT2RP2003564, NT2RP2003714, NT2RP2004013, NT2RP2004187, NT2RP2004961, NT2RP2005003, NT2RP2005037, NT2RP2005287, NT2RP2005496, NT2RP2005539, NT2RP2005722, NT2RP2006238, NT2RP200646 4, NT2RP3000050, NT2RP3000397, NT2RP3000512, NT2RP3000527, NT2RP3000590, NT2RP30006 32, NT2RP3001057, NT2RP3001120, NT2RP3001155, NT2RP3001268, NT2RP3001398, NT2RP3001 399, NT2RP3001671, NT2RP3001672, NT2RP3001688, NT2RP3001712, NT2RP3001792, NT2RP300 1855, NT2RP3002165, NT2RP3002377, NT2RP3002399, NT2RP3003157, NT2RP3003193, NT2RP30 03251, NT2RP3003327, NT2RP3004258, NT2RP3004566, NT2RP3004572, NT2RP3004594, NT2RP3 004617, NT2RP4000078, NT2RP4000210, NT2RP4000398, NT2RP4000449, NT2RP4000787, NT2RP 4000865, NT2RP4000997, NT2RP4001029, NT2RP4001213, NT2RP4001433, NT2RP4001529, NT2R P4001551, NT2RP4001638, NT2RP4001753, NT2RP4001790, NT2RP4001938, NT2RP4002078, OVA RC1000479, OVARC1000846, OVARC1001381, OVARC1001555, OVARC1001577, OVARC1001949, PL ACE1000066, PLACE1000133, PLACE1000583, PLACE1000596, PLACE1000706, PLACE1001118, P LACE1001238, PLACE1001304, PLACE1001602, PLACE1001632, PLACE1002450, PLACE1002532, PLACE1002834, PLACE1003302, PLACE1003605, PLACE1003738, PLACE1003885, PLACE1004471, PLACE1004510, PLACE1004681, PLACE1006414, PLACE1006438, PLACE1006482, PLACE100723 9, PLACE1007346, PLACE1007544, PLACE1007598, PLACE1007955, PLACE1007969, PLACE10086 27, PLACE1008941, PLACE1009099, PLACE1009246, PLACE1009398, PLACE1010261, PLACE1010491, PLACE1010702, PLACE1010771, PLACE1010870, PLACE1011576, PLACE2000072, PLACE2000359, PLACE4000128, PLACE4000156, PLACE4000259, PLACE4000431, THYRO100012 1, THYRO1000242, THYRO1000501, THYRO1000585, THYRO1001100, THYRO1001189, Y79AA10000 37, Y79AA1000627, Y79AA1000705, Y79AA1001105, Y79AA1001299, Y79AA1001391, Y79AA1001 533, Y79AA1001613, Y79AA1001848, Y79AA1001866, Y79AA1002093, Y79AA1002472, Y79AA100 2482,

BNSDOCID: <EP___1074617A2_I_>

(5) The following 436 clones were predicted to encode a protein in the category of proteins associated with diseases (including the clones belonging to plural categories).

HEMBA1000158, HEMBA1000216, HEMBA1000523, HEMBA1000561, HEMBA1000569, HEMBA1000673, HEMBA1000972, HEMBA1001017, HEMBA1001019, HEMBA1001059, HEMBA1001071, HEMBA100108 8, HEMBA1001123, HEMBA1001407, HEMBA1001569, HEMBA1001570, HEMBA1001672, HEMBA10020 35, HEMBA1002160, HEMBA1002162, HEMBA1002547, HEMBA1002939, HEMBA1003077, HEMBA1003 418, HEMBA1003433, HEMBA1003538, HEMBA1003555, HEMBA1003568, HEMBA1003569, HEMBA100 3581, HEMBA1003720, HEMBA1003760, HEMBA1004168, HEMBA1004248, HEMBA1004276, HEMBA10 04354, HEMBA1004356, HEMBA1004479, HEMBA1004534, HEMBA1004669, HEMBA1004752, HEMBA1 004753, HEMBA1004807, HEMBA1005293, HEMBA1005331, HEMBA1005359, HEMBA1005367, HEMBA 1005423, HEMBA1005443, HEMBA1005475, HEMBA1005528, HEMBA1005576, HEMBA1005581, HEMB A1005679, HEMBA1005699, HEMBA1005732, HEMBA1005931, HEMBA1006173, HEMBA1006474, HEM BA1006562, HEMBA1006648, HEMBA1006652, HEMBA1006737, HEMBA1006807, HEMBA1006976, HE MBA1007078, HEMBA1007121, HEMBA1007243, HEMBA1007301, HEMBB1000264, HEMBB1000637, H EMBB1000684, HEMBB1000693, HEMBB1000915, HEMBB1000927, HEMBB1001011, HEMBB1001051, HEMBB1001068, HEMBB1001102, HEMBB1001119, HEMBB1001133, HEMBB1001177, HEMBB1001802, HEMBB1001908, HEMBB1001922, HEMBB1001967, HEMBB1002050, HEMBB1002193, HEMBB100221 7, HEMBB1002358, HEMBB1002635, HEMBB1002683, MAMMA1000009, MAMMA1000092, MAMMA10001 03, MAMMA1000173, MAMMA1000731, MAMMA1000897, MAMMA1000956, MAMMA1001021, MAMMA1001041, MAMMA1001105, MAMMA1001198, MAMMA1001305, MAMMA1001576, MAMMA1001633, MAMMA1002140, MAMMA1002170, MAMMA1002198, MAMMA1002268, MAMMA1002352, MAMMA100239 2, MAMMA1002485, MAMMA1002530, MAMMA1002573, MAMMA1002636, MAMMA1002858, MAMMA10028 69, MAMMA1002881, MAMMA1002937, MAMMA1003047, MAMMA1003099, MAMMA1003146, MAMMA1003 166, NT2RM1000035, NT2RM1000153, NT2RM1000257, NT2RM1000318, NT2RM1000377, NT2RM100 0394, NT2RM1000555, NT2RM1000691, NT2RM1000725, NT2RM1000770, NT2RM1000826, NT2RM10 00850, NT2RM1001059, NT2RM1001072, NT2RM1001082, NT2RM1001092, NT2RM2000363, NT2RM2 000374, NT2RM2000594, NT2RM2000599, NT2RM2000714, NT2RM2000740, NT2RM2000821, NT2RM 2001035, NT2RM2001499, NT2RM2001575, NT2RM2001605, NT2RM2001664, NT2RM2001670, NT2R M2001803, NT2RM2001823, NT2RM2001839, NT2RM4000085, NT2RM4000139, NT2RM4000155, NT2 RM4000290, NT2RM4000689, NT2RM4000895, NT2RM4001320, NT2RM4001566, NT2RM4001629, NT 2RM4001741, NT2RM4001819, NT2RM4001823, NT2RM4001865, NT2RM4001940, NT2RM4002093, N T2RM4002146, NT2RM4002161, NT2RM4002189, NT2RM4002457, NT2RM4002558, NT2RM4002571, NT2RP1000086, NT2RP1000376, NT2RP1000574, NT2RP1000581, NT2RP1000629, NT2RP1000721, NT2RP1000733, NT2RP1000738, NT2RP1000825, NT2RP1000833, NT2RP1000860, NT2RP100096 6, NT2RP1001033, NT2RP1001247, NT2RP2000126, NT2RP2000147, NT2RP2000233, NT2RP20002 97, NT2RP2000310, NT2RP2000414, NT2RP2000448, NT2RP2000459, NT2RP2000603, NT2RP2000812, NT2RP2001127, NT2RP2001327, NT2RP2001440, NT2RP2001520, NT2RP2001663, NT2RP2001748, NT2RP2001876, NT2RP2001898, NT2RP2002025, NT2RP2002066, NT2RP200225 9, NT2RP2002312, NT2RP2002503, NT2RP2002618, NT2RP2003228, NT2RP2003293, NT2RP20032 95, NT2RP2003517, NT2RP2003564, NT2RP2003706, NT2RP2003737, NT2RP2003968, NT2RP2004 013, NT2RP2004098, NT2RP2004187, NT2RP2004316, NT2RP2004523, NT2RP2004538, NT2RP200 4933, NT2RP2005144, NT2RP2005288, NT2RP2005289, NT2RP2005325, NT2RP2005358, NT2RP20 05531, NT2RP2005773, NT2RP2006219, NT2RP3000050, NT2RP3000080, NT2RP3000299, NT2RP3 000397, NT2RP3000512, NT2RP3000527, NT2RP3001081, NT2RP3001216, NT2RP3001268, NT2RP 3001355, NT2RP3001427, NT2RP3001428, NT2RP3001497, NT2RP3001554, NT2RP3001724, NT2R P3001764, NT2RP3001799, NT2RP3001855, NT2RP3002045, NT2RP3002151, NT2RP3002351, NT2 RP3002352, NT2RP3002663, NT2RP3002818, NT2RP3002876, NT2RP3002909, NT2RP3002972, NT 2RP3003061, NT2RP3003157, NT2RP3003242, NT2RP3003282, NT2RP3003672, NT2RP3004078, N T2RP3004209, NT2RP3004399, NT2RP3004424, NT2RP3004475, NT2RP3004480, NT2RP3004490, NT2RP3004527, NT2RP3004578, NT2RP4000049, NT2RP4000109, NT2RP4000185, NT2RP4000312, NT2RP4000367, NT2RP4000398, NT2RP4000457, NT2RP4000855, NT2RP4000879, NT2RP400091 5, NT2RP4000928, NT2RP4001095, NT2RP4001150, NT2RP4001213, NT2RP4001483, NT2RP40014 98, NT2RP4001753, NT2RP4001838, OVARC1000014, OVARC1000114, OVARC1000139, OVARC1000241, OVARC1000440, OVARC1000543, OVARC1000722, OVARC1000771, OVARC1000834, OVARC1000850, OVARC1001113, OVARC1001244, OVARC1001296, OVARC1001357, OVARC100137 2, OVARC1001417, OVARC1001496, OVARC1001506, OVARC1001577, OVARC1001668, OVARC10017 13, OVARC1001809, OVARC1001880, OVARC1001901, OVARC1001949, OVARC1002050, PLACE1000 133, PLACE1000142, PLACE1000184, PLACE1000383, PLACE1000406, PLACE1000420, PLACE100 0583,

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PLACE1000588, PLACE1000706, PLACE1001384, PLACE1001387, PLACE1001517, PLACE10 01602, PLACE1001634, PLACE1001771, PLACE1002046, PLACE1002437, PLACE1002474, PLACE1 002665, PLACE1002834, PLACE1003302, PLACE1003493, PLACE1003704, PLACE1003888, PLACE 1003903, PLACE1003968, PLACE1004197, PLACE1004358, PLACE1004471, PLACE1004681, PLAC E1004751, PLACE1004773, PLACE1005101, PLACE1006040, PLACE1006119, PLACE1006170, PLA CE1006187, PLACE1006288, PLACE1006414, PLACE1006438, PLACE1006962, PLACE1007239, PL ACE1007257, PLACE1007488, PLACE1007511, PLACE1007737, PLACE1008000, PLACE1008402, P LACE1008643, PLACE1008696, PLACE1008941, PLACE1009027, PLACE1009200, PLACE1009230, PLACE1009298, PLACE1009319, PLACE1009444, PLACE1009524, PLACE1010083, PLACE1010089, PLACE1010599, PLACE1010833, PLACE1010856, PLACE1011054, PLACE1011057, PLACE101116 5, PLACE1011229, PLACE1011263, PLACE1011371, PLACE2000072, PLACE2000399, PLACE20004 38, PLACE2000458, PLACE3000004, PLACE3000242, PLACE3000352, PLACE3000353, PLACE3000455, PLACE3000475, PLACE4000009, PLACE4000014, PLACE4000052, PLACE4000320, PLACE4000581, SKNMC1000050, THYRO1000026, THYRO1000173, THYRO1000186, THYRO100032 0, THYRO1000327, THYRO1000387, THYRO1000471, THYRO1000934, THYRO1001458, THYRO10015 95, THYRO1001605, THYRO1001617, THYRO1001671, Y79AA1000037, Y79AA1000469, Y79AA1000 539, Y79AA1000560, Y79AA1000734, Y79AA1000985, Y79AA1001105, Y79AA1001391, Y79AA100 1394, Y79AA1001548, Y79AA1001613, Y79AA1001874, Y79AA1002258, Y79AA1002416, Y79AA10 02482,

(6) The following 301 clones were predicted to encode a protein in the category of enzyme or proteins associated with metabolism (including the clones belonging to plural categories).

HEMBA1000012, HEMBA1000459, HEMBA1000852, HEMBA1001059, HEMBA1001257, HEMBA1001620, HEMBA1001714, HEMBA1001744, HEMBA1001896, HEMBA1002003, HEMBA1002212, HEMBA100225 7, HEMBA1002513, HEMBA1002973, HEMBA1003046, HEMBA1003136, HEMBA1003179, HEMBA10032 86, HEMBA1003291, HEMBA1003538, HEMBA1003680, HEMBA1004227, HEMBA1004408, HEMBA1004 734, HEMBA1004795, HEMBA1005513, HEMBA1005737, HEMBA1005815, HEMBA1006278, HEMBA100 6347, HEMBA1006521, HEMBA1006648, HEMBA1006877, HEMBA1006941, HEMBA1006976, HEMBA10 07121, HEMBA1007243, HEMBA1007300, HEMBB1000781, HEMBB1000915, HEMBB1001288, HEMBB1 001429, HEMBB1001443, HEMBB1001915, HEMBB1002042, HEMBB1002342, HEMBB1002358, HEMBB 1002635, HEMBB1002683, MAMMA1000020, MAMMA1000085, MAMMA1000672, MAMMA1000841, MAMM A1001008, MAMMA1001139, MAMMA1001476, MAMMA1001501, MAMMA1002268, MAMMA1002530, MAM MA1002619, MAMMA1002671, MAMMA1002938, NT2RM1000132, NT2RM1000153, NT2RM1000256, NT 2RM1000280, NT2RM1000377, NT2RM1000648, NT2RM1000850, NT2RM1000867, NT2RM1000894, N T2RM1001072, NT2RM2000013, NT2RM2000124, NT2RM2000191, NT2RM2000368, NT2RM2000371, NT2RM2000577, NT2RM2000594, NT2RM2000599, NT2RM2000951, NT2RM2001238, NT2RM2001664, NT2RM2001700, NT2RM2001730, NT2RM2001785, NT2RM2001803, NT2RM2002030, NT2RM400002 4, NT2RM4000155, NT2RM4000344, NT2RM4000496, NT2RM4000616, NT2RM4000712, NT2RM40008 95, NT2RM4001313, NT2RM4001316, NT2RM4001340, NT2RM4001444, NT2RM4001758, NT2RM4001819, NT2RM4001930, NT2RM4002062, NT2RM4002063, NT2RM4002409, NT2RM4002558, NT2RM4002571, NT2RM4002623, NT2RP1000018, NT2RP1000112, NT2RP1000376, NT2RP100060 9, NT2RP1000833, NT2RP1000834, NT2RP1001079, NT2RP1001253, NT2RP1001361, NT2RP10015 43, NT2RP2000056, NT2RP2000114, NT2RP2000183, NT2RP2000329, NT2RP2000422, NT2RP2000 710, NT2RP2000764, NT2RP2000932, NT2RP2001070, NT2RP2001663, NT2RP2001839, NT2RP200 1898, NT2RP2002256, NT2RP2002312, NT2RP2002442, NT2RP2002595, NT2RP2002618, NT2RP20 02993, NT2RP2003230, NT2RP2003286, NT2RP2003506, NT2RP2003643, NT2RP2003706, NT2RP2 003737, NT2RP2003781, NT2RP2003912, NT2RP2004232, NT2RP2004239, NT2RP2004768, NT2RP 2004791, NT2RP2004799, NT2RP2005038, NT2RP2005276, NT2RP2005344, NT2RP2005457, NT2R P2005498, NT2RP2005531, NT2RP2005557, NT2RP2005690, NT2RP2005773, NT2RP2005775, NT2 RP2005942, NT2RP2006571, NT2RP3000046, NT2RP3000085, NT2RP3000359, NT2RP3000418, NT 2RP3000742, NT2RP3000845, NT2RP3000875, NT2RP3001274, NT2RP3001407, NT2RP3001495, N T2RP3002351, NT2RP3002402, NT2RP3002969, NT2RP3003301, NT2RP3003346, NT2RP3003500, NT2RP3003800, NT2RP3003825, NT2RP3003831, NT2RP3003914, NT2RP3004155, NT2RP3004209 NT2RP3004669, NT2RP3004670, NT2RP4000259, NT2RP4000417, NT2RP4000457, NT2RP400072 4, NT2RP4000855, NT2RP4000928, NT2RP4000997, NT2RP4001041, NT2RP4001079, NT2RP40010 95, NT2RP4001219, NT2RP4001345, NT2RP4001375, NT2RP4001483, NT2RP4001592, NT2RP4001644, NT2RP4001893, NT2RP4001946, NT2RP4002408, NT2RP5003500, NT2RP5003522, OVARC1000060, OVARC1000139, OVARC1000309, OVARC1000543, OVARC1000682, OVARC100072 2, OVARC1000885, OVARC1001261, OVARC1001610, OVARC1001713, OVARC1001762, OVARC10018 09,

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(7) The following 74 clones were predicted to encode a protein in the category of proteins associated with cell division or cell proliferation (including the clones belonging to plural categories).
HEMBA1001019, HEMBA1001595, HEMBA1002229, HEMBA1002363, HEMBA1003136, HEMBA1003836, HEMBA1004131, HEMBA1005241, HEMBB1000399, HEMBB1001175, HEMBB1001242, MAMMA100182 0, MAMMA1003011, NT2RM1000394, NT2RM2001256, NT2RM4000215, NT2RM4001611, NT2RM40017 14, NT2RP1000733, NT2RP1001177, NT2RP2000077, NT2RP2000346, NT2RP2001397, NT2RP2003 912, NT2RP2005520, NT2RP2005675, NT2RP2005767, NT2RP2005857, NT2RP2006464, NT2RP300 0031, NT2RP3001155, NT2RP3001730, NT2RP3002151, NT2RP3002273, NT2RP3002399, NT2RP30 04507, NT2RP3004578, NT2RP3004594, NT2RP4000210, NT2RP4000498, NT2RP4001207, NT2RP4 001414, NT2RP4001551, OVARC1000006, OVARC1000087, OVARC1000113, OVARC1000846, OVARC 1000876, OVARC1001068, OVARC1001107, OVARC1001113, OVARC1002112, PLACE1000547, PLAC E1001611, PLACE1001691, PLACE1002775, PLACE1002811, PLACE1003709, PLACE1004316, PLA CE1004674, PLACE1004814, PLACE1005287, PLACE1006187, PLACE1006368, PLACE1008808, PL ACE1008947, PLACE1009060, PLACE1010720, PLACE1010761, PLACE1010833, PLACE1011056, P LACE3000244, Y79AA1000214, Y79AA1001236,

(8) The following 92 clones were predicted to encode a protein in the category of proteins associated with cytoskeleton (including the clones belonging to plural categories).
HEMBA1000020, HEMBA1000588, HEMBA1001804, HEMBA1002102, HEMBA1002161, HEMBA1002939, HEMBA1003235, HEMBA1003581, HEMBA1004534, HEMBA1005009, HEMBA1005595, HEMBA100627 2, HEMBA1006737, HEMBA1007018, HEMBB1000404, HEMBB1001282, MAMMA1000173, MAMMA10004 29, MAMMA1001041, MAMMA1001576, MAMMA1001735, MAMMA1002622, MAMMA1002637, MAMMA1003 099, MAMMA1003127, NT2RM1000898, NT2RM1001003, NT2RM1001139, NT2RM2000691, NT2RM400 0030, NT2RM4000167, NT2RM4000689, NT2RM4001741, NT2RM4001776, NT2RM4002109, NT2RP10 00348, NT2RP1000460, NT2RP1000478, NT2RP1001033, NT2RP2000812, NT2RP2001634, NT2RP2 001900, NT2RP2002727, NT2RP2003307, NT2RP2003604, NT2RP2004538, NT2RP2005531, NT2RP 3000868, NT2RP3001216, NT2RP3001272, NT2RP3002688, NT2RP3003061, NT2RP3003138, NT2R P3003230, NT2RP3003282, NT2RP3004454, NT2RP3004569, NT2RP4001126, NT2RP4001927, OVA RC1000437, OVARC1000520, OVARC1000679, OVARC1001731, OVARC1002050, PLACE1002571, PL ACE1002591, PLACE1002655, PLACE1003669, PLACE1004777, PLACE1005287, PLACE1006368, P LACE1007105, PLACE1010310, PLACE1010743, PLACE1010960, PLACE1011263, PLACE2000039, PLACE2000216, PLACE2000274, PLACE3000145, PLACE3000322, PLACE4000009, PLACE4000612, THYRO1000072, THYRO1000666, THYRO1001121, THYRO1001458, Y79AA1000368, Y79AA100083 3, Y79AA1000962, Y79AA1000985, Y79AA1002208,

(9) The following 280 clones were predicted to encode a protein in the category of proteins associated with RNA synthesis (including the clones belonging to plural categories).
HEMBA1000201, HEMBA1000216, HEMBA1000488, HEMBA1000561, HEMBA1000591, HEMBA1000851, HEMBA1001137, HEMBA1001510, HEMBA1001579, HEMBA1001800, HEMBA1001809, HEMBA100181 9, HEMBA1001847, HEMBA1002035, HEMBA1002092, HEMBA1002569, HEMBA1002609, HEMBA10034 18, HEMBA1003545, HEMBA1003568, HEMBA1003684, HEMBA1003760, HEMBA1003953, HEMBA1004 097, HEMBA1004321, HEMBA1004353, HEMBA1004479, HEMBA1004669, HEMBA1004758, HEMBA100 5359, HEMBA1005528, HEMBA1005548, HEMBA1005931, HEMBA1006253, HEMBA1006278, HEMBA10 06359,

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HEMBA1006559, HEMBA1006639, HEMBB1000250, HEMBB1000789, HEMBB1001011, HEMBB1 001314, HEMBB1001482, HEMBB1001908, HEMBB1002134, HEMBB1002217, MAMMA1000155, MAMMA 1000183, MAMMA1000388, MAMMA1001059, MAMMA1001633, MAMMA1001820, MAMMA1001837, MAMM A1002650, MAMMA1002937, NT2RM1000055, NT2RM1000187, NT2RM1000666, NT2RM1000691, NT2 RM1000852, NT2RM1000894, NT2RM1001092, NT2RM2000013, NT2RM2000735, NT2RM2001035, NT 2RM2001424, NT2RM2001575, NT2RM2001605, NT2RM2001670, NT2RM2001771, NT2RM2001797, N T2RM2001989, NT2RM2002100, NT2RM2002580, NT2RM4000024, NT2RM4000104, NT2RM4000191, NT2RM4000421, NT2RM4000471, NT2RM4000496, NT2RM4000531, NT2RM4000734, NT2RM4000751 , NT2RM4000996, NT2RM4001140, NT2RM4001200, NT2RM4001483, NT2RM4001592, NT2RM400174 6, NT2RM4001783, NT2RM4001823, NT2RM4001828, NT2RM4001858, NT2RM4001979, NT2RM40020 93, NT2RM4002479, NT2RP1000111, NT2RP1000272, NT2RP1000333, NT2RP1000470, NT2RP1000574, NT2RP1000721, NT2RP1000860, NT2RP1001080, NT2RP2000008, NT2RP2000133 , NT2RP2000161, NT2RP2000297, NT2RP2000931, NT2RP2001174, NT2RP2001233, NT2RP200144 9, NT2RP2002099, NT2RP2002252, NT2RP2002503, NT2RP2002591, NT2RP2002928, NT2RP20031 25, NT2RP2003228, NT2RP2003293, NT2RP2003564, NT2RP2003714, NT2RP2004013, NT2RP2004 187, NT2RP2004568, NT2RP2004961, NT2RP2005003, NT2RP2005037, NT2RP2005126, NT2RP200 5168, NT2RP2005239, NT2RP2005287, NT2RP2005496, NT2RP2005539, NT2RP2005722, NT2RP20 05763, NT2RP2005942, NT2RP2006238, NT2RP2006464, NT2RP3000050, NT2RP3000361, NT2RP3 000397, NT2RP3000512, NT2RP3000527, NT2RP3000590, NT2RP3000632, NT2RP3000917, NT2RP 3001057, NT2RP3001120, NT2RP3001155, NT2RP3001268, NT2RP3001398, NT2RP3001399, NT2R P3001671, NT2RP3001672, NT2RP3001688, NT2RP3001712, NT2RP3001792, NT2RP3001855, NT2 RP3002165, NT2RP3002377, NT2RP3002399, NT2RP3003157, NT2RP3003193, NT2RP3003251, NT 2RP3003327, NT2RP3004013, NT2RP3004258, NT2RP3004504, NT2RP3004566, NT2RP3004572, N T2RP3004594, NT2RP3004617, NT2RP4000078, NT2RP4000111, NT2RP4000210, NT2RP4000398, NT2RP4000449, NT2RP4000518, NT2RP4000614, NT2RP4000787, NT2RP4000865, NT2RP4000997 , NT2RP4001029, NT2RP4001080, NT2RP4001148, NT2RP4001213, NT2RP4001433, NT2RP400152 9, NT2RP4001551, NT2RP4001638, NT2RP4001753, NT2RP4001790, NT2RP4001938, NT2RP40020 78, OVARC1000479, OVARC1000846, OVARC1001381, OVARC1001555, OVARC1001577, OVARC1001949, PLACE1000066, PLACE1000133, PLACE1000583, PLACE1000596, PLACE1000706 , PLACE1001118, PLACE1001238, PLACE1001304, PLACE1001602, PLACE1001632, PLACE100245 0, PLACE1002532, PLACE1002834, PLACE1003190, PLACE1003302, PLACE1003605, PLACE10037 04, PLACE1003738, PLACE1003885, PLACE1004471, PLACE1004510, PLACE1004564, PLACE1004 681, PLACE1004902, PLACE1005646, PLACE1005876, PLACE1006196, PLACE1006414, PLACE100 6438, PLACE1006482, PLACE1007239, PLACE1007346, PLACE1007544, PLACE1007598, PLACE10 07955, PLACE1007969, PLACE1008627, PLACE1008941, PLACE1009099, PLACE1009246, PLACE1 009398, PLACE1010053, PLACE1010194, PLACE1010261, PLACE1010491, PLACE1010580, PLACE 1010702, PLACE1010771, PLACE1010870, PLACE1011576, PLACE2000072, PLACE2000359, PLAC E4000128, PLACE4000156, PLACE4000259, PLACE4000431, THYRO1000121, THYRO1000242, THY RO1000501, THYRO1000585, THYRO1001100, THYRO1001189, Y79AA1000037, Y79AA1000349, Y7 9AA1000539, Y79AA1000627, Y79AA1000705, Y79AA1000752, Y79AA1001105, Y79AA1001299, Y 79AA1001391, Y79AA1001533, Y79AA1001613, Y79AA1001848, Y79AA1001866, Y79AA1001963, Y79AA1002093, Y79AA1002472, Y79AA1002482,

(10) The following 352 clones were predicted to encode a protein in the category of nuclear protein (including the clones belonging to plural categories).

HEMBA1000005, HEMBA1000201, HEMBA1000216, HEMBA1000488, HEMBA1000561, HEMBA1000827 , HEMBA1000851, HEMBA1001088, HEMBA1001137, HEMBA1001476, HEMBA1001510, HEMBA100157 9, HEMBA1001800, HEMBA1001809, HEMBA1001819, HEMBA1001847, HEMBA1002035, HEMBA10020 92, HEMBA1002363, HEMBA1002495, HEMBA1002569, HEMBA1002609, HEMBA1002999, HEMBA1003 148, HEMBA1003418, HEMBA1003545, HEMBA1003568, HEMBA1003684, HEMBA1003760, HEMBA100 3783, HEMBA1003953, HEMBA1004097, HEMBA1004321, HEMBA1004353, HEMBA1004479, HEMBA10 04669, HEMBA1004758, HEMBA1005359, HEMBA1005475, HEMBA1005528, HEMBA1005548, HEMBA1 005931, HEMBA1006253, HEMBA1006278, HEMBA1006359, HEMBA1006474, HEMBA1006559, HEMBA 1006914, HEMBB1000250, HEMBB1000399, HEMBB1000789, HEMBB1001011, HEMBB1001314, HEMB B1001482, HEMBB1001908, HEMBB1001915, HEMBB1002134, HEMBB1002217, MAMMA1000155, MAM MA1000183, MAMMA1000388, MAMMA1000731, MAMMA1001633, MAMMA1001820, MAMMA1001837, MA MMA1002650, MAMMA1002869, MAMMA1002937, MAMMA1003011, NT2RM1000055, NT2RM1000187, N T2RM1000257, NT2RM1000394, NT2RM1000666, NT2RM1000691, NT2RM1000852, NT2RM1000894, NT2RM1001092,

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NT2RM2000013, NT2RM2000735, NT2RM2001035, NT2RM2001575, NT2RM2001605, NT2RM2001635, NT2RM2001670, NT2RM2001771, NT2RM2001797, NT2RM2001823, NT2RM200193 6, NT2RM2001989, NT2RM2002100, NT2RM2002580, NT2RM4000024, NT2RM4000085, NT2RM40001 04, NT2RM4000191, NT2RM4000215, NT2RM4000290, NT2RM4000421, NT2RM4000496, NT2RM4000531, NT2RM4000734, NT2RM4000751, NT2RM4000996, NT2RM4001140, NT2RM4001200, NT2RM4001217, NT2RM4001382, NT2RM4001483, NT2RM4001592, NT2RM4001605, NT2RM400161 1, NT2RM4001746, NT2RM4001783, NT2RM4001823, NT2RM4001828, NT2RM4001858, NT2RM40019 79, NT2RM4002093, NT2RM4002146, NT2RM4002527, NT2RP1000035, NT2RP1000111, NT2RP1000 333, NT2RP1000493, NT2RP1000574, NT2RP1000721, NT2RP1000860, NT2RP1000966, NT2RP100 1177, NT2RP2000008, NT2RP2000126, NT2RP2000133, NT2RP2000161, NT2RP2000297, NT2RP20 00414, NT2RP2000931, NT2RP2001174, NT2RP2001233, NT2RP2001420, NT2RP2001449, NT2RP2 001536, NT2RP2001762, NT2RP2002185, NT2RP2002252, NT2RP2002259, NT2RP2002503, NT2RP 2002504, NT2RP2002591, NT2RP2002993, NT2RP2003125, NT2RP2003228, NT2RP2003277, NT2R P2003286, NT2RP2003293, NT2RP2003308, NT2RP2003564, NT2RP2003714, NT2RP2004013, NT2 RP2004187, NT2RP2004961, NT2RP2005003, NT2RP2005037, NT2RP2005287, NT2RP2005496, NT 2RP2005520, NT2RP2005539, NT2RP2005722, NT2RP2005767, NT2RP2005857, NT2RP2005942, N T2RP2006238, NT2RP2006464, NT2RP3000031, NT2RP3000050, NT2RP3000361, NT2RP3000397, NT2RP3000512, NT2RP3000527, NT2RP1000590, NT2RP3000603, NT2RP3000632, NT2RP3000917, NT2RP3001057, NT2RP3001120, NT2RP3001155, NT2RP3001268, NT2RP3001274, NT2RP300139 8, NT2RP3001399, NT2RP3001427, NT2RP3001428, NT2RP3001587, NT2RP3001671, NT2RP30016 72, NT2RP3001688, NT2RP3001712, NT2RP3001724, NT2RP3001792, NT2RP3001855, NT2RP3002056, NT2RP3002165, NT2RP3002377, NT2RP3002399, NT2RP3003157, NT2RP3003193, NT2RP3003212, NT2RP3003251, NT2RP3003327, NT2RP3004206, NT2RP3004209, NT2RP300425 8, NT2RP3004566, NT2RP3004572, NT2RP3004594, NT2RP3004617, NT2RP4000078, NT2RP40001 11, NT2RP4000150, NT2RP4000210, NT2RP4000398, NT2RP4000449, NT2RP4000457, NT2RP4000 518, NT2RP4000787, NT2RP4000865, NT2RP4000997, NT2RP4001029, NT2RP4001080, NT2RP400 1148, NT2RP4001207, NT2RP4001213, NT2RP4001433, NT2RP4001529, NT2RP4001551, NT2RP40 01638, NT2RP4001753, NT2RP4001790, NT2RP4001938, NT2RP4002078, OVARC1000006, OVARC1 000087, OVARC1000139, OVARC1000326, OVARC1000440, OVARC1000479, OVARC1000846, OVARC 1000883, OVARC1001180, OVARC1001244, OVARC1001381, OVARC1001555, OVARC1001577, OVAR C1001702, OVARC1001949, OVARC1002112, PLACE1000066, PLACE1000133, PLACE1000406, PLA CE1000583, PLACE1000596, PLACE1000706, PLACE1001118, PLACE1001238, PLACE1001304, PL ACE1001602, PLACE1001611, PLACE1001632, PLACE1002450, PLACE1002532, PLACE1002834, P LACE1003100, PLACE1003190, PLACE1003302, PLACE1003605, PLACE1003704, PLACE1003738, PLACE1003885, PLACE1004471, PLACE1004510, PLACE1004564, PLACE1004681, PLACE1004902, PLACE1005287, PLACE1005876, PLACE1006011, PLACE1006119, PLACE1006414, PLACE100643 8, PLACE1006482, PLACE1007239, PLACE1007346, PLACE1007544, PLACE1007598, PLACE10079 55, PLACE1007969, PLACE1008044, PLACE1008177, PLACE1008603, PLACE1008627, PLACE1008941, PLACE1008947, PLACE1009099, PLACE1009113, PLACE1009246, PLACE1009398, PLACE1010152, PLACE1010194, PLACE1010261, PLACE1010491, PLACE1010702, PLACE101072 0, PLACE1010771, PLACE1010870, PLACE1011056, PLACE1011229, PLACE1011576, PLACE10116 64, PLACE2000072, PLACE2000359, PLACE2000411, PLACE4000014, PLACE4000128, PLACE4000 156, PLACE4000259, PLACE4000261, PLACE4000431, THYRO1000121, THYRO1000242, THYRO100 0501, THYRO1000585, THYRO1001100, THYRO1001189, Y79AA1000037, Y79AA1000214, Y79AA10 00539, Y79AA1000589, Y79AA1000627, Y79AA1000705, Y79AA1000752, Y79AA1000784, Y79AA1 001105, Y79AA1001299, Y79AA1001391, Y79AA1001533, Y79AA1001613, Y79AA1001848, Y79AA 1001866, Y79AA1001963, Y79AA1002093, Y79AA1002472, Y79AA1002482,

(11) The following 111 clones were predicted to encode a protein in the category of proteins associated with protein synthesis or transport (including the clones belonging to plural categories).

HEMBA1000012, HEMBA1000542, HEMBA1001913, HEMBA1003773, HEMBA1004202, HEMBA1004356, HEMBA1004847, HEMBA1005047,HEMBA1005202, HEMBA1005963, HEMBA1006310, HEMBA100665 2, HEMBA1006914, HEMBB1000217, HEMBB1000725, HEMBB1001346, HEMBB1001831, MAMMA10000 85, MAMMA1000734, MAMMA1002170, MAMMA1002236, MAMMA1002598, NT2RM1000661, NT2RM2000 504, NT2RM2000577, NT2RM2001131, NT2RM4000155, NT2RM4001444, NT2RM4002062, NT2RM400 2205, NT2RM4002623, NT2RP1000326, NT2RP1000947, NT2RP1001569, NT2RP2000710, NT2RP20 00880, NT2RP2001290, NT2RP2001511, NT2RP2001660, NT2RP2002185, NT2RP2002606, NT2RP2 002959, NT2RP2002980, NT2RP2003158, NT2RP2003760, NT2RP2004194, NT2RP2004791, NT2RP 2005012,

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NT2RP2005116, NT2RP2005204, NT2RP2006565, NT2RP2006598, NT2RP3000047, NT2R P3000366, NT2RP3000759, NT2RP3000968, NT2RP3001587, NT2RP3002529, NT2RP3003385, NT2 RP3003589, NT2RP3003876, NT2RP3004618, NT2RP4000370, NT2RP4000524, NT2RP4000528, NT 2RP4001041, NT2RP4001574, NT2RP4001592, NT2RP4002047, OVARC1000004, OVARC1000771, O VARC1000862, OVARC1001180, OVARC1001342, OVARC1001766, OVARC1002138, PLACE1000061, PLACE1000492, PLACE1000863, PLACE1001748, PLACE1002090, PLACE1003394, PLACE1003915, PLACE1004149, PLACE1004743, PLACE1005557, PLACE1005813, PLACE1006488, PLACE100653 1, PLACE1006615, PLACE1007706, PLACE1008273, PLACE1008790, PLACE1008813, PLACE10097 21, PLACE1009763, PLACE1009845, PLACE1010074, PLACE1011109, PLACE1011477, PLACE2000404, PLACE3000059, PLACE3000121, PLACE4000558, PLACE4000654, SKNMC1000011, THYRO1000288, THYRO1000974, Y79AA1000346, Y79AA1000968, Y79AA1002209,

(12) The following 23 clones were predicted to encode a protein in the category of proteins associated with cellular defense (including the clones belonging to plural categories).
HEMBA1000005, HEMBA1000531, HEMBB1000217, HEMBB1000399, MAMMA1000734, NT2RP1000493, NT2RP1000493, NT2RP2000006, NT2RP2000045, NT2RP2001536, NT2RP2005204, NT2RP300059 0, NT2RP3001426, NT2RP3002056, NT2RP3004262, NT2RP4001638, OVARC1001900, PLACE10056 11, PLACE1006958, PLACE1008275, PLACE1009113, PLACE4000014, Y79AA1002139,

(13) The following 23 clones were predicted to encode a protein in the category of proteins associated with development or growth (including the clones belonging to plural categories).
HEMBB1001802, HEMBB1002442, NT2RM2002142, NT2RM4001047, NT2RP2003308, NT2RP2004816, NT2RP3000994, NT2RP3001340, NT2RP3004206, NT2RP3004472, NT2RP4000246, NT2RP400100 6, OVARC1000304, OVARC1000746, OVARC1000996, PLACE1006037, PLACE1009622, PLACE10116 64, Y79AA1001692,

Table 9

Selected clones having the maximal ATGpr1 score of 0.3 or higher (3690 clones).

clone name	name of sequence	maximal ATGpr1 score
HEMBA1000005	F-HEMBA1000005	0.84
HEMBA1000012	F-HEMBA1000012	0.56
HEMBA1000020	F-HEMBA1000020	0.94
HEMBA1000030	F-HEMBA1000030	0.44
HEMBA1000046	F-HEMBA1000046	0.50
HEMBA1000050	F-HEMBA1000050	0.94
HEMBA1000076	F-HEMBA1000076	0.48
HEMBA1000129	F-HEMBA1000129	0.74
HEMBA1000141	F-HEMBA1000141	0.55
HEMBA1000150	F-HEMBA1000150	0.72
HEMBA1000156	F-HEMBA1000156	0.94
HEMBA1000158	F-HEMBA1000158	0.62
HEMBA1000168	F-HEMBA1000168	0.94
HEMBA1000185	F-HEMBA1000185	0.86
HEMBA1000193	F-HEMBA1000193	0.94

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HEMBA1000201	F-HEMBA1000201	0.83
HEMBA1000216	F-HEMBA1000216	0.32
HEMBA1000227	F-HEMBA1000227	0.72
HEMBA1000231	F-HEMBA1000231	0.34
HEMBA1000244	F-HEMBA1000244	0.51
HEMBA1000288	F-HEMBA1000288	0.36
HEMBA1000290	F-HEMBA1000290	0.45
HEMBA1000302	F-HEMBA1000302	0.71
HEMBA1000303	F-HEMBA1000303	0.42
HEMBA1000304	F-HEMBA1000304	0.45
HEMBA1000307	F-HEMBA1000307	0.48
HEMBA1000327	F-HEMBA1000327	0.94
HEMBA1000356	F-HEMBA1000356	0.90
HEMBA1000369	F-HEMBA1000369	0.94
HEMBA1000387	F-HEMBA1000387	0.66
HEMBA1000392	F-HEMBA1000392	0.60
HEMBA1000396	F-HEMBA1000396	0.81
HEMBA1000456	F-HEMBA1000456	0.90
HEMBA1000460	F-HEMBA1000460	0.31
HEMBA1000488	F-HEMBA1000488	0.47
HEMBA1000490	F-HEMBA1000490	0.89
HEMBA1000491	F-HEMBA1000491	0.94
HEMBA1000501	F-HEMBA1000501	0.67
HEMBA1000505	F-HEMBA1000505	0.65
HEMBA1000508	F-HEMBA1000508	0.39
HEMBA1000520	F-HEMBA1000520	0.94
HEMBA1000523	F-HEMBA1000523	0.86
HEMBA1000531	F-HEMBA1000531	0.49
HEMBA1000534	F-HEMBA1000534	0.52
HEMBA1000542	F-HEMBA1000542	0.81
HEMBA1000555	F-HEMBA1000555	0.67
HEMBA1000561	F-HEMBA1000561	0.34
HEMBA1000568	F-HEMBA1000568	0.66
HEMBA1000588	F-HEMBA1000588	0.79
HEMBA1000591	F-HEMBA1000591	0.92
HEMBA1000592	F-HEMBA1000592	0.73
HEMBA1000594	F-HEMBA1000594	0.89
HEMBA1000608	F-HEMBA1000608	0.94
HEMBA1000636	F-HEMBA1000636	0.94
HEMBA1000637	F-HEMBA1000637	0.92
HEMBA1000657	F-HEMBA1000657	0.85
HEMBA1000682	F-HEMBA1000682	0.94
HEMBA1000686	F-HEMBA1000686	0.90
HEMBA1000719	F-HEMBA1000719	0.94
HEMBA1000727	F-HEMBA1000727	0.40
HEMBA1000752	F-HEMBA1000752	0.31

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HEMBA1000817	F-HEMBA1000817	0.94
HEMBA1000851	F-HEMBA1000851	0.63
HEMBA1000867	F-HEMBA1000867	0.68
HEMBA1000869	F-HEMBA1000869	0.82
HEMBA1000872	F-HEMBA1000872	0.54
HEMBA1000910	F-HEMBA1000910	0.91
HEMBA1000918	F-HEMBA1000918	0.38
HEMBA1000919	F-HEMBA1000919	0.83
HEMBA1000942	F-HEMBA1000942	0.31
HEMBA1000946	F-HEMBA1000946	0.75
HEMBA1000968	F-HEMBA1000968	0.39
HEMBA1000971	F-HEMBA1000971	0.74
HEMBA1000975	F-HEMBA1000975	0.46
HEMBA1000986	F-HEMBA1000986	0.89
HEMBA1001008	F-HEMBA1001008	0.47
HEMBA1001009	F-HEMBA1001009	0.86
HEMBA1001022	F-HEMBA1001022	0.57
HEMBA1001043	F-HEMBA1001043	0.79
HEMBA1001052	F-HEMBA1001052	0.83
HEMBA1001059	F-HEMBA1001059	0.78
HEMBA1001080	F-HEMBA1001080	0.77
HEMBA1001085	F-HEMBA1001085	0.92
HEMBA1001088	F-HEMBA1001088	0.94
HEMBA1001109	F-HEMBA1001109	0.50
HEMBA1001122	F-HEMBA1001122	0.74
HEMBA1001133	F-HEMBA1001133	0.45
HEMBA1001137	F-HEMBA1001137	0.37
HEMBA1001140	F-HEMBA1001140	0.43
HEMBA1001174	F-HEMBA1001174	0.44
HEMBA1001197	F-HEMBA1001197	0.65
HEMBA1001213	F-HEMBA1001213	0.61
HEMBA1001235	F-HEMBA1001235	0.94
HEMBA1001247	F-HEMBA1001247	0.31
HEMBA1001257	F-HEMBA1001257	0.92
HEMBA1001281	F-HEMBA1001281	0.94
HEMBA1001286	F-HEMBA1001286	0.49
HEMBA1001289	F-HEMBA1001289	0.94
HEMBA1001302	F-HEMBA1001302	0.62
HEMBA1001303	F-HEMBA1001303	0.79
HEMBA1001310	F-HEMBA1001310	0.66
HEMBA1001326	F-HEMBA1001326	0.59
HEMBA1001351	F-HEMBA1001351	0.65
HEMBA1001361	F-HEMBA1001361	0.94
HEMBA1001377	F-HEMBA1001377	0.87
HEMBA1001387	F-HEMBA1001387	0.94
HEMBA1001388	F-HEMBA1001388	0.57

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HEMBA1001398	F-HEMBA1001398	0.74
HEMBA1001405	F-HEMBA1001405	0.61
HEMBA1001407	F-HEMBA1001407	0.43
HEMBA1001413	F-HEMBA1001413	0.40
HEMBA1001415	F-HEMBA1001415	0.94
HEMBA1001446	F-HEMBA1001446	0.90
HEMBA1001450	F-HEMBA1001450	0.40
HEMBA1001455	F-HEMBA1001455	0.73
HEMBA1001476	F-HEMBA1001476	0.65
HEMBA1001497	F-HEMBA1001497	0.48
HEMBA1001510	F-HEMBA1001510	0.36
HEMBA1001526	F-HEMBA1001526	0.66
HEMBA1001533	F-HEMBA1001533	0.46
HEMBA1001569	F-HEMBA1001569	0.73
HEMBA1001570	F-HEMBA1001570	0.53
HEMBA1001579	F-HEMBA1001579	0.82
HEMBA1001581	F-HEMBA1001581	0.80
HEMBA1001595	F-HEMBA1001595	0.72
HEMBA1001620	F-HEMBA1001620	0.94
HEMBA1001635	F-HEMBA1001635	0.87
HEMBA1001640	F-HEMBA1001640	0.82
HEMBA1001647	F-HEMBA1001647	0.91
HEMBA1001655	F-HEMBA1001655	0.39
HEMBA1001661	F-HEMBA1001661	0.86
HEMBA1001672	F-HEMBA1001672	0.94
HEMBA1001702	F-HEMBA1001702	0.72
HEMBA1001711	F-HEMBA1001711	0.74
HEMBA1001714	F-HEMBA1001714	0.89
HEMBA1001723	F-HEMBA1001723	0.94
HEMBA1001731	F-HEMBA1001731	0.37
HEMBA1001744	F-HEMBA1001744	0.31
HEMBA1001746	F-HEMBA1001746	0.39
HEMBA1001781	F-HEMBA1001781	0.67
HEMBA1001800	F-HEMBA1001800	0.69
HEMBA1001804	F-HEMBA1001804	0.85
HEMBA1001809	F-HEMBA1001809	0.78
HEMBA1001815	F-HEMBA1001815	0.49
HEMBA1001819	F-HEMBA1001819	0.90
HEMBA1001822	F-HEMBA1001822	0.80
HEMBA1001824	F-HEMBA1001824	0.68
HEMBA1001847	F-HEMBA1001847	0.46
HEMBA1001864	F-HEMBA1001864	0.34
HEMBA1001866	F-HEMBA1001866	0.53
HEMBA1001869	F-HEMBA1001869	0.69
HEMBA1001896	F-HEMBA1001896	0.48
HEMBA1001910	F-HEMBA1001910	0.84

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HEMBA1001912	F-HEMBA1001912	0.48
HEMBA1001913	F-HEMBA1001913	0.94
HEMBA1001915	F-HEMBA1001915	0.41
HEMBA1001921	F-HEMBA1001921	0.94
HEMBA1001939	F-HEMBA1001939	0.87
HEMBA1001950	F-HEMBA1001950	0.36
HEMBA1001967	F-HEMBA1001967	0.94
HEMBA1001987	F-HEMBA1001987	0.41
HEMBA1002018	F-HEMBA1002018	0.41
HEMBA1002035	F-HEMBA1002035	0.36
HEMBA1002049	F-HEMBA1002049	0.39
HEMBA1002084	F-HEMBA1002084	0.45
HEMBA1002092	F-HEMBA1002092	0.94
HEMBA1002102	F-HEMBA1002102	0.94
HEMBA1002119	F-HEMBA1002119	0.60
HEMBA1002125	F-HEMBA1002125	0.88
HEMBA1002150	F-HEMBA1002150	0.31
HEMBA1002151	F-HEMBA1002151	0.82
HEMBA1002161	F-HEMBA1002161	0.94
HEMBA1002177	F-HEMBA1002177	0.38
HEMBA1002189	F-HEMBA1002189	0.43
HEMBA1002191	F-HEMBA1002191	0.94
HEMBA1002199	F-HEMBA1002199	0.85
HEMBA1002212	F-HEMBA1002212	0.39
HEMBA1002215	F-HEMBA1002215	0.94
HEMBA1002229	F-HEMBA1002229	0.83
HEMBA1002237	F-HEMBA1002237	0.86
HEMBA1002241	F-HEMBA1002241	0.66
HEMBA1002265	F-HEMBA1002265	0.38
HEMBA1002267	F-HEMBA1002267	0.33
HEMBA1002341	F-HEMBA1002341	0.53
HEMBA1002363	F-HEMBA1002363	0.88
HEMBA1002417	F-HEMBA1002417	0.83
HEMBA1002419	F-HEMBA1002419	0.92
HEMBA1002430	F-HEMBA1002430	0.45
HEMBA1002439	F-HEMBA1002439	0.83
HEMBA1002458	F-HEMBA1002458	0.47
HEMBA1002460	F-HEMBA1002460	0.48
HEMBA1002462	F-HEMBA1002462	0.55
HEMBA1002469	F-HEMBA1002469	0.79
HEMBA1002475	F-HEMBA1002475	0.88
HEMBA1002477	F-HEMBA1002477	0.45
HEMBA1002495	F-HEMBA1002495	0.78
HEMBA1002503	F-HEMBA1002503	0.94
HEMBA1002508	F-HEMBA1002508	0.33
HEMBA1002513	F-HEMBA1002513	0.41

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HEMBA1002515	F-HEMBA1002515	0.94
HEMBA1002542	F-HEMBA1002542	0.46
HEMBA1002547	F-HEMBA1002547	0.45
HEMBA1002569	F-HEMBA1002569	0.86
HEMBA1002583	F-HEMBA1002583	0.86
HEMBA1002609	F-HEMBA1002609	0.75
HEMBA1002624	F-HEMBA1002624	0.59
HEMBA1002688	F-HEMBA1002688	0.88
HEMBA1002696	F-HEMBA1002696	0.82
HEMBA1002703	F-HEMBA1002703	0.94
HEMBA1002746	F-HEMBA1002746	0.33
HEMBA1002750	F-HEMBA1002750	0.53
HEMBA1002768	F-HEMBA1002768	0.94
HEMBA1002770	F-HEMBA1002770	0.61
HEMBA1002777	F-HEMBA1002777	0.90
HEMBA1002779	F-HEMBA1002779	0.92
HEMBA1002794	F-HEMBA1002794	0.86
HEMBA1002810	F-HEMBA1002810	0.87
HEMBA1002816	F-HEMBA1002816	0.91
HEMBA1002818	F-HEMBA1002818	0.94
HEMBA1002850	F-HEMBA1002850	0.57
HEMBA1002863	F-HEMBA1002863	0.48
HEMBA1002876	F-HEMBA1002876	0.86
HEMBA1002935	F-HEMBA1002935	0.91
HEMBA1002937	F-HEMBA1002937	0.61
HEMBA1002939	F-HEMBA1002939	0.32
HEMBA1002951	F-HEMBA1002951	0.83
HEMBA1002954	F-HEMBA1002954	0.67
HEMBA1002970	F-HEMBA1002970	0.33
HEMBA1002971	F-HEMBA1002971	0.57
HEMBA1002973	F-HEMBA1002973	0.33
HEMBA1002997	F-HEMBA1002997	0.46
HEMBA1002999	F-HEMBA1002999	0.49
HEMBA1003021	F-HEMBA1003021	0.74
HEMBA1003033	F-HEMBA1003033	0.94
HEMBA1003035	F-HEMBA1003035	0.61
HEMBA1003041	F-HEMBA1003041	0.40
HEMBA1003046	F-HEMBA1003046	0.94
HEMBA1003067	F-HEMBA1003067	0.34
HEMBA1003077	F-HEMBA1003077	0.83
HEMBA1003078	F-HEMBA1003078	0.89
HEMBA1003079	F-HEMBA1003079	0.49
HEMBA1003096	F-HEMBA1003096	0.34
HEMBA1003117	F-HEMBA1003117	0.94
HEMBA1003129	F-HEMBA1003129	0.81
HEMBA1003136	F-HEMBA1003136	0.77

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HEMBA1003148	F-HEMBA1003148	0.91
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HEMBA1003179	F-HEMBA1003179	0.42
HEMBA1003199	F-HEMBA1003199	0.84
HEMBA1003222	F-HEMBA1003222	0.47
HEMBA1003235	F-HEMBA1003235	0.94
HEMBA1003250	F-HEMBA1003250	0.39
HEMBA1003257	F-HEMBA1003257	0.88
HEMBA1003281	F-HEMBA1003281	0.67
HEMBA1003286	F-HEMBA1003286	0.57
HEMBA1003291	F-HEMBA1003291	0.89
HEMBA1003322	F-HEMBA1003322	0.60
HEMBA1003327	F-HEMBA1003327	0.88
HEMBA1003369	F-HEMBA1003369	0.89
HEMBA1003370	F-HEMBA1003370	0.75
HEMBA1003380	F-HEMBA1003380	0.68
HEMBA1003395	F-HEMBA1003395	0.88
HEMBA1003402	F-HEMBA1003402	0.45
HEMBA1003403	F-HEMBA1003403	0.44
HEMBA1003408	F-HEMBA1003408	0.34
HEMBA1003417	F-HEMBA1003417	0.78
HEMBA1003418	F-HEMBA1003418	0.94
HEMBA1003433	F-HEMBA1003433	0.70
HEMBA1003447	F-HEMBA1003447	0.49
HEMBA1003461	F-HEMBA1003461	0.85
HEMBA1003463	F-HEMBA1003463	0.59
HEMBA1003480	F-HEMBA1003480	0.94
HEMBA1003528	F-HEMBA1003528	0.90
HEMBA1003538	F-HEMBA1003538	0.47
HEMBA1003545	F-HEMBA1003545	0.74
HEMBA1003555	F-HEMBA1003555	0.94
HEMBA1003556	F-HEMBA1003556	0.44
HEMBA1003560	F-HEMBA1003560	0.40
HEMBA1003568	F-HEMBA1003568	0.94
HEMBA1003569	F-HEMBA1003569	0.82
HEMBA1003581	F-HEMBA1003581	0.83
HEMBA1003591	F-HEMBA1003591	0.68
HEMBA1003615	F-HEMBA1003615	0.94
HEMBA1003617	F-HEMBA1003617	0.88
HEMBA1003621	F-HEMBA1003621	0.47
HEMBA1003645	F-HEMBA1003645	0.75
HEMBA1003646	F-HEMBA1003646	0.51
HEMBA1003662	F-HEMBA1003662	0.61
HEMBA1003667	F-HEMBA1003667	0.54
HEMBA1003679	F-HEMBA1003679	0.72
HEMBA1003680	F-HEMBA1003680	0.52

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HEMBA1003684	F-HEMBA1003684	0.94
HEMBA1003690	F-HEMBA1003690	0.93
HEMBA1003692	F-HEMBA1003692	0.46
HEMBA1003711	F-HEMBA1003711	0.94
HEMBA1003720	F-HEMBA1003720	0.94
HEMBA1003729	F-HEMBA1003729	0.73
HEMBA1003742	F-HEMBA1003742	0.94
HEMBA1003760	F-HEMBA1003760	0.75
HEMBA1003783	F-HEMBA1003783	0.31
HEMBA1003799	F-HEMBA1003799	0.70
HEMBA1003803	F-HEMBA1003803	0.87
HEMBA1003804	F-HEMBA1003804	0.94
HEMBA1003805	F-HEMBA1003805	0.94
HEMBA1003807	F-HEMBA1003807	0.91
HEMBA1003827	F-HEMBA1003827	0.62
HEMBA1003836	F-HEMBA1003836	0.69
HEMBA1003838	F-HEMBA1003838	0.80
HEMBA1003864	F-HEMBA1003864	0.94
HEMBA1003866	F-HEMBA1003866	0.32
HEMBA1003879	F-HEMBA1003879	0.82
HEMBA1003880	F-HEMBA1003880	0.59
HEMBA1003893	F-HEMBA1003893	0.47
HEMBA1003953	F-HEMBA1003953	0.77
HEMBA1003959	F-HEMBA1003959	0.32
HEMBA1003978	F-HEMBA1003978	0.37
HEMBA1003985	F-HEMBA1003985	0.31
HEMBA1003989	F-HEMBA1003989	0.75
HEMBA1004011	F-HEMBA1004011	0.34
HEMBA1004048	F-HEMBA1004048	0.32
HEMBA1004055	F-HEMBA1004055	0.74
HEMBA1004056	F-HEMBA1004056	0.49
HEMBA1004074	F-HEMBA1004074	0.39
HEMBA1004086	F-HEMBA1004086	0.45
HEMBA1004097	F-HEMBA1004097	0.82
HEMBA1004111	F-HEMBA1004111	0.94
HEMBA1004131	F-HEMBA1004131	0.84
HEMBA1004133	F-HEMBA1004133	0.40
HEMBA1004143	F-HEMBA1004143	0.33
HEMBA1004146	F-HEMBA1004146	0.31
HEMBA1004150	F-HEMBA1004150	0.70
HEMBA1004168	F-HEMBA1004168	0.34
HEMBA1004199	F-HEMBA1004199	0.34
HEMBA1004200	F-HEMBA1004200	0.40
HEMBA1004202	F-HEMBA1004202	0.88
HEMBA1004203	F-HEMBA1004203	0.94
HEMBA1004207	F-HEMBA1004207	0.53

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HEMBA1004227	F-HEMBA1004227	0.94
HEMBA1004238	F-HEMBA1004238	0.44
HEMBA1004246	F-HEMBA1004246	0.71
HEMBA1004248	F-HEMBA1004248	0.40
HEMBA1004264	F-HEMBA1004264	0.94
HEMBA1004274	F-HEMBA1004274	0.88
HEMBA1004275	F-HEMBA1004275	0.85
HEMBA1004276	F-HEMBA1004276	0.32
HEMBA1004286	F-HEMBA1004286	0.37
HEMBA1004289	F-HEMBA1004289	0.76
HEMBA1004321	F-HEMBA1004321	0.82
HEMBA1004327	F-HEMBA1004327	0.40
HEMBA1004330	F-HEMBA1004330	0.84
HEMBA1004335	F-HEMBA1004335	0.79
HEMBA1004341	F-HEMBA1004341	0.38
HEMBA1004353	F-HEMBA1004353	0.79
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HEMBA1004389	F-HEMBA1004389	0.32
HEMBA1004408	F-HEMBA1004408	0.70
HEMBA1004479	F-HEMBA1004479	0.55
HEMBA1004499	F-HEMBA1004499	0.62
HEMBA1004502	F-HEMBA1004502	0.31
HEMBA1004507	F-HEMBA1004507	0.71
HEMBA1004509	F-HEMBA1004509	0.68
HEMBA1004534	F-HEMBA1004534	0.56
HEMBA1004542	F-HEMBA1004542	0.36
HEMBA1004554	F-HEMBA1004554	0.90
HEMBA1004560	F-HEMBA1004560	0.57
HEMBA1004573	F-HEMBA1004573	0.93
HEMBA1004596	F-HEMBA1004596	0.45
HEMBA1004604	F-HEMBA1004604	0.91
HEMBA1004610	F-HEMBA1004610	0.59
HEMBA1004632	F-HEMBA1004632	0.59
HEMBA1004637	F-HEMBA1004637	0.38
HEMBA1004638	F-HEMBA1004638	0.40
HEMBA1004669	F-HEMBA1004669	0.94
HEMBA1004693	F-HEMBA1004693	0.52
HEMBA1004697	F-HEMBA1004697	0.94
HEMBA1004705	F-HEMBA1004705	0.94
HEMBA1004709	F-HEMBA1004709	0.77
HEMBA1004711	F-HEMBA1004711	0.73
HEMBA1004725	F-HEMBA1004725	0.94
HEMBA1004734	F-HEMBA1004734	0.94
HEMBA1004736	F-HEMBA1004736	0.94
HEMBA1004751	F-HEMBA1004751	0.64
HEMBA1004752	F-HEMBA1004752	0.87

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HEMBA1004753	F-HEMBA1004753	0.54
HEMBA1004756	F-HEMBA1004756	0.54
HEMBA1004758	F-HEMBA1004758	0.69
HEMBA1004763	F-HEMBA1004763	0.94
HEMBA1004768	F-HEMBA1004768	0.66
HEMBA1004771	F-HEMBA1004771	0.72
HEMBA1004776	F-HEMBA1004776	0.49
HEMBA1004795	F-HEMBA1004795	0.46
HEMBA1004806	F-HEMBA1004806	0.32
HEMBA1004847	F-HEMBA1004847	0.79
HEMBA1004850	F-HEMBA1004850	0.94
HEMBA1004863	F-HEMBA1004863	0.32
HEMBA1004864	F-HEMBA1004864	0.94
HEMBA1004889	F-HEMBA1004889	0.94
HEMBA1004923	F-HEMBA1004923	0.70
HEMBA1004929	F-HEMBA1004929	0.31
HEMBA1004930	F-HEMBA1004930	0.90
HEMBA1004933	F-HEMBA1004933	0.84
HEMBA1004934	F-HEMBA1004934	0.34
HEMBA1004944	F-HEMBA1004944	0.40
HEMBA1004954	F-HEMBA1004954	0.62
HEMBA1004972	F-HEMBA1004972	0.90
HEMBA1004973	F-HEMBA1004973	0.94
HEMBA1004977	F-HEMBA1004977	0.77
HEMBA1004980	F-HEMBA1004980	0.33
HEMBA1005009	F-HEMBA1005009	0.94
HEMBA1005019	F-HEMBA1005019	0.32
HEMBA1005029	F-HEMBA1005029	0.84
HEMBA1005035	F-HEMBA1005035	0.91
HEMBA1005047	F-HEMBA1005047	0.94
HEMBA1005050	F-HEMBA1005050	0.88
HEMBA1005066	F-HEMBA1005066	0.79
HEMBA1005075	F-HEMBA1005075	0.31
HEMBA1005079	F-HEMBA1005079	0.35
HEMBA1005083	F-HEMBA1005083	0.43
HEMBA1005101	F-HEMBA1005101	0.94
HEMBA1005113	F-HEMBA1005113	0.38
HEMBA1005133	F-HEMBA1005133	0.34
HEMBA1005149	F-HEMBA1005149	0.36
HEMBA1005185	F-HEMBA1005185	0.64
HEMBA1005201	F-HEMBA1005201	0.83
HEMBA1005202	F-HEMBA1005202	0.94
HEMBA1005206	F-HEMBA1005206	0.94
HEMBA1005219	F-HEMBA1005219	0.57
HEMBA1005223	F-HEMBA1005223	0.33
HEMBA1005244	F-HEMBA1005244	0.35

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HEMBA1005252	F-HEMBA1005252	0.80
HEMBA1005296	F-HEMBA1005296	0.94
HEMBA1005314	F-HEMBA1005314	0.94
HEMBA1005331	F-HEMBA1005331	0.69
HEMBA1005338	F-HEMBA1005338	0.94
HEMBA1005367	F-HEMBA1005367	0.50
HEMBA1005382	F-HEMBA1005382	0.91
HEMBA1005394	F-HEMBA1005394	0.45
HEMBA1005403	F-HEMBA1005403	0.94
HEMBA1005411	F-HEMBA1005411	0.33
HEMBA1005423	F-HEMBA1005423	0.64
HEMBA1005468	F-HEMBA1005468	0.33
HEMBA1005469	F-HEMBA1005469	0.59
HEMBA1005472	F-HEMBA1005472	0.32
HEMBA1005474	F-HEMBA1005474	0.51
HEMBA1005475	F-HEMBA1005475	0.36
HEMBA1005513	F-HEMBA1005513	0.94
HEMBA1005517	F-HEMBA1005517	0.94
HEMBA1005518	F-HEMBA1005518	0.39
HEMBA1005526	F-HEMBA1005526	0.62
HEMBA1005528	F-HEMBA1005528	0.81
HEMBA1005530	F-HEMBA1005530	0.62
HEMBA1005548	F-HEMBA1005548	0.94
HEMBA1005558	F-HEMBA1005558	0.94
HEMBA1005576	F-HEMBA1005576	0.49
HEMBA1005581	F-HEMBA1005581	0.53
HEMBA1005582	F-HEMBA1005582	0.34
HEMBA1005583	F-HEMBA1005583	0.94
HEMBA1005595	F-HEMBA1005595	0.93
HEMBA1005609	F-HEMBA1005609	0.34
HEMBA1005621	F-HEMBA1005621	0.94
HEMBA1005666	F-HEMBA1005666	0.57
HEMBA1005680	F-HEMBA1005680	0.38
HEMBA1005685	F-HEMBA1005685	0.32
HEMBA1005732	F-HEMBA1005732	0.33
HEMBA1005737	F-HEMBA1005737	0.92
HEMBA1005746	F-HEMBA1005746	0.37
HEMBA1005755	F-HEMBA1005755	0.94
HEMBA1005813	F-HEMBA1005813	0.33
HEMBA1005815	F-HEMBA1005815	0.82
HEMBA1005822	F-HEMBA1005822	0.83
HEMBA1005834	F-HEMBA1005834	0.70
HEMBA1005852	F-HEMBA1005852	0.76
HEMBA1005884	F-HEMBA1005884	0.79
HEMBA1005891	F-HEMBA1005891	0.94
HEMBA1005963	F-HEMBA1005963	0.40

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HEMBA1005991	F-HEMBA1005991	0. 43
HEMBA1006031	F-HEMBA1006031	0. 55
HEMBA1006035	F-HEMBA1006035	0. 43
HEMBA1006081	F-HEMBA1006081	0. 36
HEMBA1006091	F-HEMBA1006091	0. 81
HEMBA1006100	F-HEMBA1006100	0. 31
HEMBA1006108	F-HEMBA1006108	0. 80
HEMBA1006121	F-HEMBA1006121	0. 45
HEMBA1006130	F-HEMBA1006130	0. 46
HEMBA1006138	F-HEMBA1006138	0. 48
HEMBA1006155	F-HEMBA1006155	0. 72
HEMBA1006173	F-HEMBA1006173	0. 42
HEMBA1006182	F-HEMBA1006182	0. 73
HEMBA1006198	F-HEMBA1006198	0. 94
HEMBA1006235	F-HEMBA1006235	0. 58
HEMBA1006248	F-HEMBA1006248	0. 57
HEMBA1006252	F-HEMBA1006252	0. 31
HEMBA1006272	F-HEMBA1006272	0. 54
HEMBA1006278	F-HEMBA1006278	0. 92
HEMBA1006283	F-HEMBA1006283	0. 90
HEMBA1006284	F-HEMBA1006284	0. 93
HEMBA1006291	F-HEMBA1006291	0. 38
HEMBA1006293	F-HEMBA1006293	0. 89
HEMBA1006309	F-HEMBA1006309	0. 94
HEMBA1006310	F-HEMBA1006310	0. 67
HEMBA1006344	F-HEMBA1006344	0. 94
HEMBA1006347	F-HEMBA1006347	0. 94
HEMBA1006349	F-HEMBA1006349	0. 56
HEMBA1006377	F-HEMBA1006377	0. 94
HEMBA1006381	F-HEMBA1006381	0. 33
HEMBA1006398	F-HEMBA1006398	0. 71
HEMBA1006424	F-HEMBA1006424	0. 40
HEMBA1006445	F-HEMBA1006445	0. 86
HEMBA1006467	F-HEMBA1006467	0. 55
HEMBA1006474	F-HEMBA1006474	0. 66
HEMBA1006483	F-HEMBA1006483	0. 71
HEMBA1006485	F-HEMBA1006485	0. 87
HEMBA1006492	F-HEMBA1006492	0. 73
HEMBA1006494	F-HEMBA1006494	0. 90
HEMBA1006497	F-HEMBA1006497	0. 77
HEMBA1006502	F-HEMBA1006502	0. 80
HEMBA1006507	F-HEMBA1006507	0. 56
HEMBA1006521	F-HEMBA1006521	0. 91
HEMBA1006530	F-HEMBA1006530	0. 37
HEMBA1006535	F-HEMBA1006535	0. 56

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HEMBA1006566	F-HEMBA1006566	0.41
HEMBA1006579	F-HEMBA1006579	0.83
HEMBA1006583	F-HEMBA1006583	0.31
HEMBA1006612	F-HEMBA1006612	0.55
HEMBA1006624	F-HEMBA1006624	0.94
HEMBA1006631	F-HEMBA1006631	0.74
HEMBA1006643	F-HEMBA1006643	0.38
HEMBA1006652	F-HEMBA1006652	0.93
HEMBA1006659	F-HEMBA1006659	0.63
HEMBA1006674	F-HEMBA1006674	0.54
HEMBA1006682	F-HEMBA1006682	0.34
HEMBA1006708	F-HEMBA1006708	0.40
HEMBA1006709	F-HEMBA1006709	0.41
HEMBA1006717	F-HEMBA1006717	0.43
HEMBA1006737	F-HEMBA1006737	0.72
HEMBA1006754	F-HEMBA1006754	0.45
HEMBA1006758	F-HEMBA1006758	0.60
HEMBA1006767	F-HEMBA1006767	0.61
HEMBA1006789	F-HEMBA1006789	0.34
HEMBA1006795	F-HEMBA1006795	0.48
HEMBA1006796	F-HEMBA1006796	0.41
HEMBA1006807	F-HEMBA1006807	0.34
HEMBA1006832	F-HEMBA1006832	0.59
HEMBA1006877	F-HEMBA1006877	0.90
HEMBA1006885	F-HEMBA1006885	0.80
HEMBA1006900	F-HEMBA1006900	0.34
HEMBA1006914	F-HEMBA1006914	0.78
HEMBA1006926	F-HEMBA1006926	0.67
HEMBA1006936	F-HEMBA1006936	0.65
HEMBA1006941	F-HEMBA1006941	0.94
HEMBA1006973	F-HEMBA1006973	0.64
HEMBA1006976	F-HEMBA1006976	0.40
HEMBA1006993	F-HEMBA1006993	0.81
HEMBA1006996	F-HEMBA1006996	0.77
HEMBA1007002	F-HEMBA1007002	0.72
HEMBA1007018	F-HEMBA1007018	0.31
HEMBA1007052	F-HEMBA1007052	0.41
HEMBA1007062	F-HEMBA1007062	0.39
HEMBA1007066	F-HEMBA1007066	0.35
HEMBA1007080	F-HEMBA1007080	0.43
HEMBA1007085	F-HEMBA1007085	0.73
HEMBA1007087	F-HEMBA1007087	0.94
HEMBA1007112	F-HEMBA1007112	0.49
HEMBA1007121	F-HEMBA1007121	0.70
HEMBA1007149	F-HEMBA1007149	0.94

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HEMBA1007151	F-HEMBA1007151	0.80
HEMBA1007174	F-HEMBA1007174	0.63
HEMBA1007178	F-HEMBA1007178	0.47
HEMBA1007194	F-HEMBA1007194	0.94
HEMBA1007203	F-HEMBA1007203	0.48
HEMBA1007224	F-HEMBA1007224	0.74
HEMBA1007243	F-HEMBA1007243	0.94
HEMBA1007251	F-HEMBA1007251	0.79
HEMBA1007267	F-HEMBA1007267	0.86
HEMBA1007281	F-HEMBA1007281	0.61
HEMBA1007300	F-HEMBA1007300	0.87
HEMBA1007301	F-HEMBA1007301	0.38
HEMBA1007319	F-HEMBA1007319	0.47
HEMBA1007320	F-HEMBA1007320	0.69
HEMBA1007342	F-HEMBA1007342	0.80
HEMBB1000008	F-HEMBB1000008	0.39
HEMBB1000018	F-HEMBB1000018	0.79
HEMBB1000024	F-HEMBB1000024	0.62
HEMBB1000025	F-HEMBB1000025	0.66
HEMBB1000030	F-HEMBB1000030	0.33
HEMBB1000036	F-HEMBB1000036	0.75
HEMBB1000037	F-HEMBB1000037	0.94
HEMBB1000048	F-HEMBB1000048	0.87
HEMBB1000083	F-HEMBB1000083	0.48
HEMBB1000103	F-HEMBB1000103	0.63
HEMBB1000119	F-HEMBB1000119	0.94
HEMBB1000136	F-HEMBB1000136	0.92
HEMBB1000173	F-HEMBB1000173	0.46
HEMBB1000175	F-HEMBB1000175	0.48
HEMBB1000198	F-HEMBB1000198	0.74
HEMBB1000215	F-HEMBB1000215	0.61
HEMBB1000217	F-HEMBB1000217	0.94
HEMBB1000226	F-HEMBB1000226	0.94
HEMBB1000240	F-HEMBB1000240	0.40
HEMBB1000244	F-HEMBB1000244	0.81
HEMBB1000266	F-HEMBB1000266	0.92
HEMBB1000338	F-HEMBB1000338	0.33
HEMBB1000339	F-HEMBB1000339	0.40
HEMBB1000391	F-HEMBB1000391	0.43
HEMBB1000438	F-HEMBB1000438	0.79
HEMBB1000449	F-HEMBB1000449	0.48
HEMBB1000510	F-HEMBB1000510	0.35
HEMBB1000550	F-HEMBB1000550	0.94
HEMBB1000556	F-HEMBB1000556	0.89
HEMBB1000589	F-HEMBB1000589	0.77
HEMBB1000591	F-HEMBB1000591	0.33

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HEMBB1000592	F-HEMBB1000592	0.77
HEMBB1000593	F-HEMBB1000593	0.68
HEMBB1000623	F-HEMBB1000623	0.94
HEMBB1000630	F-HEMBB1000630	0.59
HEMBB1000631	F-HEMBB1000631	0.71
HEMBB1000632	F-HEMBB1000632	0.38
HEMBB1000671	F-HEMBB1000671	0.36
HEMBB1000673	F-HEMBB1000673	0.54
HEMBB1000693	F-HEMBB1000693	0.68
HEMBB1000705	F-HEMBB1000705	0.44
HEMBB1000706	F-HEMBB1000706	0.45
HEMBB1000725	F-HEMBB1000725	0.91
HEMBB1000763	F-HEMBB1000763	0.87
HEMBB1000774	F-HEMBB1000774	0.80
HEMBB1000781	F-HEMBB1000781	0.94
HEMBB1000789	F-HEMBB1000789	0.34
HEMBB1000807	F-HEMBB1000807	0.94
HEMBB1000810	F-HEMBB1000810	0.33
HEMBB1000826	F-HEMBB1000826	0.36
HEMBB1000835	F-HEMBB1000835	0.81
HEMBB1000848	F-HEMBB1000848	0.66
HEMBB1000852	F-HEMBB1000852	0.85
HEMBB1000870	F-HEMBB1000870	0.34
HEMBB1000887	F-HEMBB1000887	0.58
HEMBB1000908	F-HEMBB1000908	0.31
HEMBB1000927	F-HEMBB1000927	0.94
HEMBB1000947	F-HEMBB1000947	0.33
HEMBB1000973	F-HEMBB1000973	0.72
HEMBB1000975	F-HEMBB1000975	0.68
HEMBB1000985	F-HEMBB1000985	0.62
HEMBB1000991	F-HEMBB1000991	0.45
HEMBB1001011	F-HEMBB1001011	0.58
HEMBB1001014	F-HEMBB1001014	0.86
HEMBB1001020	F-HEMBB1001020	0.87
HEMBB1001024	F-HEMBB1001024	0.64
HEMBB1001056	F-HEMBB1001056	0.94
HEMBB1001058	F-HEMBB1001058	0.39
HEMBB1001068	F-HEMBB1001068	0.57
HEMBB1001096	F-HEMBB1001096	0.48
HEMBB1001105	F-HEMBB1001105	0.45
HEMBB1001112	F-HEMBB1001112	0.47
HEMBB1001117	F-HEMBB1001117	0.83
HEMBB1001126	F-HEMBB1001126	0.76
HEMBB1001137	F-HEMBB1001137	0.53
HEMBB1001151	F-HEMBB1001151	0.94
HEMBB1001153	F-HEMBB1001153	0.77

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HEMBB1001169	F-HEMBB1001169	0.39
HEMBB1001175	F-HEMBB1001175	0.91
HEMBB1001182	F-HEMBB1001182	0.94
HEMBB1001199	F-HEMBB1001199	0.54
HEMBB1001210	F-HEMBB1001210	0.88
HEMBB1001234	F-HEMBB1001234	0.67
HEMBB1001242	F-HEMBB1001242	0.33
HEMBB1001288	F-HEMBB1001288	0.33
HEMBB1001289	F-HEMBB1001289	0.58
HEMBB1001294	F-HEMBB1001294	0.86
HEMBB1001314	F-HEMBB1001314	0.76
HEMBB1001331	F-HEMBB1001331	0.44
HEMBB1001339	F-HEMBB1001339	0.40
HEMBB1001346	F-HEMBB1001346	0.83
HEMBB1001364	F-HEMBB1001364	0.69
HEMBB1001369	F-HEMBB1001369	0.47
HEMBB1001384	F-HEMBB1001384	0.80
HEMBB1001387	F-HEMBB1001387	0.36
HEMBB1001394	F-HEMBB1001394	0.94
HEMBB1001410	F-HEMBB1001410	0.51
HEMBB1001426	F-HEMBB1001426	0.80
HEMBB1001429	F-HEMBB1001429	0.91
HEMBB1001449	F-HEMBB1001449	0.31
HEMBB1001482	F-HEMBB1001482	0.44
HEMBB1001531	F-HEMBB1001531	0.58
HEMBB1001562	F-HEMBB1001562	0.65
HEMBB1001564	F-HEMBB1001564	0.46
HEMBB1001585	F-HEMBB1001585	0.74
HEMBB1001603	F-HEMBB1001603	0.81
HEMBB1001635	F-HEMBB1001635	0.46
HEMBB1001653	F-HEMBB1001653	0.33
HEMBB1001665	F-HEMBB1001665	0.39
HEMBB1001668	F-HEMBB1001668	0.38
HEMBB1001673	F-HEMBB1001673	0.83
HEMBB1001684	F-HEMBB1001684	0.44
HEMBB1001685	F-HEMBB1001685	0.90
HEMBB1001695	F-HEMBB1001695	0.92
HEMBB1001707	F-HEMBB1001707	0.51
HEMBB1001736	F-HEMBB1001736	0.94
HEMBB1001760	F-HEMBB1001760	0.88
HEMBB1001785	F-HEMBB1001785	0.74
HEMBB1001812	F-HEMBB1001812	0.33
HEMBB1001816	F-HEMBB1001816	0.41
HEMBB1001831	F-HEMBB1001831	0.93
HEMBB1001834	F-HEMBB1001834	0.78
HEMBB1001839	F-HEMBB1001839	0.32

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HEMBB1001869	F-HEMBB1001869	0. 48
HEMBB1001872	F-HEMBB1001872	0. 93
HEMBB1001874	F-HEMBB1001874	0. 31
HEMBB1001905	F-HEMBB1001905	0. 87
HEMBB1001906	F-HEMBB1001906	0. 88
HEMBB1001908	F-HEMBB1001908	0. 69
HEMBB1001910	F-HEMBB1001910	0. 77
HEMBB1001915	F-HEMBB1001915	0. 76
HEMBB1001945	F-HEMBB1001945	0. 64
HEMBB1001947	F-HEMBB1001947	0. 94
HEMBB1001950	F-HEMBB1001950	0. 73
HEMBB1001957	F-HEMBB1001957	0. 64
HEMBB1001962	F-HEMBB1001962	0. 90
HEMBB1001990	F-HEMBB1001990	0. 83
HEMBB1002044	F-HEMBB1002044	0. 82
HEMBB1002050	F-HEMBB1002050	0. 91
HEMBB1002068	F-HEMBB1002068	0. 48
HEMBB1002134	F-HEMBB1002134	0. 80
HEMBB1002142	F-HEMBB1002142	0. 39
HEMBB1002152	F-HEMBB1002152	0. 31
HEMBB1002193	F-HEMBB1002193	0. 35
HEMBB1002217	F-HEMBB1002217	0. 49
HEMBB1002218	F-HEMBB1002218	0. 32
HEMBB1002249	F-HEMBB1002249	0. 72
HEMBB1002300	F-HEMBB1002300	0. 75
HEMBB1002327	F-HEMBB1002327	0. 86
HEMBB1002329	F-HEMBB1002329	0. 31
HEMBB1002340	F-HEMBB1002340	0. 42
HEMBB1002342	F-HEMBB1002342	0. 76
HEMBB1002358	F-HEMBB1002358	0. 70
HEMBB1002359	F-HEMBB1002359	0. 75
HEMBB1002383	F-HEMBB1002383	0. 78
HEMBB1002409	F-HEMBB1002409	0. 52
HEMBB1002415	F-HEMBB1002415	0. 82
HEMBB1002442	F-HEMBB1002442	0. 31
HEMBB1002457	F-HEMBB1002457	0. 46
HEMBB1002489	F-HEMBB1002489	0. 69
HEMBB1002492	F-HEMBB1002492	0. 68
HEMBB1002495	F-HEMBB1002495	0. 94
HEMBB1002502	F-HEMBB1002502	0. 39
HEMBB1002510	F-HEMBB1002510	0. 94
HEMBB1002545	F-HEMBB1002545	0. 44
HEMBB1002550	F-HEMBB1002550	0. 57
HEMBB1002600	F-HEMBB1002600	0. 91
HEMBB1002607	F-HEMBB1002607	0. 83
HEMBB1002614	F-HEMBB1002614	0. 75

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HEMBB1002684	F-HEMBB1002684	0.84
HEMBB1002692	F-HEMBB1002692	0.52
HEMBB1002697	F-HEMBB1002697	0.86
HEMBB1002705	F-HEMBB1002705	0.32
MAMMA1000019	F-MAMMA1000019	0.48
MAMMA1000020	F-MAMMA1000020	0.36
MAMMA1000025	F-MAMMA1000025	0.31
MAMMA1000055	F-MAMMA1000055	0.39
MAMMA1000057	F-MAMMA1000057	0.35
MAMMA1000069	F-MAMMA1000069	0.78
MAMMA1000084	F-MAMMA1000084	0.61
MAMMA1000085	F-MAMMA1000085	0.72
MAMMA1000139	F-MAMMA1000139	0.33
MAMMA1000143	F-MAMMA1000143	0.40
MAMMA1000163	F-MAMMA1000163	0.94
MAMMA1000171	F-MAMMA1000171	0.78
MAMMA1000173	F-MAMMA1000173	0.94
MAMMA1000183	F-MAMMA1000183	0.77
MAMMA1000251	F-MAMMA1000251	0.94
MAMMA1000257	F-MAMMA1000257	0.75
MAMMA1000277	F-MAMMA1000277	0.94
MAMMA1000278	F-MAMMA1000278	0.35
MAMMA1000279	F-MAMMA1000279	0.62
MAMMA1000284	F-MAMMA1000284	0.35
MAMMA1000309	F-MAMMA1000309	0.53
MAMMA1000312	F-MAMMA1000312	0.68
MAMMA1000313	F-MAMMA1000313	0.32
MAMMA1000339	F-MAMMA1000339	0.35
MAMMA1000361	F-MAMMA1000361	0.61
MAMMA1000372	F-MAMMA1000372	0.60
MAMMA1000388	F-MAMMA1000388	0.93
MAMMA1000395	F-MAMMA1000395	0.94
MAMMA1000410	F-MAMMA1000410	0.94
MAMMA1000416	F-MAMMA1000416	0.89
MAMMA1000421	F-MAMMA1000421	0.50
MAMMA1000422	F-MAMMA1000422	0.92
MAMMA1000429	F-MAMMA1000429	0.92
MAMMA1000458	F-MAMMA1000458	0.88
MAMMA1000468	F-MAMMA1000468	0.60
MAMMA1000472	F-MAMMA1000472	0.33
MAMMA1000490	F-MAMMA1000490	0.34
MAMMA1000524	F-MAMMA1000524	0.39
MAMMA1000567	F-MAMMA1000567	0.40
MAMMA1000583	F-MAMMA1000583	0.45
MAMMA1000612	F-MAMMA1000612	0.89
MAMMA1000623	F-MAMMA1000623	0.44

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MAMMA1000625	F-MAMMA1000625	0.52
MAMMA1000664	F-MAMMA1000664	0.42
MAMMA1000670	F-MAMMA1000670	0.94
MAMMA1000672	F-MAMMA1000672	0.44
MAMMA1000684	F-MAMMA1000684	0.94
MAMMA1000713	F-MAMMA1000713	0.88
MAMMA1000731	F-MAMMA1000731	0.67
MAMMA1000734	F-MAMMA1000734	0.40
MAMMA1000738	F-MAMMA1000738	0.93
MAMMA1000746	F-MAMMA1000746	0.48
MAMMA1000760	F-MAMMA1000760	0.94
MAMMA1000776	F-MAMMA1000776	0.94
MAMMA1000824	F-MAMMA1000824	0.81
MAMMA1000831	F-MAMMA1000831	0.39
MAMMA1000841	F-MAMMA1000841	0.41
MAMMA1000842	F-MAMMA1000842	0.61
MAMMA1000843	F-MAMMA1000843	0.48
MAMMA1000856	F-MAMMA1000856	0.31
MAMMA1000859	F-MAMMA1000859	0.44
MAMMA1000865	F-MAMMA1000865	0.94
MAMMA1000875	F-MAMMA1000875	0.49
MAMMA1000897	F-MAMMA1000897	0.94
MAMMA1000906	F-MAMMA1000906	0.45
MAMMA1000908	F-MAMMA1000908	0.39
MAMMA1000914	F-MAMMA1000914	0.94
MAMMA1000921	F-MAMMA1000921	0.34
MAMMA1000956	F-MAMMA1000956	0.39
MAMMA1000968	F-MAMMA1000968	0.35
MAMMA1000979	F-MAMMA1000979	0.68
MAMMA1001008	F-MAMMA1001008	0.36
MAMMA1001021	F-MAMMA1001021	0.48
MAMMA1001041	F-MAMMA1001041	0.34
MAMMA1001059	F-MAMMA1001059	0.94
MAMMA1001073	F-MAMMA1001073	0.94
MAMMA1001075	F-MAMMA1001075	0.94
MAMMA1001078	F-MAMMA1001078	0.52
MAMMA1001080	F-MAMMA1001080	0.87
MAMMA1001091	F-MAMMA1001091	0.53
MAMMA1001105	F-MAMMA1001105	0.94
MAMMA1001110	F-MAMMA1001110	0.78
MAMMA1001126	F-MAMMA1001126	0.85
MAMMA1001139	F-MAMMA1001139	0.38
MAMMA1001143	F-MAMMA1001143	0.79
MAMMA1001154	F-MAMMA1001154	0.31
MAMMA1001181	F-MAMMA1001181	0.69
MAMMA1001198	F-MAMMA1001198	0.88

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MAMMA1001202	F-MAMMA1001202	0.38
MAMMA1001215	F-MAMMA1001215	0.94
MAMMA1001222	F-MAMMA1001222	0.89
MAMMA1001244	F-MAMMA1001244	0.87
MAMMA1001259	F-MAMMA1001259	0.91
MAMMA1001260	F-MAMMA1001260	0.75
MAMMA1001271	F-MAMMA1001271	0.77
MAMMA1001292	F-MAMMA1001292	0.94
MAMMA1001296	F-MAMMA1001296	0.75
MAMMA1001305	F-MAMMA1001305	0.66
MAMMA1001343	F-MAMMA1001343	0.38
MAMMA1001346	F-MAMMA1001346	0.81
MAMMA1001388	F-MAMMA1001388	0.94
MAMMA1001411	F-MAMMA1001411	0.42
MAMMA1001419	F-MAMMA1001419	0.45
MAMMA1001465	F-MAMMA1001465	0.94
MAMMA1001476	F-MAMMA1001476	0.90
MAMMA1001487	F-MAMMA1001487	0.78
MAMMA1001510	F-MAMMA1001510	0.82
MAMMA1001522	F-MAMMA1001522	0.63
MAMMA1001551	F-MAMMA1001551	0.81
MAMMA1001576	F-MAMMA1001576	0.94
MAMMA1001600	F-MAMMA1001600	0.72
MAMMA1001604	F-MAMMA1001604	0.87
MAMMA1001620	F-MAMMA1001620	0.43
MAMMA1001627	F-MAMMA1001627	0.39
MAMMA1001630	F-MAMMA1001630	0.46
MAMMA1001633	F-MAMMA1001633	0.58
MAMMA1001635	F-MAMMA1001635	0.89
MAMMA1001649	F-MAMMA1001649	0.62
MAMMA1001654	F-MAMMA1001654	0.94
MAMMA1001692	F-MAMMA1001692	0.83
MAMMA1001730	F-MAMMA1001730	0.48
MAMMA1001735	F-MAMMA1001735	0.94
MAMMA1001743	F-MAMMA1001743	0.94
MAMMA1001744	F-MAMMA1001744	0.33
MAMMA1001751	F-MAMMA1001751	0.94
MAMMA1001754	F-MAMMA1001754	0.47
MAMMA1001757	F-MAMMA1001757	0.38
MAMMA1001764	F-MAMMA1001764	0.57
MAMMA1001768	F-MAMMA1001768	0.85
MAMMA1001771	F-MAMMA1001771	0.39
MAMMA1001783	F-MAMMA1001783	0.61
MAMMA1001785	F-MAMMA1001785	0.41
MAMMA1001790	F-MAMMA1001790	0.69
MAMMA1001812	F-MAMMA1001812	0.32

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MAMMA1001817	F-MAMMA1001817	0.55
MAMMA1001824	F-MAMMA1001824	0.57
MAMMA1001837	F-MAMMA1001837	0.35
MAMMA1001848	F-MAMMA1001848	0.38
MAMMA1001851	F-MAMMA1001851	0.46
MAMMA1001858	F-MAMMA1001858	0.53
MAMMA1001864	F-MAMMA1001864	0.32
MAMMA1001868	F-MAMMA1001868	0.48
MAMMA1001874	F-MAMMA1001874	0.94
MAMMA1001956	F-MAMMA1001956	0.47
MAMMA1001969	F-MAMMA1001969	0.31
MAMMA1001970	F-MAMMA1001970	0.34
MAMMA1002009	F-MAMMA1002009	0.45
MAMMA1002011	F-MAMMA1002011	0.94
MAMMA1002033	F-MAMMA1002033	0.33
MAMMA1002041	F-MAMMA1002041	0.86
MAMMA1002042	F-MAMMA1002042	0.88
MAMMA1002047	F-MAMMA1002047	0.41
MAMMA1002068	F-MAMMA1002068	0.38
MAMMA1002143	F-MAMMA1002143	0.91
MAMMA1002153	F-MAMMA1002153	0.94
MAMMA1002156	F-MAMMA1002156	0.73
MAMMA1002170	F-MAMMA1002170	0.43
MAMMA1002174	F-MAMMA1002174	0.69
MAMMA1002198	F-MAMMA1002198	0.65
MAMMA1002209	F-MAMMA1002209	0.80
MAMMA1002219	F-MAMMA1002219	0.85
MAMMA1002236	F-MAMMA1002236	0.55
MAMMA1002243	F-MAMMA1002243	0.50
MAMMA1002268	F-MAMMA1002268	0.43
MAMMA1002269	F-MAMMA1002269	0.33
MAMMA1002292	F-MAMMA1002292	0.76
MAMMA1002294	F-MAMMA1002294	0.94
MAMMA1002297	F-MAMMA1002297	0.91
MAMMA1002308	F-MAMMA1002308	0.68
MAMMA1002312	F-MAMMA1002312	0.77
MAMMA1002317	F-MAMMA1002317	0.46
MAMMA1002319	F-MAMMA1002319	0.31
MAMMA1002329	F-MAMMA1002329	0.34
MAMMA1002333	F-MAMMA1002333	0.65
MAMMA1002351	F-MAMMA1002351	0.89
MAMMA1002353	F-MAMMA1002353	0.94
MAMMA1002355	F-MAMMA1002355	0.55
MAMMA1002356	F-MAMMA1002356	0.32
MAMMA1002362	F-MAMMA1002362	0.83
MAMMA1002380	F-MAMMA1002380	0.94

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MAMMA1002384	F-MAMMA1002384	0.42
MAMMA1002385	F-MAMMA1002385	0.82
MAMMA1002413	F-MAMMA1002413	0.94
MAMMA1002427	F-MAMMA1002427	0.40
MAMMA1002434	F-MAMMA1002434	0.74
MAMMA1002454	F-MAMMA1002454	0.82
MAMMA1002461	F-MAMMA1002461	0.49
MAMMA1002470	F-MAMMA1002470	0.89
MAMMA1002485	F-MAMMA1002485	0.55
MAMMA1002524	F-MAMMA1002524	0.33
MAMMA1002530	F-MAMMA1002530	0.75
MAMMA1002554	F-MAMMA1002554	0.41
MAMMA1002585	F-MAMMA1002585	0.31
MAMMA1002590	F-MAMMA1002590	0.72
MAMMA1002598	F-MAMMA1002598	0.76
MAMMA1002617	F-MAMMA1002617	0.49
MAMMA1002619	F-MAMMA1002619	0.88
MAMMA1002637	F-MAMMA1002637	0.94
MAMMA1002650	F-MAMMA1002650	0.54
MAMMA1002655	F-MAMMA1002655	0.39
MAMMA1002665	F-MAMMA1002665	0.33
MAMMA1002671	F-MAMMA1002671	0.94
MAMMA1002673	F-MAMMA1002673	0.70
MAMMA1002684	F-MAMMA1002684	0.94
MAMMA1002685	F-MAMMA1002685	0.88
MAMMA1002699	F-MAMMA1002699	0.94
MAMMA1002711	F-MAMMA1002711	0.39
MAMMA1002769	F-MAMMA1002769	0.88
MAMMA1002775	F-MAMMA1002775	0.81
MAMMA1002782	F-MAMMA1002782	0.87
MAMMA1002796	F-MAMMA1002796	0.40
MAMMA1002807	F-MAMMA1002807	0.64
MAMMA1002842	F-MAMMA1002842	0.94
MAMMA1002843	F-MAMMA1002843	0.32
MAMMA1002868	F-MAMMA1002868	0.54
MAMMA1002869	F-MAMMA1002869	0.94
MAMMA1002881	F-MAMMA1002881	0.94
MAMMA1002886	F-MAMMA1002886	0.61
MAMMA1002890	F-MAMMA1002890	0.94
MAMMA1002895	F-MAMMA1002895	0.94
MAMMA1002937	F-MAMMA1002937	0.91
MAMMA1002938	F-MAMMA1002938	0.78
MAMMA1002947	F-MAMMA1002947	0.94
MAMMA1002964	F-MAMMA1002964	0.34
MAMMA1002987	F-MAMMA1002987	0.74
MAMMA1003011	F-MAMMA1003011	0.90

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MAMMA1003013	F-MAMMA1003013	0.36
MAMMA1003015	F-MAMMA1003015	0.92
MAMMA1003035	F-MAMMA1003035	0.94
MAMMA1003044	F-MAMMA1003044	0.61
MAMMA1003047	F-MAMMA1003047	0.94
MAMMA1003049	F-MAMMA1003049	0.31
MAMMA1003056	F-MAMMA1003056	0.75
MAMMA1003057	F-MAMMA1003057	0.33
MAMMA1003066	F-MAMMA1003066	0.38
MAMMA1003099	F-MAMMA1003099	0.79
MAMMA1003104	F-MAMMA1003104	0.44
MAMMA1003113	F-MAMMA1003113	0.90
MAMMA1003127	F-MAMMA1003127	0.53
MAMMA1003135	F-MAMMA1003135	0.94
MAMMA1003146	F-MAMMA1003146	0.88
MAMMA1003150	F-MAMMA1003150	0.73
MAMMA1003166	F-MAMMA1003166	0.94
NT2RM1000001	F-NT2RM1000001	0.66
NT2RM1000018	F-NT2RM1000018	0.55
NT2RM1000032	F-NT2RM1000032	0.74
NT2RM1000035	F-NT2RM1000035	0.52
NT2RM1000037	F-NT2RM1000037	0.94
NT2RM1000039	F-NT2RM1000039	0.77
NT2RM1000055	F-NT2RM1000055	0.89
NT2RM1000059	F-NT2RM1000059	0.41
NT2RM1000062	F-NT2RM1000062	0.65
NT2RM1000080	F-NT2RM1000080	0.61
NT2RM1000086	F-NT2RM1000086	0.94
NT2RM1000092	F-NT2RM1000092	0.94
NT2RM1000118	F-NT2RM1000118	0.76
NT2RM1000119	F-NT2RM1000119	0.41
NT2RM1000127	F-NT2RM1000127	0.94
NT2RM1000131	F-NT2RM1000131	0.90
NT2RM1000132	F-NT2RM1000132	0.94
NT2RM1000153	F-NT2RM1000153	0.90
NT2RM1000186	F-NT2RM1000186	0.78
NT2RM1000187	F-NT2RM1000187	0.54
NT2RM1000199	F-NT2RM1000199	0.33
NT2RM1000242	F-NT2RM1000242	0.78
NT2RM1000244	F-NT2RM1000244	0.31
NT2RM1000252	F-NT2RM1000252	0.76
NT2RM1000256	F-NT2RM1000256	0.94
NT2RM1000257	F-NT2RM1000257	0.89
NT2RM1000260	F-NT2RM1000260	0.42
NT2RM1000271	F-NT2RM1000271	0.74
NT2RM1000272	F-NT2RM1000272	0.78

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NT2RM1000280	F-NT2RM1000280	0.94
NT2RM1000300	F-NT2RM1000300	0.47
NT2RM1000314	F-NT2RM1000314	0.61
NT2RM1000318	F-NT2RM1000318	0.94
NT2RM1000341	F-NT2RM1000341	0.70
NT2RM1000354	F-NT2RM1000354	0.82
NT2RM1000355	F-NT2RM1000355	0.94
NT2RM1000365	F-NT2RM1000365	0.31
NT2RM1000377	F-NT2RM1000377	0.87
NT2RM1000388	F-NT2RM1000388	0.94
NT2RM1000394	F-NT2RM1000394	0.58
NT2RM1000399	F-NT2RM1000399	0.86
NT2RM1000421	F-NT2RM1000421	0.39
NT2RM1000430	F-NT2RM1000430	0.94
NT2RM1000499	F-NT2RM1000499	0.44
NT2RM1000539	F-NT2RM1000539	0.87
NT2RM1000553	F-NT2RM1000553	0.88
NT2RM1000555	F-NT2RM1000555	0.37
NT2RM1000563	F-NT2RM1000563	0.63
NT2RM1000623	F-NT2RM1000623	0.34
NT2RM1000648	F-NT2RM1000648	0.94
NT2RM1000661	F-NT2RM1000661	0.61
NT2RM1000666	F-NT2RM1000666	0.94
NT2RM1000669	F-NT2RM1000669	0.94
NT2RM1000672	F-NT2RM1000672	0.53
NT2RM1000691	F-NT2RM1000691	0.38
NT2RM1000699	F-NT2RM1000699	0.32
NT2RM1000702	F-NT2RM1000702	0.74
NT2RM1000725	F-NT2RM1000725	0.75
NT2RM1000741	F-NT2RM1000741	0.94
NT2RM1000742	F-NT2RM1000742	0.54
NT2RM1000746	F-NT2RM1000746	0.94
NT2RM1000770	F-NT2RM1000770	0.48
NT2RM1000772	F-NT2RM1000772	0.39
NT2RM1000780	F-NT2RM1000780	0.66
NT2RM1000781	F-NT2RM1000781	0.49
NT2RM1000800	F-NT2RM1000800	0.72
NT2RM1000802	F-NT2RM1000802	0.89
NT2RM1000811	F-NT2RM1000811	0.53
NT2RM1000826	F-NT2RM1000826	0.39
NT2RM1000829	F-NT2RM1000829	0.63
NT2RM1000833	F-NT2RM1000833	0.94
NT2RM1000850	F-NT2RM1000850	0.89
NT2RM1000852	F-NT2RM1000852	0.88
NT2RM1000857	F-NT2RM1000857	0.58
NT2RM1000867	F-NT2RM1000867	0.90

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NT2RM1000874	F-NT2RM1000874	0.89
NT2RM1000882	F-NT2RM1000882	0.63
NT2RM1000883	F-NT2RM1000883	0.71
NT2RM1000885	F-NT2RM1000885	0.89
NT2RM1000894	F-NT2RM1000894	0.57
NT2RM1000898	F-NT2RM1000898	0.87
NT2RM1000905	F-NT2RM1000905	0.94
NT2RM1000924	F-NT2RM1000924	0.88
NT2RM1000927	F-NT2RM1000927	0.70
NT2RM1000962	F-NT2RM1000962	0.84
NT2RM1000978	F-NT2RM1000978	0.39
NT2RM1001003	F-NT2RM1001003	0.81
NT2RM1001008	F-NT2RM1001008	0.94
NT2RM1001043	F-NT2RM1001043	0.94
NT2RM1001044	F-NT2RM1001044	0.94
NT2RM1001059	F-NT2RM1001059	0.94
NT2RM1001066	F-NT2RM1001066	0.94
NT2RM1001072	F-NT2RM1001072	0.77
NT2RM1001074	F-NT2RM1001074	0.94
NT2RM1001082	F-NT2RM1001082	0.94
NT2RM1001085	F-NT2RM1001085	0.83
NT2RM1001092	F-NT2RM1001092	0.77
NT2RM1001102	F-NT2RM1001102	0.59
NT2RM1001105	F-NT2RM1001105	0.94
NT2RM1001112	F-NT2RM1001112	0.50
NT2RM1001115	F-NT2RM1001115	0.32
NT2RM1001139	F-NT2RM1001139	0.77
NT2RM2000006	F-NT2RM2000006	0.34
NT2RM2000013	F-NT2RM2000013	0.70
NT2RM2000030	F-NT2RM2000030	0.89
NT2RM2000032	F-NT2RM2000032	0.36
NT2RM2000042	F-NT2RM2000042	0.32
NT2RM2000092	F-NT2RM2000092	0.55
NT2RM2000093	F-NT2RM2000093	0.33
NT2RM2000101	F-NT2RM2000101	0.77
NT2RM2000124	F-NT2RM2000124	0.94
NT2RM2000191	F-NT2RM2000191	0.80
NT2RM2000192	F-NT2RM2000192	0.93
NT2RM2000239	F-NT2RM2000239	0.68
NNNNNNNNNNNN	F-NNNNNNNNNNNN	0.94
NT2RM2000250	F-NT2RM2000250	0.94
NT2RM2000259	F-NT2RM2000259	0.68
NT2RM2000260	F-NT2RM2000260	0.37
NT2RM2000287	F-NT2RM2000287	0.46
NT2RM2000322	F-NT2RM2000322	0.83
NT2RM2000359	F-NT2RM2000359	0.94

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NT2RM2000363	F-NT2RM2000363	0.91
NT2RM2000368	F-NT2RM2000368	0.34
NT2RM2000371	F-NT2RM2000371	0.94
NT2RM2000374	F-NT2RM2000374	0.65
NT2RM2000395	F-NT2RM2000395	0.33
NT2RM2000402	F-NT2RM2000402	0.80
NT2RM2000407	F-NT2RM2000407	0.88
NT2RM2000420	F-NT2RM2000420	0.92
NT2RM2000422	F-NT2RM2000422	0.49
NT2RM2000452	F-NT2RM2000452	0.93
NT2RM2000469	F-NT2RM2000469	0.39
NT2RM2000490	F-NT2RM2000490	0.90
NT2RM2000502	F-NT2RM2000502	0.64
NT2RM2000504	F-NT2RM2000504	0.71
NT2RM2000522	F-NT2RM2000522	0.91
NT2RM2000540	F-NT2RM2000540	0.87
NT2RM2000556	F-NT2RM2000556	0.91
NT2RM2000566	F-NT2RM2000566	0.39
NT2RM2000567	F-NT2RM2000567	0.44
NT2RM2000569	F-NT2RM2000569	0.49
NT2RM2000577	F-NT2RM2000577	0.45
NT2RM2000581	F-NT2RM2000581	0.72
NT2RM2000588	F-NT2RM2000588	0.31
NT2RM2000594	F-NT2RM2000594	0.79
NT2RM2000599	F-NT2RM2000599	0.80
NT2RM2000612	F-NT2RM2000612	0.75
NT2RM2000623	F-NT2RM2000623	0.72
NT2RM2000624	F-NT2RM2000624	0.94
NT2RM2000635	F-NT2RM2000635	0.73
NT2RM2000636	F-NT2RM2000636	0.45
NT2RM2000639	F-NT2RM2000639	0.43
NT2RM2000649	F-NT2RM2000649	0.74
NT2RM2000669	F-NT2RM2000669	0.94
NT2RM2000691	F-NT2RM2000691	0.84
NT2RM2000714	F-NT2RM2000714	0.92
NT2RM2000718	F-NT2RM2000718	0.52
NT2RM2000735	F-NT2RM2000735	0.33
NT2RM2000740	F-NT2RM2000740	0.94
NT2RM2000795	F-NT2RM2000795	0.44
NT2RM2000821	F-NT2RM2000821	0.33
NT2RM2000837	F-NT2RM2000837	0.57
NT2RM2000951	F-NT2RM2000951	0.32
NT2RM2000952	F-NT2RM2000952	0.50
NT2RM2000984	F-NT2RM2000984	0.76
NT2RM2001004	F-NT2RM2001004	0.55
NT2RM2001035	F-NT2RM2001035	0.82

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NT2RM2001065	F-NT2RM2001065	0.65
NT2RM2001100	F-NT2RM2001100	0.89
NT2RM2001105	F-NT2RM2001105	0.94
NT2RM2001131	F-NT2RM2001131	0.94
NT2RM2001141	F-NT2RM2001141	0.74
NT2RM2001152	F-NT2RM2001152	0.33
NT2RM2001177	F-NT2RM2001177	0.32
NT2RM2001194	F-NT2RM2001194	0.83
NT2RM2001196	F-NT2RM2001196	0.42
NT2RM2001201	F-NT2RM2001201	0.90
NT2RM2001221	F-NT2RM2001221	0.39
NT2RM2001238	F-NT2RM2001238	0.94
NT2RM2001243	F-NT2RM2001243	0.44
NT2RM2001247	F-NT2RM2001247	0.42
NT2RM2001256	F-NT2RM2001256	0.60
NT2RM2001291	F-NT2RM2001291	0.39
NT2RM2001306	F-NT2RM2001306	0.81
NT2RM2001312	F-NT2RM2001312	0.64
NT2RM2001319	F-NT2RM2001319	0.53
NT2RM2001324	F-NT2RM2001324	0.94
NT2RM2001345	F-NT2RM2001345	0.94
NT2RM2001360	F-NT2RM2001360	0.69
NT2RM2001370	F-NT2RM2001370	0.44
NT2RM2001393	F-NT2RM2001393	0.94
NT2RM2001420	F-NT2RM2001420	0.46
NT2RM2001424	F-NT2RM2001424	0.94
NT2RM2001499	F-NT2RM2001499	0.63
NT2RM2001504	F-NT2RM2001504	0.94
NT2RM2001524	F-NT2RM2001524	0.76
NT2RM2001544	F-NT2RM2001544	0.59
NT2RM2001547	F-NT2RM2001547	0.48
NT2RM2001575	F-NT2RM2001575	0.91
NT2RM2001582	F-NT2RM2001582	0.34
NT2RM2001588	F-NT2RM2001588	0.48
NT2RM2001592	F-NT2RM2001592	0.64
NT2RM2001605	F-NT2RM2001605	0.47
NT2RM2001613	F-NT2RM2001613	0.61
NT2RM2001632	F-NT2RM2001632	0.31
NT2RM2001635	F-NT2RM2001635	0.39
NT2RM2001637	F-NT2RM2001637	0.71
NT2RM2001641	F-NT2RM2001641	0.73
NT2RM2001648	F-NT2RM2001648	0.44
NT2RM2001652	F-NT2RM2001652	0.40
NT2RM2001659	F-NT2RM2001659	0.35
NT2RM2001664	F-NT2RM2001664	0.53
NT2RM2001668	F-NT2RM2001668	0.64

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NT2RM2001670	F-NT2RM2001670	0.59
NT2RM2001671	F-NT2RM2001671	0.41
NT2RM2001675	F-NT2RM2001675	0.51
NT2RM2001681	F-NT2RM2001681	0.33
NT2RM2001688	F-NT2RM2001688	0.74
NT2RM2001695	F-NT2RM2001695	0.31
NT2RM2001696	F-NT2RM2001696	0.94
NT2RM2001698	F-NT2RM2001698	0.69
NT2RM2001699	F-NT2RM2001699	0.85
NT2RM2001700	F-NT2RM2001700	0.71
NT2RM2001706	F-NT2RM2001706	0.38
NT2RM2001716	F-NT2RM2001716	0.78
NT2RM2001718	F-NT2RM2001718	0.81
NT2RM2001723	F-NT2RM2001723	0.83
NT2RM2001727	F-NT2RM2001727	0.87
NT2RM2001730	F-NT2RM2001730	0.94
NT2RM2001743	F-NT2RM2001743	0.94
NT2RM2001753	F-NT2RM2001753	0.75
NT2RM2001760	F-NT2RM2001760	0.75
NT2RM2001768	F-NT2RM2001768	0.71
NT2RM2001771	F-NT2RM2001771	0.33
NT2RM2001782	F-NT2RM2001782	0.34
NT2RM2001784	F-NT2RM2001784	0.45
NT2RM2001785	F-NT2RM2001785	0.94
NT2RM2001797	F-NT2RM2001797	0.74
NT2RM2001800	F-NT2RM2001800	0.90
NT2RM2001803	F-NT2RM2001803	0.36
NT2RM2001805	F-NT2RM2001805	0.81
NT2RM2001813	F-NT2RM2001813	0.94
NT2RM2001823	F-NT2RM2001823	0.94
NT2RM2001839	F-NT2RM2001839	0.39
NT2RM2001840	F-NT2RM2001840	0.94
NT2RM2001855	F-NT2RM2001855	0.92
NT2RM2001867	F-NT2RM2001867	0.82
NT2RM2001879	F-NT2RM2001879	0.86
NT2RM2001886	F-NT2RM2001886	0.91
NT2RM2001896	F-NT2RM2001896	0.94
NT2RM2001903	F-NT2RM2001903	0.61
NT2RM2001930	F-NT2RM2001930	0.94
NT2RM2001935	F-NT2RM2001935	0.77
NT2RM2001936	F-NT2RM2001936	0.94
NT2RM2001950	F-NT2RM2001950	0.34
NT2RM2001982	F-NT2RM2001982	0.48
NT2RM2001983	F-NT2RM2001983	0.59
NT2RM2001989	F-NT2RM2001989	0.94
NT2RM2001997	F-NT2RM2001997	0.90

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NT2RM2001998	F-NT2RM2001998	0.72
NT2RM2002004	F-NT2RM2002004	0.46
NT2RM2002014	F-NT2RM2002014	0.32
NT2RM2002030	F-NT2RM2002030	0.54
NT2RM2002049	F-NT2RM2002049	0.59
NT2RM2002055	F-NT2RM2002055	0.94
NT2RM2002088	F-NT2RM2002088	0.47
NT2RM2002091	F-NT2RM2002091	0.78
NT2RM2002100	F-NT2RM2002100	0.87
NT2RM2002109	F-NT2RM2002109	0.86
NT2RM2002128	F-NT2RM2002128	0.42
NT2RM2002142	F-NT2RM2002142	0.94
NT2RM2002145	F-NT2RM2002145	0.94
NT2RM2002178	F-NT2RM2002178	0.44
NT2RM2002580	F-NT2RM2002580	0.94
NT2RM4000024	F-NT2RM4000024	0.76
NT2RM4000027	F-NT2RM4000027	0.40
NT2RM4000030	F-NT2RM4000030	0.66
NT2RM4000061	F-NT2RM4000061	0.33
NT2RM4000104	F-NT2RM4000104	0.93
NT2RM4000139	F-NT2RM4000139	0.87
NT2RM4000155	F-NT2RM4000155	0.51
NT2RM4000156	F-NT2RM4000156	0.39
NT2RM4000167	F-NT2RM4000167	0.50
NT2RM4000169	F-NT2RM4000169	0.44
NT2RM4000191	F-NT2RM4000191	0.94
NT2RM4000197	F-NT2RM4000197	0.41
NT2RM4000199	F-NT2RM4000199	0.76
NT2RM4000202	F-NT2RM4000202	0.47
NT2RM4000210	F-NT2RM4000210	0.44
NT2RM4000215	F-NT2RM4000215	0.94
NT2RM4000229	F-NT2RM4000229	0.93
NT2RM4000233	F-NT2RM4000233	0.74
NT2RM4000251	F-NT2RM4000251	0.48
NT2RM4000290	F-NT2RM4000290	0.94
NT2RM4000324	F-NT2RM4000324	0.32
NT2RM4000344	F-NT2RM4000344	0.94
NT2RM4000349	F-NT2RM4000349	0.78
NT2RM4000354	F-NT2RM4000354	0.36
NT2RM4000356	F-NT2RM4000356	0.58
NT2RM4000386	F-NT2RM4000386	0.90
NT2RM4000395	F-NT2RM4000395	0.47
NT2RM4000421	F-NT2RM4000421	0.46
NT2RM4000433	F-NT2RM4000433	0.48
NT2RM4000457	F-NT2RM4000457	0.75
NT2RM4000471	F-NT2RM4000471	0.92

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NT2RM4000486	F-NT2RM4000486	0.55
NT2RM4000496	F-NT2RM4000496	0.62
NT2RM4000511	F-NT2RM4000511	0.74
NT2RM4000514	F-NT2RM4000514	0.72
NT2RM4000515	F-NT2RM4000515	0.66
NT2RM4000520	F-NT2RM4000520	0.69
NT2RM4000531	F-NT2RM4000531	0.62
NT2RM4000534	F-NT2RM4000534	0.94
NT2RM4000585	F-NT2RM4000585	0.52
NT2RM4000590	F-NT2RM4000590	0.94
NT2RM4000595	F-NT2RM4000595	0.44
NT2RM4000603	F-NT2RM4000603	0.94
NT2RM4000611	F-NT2RM4000611	0.46
NT2RM4000616	F-NT2RM4000616	0.94
NT2RM4000674	F-NT2RM4000674	0.80
NT2RM4000689	F-NT2RM4000689	0.58
NT2RM4000698	F-NT2RM4000698	0.71
NT2RM4000700	F-NT2RM4000700	0.59
NT2RM4000712	F-NT2RM4000712	0.94
NT2RM4000717	F-NT2RM4000717	0.69
NT2RM4000733	F-NT2RM4000733	0.94
NT2RM4000734	F-NT2RM4000734	0.42
NT2RM4000741	F-NT2RM4000741	0.83
NT2RM4000751	F-NT2RM4000751	0.91
NT2RM4000764	F-NT2RM4000764	0.35
NT2RM4000778	F-NT2RM4000778	0.90
NT2RM4000787	F-NT2RM4000787	0.40
NT2RM4000790	F-NT2RM4000790	0.62
NT2RM4000795	F-NT2RM4000795	0.94
NT2RM4000796	F-NT2RM4000796	0.93
NT2RM4000798	F-NT2RM4000798	0.61
NT2RM4000813	F-NT2RM4000813	0.58
NT2RM4000820	F-NT2RM4000820	0.39
NT2RM4000833	F-NT2RM4000833	0.80
NT2RM4000848	F-NT2RM4000848	0.73
NT2RM4000852	F-NT2RM4000852	0.74
NT2RM4000887	F-NT2RM4000887	0.42
NT2RM4000895	F-NT2RM4000895	0.47
NT2RM4000950	F-NT2RM4000950	0.53
NT2RM4000971	F-NT2RM4000971	0.73
NT2RM4000996	F-NT2RM4000996	0.42
NT2RM4001002	F-NT2RM4001002	0.57
NT2RM4001032	F-NT2RM4001032	0.94
NT2RM4001047	F-NT2RM4001047	0.76
NT2RM4001054	F-NT2RM4001054	0.91
NT2RM4001084	F-NT2RM4001084	0.94

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NT2RM4001092	F-NT2RM4001092	0.94
NT2RM4001116	F-NT2RM4001116	0.36
NT2RM4001140	F-NT2RM4001140	0.82
NT2RM4001151	F-NT2RM4001151	0.94
NT2RM4001155	F-NT2RM4001155	0.94
NT2RM4001187	F-NT2RM4001187	0.61
NT2RM4001191	F-NT2RM4001191	0.77
NT2RM4001200	F-NT2RM4001200	0.72
NT2RM4001203	F-NT2RM4001203	0.60
NT2RM4001204	F-NT2RM4001204	0.89
NT2RM4001217	F-NT2RM4001217	0.93
NT2RM4001256	F-NT2RM4001256	0.89
NT2RM4001258	F-NT2RM4001258	0.94
NT2RM4001309	F-NT2RM4001309	0.88
NT2RM4001316	F-NT2RM4001316	0.38
NT2RM4001320	F-NT2RM4001320	0.33
NT2RM4001340	F-NT2RM4001340	0.83
NT2RM4001344	F-NT2RM4001344	0.94
NT2RM4001347	F-NT2RM4001347	0.88
NT2RM4001371	F-NT2RM4001371	0.61
NT2RM4001382	F-NT2RM4001382	0.93
NT2RM4001384	F-NT2RM4001384	0.32
NT2RM4001410	F-NT2RM4001410	0.94
NT2RM4001411	F-NT2RM4001411	0.47
NT2RM4001412	F-NT2RM4001412	0.85
NT2RM4001444	F-NT2RM4001444	0.94
NT2RM4001454	F-NT2RM4001454	0.72
NT2RM4001455	F-NT2RM4001455	0.39
NT2RM4001483	F-NT2RM4001483	0.76
NT2RM4001489	F-NT2RM4001489	0.94
NT2RM4001522	F-NT2RM4001522	0.88
NT2RM4001565	F-NT2RM4001565	0.78
NT2RM4001566	F-NT2RM4001566	0.87
NT2RM4001569	F-NT2RM4001569	0.70
NT2RM4001582	F-NT2RM4001582	0.76
NT2RM4001592	F-NT2RM4001592	0.31
NT2RM4001594	F-NT2RM4001594	0.86
NT2RM4001597	F-NT2RM4001597	0.91
NT2RM4001611	F-NT2RM4001611	0.91
NT2RM4001629	F-NT2RM4001629	0.72
NT2RM4001650	F-NT2RM4001650	0.37
NT2RM4001662	F-NT2RM4001662	0.70
NT2RM4001666	F-NT2RM4001666	0.37
NT2RM4001682	F-NT2RM4001682	0.91
NT2RM4001710	F-NT2RM4001710	0.45
NT2RM4001714	F-NT2RM4001714	0.94

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NT2RM4001715	F-NT2RM4001715	0.33
NT2RM4001731	F-NT2RM4001731	0.94
NT2RM4001741	F-NT2RM4001741	0.87
NT2RM4001746	F-NT2RM4001746	0.81
NT2RM4001758	F-NT2RM4001758	0.59
NT2RM4001783	F-NT2RM4001783	0.68
NT2RM4001813	F-NT2RM4001813	0.39
NT2RM4001819	F-NT2RM4001819	0.43
NT2RM4001823	F-NT2RM4001823	0.94
NT2RM4001828	F-NT2RM4001828	0.83
NT2RM4001836	F-NT2RM4001836	0.61
NT2RM4001841	F-NT2RM4001841	0.37
NT2RM4001842	F-NT2RM4001842	0.68
NT2RM4001865	F-NT2RM4001865	0.91
NT2RM4001876	F-NT2RM4001876	0.88
NT2RM4001880	F-NT2RM4001880	0.43
NT2RM4001905	F-NT2RM4001905	0.94
NT2RM4001922	F-NT2RM4001922	0.48
NT2RM4001938	F-NT2RM4001938	0.67
NT2RM4001940	F-NT2RM4001940	0.92
NT2RM4001965	F-NT2RM4001965	0.94
NT2RM4001969	F-NT2RM4001969	0.88
NT2RM4001979	F-NT2RM4001979	0.42
NT2RM4001987	F-NT2RM4001987	0.86
NT2RM4002013	F-NT2RM4002013	0.94
NT2RM4002018	F-NT2RM4002018	0.92
NT2RM4002034	F-NT2RM4002034	0.43
NT2RM4002044	F-NT2RM4002044	0.42
NT2RM4002054	F-NT2RM4002054	0.88
NT2RM4002055	F-NT2RM4002055	0.32
NT2RM4002062	F-NT2RM4002062	0.87
NT2RM4002063	F-NT2RM4002063	0.49
NT2RM4002066	F-NT2RM4002066	0.39
NT2RM4002073	F-NT2RM4002073	0.78
NT2RM4002075	F-NT2RM4002075	0.87
NT2RM4002093	F-NT2RM4002093	0.82
NT2RM4002109	F-NT2RM4002109	0.52
NT2RM4002128	F-NT2RM4002128	0.68
NT2RM4002140	F-NT2RM4002140	0.94
NT2RM4002145	F-NT2RM4002145	0.94
NT2RM4002146	F-NT2RM4002146	0.89
NT2RM4002161	F-NT2RM4002161	0.49
NT2RM4002174	F-NT2RM4002174	0.36
NT2RM4002189	F-NT2RM4002189	0.34
NT2RM4002194	F-NT2RM4002194	0.73
NT2RM4002205	F-NT2RM4002205	0.94

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NT2RM4002213	F-NT2RM4002213	0.52
NT2RM4002226	F-NT2RM4002226	0.48
NT2RM4002251	F-NT2RM4002251	0.94
NT2RM4002256	F-NT2RM4002256	0.93
NT2RM4002266	F-NT2RM4002266	0.73
NT2RM4002294	F-NT2RM4002294	0.86
NT2RM4002301	F-NT2RM4002301	0.40
NT2RM4002323	F-NT2RM4002323	0.81
NT2RM4002339	F-NT2RM4002339	0.32
NT2RM4002344	F-NT2RM4002344	0.87
NT2RM4002373	F-NT2RM4002373	0.41
NT2RM4002374	F-NT2RM4002374	0.33
NT2RM4002398	F-NT2RM4002398	0.94
NT2RM4002409	F-NT2RM4002409	0.82
NT2RM4002446	F-NT2RM4002446	0.61
NT2RM4002452	F-NT2RM4002452	0.47
NT2RM4002457	F-NT2RM4002457	0.92
NT2RM4002460	F-NT2RM4002460	0.61
NT2RM4002482	F-NT2RM4002482	0.94
NT2RM4002493	F-NT2RM4002493	0.39
NT2RM4002527	F-NT2RM4002527	0.64
NT2RM4002534	F-NT2RM4002534	0.76
NT2RM4002558	F-NT2RM4002558	0.62
NT2RM4002565	F-NT2RM4002565	0.54
NT2RM4002571	F-NT2RM4002571	0.90
NT2RM4002593	F-NT2RM4002593	0.91
NT2RM4002594	F-NT2RM4002594	0.70
NT2RM4002623	F-NT2RM4002623	0.81
NT2RP1000018	F-NT2RP1000018	0.31
NT2RP1000035	F-NT2RP1000035	0.49
NT2RP1000040	F-NT2RP1000040	0.45
NT2RP1000063	F-NT2RP1000063	0.90
NT2RP1000086	F-NT2RP1000086	0.89
NT2RP1000101	F-NT2RP1000101	0.76
NT2RP1000111	F-NT2RP1000111	0.94
NT2RP1000112	F-NT2RP1000112	0.45
NT2RP1000124	F-NT2RP1000124	0.94
NT2RP1000130	F-NT2RP1000130	0.69
NT2RP1000163	F-NT2RP1000163	0.90
NT2RP1000170	F-NT2RP1000170	0.94
NT2RP1000174	F-NT2RP1000174	0.74
NT2RP1000191	F-NT2RP1000191	0.76
NT2RP1000202	F-NT2RP1000202	0.60
NT2RP1000243	F-NT2RP1000243	0.81
NT2RP1000259	F-NT2RP1000259	0.79
NT2RP1000272	F-NT2RP1000272	0.94

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NT2RP1000324	F-NT2RP1000324	0.32
NT2RP1000326	F-NT2RP1000326	0.94
NT2RP1000333	F-NT2RP1000333	0.94
NT2RP1000348	F-NT2RP1000348	0.94
NT2RP1000357	F-NT2RP1000357	0.87
NT2RP1000358	F-NT2RP1000358	0.79
NT2RP1000363	F-NT2RP1000363	0.40
NT2RP1000376	F-NT2RP1000376	0.61
NT2RP1000409	F-NT2RP1000409	0.85
NT2RP1000413	F-NT2RP1000413	0.42
NT2RP1000416	F-NT2RP1000416	0.68
NT2RP1000418	F-NT2RP1000418	0.88
NT2RP1000439	F-NT2RP1000439	0.69
NT2RP1000443	F-NT2RP1000443	0.59
NT2RP1000460	F-NT2RP1000460	0.86
NT2RP1000470	F-NT2RP1000470	0.56
NT2RP1000478	F-NT2RP1000478	0.87
NT2RP1000481	F-NT2RP1000481	0.58
NT2RP1000493	F-NT2RP1000493	0.34
NT2RP1000513	F-NT2RP1000513	0.89
NT2RP1000522	F-NT2RP1000522	0.34
NT2RP1000547	F-NT2RP1000547	0.89
NT2RP1000574	F-NT2RP1000574	0.74
NT2RP1000577	F-NT2RP1000577	0.53
NT2RP1000581	F-NT2RP1000581	0.66
NT2RP1000609	F-NT2RP1000609	0.90
NT2RP1000629	F-NT2RP1000629	0.94
NT2RP1000630	F-NT2RP1000630	0.93
NT2RP1000677	F-NT2RP1000677	0.94
NT2RP1000688	F-NT2RP1000688	0.94
NT2RP1000695	F-NT2RP1000695	0.89
NT2RP1000701	F-NT2RP1000701	0.89
NT2RP1000721	F-NT2RP1000721	0.91
NT2RP1000730	F-NT2RP1000730	0.94
NT2RP1000733	F-NT2RP1000733	0.90
NT2RP1000738	F-NT2RP1000738	0.64
NT2RP1000746	F-NT2RP1000746	0.92
NT2RP1000767	F-NT2RP1000767	0.82
NT2RP1000782	F-NT2RP1000782	0.94
NT2RP1000796	F-NT2RP1000796	0.33
NT2RP1000825	F-NT2RP1000825	0.74
NT2RP1000833	F-NT2RP1000833	0.94
NT2RP1000834	F-NT2RP1000834	0.88
NT2RP1000836	F-NT2RP1000836	0.59
NT2RP1000846	F-NT2RP1000846	0.46
NT2RP1000851	F-NT2RP1000851	0.82

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NT2RP1000856	F-NT2RP1000856	0.94
NT2RP1000860	F-NT2RP1000860	0.60
NT2RP1000902	F-NT2RP1000902	0.42
NT2RP1000915	F-NT2RP1000915	0.90
NT2RP1000916	F-NT2RP1000916	0.67
NT2RP1000943	F-NT2RP1000943	0.77
NT2RP1000944	F-NT2RP1000944	0.94
NT2RP1000947	F-NT2RP1000947	0.38
NT2RP1000954	F-NT2RP1000954	0.59
NT2RP1000958	F-NT2RP1000958	0.59
NT2RP1000959	F-NT2RP1000959	0.74
NT2RP1000966	F-NT2RP1000966	0.93
NT2RP1000980	F-NT2RP1000980	0.31
NT2RP1000988	F-NT2RP1000988	0.53
NT2RP1001011	F-NT2RP1001011	0.65
NT2RP1001013	F-NT2RP1001013	0.34
NT2RP1001014	F-NT2RP1001014	0.94
NT2RP1001033	F-NT2RP1001033	0.40
NT2RP1001073	F-NT2RP1001073	0.74
NT2RP1001079	F-NT2RP1001079	0.48
NT2RP1001080	F-NT2RP1001080	0.91
NT2RP1001113	F-NT2RP1001113	0.94
NT2RP1001173	F-NT2RP1001173	0.57
NT2RP1001177	F-NT2RP1001177	0.75
NT2RP1001185	F-NT2RP1001185	0.94
NT2RP1001199	F-NT2RP1001199	0.42
NT2RP1001247	F-NT2RP1001247	0.67
NT2RP1001248	F-NT2RP1001248	0.89
NT2RP1001253	F-NT2RP1001253	0.94
NT2RP1001286	F-NT2RP1001286	0.59
NT2RP1001294	F-NT2RP1001294	0.81
NT2RP1001302	F-NT2RP1001302	0.86
NT2RP1001310	F-NT2RP1001310	0.91
NT2RP1001311	F-NT2RP1001311	0.87
NT2RP1001313	F-NT2RP1001313	0.91
NT2RP1001361	F-NT2RP1001361	0.83
NT2RP1001385	F-NT2RP1001385	0.36
NT2RP1001395	F-NT2RP1001395	0.84
NT2RP1001410	F-NT2RP1001410	0.72
NT2RP1001424	F-NT2RP1001424	0.81
NT2RP1001432	F-NT2RP1001432	0.81
NT2RP1001449	F-NT2RP1001449	0.77
NT2RP1001457	F-NT2RP1001457	0.92
NT2RP1001466	F-NT2RP1001466	0.44
NT2RP1001475	F-NT2RP1001475	0.53
NT2RP1001482	F-NT2RP1001482	0.34

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NT2RP1001494	F-NT2RP1001494	0.93
NT2RP1001543	F-NT2RP1001543	0.94
NT2RP1001546	F-NT2RP1001546	0.94
NT2RP1001569	F-NT2RP1001569	0.93
NT2RP1001616	F-NT2RP1001616	0.46
NT2RP1001665	F-NT2RP1001665	0.94
NT2RP2000001	F-NT2RP2000001	0.94
NT2RP2000006	F-NT2RP2000006	0.74
NT2RP2000007	F-NT2RP2000007	0.94
NT2RP2000008	F-NT2RP2000008	0.83
NT2RP2000032	F-NT2RP2000032	0.94
NT2RP2000040	F-NT2RP2000040	0.92
NT2RP2000045	F-NT2RP2000045	0.94
NT2RP2000054	F-NT2RP2000054	0.53
NT2RP2000056	F-NT2RP2000056	0.42
NT2RP2000067	F-NT2RP2000067	0.88
NT2RP2000070	F-NT2RP2000070	0.48
NT2RP2000079	F-NT2RP2000079	0.85
NT2RP2000088	F-NT2RP2000088	0.94
NT2RP2000091	F-NT2RP2000091	0.79
NT2RP2000097	F-NT2RP2000097	0.66
NT2RP2000114	F-NT2RP2000114	0.86
NT2RP2000120	F-NT2RP2000120	0.48
NT2RP2000126	F-NT2RP2000126	0.77
NT2RP2000133	F-NT2RP2000133	0.64
NT2RP2000147	F-NT2RP2000147	0.94
NT2RP2000153	F-NT2RP2000153	0.87
NT2RP2000157	F-NT2RP2000157	0.48
NT2RP2000161	F-NT2RP2000161	0.79
NT2RP2000173	F-NT2RP2000173	0.75
NT2RP2000175	F-NT2RP2000175	0.79
NT2RP2000195	F-NT2RP2000195	0.91
NT2RP2000205	F-NT2RP2000205	0.94
NT2RP2000208	F-NT2RP2000208	0.84
NT2RP2000224	F-NT2RP2000224	0.52
NT2RP2000232	F-NT2RP2000232	0.33
NT2RP2000233	F-NT2RP2000233	0.57
NT2RP2000239	F-NT2RP2000239	0.52
NT2RP2000248	F-NT2RP2000248	0.36
NT2RP2000274	F-NT2RP2000274	0.55
NT2RP2000283	F-NT2RP2000283	0.61
NT2RP2000288	F-NT2RP2000288	0.31
NT2RP2000297	F-NT2RP2000297	0.78
NT2RP2000298	F-NT2RP2000298	0.94
NT2RP2000310	F-NT2RP2000310	0.52
NT2RP2000328	F-NT2RP2000328	0.75

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NT2RP2000329	F-NT2RP2000329	0.94
NT2RP2000346	F-NT2RP2000346	0.62
NT2RP2000369	F-NT2RP2000369	0.87
NT2RP2000412	F-NT2RP2000412	0.75
NT2RP2000414	F-NT2RP2000414	0.79
NT2RP2000422	F-NT2RP2000422	0.46
NT2RP2000438	F-NT2RP2000438	0.94
NT2RP2000448	F-NT2RP2000448	0.94
NT2RP2000503	F-NT2RP2000503	0.94
NT2RP2000510	F-NT2RP2000510	0.87
NT2RP2000516	F-NT2RP2000516	0.42
NT2RP2000617	F-NT2RP2000617	0.94
NT2RP2000634	F-NT2RP2000634	0.74
NT2RP2000656	F-NT2RP2000656	0.68
NT2RP2000658	F-NT2RP2000658	0.55
NT2RP2000668	F-NT2RP2000668	0.81
NT2RP2000704	F-NT2RP2000704	0.88
NT2RP2000710	F-NT2RP2000710	0.58
NT2RP2000764	F-NT2RP2000764	0.59
NT2RP2000809	F-NT2RP2000809	0.51
NT2RP2000812	F-NT2RP2000812	0.37
NT2RP2000814	F-NT2RP2000814	0.66
NT2RP2000816	F-NT2RP2000816	0.50
NT2RP2000819	F-NT2RP2000819	0.35
NT2RP2000841	F-NT2RP2000841	0.93
NT2RP2000845	F-NT2RP2000845	0.78
NT2RP2000863	F-NT2RP2000863	0.41
NT2RP2000880	F-NT2RP2000880	0.79
NT2RP2000892	F-NT2RP2000892	0.94
NT2RP2000931	F-NT2RP2000931	0.89
NT2RP2000932	F-NT2RP2000932	0.94
NT2RP2000938	F-NT2RP2000938	0.90
NT2RP2000943	F-NT2RP2000943	0.61
NT2RP2000965	F-NT2RP2000965	0.80
NT2RP2000985	F-NT2RP2000985	0.94
NT2RP2001036	F-NT2RP2001036	0.86
NT2RP2001044	F-NT2RP2001044	0.93
NT2RP2001056	F-NT2RP2001056	0.77
NT2RP2001065	F-NT2RP2001065	0.73
NT2RP2001070	F-NT2RP2001070	0.91
NT2RP2001081	F-NT2RP2001081	0.94
NT2RP2001094	F-NT2RP2001094	0.93
NT2RP2001119	F-NT2RP2001119	0.31
NT2RP2001127	F-NT2RP2001127	0.41
NT2RP2001137	F-NT2RP2001137	0.93
NT2RP2001168	F-NT2RP2001168	0.71

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NT2RP2001173	F-NT2RP2001173	0.94
NT2RP2001174	F-NT2RP2001174	0.71
NT2RP2001218	F-NT2RP2001218	0.76
NT2RP2001233	F-NT2RP2001233	0.31
NT2RP2001245	F-NT2RP2001245	0.33
NT2RP2001268	F-NT2RP2001268	0.61
NT2RP2001327	F-NT2RP2001327	0.86
NT2RP2001328	F-NT2RP2001328	0.94
NT2RP2001366	F-NT2RP2001366	0.52
NT2RP2001378	F-NT2RP2001378	0.64
NT2RP2001381	F-NT2RP2001381	0.80
NT2RP2001392	F-NT2RP2001392	0.69
NT2RP2001394	F-NT2RP2001394	0.38
NT2RP2001397	F-NT2RP2001397	0.79
NT2RP2001420	F-NT2RP2001420	0.88
NT2RP2001427	F-NT2RP2001427	0.73
NT2RP2001436	F-NT2RP2001436	0.32
NT2RP2001440	F-NT2RP2001440	0.94
NT2RP2001450	F-NT2RP2001450	0.38
NT2RP2001511	F-NT2RP2001511	0.53
NT2RP2001520	F-NT2RP2001520	0.88
NT2RP2001536	F-NT2RP2001536	0.64
NT2RP2001560	F-NT2RP2001560	0.79
NT2RP2001576	F-NT2RP2001576	0.62
NT2RP2001581	F-NT2RP2001581	0.48
NT2RP2001597	F-NT2RP2001597	0.94
NT2RP2001601	F-NT2RP2001601	0.33
NT2RP2001613	F-NT2RP2001613	0.41
NT2RP2001628	F-NT2RP2001628	0.79
NT2RP2001634	F-NT2RP2001634	0.87
NT2RP2001660	F-NT2RP2001660	0.86
NT2RP2001675	F-NT2RP2001675	0.90
NT2RP2001721	F-NT2RP2001721	0.32
NT2RP2001748	F-NT2RP2001748	0.32
NT2RP2001839	F-NT2RP2001839	0.83
NT2RP2001861	F-NT2RP2001861	0.33
NT2RP2001876	F-NT2RP2001876	0.94
NT2RP2001883	F-NT2RP2001883	0.90
NT2RP2001898	F-NT2RP2001898	0.94
NT2RP2001900	F-NT2RP2001900	0.93
NT2RP2001907	F-NT2RP2001907	0.94
NT2RP2001946	F-NT2RP2001946	0.63
NT2RP2001947	F-NT2RP2001947	0.75
NT2RP2001969	F-NT2RP2001969	0.94
NT2RP2001976	F-NT2RP2001976	0.48
NT2RP2001985	F-NT2RP2001985	0.44

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NT2RP2001991	F-NT2RP2001991	0. 39
NT2RP2002025	F-NT2RP2002025	0. 94
NT2RP2002033	F-NT2RP2002033	0. 40
NT2RP2002046	F-NT2RP2002046	0. 56
NT2RP2002058	F-NT2RP2002058	0. 64
NT2RP2002076	F-NT2RP2002076	0. 40
NT2RP2002078	F-NT2RP2002078	0. 81
NT2RP2002079	F-NT2RP2002079	0. 82
NT2RP2002099	F-NT2RP2002099	0. 92
NT2RP2002154	F-NT2RP2002154	0. 44
NT2RP2002185	F-NT2RP2002185	0. 94
NT2RP2002193	F-NT2RP2002193	0. 48
NT2RP2002208	F-NT2RP2002208	0. 49
NT2RP2002231	F-NT2RP2002231	0. 61
NT2RP2002235	F-NT2RP2002235	0. 87
NT2RP2002252	F-NT2RP2002252	0. 51
NT2RP2002270	F-NT2RP2002270	0. 78
NT2RP2002292	F-NT2RP2002292	0. 94
NT2RP2002312	F-NT2RP2002312	0. 33
NT2RP2002325	F-NT2RP2002325	0. 53
NT2RP2002333	F-NT2RP2002333	0. 60
NT2RP2002373	F-NT2RP2002373	0. 91
NT2RP2002385	F-NT2RP2002385	0. 94
NT2RP2002408	F-NT2RP2002408	0. 44
NT2RP2002426	F-NT2RP2002426	0. 54
NT2RP2002442	F-NT2RP2002442	0. 37
NT2RP2002464	F-NT2RP2002464	0. 79
NT2RP2002479	F-NT2RP2002479	0. 92
NT2RP2002498	F-NT2RP2002498	0. 94
NT2RP2002503	F-NT2RP2002503	0. 90
NT2RP2002520	F-NT2RP2002520	0. 37
NT2RP2002537	F-NT2RP2002537	0. 42
NT2RP2002549	F-NT2RP2002549	0. 75
NT2RP2002595	F-NT2RP2002595	0. 90
NT2RP2002609	F-NT2RP2002609	0. 33
NT2RP2002618	F-NT2RP2002618	0. 52
NT2RP2002621	F-NT2RP2002621	0. 67
NT2RP2002672	F-NT2RP2002672	0. 43
NT2RP2002701	F-NT2RP2002701	0. 69
NT2RP2002706	F-NT2RP2002706	0. 51
NT2RP2002710	F-NT2RP2002710	0. 94
NT2RP2002769	F-NT2RP2002769	0. 42
NT2RP2002800	F-NT2RP2002800	0. 47
NT2RP2002862	F-NT2RP2002862	0. 88
NT2RP2002880	F-NT2RP2002880	0. 78
NT2RP2002891	F-NT2RP2002891	0. 69

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NT2RP2002925	F-NT2RP2002925	0.65
NT2RP2002928	F-NT2RP2002928	0.47
NT2RP2002929	F-NT2RP2002929	0.94
NT2RP2002939	F-NT2RP2002939	0.94
NT2RP2002954	F-NT2RP2002954	0.94
NT2RP2002959	F-NT2RP2002959	0.45
NT2RP2002979	F-NT2RP2002979	0.51
NT2RP2002980	F-NT2RP2002980	0.38
NT2RP2002986	F-NT2RP2002986	0.34
NT2RP2002993	F-NT2RP2002993	0.94
NT2RP2003034	F-NT2RP2003034	0.34
NT2RP2003099	F-NT2RP2003099	0.46
NT2RP2003108	F-NT2RP2003108	0.67
NT2RP2003117	F-NT2RP2003117	0.57
NT2RP2003121	F-NT2RP2003121	0.94
NT2RP2003125	F-NT2RP2003125	0.94
NT2RP2003137	F-NT2RP2003137	0.60
NT2RP2003157	F-NT2RP2003157	0.94
NT2RP2003158	F-NT2RP2003158	0.75
NT2RP2003165	F-NT2RP2003165	0.90
NT2RP2003177	F-NT2RP2003177	0.85
NT2RP2003194	F-NT2RP2003194	0.94
NT2RP2003228	F-NT2RP2003228	0.57
NT2RP2003243	F-NT2RP2003243	0.94
NT2RP2003265	F-NT2RP2003265	0.68
NT2RP2003272	F-NT2RP2003272	0.94
NT2RP2003277	F-NT2RP2003277	0.73
NT2RP2003280	F-NT2RP2003280	0.94
NT2RP2003286	F-NT2RP2003286	0.44
NT2RP2003293	F-NT2RP2003293	0.42
NT2RP2003295	F-NT2RP2003295	0.89
NT2RP2003297	F-NT2RP2003297	0.94
NT2RP2003307	F-NT2RP2003307	0.79
NT2RP2003308	F-NT2RP2003308	0.49
NT2RP2003329	F-NT2RP2003329	0.33
NT2RP2003347	F-NT2RP2003347	0.79
NT2RP2003367	F-NT2RP2003367	0.94
NT2RP2003391	F-NT2RP2003391	0.90
NT2RP2003393	F-NT2RP2003393	0.94
NT2RP2003401	F-NT2RP2003401	0.80
NT2RP2003433	F-NT2RP2003433	0.40
NT2RP2003445	F-NT2RP2003445	0.94
NT2RP2003446	F-NT2RP2003446	0.40
NT2RP2003466	F-NT2RP2003466	0.58
NT2RP2003480	F-NT2RP2003480	0.59
NT2RP2003506	F-NT2RP2003506	0.94

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NT2RP2003511	F-NT2RP2003511	0.31
NT2RP2003513	F-NT2RP2003513	0.67
NT2RP2003533	F-NT2RP2003533	0.57
NT2RP2003543	F-NT2RP2003543	0.94
NT2RP2003564	F-NT2RP2003564	0.88
NT2RP2003567	F-NT2RP2003567	0.69
NT2RP2003581	F-NT2RP2003581	0.40
NT2RP2003596	F-NT2RP2003596	0.83
NT2RP2003604	F-NT2RP2003604	0.87
NT2RP2003629	F-NT2RP2003629	0.87
NT2RP2003643	F-NT2RP2003643	0.94
NT2RP2003687	F-NT2RP2003687	0.31
NT2RP2003691	F-NT2RP2003691	0.34
NT2RP2003702	F-NT2RP2003702	0.80
NT2RP2003713	F-NT2RP2003713	0.53
NT2RP2003714	F-NT2RP2003714	0.61
NT2RP2003737	F-NT2RP2003737	0.88
NT2RP2003751	F-NT2RP2003751	0.36
NT2RP2003760	F-NT2RP2003760	0.62
NT2RP2003764	F-NT2RP2003764	0.94
NT2RP2003769	F-NT2RP2003769	0.69
NT2RP2003777	F-NT2RP2003777	0.93
NT2RP2003781	F-NT2RP2003781	0.37
NT2RP2003793	F-NT2RP2003793	0.92
NT2RP2003825	F-NT2RP2003825	0.49
NT2RP2003840	F-NT2RP2003840	0.88
NT2RP2003857	F-NT2RP2003857	0.34
NT2RP2003952	F-NT2RP2003952	0.89
NT2RP2003976	F-NT2RP2003976	0.33
NT2RP2003981	F-NT2RP2003981	0.64
NT2RP2003984	F-NT2RP2003984	0.41
NT2RP2003986	F-NT2RP2003986	0.32
NT2RP2004013	F-NT2RP2004013	0.48
NT2RP2004041	F-NT2RP2004041	0.78
NT2RP2004042	F-NT2RP2004042	0.66
NT2RP2004066	F-NT2RP2004066	0.56
NT2RP2004081	F-NT2RP2004081	0.94
NT2RP2004098	F-NT2RP2004098	0.39
NT2RP2004124	F-NT2RP2004124	0.75
NT2RP2004152	F-NT2RP2004152	0.54
NT2RP2004165	F-NT2RP2004165	0.68
NT2RP2004187	F-NT2RP2004187	0.92
NT2RP2004194	F-NT2RP2004194	0.90
NT2RP2004196	F-NT2RP2004196	0.94
NT2RP2004226	F-NT2RP2004226	0.80
NT2RP2004239	F-NT2RP2004239	0.63

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NT2RP2004240	F-NT2RP2004240	0.86
NT2RP2004242	F-NT2RP2004242	0.94
NT2RP2004245	F-NT2RP2004245	0.92
NT2RP2004316	F-NT2RP2004316	0.33
NT2RP2004364	F-NT2RP2004364	0.75
NT2RP2004365	F-NT2RP2004365	0.43
NT2RP2004366	F-NT2RP2004366	0.32
NT2RP2004373	F-NT2RP2004373	0.60
NT2RP2004389	F-NT2RP2004389	0.94
NT2RP2004392	F-NT2RP2004392	0.93
NT2RP2004399	F-NT2RP2004399	0.36
NT2RP2004463	F-NT2RP2004463	0.43
NT2RP2004476	F-NT2RP2004476	0.80
NT2RP2004538	F-NT2RP2004538	0.94
NT2RP2004551	F-NT2RP2004551	0.47
NT2RP2004568	F-NT2RP2004568	0.73
NT2RP2004594	F-NT2RP2004594	0.64
NT2RP2004600	F-NT2RP2004600	0.53
NT2RP2004602	F-NT2RP2004602	0.33
NT2RP2004614	F-NT2RP2004614	0.34
NT2RP2004655	F-NT2RP2004655	0.77
NT2RP2004664	F-NT2RP2004664	0.94
NT2RP2004689	F-NT2RP2004689	0.83
NT2RP2004710	F-NT2RP2004710	0.94
NT2RP2004743	F-NT2RP2004743	0.32
NT2RP2004768	F-NT2RP2004768	0.53
NT2RP2004791	F-NT2RP2004791	0.64
NT2RP2004799	F-NT2RP2004799	0.42
NT2RP2004802	F-NT2RP2004802	0.88
NT2RP2004816	F-NT2RP2004816	0.78
NT2RP2004841	F-NT2RP2004841	0.61
NT2RP2004861	F-NT2RP2004861	0.32
NT2RP2004897	F-NT2RP2004897	0.67
NT2RP2004933	F-NT2RP2004933	0.94
NT2RP2004936	F-NT2RP2004936	0.53
NT2RP2004959	F-NT2RP2004959	0.78
NT2RP2004978	F-NT2RP2004978	0.86
NT2RP2004985	F-NT2RP2004985	0.42
NT2RP2004999	F-NT2RP2004999	0.55
NT2RP2005000	F-NT2RP2005000	0.40
NT2RP2005001	F-NT2RP2005001	0.94
NT2RP2005003	F-NT2RP2005003	0.44
NT2RP2005012	F-NT2RP2005012	0.73
NT2RP2005018	F-NT2RP2005018	0.43
NT2RP2005022	F-NT2RP2005022	0.34
NT2RP2005037	F-NT2RP2005037	0.94

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NT2RP2005038	F-NT2RP2005038	0.56
NT2RP2005116	F-NT2RP2005116	0.94
NT2RP2005126	F-NT2RP2005126	0.69
NT2RP2005139	F-NT2RP2005139	0.94
NT2RP2005140	F-NT2RP2005140	0.32
NT2RP2005144	F-NT2RP2005144	0.39
NT2RP2005147	F-NT2RP2005147	0.32
NT2RP2005159	F-NT2RP2005159	0.52
NT2RP2005162	F-NT2RP2005162	0.86
NT2RP2005168	F-NT2RP2005168	0.53
NT2RP2005204	F-NT2RP2005204	0.94
NT2RP2005227	F-NT2RP2005227	0.53
NT2RP2005239	F-NT2RP2005239	0.91
NT2RP2005270	F-NT2RP2005270	0.72
NT2RP2005276	F-NT2RP2005276	0.41
NT2RP2005287	F-NT2RP2005287	0.44
NT2RP2005288	F-NT2RP2005288	0.82
NT2RP2005315	F-NT2RP2005315	0.79
NT2RP2005358	F-NT2RP2005358	0.94
NT2RP2005393	F-NT2RP2005393	0.41
NT2RP2005436	F-NT2RP2005436	0.45
NT2RP2005441	F-NT2RP2005441	0.88
NT2RP2005453	F-NT2RP2005453	0.59
NT2RP2005457	F-NT2RP2005457	0.56
NT2RP2005464	F-NT2RP2005464	0.72
NT2RP2005465	F-NT2RP2005465	0.40
NT2RP2005472	F-NT2RP2005472	0.42
NT2RP2005490	F-NT2RP2005490	0.52
NT2RP2005495	F-NT2RP2005495	0.94
NT2RP2005496	F-NT2RP2005496	0.52
NT2RP2005498	F-NT2RP2005498	0.74
NT2RP2005509	F-NT2RP2005509	0.55
NT2RP2005520	F-NT2RP2005520	0.54
NT2RP2005525	F-NT2RP2005525	0.41
NT2RP2005539	F-NT2RP2005539	0.94
NT2RP2005540	F-NT2RP2005540	0.32
NT2RP2005549	F-NT2RP2005549	0.79
NT2RP2005555	F-NT2RP2005555	0.63
NT2RP2005557	F-NT2RP2005557	0.79
NT2RP2005600	F-NT2RP2005600	0.76
NT2RP2005605	F-NT2RP2005605	0.56
NT2RP2005620	F-NT2RP2005620	0.66
NT2RP2005622	F-NT2RP2005622	0.37
NT2RP2005635	F-NT2RP2005635	0.87
NT2RP2005637	F-NT2RP2005637	0.94
NT2RP2005640	F-NT2RP2005640	0.87

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NT2RP2005654	F-NT2RP2005654	0. 94
NT2RP2005669	F-NT2RP2005669	0. 94
NT2RP2005675	F-NT2RP2005675	0. 72
NT2RP2005683	F-NT2RP2005683	0. 34
NT2RP2005690	F-NT2RP2005690	0. 54
NT2RP2005712	F-NT2RP2005712	0. 93
NT2RP2005722	F-NT2RP2005722	0. 50
NT2RP2005723	F-NT2RP2005723	0. 45
NT2RP2005732	F-NT2RP2005732	0. 54
NT2RP2005748	F-NT2RP2005748	0. 76
NT2RP2005752	F-NT2RP2005752	0. 47
NT2RP2005763	F-NT2RP2005763	0. 87
NT2RP2005767	F-NT2RP2005767	0. 58
NT2RP2005773	F-NT2RP2005773	0. 49
NT2RP2005775	F-NT2RP2005775	0. 34
NT2RP2005781	F-NT2RP2005781	0. 81
NT2RP2005784	F-NT2RP2005784	0. 94
NT2RP2005804	F-NT2RP2005804	0. 94
NT2RP2005812	F-NT2RP2005812	0. 90
NT2RP2005835	F-NT2RP2005835	0. 94
NT2RP2005853	F-NT2RP2005853	0. 77
NT2RP2005859	F-NT2RP2005859	0. 68
NT2RP2005868	F-NT2RP2005868	0. 76
NT2RP2005886	F-NT2RP2005886	0. 62
NT2RP2005890	F-NT2RP2005890	0. 79
NT2RP2005901	F-NT2RP2005901	0. 94
NT2RP2005933	F-NT2RP2005933	0. 55
NT2RP2006023	F-NT2RP2006023	0. 47
NT2RP2006038	F-NT2RP2006038	0. 73
NT2RP2006043	F-NT2RP2006043	0. 50
NT2RP2006052	F-NT2RP2006052	0. 74
NT2RP2006069	F-NT2RP2006069	0. 85
NT2RP2006071	F-NT2RP2006071	0. 94
NT2RP2006100	F-NT2RP2006100	0. 42
NT2RP2006106	F-NT2RP2006106	0. 94
NT2RP2006141	F-NT2RP2006141	0. 92
NT2RP2006186	F-NT2RP2006186	0. 94
NT2RP2006196	F-NT2RP2006196	0. 32
NT2RP2006200	F-NT2RP2006200	0. 70
NT2RP2006219	F-NT2RP2006219	0. 94
NT2RP2006237	F-NT2RP2006237	0. 59
NT2RP2006238	F-NT2RP2006238	0. 47
NT2RP2006275	F-NT2RP2006275	0. 89
NT2RP2006312	F-NT2RP2006312	0. 75
NT2RP2006333	F-NT2RP2006333	0. 73
NT2RP2006334	F-NT2RP2006334	0. 72

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NT2RP2006365	F-NT2RP2006365	0.48
NT2RP2006436	F-NT2RP2006436	0.75
NT2RP2006441	F-NT2RP2006441	0.61
NT2RP2006456	F-NT2RP2006456	0.60
NT2RP2006464	F-NT2RP2006464	0.51
NT2RP2006472	F-NT2RP2006472	0.76
NT2RP2006565	F-NT2RP2006565	0.34
NT2RP2006571	F-NT2RP2006571	0.94
NT2RP2006573	F-NT2RP2006573	0.35
NT2RP3000002	F-NT2RP3000002	0.40
NT2RP3000031	F-NT2RP3000031	0.49
NT2RP3000046	F-NT2RP3000046	0.90
NT2RP3000047	F-NT2RP3000047	0.69
NT2RP3000050	F-NT2RP3000050	0.78
NT2RP3000068	F-NT2RP3000068	0.94
NT2RP3000072	F-NT2RP3000072	0.34
NT2RP3000080	F-NT2RP3000080	0.32
NT2RP3000085	F-NT2RP3000085	0.92
NT2RP3000092	F-NT2RP3000092	0.40
NT2RP3000134	F-NT2RP3000134	0.42
NT2RP3000142	F-NT2RP3000142	0.58
NT2RP3000149	F-NT2RP3000149	0.83
NT2RP3000197	F-NT2RP3000197	0.59
NT2RP3000207	F-NT2RP3000207	0.48
NT2RP3000220	F-NT2RP3000220	0.75
NT2RP3000251	F-NT2RP3000251	0.82
NT2RP3000252	F-NT2RP3000252	0.88
NT2RP3000255	F-NT2RP3000255	0.94
NT2RP3000267	F-NT2RP3000267	0.92
NT2RP3000299	F-NT2RP3000299	0.94
NT2RP3000312	F-NT2RP3000312	0.57
NT2RP3000320	F-NT2RP3000320	0.94
NT2RP3000324	F-NT2RP3000324	0.32
NT2RP3000333	F-NT2RP3000333	0.94
NT2RP3000348	F-NT2RP3000348	0.32
NT2RP3000350	F-NT2RP3000350	0.67
NT2RP3000359	F-NT2RP3000359	0.94
NT2RP3000361	F-NT2RP3000361	0.94
NT2RP3000366	F-NT2RP3000366	0.94
NT2RP3000393	F-NT2RP3000393	0.53
NT2RP3000397	F-NT2RP3000397	0.89
NT2RP3000403	F-NT2RP3000403	0.87
NT2RP3000439	F-NT2RP3000439	0.77
NT2RP3000456	F-NT2RP3000456	0.88
NT2RP3000484	F-NT2RP3000484	0.59
NT2RP3000487	F-NT2RP3000487	0.32

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NT2RP3000526	F-NT2RP3000526	0. 32
NT2RP3000527	F-NT2RP3000527	0. 69
NT2RP3000531	F-NT2RP3000531	0. 56
NT2RP3000562	F-NT2RP3000562	0. 44
NT2RP3000590	F-NT2RP3000590	0. 88
NT2RP3000592	F-NT2RP3000592	0. 92
NT2RP3000596	F-NT2RP3000596	0. 50
NT2RP3000599	F-NT2RP3000599	0. 69
NT2RP3000603	F-NT2RP3000603	0. 94
NT2RP3000605	F-NT2RP3000605	0. 92
NT2RP3000624	F-NT2RP3000624	0. 71
NT2RP3000632	F-NT2RP3000632	0. 43
NT2RP3000644	F-NT2RP3000644	0. 94
NT2RP3000661	F-NT2RP3000661	0. 60
NT2RP3000665	F-NT2RP3000665	0. 46
NT2RP3000690	F-NT2RP3000690	0. 79
NT2RP3000739	F-NT2RP3000739	0. 94
NT2RP3000753	F-NT2RP3000753	0. 42
NT2RP3000759	F-NT2RP3000759	0. 94
NT2RP3000825	F-NT2RP3000825	0. 73
NT2RP3000826	F-NT2RP3000826	0. 94
NT2RP3000836	F-NT2RP3000836	0. 39
NT2RP3000841	F-NT2RP3000841	0. 55
NT2RP3000845	F-NT2RP3000845	0. 38
NT2RP3000847	F-NT2RP3000847	0. 67
NT2RP3000850	F-NT2RP3000850	0. 59
NT2RP3000852	F-NT2RP3000852	0. 39
NT2RP3000859	F-NT2RP3000859	0. 83
NT2RP3000868	F-NT2RP3000868	0. 49
NT2RP3000869	F-NT2RP3000869	0. 94
NT2RP3000901	F-NT2RP3000901	0. 34
NT2RP3000917	F-NT2RP3000917	0. 73
NT2RP3000919	F-NT2RP3000919	0. 94
NT2RP3000968	F-NT2RP3000968	0. 94
NT2RP3000980	F-NT2RP3000980	0. 61
NT2RP3000994	F-NT2RP3000994	0. 45
NT2RP3001004	F-NT2RP3001004	0. 86
NT2RP3001055	F-NT2RP3001055	0. 38
NT2RP3001057	F-NT2RP3001057	0. 84
NT2RP3001081	F-NT2RP3001081	0. 57
NT2RP3001084	F-NT2RP3001084	0. 94
NT2RP3001096	F-NT2RP3001096	0. 94
NT2RP3001107	F-NT2RP3001107	0. 88
NT2RP3001109	F-NT2RP3001109	0. 67
NT2RP3001111	F-NT2RP3001111	0. 87
NT2RP3001113	F-NT2RP3001113	0. 40

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NT2RP3001116	F-NT2RP3001116	0.73
NT2RP3001119	F-NT2RP3001119	0.62
NT2RP3001120	F-NT2RP3001120	0.59
NT2RP3001126	F-NT2RP3001126	0.94
NT2RP3001133	F-NT2RP3001133	0.89
NT2RP3001140	F-NT2RP3001140	0.59
NT2RP3001147	F-NT2RP3001147	0.94
NT2RP3001150	F-NT2RP3001150	0.92
NT2RP3001155	F-NT2RP3001155	0.94
NT2RP3001176	F-NT2RP3001176	0.82
NT2RP3001214	F-NT2RP3001214	0.41
NT2RP3001216	F-NT2RP3001216	0.32
NT2RP3001221	F-NT2RP3001221	0.46
NT2RP3001236	F-NT2RP3001236	0.79
NT2RP3001239	F-NT2RP3001239	0.94
NT2RP3001253	F-NT2RP3001253	0.59
NT2RP3001260	F-NT2RP3001260	0.94
NT2RP3001268	F-NT2RP3001268	0.75
NT2RP3001272	F-NT2RP3001272	0.94
NT2RP3001274	F-NT2RP3001274	0.94
NT2RP3001297	F-NT2RP3001297	0.94
NT2RP3001307	F-NT2RP3001307	0.87
NT2RP3001325	F-NT2RP3001325	0.71
NT2RP3001338	F-NT2RP3001338	0.90
NT2RP3001355	F-NT2RP3001355	0.40
NT2RP3001356	F-NT2RP3001356	0.88
NT2RP3001384	F-NT2RP3001384	0.91
NT2RP3001392	F-NT2RP3001392	0.42
NT2RP3001396	F-NT2RP3001396	0.56
NT2RP3001398	F-NT2RP3001398	0.94
NT2RP3001399	F-NT2RP3001399	0.94
NT2RP3001407	F-NT2RP3001407	0.54
NT2RP3001420	F-NT2RP3001420	0.74
NT2RP3001426	F-NT2RP3001426	0.92
NT2RP3001427	F-NT2RP3001427	0.40
NT2RP3001428	F-NT2RP3001428	0.94
NT2RP3001447	F-NT2RP3001447	0.57
NT2RP3001449	F-NT2RP3001449	0.62
NT2RP3001453	F-NT2RP3001453	0.94
NT2RP3001457	F-NT2RP3001457	0.89
NT2RP3001472	F-NT2RP3001472	0.82
NT2RP3001490	F-NT2RP3001490	0.53
NT2RP3001495	F-NT2RP3001495	0.94
NT2RP3001497	F-NT2RP3001497	0.40
NT2RP3001529	F-NT2RP3001529	0.94
NT2RP3001538	F-NT2RP3001538	0.93

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NT2RP3001554	F-NT2RP3001554	0. 91
NT2RP3001587	F-NT2RP3001587	0. 94
NT2RP3001608	F-NT2RP3001608	0. 94
NT2RP3001621	F-NT2RP3001621	0. 78
NT2RP3001629	F-NT2RP3001629	0. 42
NT2RP3001642	F-NT2RP3001642	0. 94
NT2RP3001646	F-NT2RP3001646	0. 94
NT2RP3001671	F-NT2RP3001671	0. 77
NT2RP3001672	F-NT2RP3001672	0. 88
NT2RP3001676	F-NT2RP3001676	0. 88
NT2RP3001678	F-NT2RP3001678	0. 44
NT2RP3001679	F-NT2RP3001679	0. 44
NT2RP3001688	F-NT2RP3001688	0. 67
NT2RP3001690	F-NT2RP3001690	0. 58
NT2RP3001698	F-NT2RP3001698	0. 86
NT2RP3001708	F-NT2RP3001708	0. 38
NT2RP3001712	F-NT2RP3001712	0. 75
NT2RP3001716	F-NT2RP3001716	0. 77
NT2RP3001724	F-NT2RP3001724	0. 65
NT2RP3001727	F-NT2RP3001727	0. 84
NT2RP3001730	F-NT2RP3001730	0. 77
NT2RP3001739	F-NT2RP3001739	0. 78
NT2RP3001753	F-NT2RP3001753	0. 79
NT2RP3001764	F-NT2RP3001764	0. 33
NT2RP3001777	F-NT2RP3001777	0. 87
NT2RP3001792	F-NT2RP3001792	0. 86
NT2RP3001799	F-NT2RP3001799	0. 79
NT2RP3001819	F-NT2RP3001819	0. 31
NT2RP3001844	F-NT2RP3001844	0. 34
NT2RP3001854	F-NT2RP3001854	0. 94
NT2RP3001855	F-NT2RP3001855	0. 88
NT2RP3001857	F-NT2RP3001857	0. 41
NT2RP3001896	F-NT2RP3001896	0. 94
NT2RP3001915	F-NT2RP3001915	0. 42
NT2RP3001929	F-NT2RP3001929	0. 49
NT2RP3001931	F-NT2RP3001931	0. 94
NT2RP3001938	F-NT2RP3001938	0. 32
NT2RP3001943	F-NT2RP3001943	0. 70
NT2RP3001944	F-NT2RP3001944	0. 94
NT2RP3001969	F-NT2RP3001969	0. 54
NT2RP3002007	F-NT2RP3002007	0. 56
NT2RP3002014	F-NT2RP3002014	0. 94
NT2RP3002033	F-NT2RP3002033	0. 94
NT2RP3002045	F-NT2RP3002045	0. 91
NT2RP3002054	F-NT2RP3002054	0. 94
NT2RP3002062	F-NT2RP3002062	0. 62

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NT2RP3002063	F-NT2RP3002063	0. 34
NT2RP3002081	F-NT2RP3002081	0. 57
NT2RP3002097	F-NT2RP3002097	0. 72
NT2RP3002102	F-NT2RP3002102	0. 90
NT2RP3002108	F-NT2RP3002108	0. 74
NT2RP3002142	F-NT2RP3002142	0. 61
NT2RP3002146	F-NT2RP3002146	0. 91
NT2RP3002147	F-NT2RP3002147	0. 37
NT2RP3002151	F-NT2RP3002151	0. 90
NT2RP3002163	F-NT2RP3002163	0. 76
NT2RP3002165	F-NT2RP3002165	0. 89
NT2RP3002181	F-NT2RP3002181	0. 78
NT2RP3002244	F-NT2RP3002244	0. 81
NT2RP3002248	F-NT2RP3002248	0. 36
NT2RP3002255	F-NT2RP3002255	0. 53
NT2RP3002273	F-NT2RP3002273	0. 90
NT2RP3002276	F-NT2RP3002276	0. 39
NT2RP3002303	F-NT2RP3002303	0. 40
NT2RP3002304	F-NT2RP3002304	0. 44
NT2RP3002330	F-NT2RP3002330	0. 94
NT2RP3002343	F-NT2RP3002343	0. 94
NT2RP3002351	F-NT2RP3002351	0. 94
NT2RP3002377	F-NT2RP3002377	0. 52
NT2RP3002399	F-NT2RP3002399	0. 91
NT2RP3002402	F-NT2RP3002402	0. 33
NT2RP3002455	F-NT2RP3002455	0. 42
NT2RP3002484	F-NT2RP3002484	0. 52
NT2RP3002501	F-NT2RP3002501	0. 57
NT2RP3002512	F-NT2RP3002512	0. 63
NT2RP3002529	F-NT2RP3002529	0. 74
NT2RP3002545	F-NT2RP3002545	0. 94
NT2RP3002549	F-NT2RP3002549	0. 94
NT2RP3002566	F-NT2RP3002566	0. 74
NT2RP3002587	F-NT2RP3002587	0. 94
NT2RP3002590	F-NT2RP3002590	0. 37
NT2RP3002602	F-NT2RP3002602	0. 39
NT2RP3002603	F-NT2RP3002603	0. 46
NT2RP3002628	F-NT2RP3002628	0. 31
NT2RP3002631	F-NT2RP3002631	0. 79
NT2RP3002650	F-NT2RP3002650	0. 94
NT2RP3002659	F-NT2RP3002659	0. 93
NT2RP3002660	F-NT2RP3002660	0. 46
NT2RP3002663	F-NT2RP3002663	0. 79
NT2RP3002671	F-NT2RP3002671	0. 34
NT2RP3002682	F-NT2RP3002682	0. 52
NT2RP3002688	F-NT2RP3002688	0. 82

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NT2RP3002701	F-NT2RP3002701	0. 62
NT2RP3002763	F-NT2RP3002763	0. 83
NT2RP3002785	F-NT2RP3002785	0. 33
NT2RP3002818	F-NT2RP3002818	0. 91
NT2RP3002861	F-NT2RP3002861	0. 31
NT2RP3002869	F-NT2RP3002869	0. 47
NT2RP3002876	F-NT2RP3002876	0. 58
NT2RP3002877	F-NT2RP3002877	0. 41
NT2RP3002909	F-NT2RP3002909	0. 52
NT2RP3002911	F-NT2RP3002911	0. 73
NT2RP3002948	F-NT2RP3002948	0. 60
NT2RP3002953	F-NT2RP3002953	0. 37
NT2RP3002969	F-NT2RP3002969	0. 47
NT2RP3002972	F-NT2RP3002972	0. 87
NT2RP3002985	F-NT2RP3002985	0. 55
NT2RP3002988	F-NT2RP3002988	0. 82
NT2RP3003008	F-NT2RP3003008	0. 94
NT2RP3003061	F-NT2RP3003061	0. 93
NT2RP3003068	F-NT2RP3003068	0. 45
NT2RP3003071	F-NT2RP3003071	0. 76
NT2RP3003078	F-NT2RP3003078	0. 40
NT2RP3003101	F-NT2RP3003101	0. 41
NT2RP3003139	F-NT2RP3003139	0. 43
NT2RP3003145	F-NT2RP3003145	0. 94
NT2RP3003150	F-NT2RP3003150	0. 94
NT2RP3003157	F-NT2RP3003157	0. 81
NT2RP3003185	F-NT2RP3003185	0. 87
NT2RP3003193	F-NT2RP3003193	0. 94
NT2RP3003197	F-NT2RP3003197	0. 74
NT2RP3003203	F-NT2RP3003203	0. 94
NT2RP3003204	F-NT2RP3003204	0. 74
NT2RP3003210	F-NT2RP3003210	0. 45
NT2RP3003212	F-NT2RP3003212	0. 51
NT2RP3003230	F-NT2RP3003230	0. 94
NT2RP3003242	F-NT2RP3003242	0. 92
NT2RP3003251	F-NT2RP3003251	0. 93
NT2RP3003278	F-NT2RP3003278	0. 83
NT2RP3003282	F-NT2RP3003282	0. 67
NT2RP3003290	F-NT2RP3003290	0. 62
NT2RP3003301	F-NT2RP3003301	0. 49
NT2RP3003302	F-NT2RP3003302	0. 32
NT2RP3003311	F-NT2RP3003311	0. 34
NT2RP3003313	F-NT2RP3003313	0. 88
NT2RP3003327	F-NT2RP3003327	0. 88
NT2RP3003330	F-NT2RP3003330	0. 94
NT2RP3003344	F-NT2RP3003344	0. 67

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NT2RP3003353	F-NT2RP3003353	0.65
NT2RP3003377	F-NT2RP3003377	0.87
NT2RP3003385	F-NT2RP3003385	0.94
NT2RP3003409	F-NT2RP3003409	0.41
NT2RP3003411	F-NT2RP3003411	0.47
NT2RP3003427	F-NT2RP3003427	0.33
NT2RP3003490	F-NT2RP3003490	0.56
NT2RP3003491	F-NT2RP3003491	0.37
NT2RP3003543	F-NT2RP3003543	0.92
NT2RP3003552	F-NT2RP3003552	0.64
NT2RP3003555	F-NT2RP3003555	0.94
NT2RP3003564	F-NT2RP3003564	0.86
NT2RP3003589	F-NT2RP3003589	0.88
NT2RP3003621	F-NT2RP3003621	0.49
NT2RP3003656	F-NT2RP3003656	0.77
NT2RP3003659	F-NT2RP3003659	0.32
NT2RP3003672	F-NT2RP3003672	0.49
NT2RP3003680	F-NT2RP3003680	0.94
NT2RP3003686	F-NT2RP3003686	0.78
NT2RP3003701	F-NT2RP3003701	0.36
NT2RP3003716	F-NT2RP3003716	0.34
NT2RP3003726	F-NT2RP3003726	0.72
NT2RP3003795	F-NT2RP3003795	0.34
NT2RP3003805	F-NT2RP3003805	0.74
NT2RP3003809	F-NT2RP3003809	0.73
NT2RP3003825	F-NT2RP3003825	0.94
NT2RP3003831	F-NT2RP3003831	0.52
NT2RP3003833	F-NT2RP3003833	0.31
NT2RP3003846	F-NT2RP3003846	0.54
NT2RP3003870	F-NT2RP3003870	0.91
NT2RP3003876	F-NT2RP3003876	0.42
NT2RP3003914	F-NT2RP3003914	0.94
NT2RP3003918	F-NT2RP3003918	0.90
NT2RP3003932	F-NT2RP3003932	0.64
NT2RP3003992	F-NT2RP3003992	0.94
NT2RP3004013	F-NT2RP3004013	0.60
NT2RP3004041	F-NT2RP3004041	0.52
NT2RP3004051	F-NT2RP3004051	0.75
NT2RP3004078	F-NT2RP3004078	0.73
NT2RP3004093	F-NT2RP3004093	0.64
NT2RP3004125	F-NT2RP3004125	0.94
NT2RP3004155	F-NT2RP3004155	0.89
NT2RP3004189	F-NT2RP3004189	0.46
NT2RP3004206	F-NT2RP3004206	0.59
NT2RP3004207	F-NT2RP3004207	0.39
NT2RP3004209	F-NT2RP3004209	0.54

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NT2RP3004242	F-NT2RP3004242	0.61
NT2RP3004246	F-NT2RP3004246	0.91
NT2RP3004253	F-NT2RP3004253	0.41
NT2RP3004258	F-NT2RP3004258	0.41
NT2RP3004262	F-NT2RP3004262	0.56
NT2RP3004282	F-NT2RP3004282	0.90
NT2RP3004332	F-NT2RP3004332	0.53
NT2RP3004341	F-NT2RP3004341	0.40
NT2RP3004348	F-NT2RP3004348	0.94
NT2RP3004378	F-NT2RP3004378	0.40
NT2RP3004424	F-NT2RP3004424	0.75
NT2RP3004428	F-NT2RP3004428	0.85
NT2RP3004451	F-NT2RP3004451	0.85
NT2RP3004454	F-NT2RP3004454	0.93
NT2RP3004466	F-NT2RP3004466	0.80
NT2RP3004472	F-NT2RP3004472	0.46
NT2RP3004480	F-NT2RP3004480	0.77
NT2RP3004490	F-NT2RP3004490	0.65
NT2RP3004498	F-NT2RP3004498	0.91
NT2RP3004504	F-NT2RP3004504	0.88
NT2RP3004507	F-NT2RP3004507	0.86
NT2RP3004534	F-NT2RP3004534	0.32
NT2RP3004539	F-NT2RP3004539	0.76
NT2RP3004544	F-NT2RP3004544	0.94
NT2RP3004566	F-NT2RP3004566	0.94
NT2RP3004569	F-NT2RP3004569	0.69
NT2RP3004572	F-NT2RP3004572	0.65
NT2RP3004578	F-NT2RP3004578	0.52
NT2RP3004594	F-NT2RP3004594	0.39
NT2RP3004617	F-NT2RP3004617	0.94
NT2RP3004618	F-NT2RP3004618	0.41
NT2RP3004669	F-NT2RP3004669	0.82
NT2RP3004670	F-NT2RP3004670	0.32
NT2RP4000008	F-NT2RP4000008	0.94
NT2RP4000051	F-NT2RP4000051	0.94
NT2RP4000109	F-NT2RP4000109	0.84
NT2RP4000111	F-NT2RP4000111	0.49
NT2RP4000129	F-NT2RP4000129	0.94
NT2RP4000147	F-NT2RP4000147	0.92
NT2RP4000150	F-NT2RP4000150	0.41
NT2RP4000151	F-NT2RP4000151	0.33
NT2RP4000159	F-NT2RP4000159	0.75
NT2RP4000185	F-NT2RP4000185	0.94
NT2RP4000210	F-NT2RP4000210	0.83
NT2RP4000212	F-NT2RP4000212	0.94
NT2RP4000243	F-NT2RP4000243	0.94

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NT2RP4000246	F-NT2RP4000246	0.59
NT2RP4000259	F-NT2RP4000259	0.94
NT2RP4000263	F-NT2RP4000263	0.62
NT2RP4000290	F-NT2RP4000290	0.92
NT2RP4000312	F-NT2RP4000312	0.39
NT2RP4000323	F-NT2RP4000323	0.73
NT2RP4000355	F-NT2RP4000355	0.94
NT2RP4000360	F-NT2RP4000360	0.55
NT2RP4000367	F-NT2RP4000367	0.60
NT2RP4000370	F-NT2RP4000370	0.93
NT2RP4000376	F-NT2RP4000376	0.88
NT2RP4000381	F-NT2RP4000381	0.39
NT2RP4000398	F-NT2RP4000398	0.64
NT2RP4000415	F-NT2RP4000415	0.94
NT2RP4000417	F-NT2RP4000417	0.33
NT2RP4000448	F-NT2RP4000448	0.33
NT2RP4000449	F-NT2RP4000449	0.33
NT2RP4000455	F-NT2RP4000455	0.37
NT2RP4000457	F-NT2RP4000457	0.36
NT2RP4000480	F-NT2RP4000480	0.88
NT2RP4000481	F-NT2RP4000481	0.51
NT2RP4000498	F-NT2RP4000498	0.64
NT2RP4000500	F-NT2RP4000500	0.67
NT2RP4000518	F-NT2RP4000518	0.34
NT2RP4000524	F-NT2RP4000524	0.94
NT2RP4000528	F-NT2RP4000528	0.65
NT2RP4000541	F-NT2RP4000541	0.44
NT2RP4000556	F-NT2RP4000556	0.69
NT2RP4000560	F-NT2RP4000560	0.67
NT2RP4000588	F-NT2RP4000588	0.94
NT2RP4000614	F-NT2RP4000614	0.94
NT2RP4000638	F-NT2RP4000638	0.74
NT2RP4000648	F-NT2RP4000648	0.40
NT2RP4000657	F-NT2RP4000657	0.94
NT2RP4000704	F-NT2RP4000704	0.69
NT2RP4000713	F-NT2RP4000713	0.93
NT2RP4000724	F-NT2RP4000724	0.32
NT2RP4000728	F-NT2RP4000728	0.34
NT2RP4000737	F-NT2RP4000737	0.48
NT2RP4000739	F-NT2RP4000739	0.40
NT2RP4000781	F-NT2RP4000781	0.94
NT2RP4000787	F-NT2RP4000787	0.94
NT2RP4000817	F-NT2RP4000817	0.60
NT2RP4000833	F-NT2RP4000833	0.35
NT2RP4000837	F-NT2RP4000837	0.80
NT2RP4000839	F-NT2RP4000839	0.33

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NT2RP4000855	F-NT2RP4000855	0. 74
NT2RP4000865	F-NT2RP4000865	0. 77
NT2RP4000878	F-NT2RP4000878	0. 79
NT2RP4000879	F-NT2RP4000879	0. 41
NT2RP4000907	F-NT2RP4000907	0. 44
NT2RP4000918	F-NT2RP4000918	0. 88
NT2RP4000925	F-NT2RP4000925	0. 89
NT2RP4000927	F-NT2RP4000927	0. 81
NT2RP4000928	F-NT2RP4000928	0. 39
NT2RP4000929	F-NT2RP4000929	0. 34
NT2RP4000955	F-NT2RP4000955	0. 77
NT2RP4000973	F-NT2RP4000973	0. 36
NT2RP4000975	F-NT2RP4000975	0. 87
NT2RP4000979	F-NT2RP4000979	0. 50
NT2RP4000984	F-NT2RP4000984	0. 66
NT2RP4000989	F-NT2RP4000989	0. 94
NT2RP4000997	F-NT2RP4000997	0. 68
NT2RP4001004	F-NT2RP4001004	0. 40
NT2RP4001006	F-NT2RP4001006	0. 91
NT2RP4001010	F-NT2RP4001010	0. 64
NT2RP4001029	F-NT2RP4001029	0. 77
NT2RP4001041	F-NT2RP4001041	0. 79
NT2RP4001057	F-NT2RP4001057	0. 65
NT2RP4001064	F-NT2RP4001064	0. 94
NT2RP4001078	F-NT2RP4001078	0. 39
NT2RP4001079	F-NT2RP4001079	0. 94
NT2RP4001080	F-NT2RP4001080	0. 58
NT2RP4001086	F-NT2RP4001086	0. 78
NT2RP4001095	F-NT2RP4001095	0. 80
NT2RP4001100	F-NT2RP4001100	0. 79
NT2RP4001117	F-NT2RP4001117	0. 60
NT2RP4001122	F-NT2RP4001122	0. 82
NT2RP4001126	F-NT2RP4001126	0. 55
NT2RP4001138	F-NT2RP4001138	0. 94
NT2RP4001143	F-NT2RP4001143	0. 41
NT2RP4001148	F-NT2RP4001148	0. 37
NT2RP4001149	F-NT2RP4001149	0. 50
NT2RP4001150	F-NT2RP4001150	0. 94
NT2RP4001159	F-NT2RP4001159	0. 78
NT2RP4001174	F-NT2RP4001174	0. 94
NT2RP4001206	F-NT2RP4001206	0. 80
NT2RP4001207	F-NT2RP4001207	0. 38
NT2RP4001210	F-NT2RP4001210	0. 94
NT2RP4001213	F-NT2RP4001213	0. 46
NT2RP4001219	F-NT2RP4001219	0. 38
NT2RP4001228	F-NT2RP4001228	0. 61

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NT2RP4001235	F-NT2RP4001235	0.88
NT2RP4001256	F-NT2RP4001256	0.60
NT2RP4001260	F-NT2RP4001260	0.94
NT2RP4001274	F-NT2RP4001274	0.82
NT2RP4001276	F-NT2RP4001276	0.68
NT2RP4001313	F-NT2RP4001313	0.77
NT2RP4001315	F-NT2RP4001315	0.87
NT2RP4001336	F-NT2RP4001336	0.48
NT2RP4001339	F-NT2RP4001339	0.41
NT2RP4001343	F-NT2RP4001343	0.63
NT2RP4001345	F-NT2RP4001345	0.89
NT2RP4001351	F-NT2RP4001351	0.87
NT2RP4001353	F-NT2RP4001353	0.72
NT2RP4001372	F-NT2RP4001372	0.78
NT2RP4001373	F-NT2RP4001373	0.60
NT2RP4001375	F-NT2RP4001375	0.43
NT2RP4001379	F-NT2RP4001379	0.77
NT2RP4001389	F-NT2RP4001389	0.41
NT2RP4001414	F-NT2RP4001414	0.90
NT2RP4001433	F-NT2RP4001433	0.39
NT2RP4001442	F-NT2RP4001442	0.59
NT2RP4001447	F-NT2RP4001447	0.33
NT2RP4001474	F-NT2RP4001474	0.89
NT2RP4001483	F-NT2RP4001483	0.94
NT2RP4001498	F-NT2RP4001498	0.59
NT2RP4001502	F-NT2RP4001502	0.61
NT2RP4001507	F-NT2RP4001507	0.91
NT2RP4001524	F-NT2RP4001524	0.61
NT2RP4001529	F-NT2RP4001529	0.75
NT2RP4001547	F-NT2RP4001547	0.77
NT2RP4001551	F-NT2RP4001551	0.79
NT2RP4001555	F-NT2RP4001555	0.79
NT2RP4001567	F-NT2RP4001567	0.39
NT2RP4001568	F-NT2RP4001568	0.45
NT2RP4001571	F-NT2RP4001571	0.76
NT2RP4001574	F-NT2RP4001574	0.91
NT2RP4001575	F-NT2RP4001575	0.57
NT2RP4001592	F-NT2RP4001592	0.71
NT2RP4001610	F-NT2RP4001610	0.94
NT2RP4001614	F-NT2RP4001614	0.73
NT2RP4001634	F-NT2RP4001634	0.40
NT2RP4001638	F-NT2RP4001638	0.37
NT2RP4001644	F-NT2RP4001644	0.94
NT2RP4001656	F-NT2RP4001656	0.92
NT2RP4001677	F-NT2RP4001677	0.47
NT2RP4001679	F-NT2RP4001679	0.54

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NT2RP4001696	F-NT2RP4001696	0.62
NT2RP4001725	F-NT2RP4001725	0.94
NT2RP4001730	F-NT2RP4001730	0.94
NT2RP4001739	F-NT2RP4001739	0.82
NT2RP4001753	F-NT2RP4001753	0.66
NT2RP4001760	F-NT2RP4001760	0.39
NT2RP4001790	F-NT2RP4001790	0.64
NT2RP4001803	F-NT2RP4001803	0.87
NT2RP4001822	F-NT2RP4001822	0.84
NT2RP4001823	F-NT2RP4001823	0.56
NT2RP4001828	F-NT2RP4001828	0.45
NT2RP4001838	F-NT2RP4001838	0.87
NT2RP4001841	F-NT2RP4001841	0.58
NT2RP4001849	F-NT2RP4001849	0.88
NT2RP4001861	F-NT2RP4001861	0.80
NT2RP4001893	F-NT2RP4001893	0.94
NT2RP4001896	F-NT2RP4001896	0.93
NT2RP4001901	F-NT2RP4001901	0.89
NT2RP4001927	F-NT2RP4001927	0.77
NT2RP4001938	F-NT2RP4001938	0.94
NT2RP4001946	F-NT2RP4001946	0.74
NT2RP4001950	F-NT2RP4001950	0.45
NT2RP4001953	F-NT2RP4001953	0.49
NT2RP4001966	F-NT2RP4001966	0.86
NT2RP4001975	F-NT2RP4001975	0.94
NT2RP4002018	F-NT2RP4002018	0.67
NT2RP4002047	F-NT2RP4002047	0.67
NT2RP4002052	F-NT2RP4002052	0.42
NT2RP4002058	F-NT2RP4002058	0.78
NT2RP4002071	F-NT2RP4002071	0.94
NT2RP4002078	F-NT2RP4002078	0.38
NT2RP4002081	F-NT2RP4002081	0.55
NT2RP4002083	F-NT2RP4002083	0.86
NT2RP4002408	F-NT2RP4002408	0.64
NT2RP4002791	F-NT2RP4002791	0.84
NT2RP4002888	F-NT2RP4002888	0.31
NT2RP5003459	F-NT2RP5003459	0.94
NT2RP5003461	F-NT2RP5003461	0.94
NT2RP5003477	F-NT2RP5003477	0.44
NT2RP5003492	F-NT2RP5003492	0.57
NT2RP5003500	F-NT2RP5003500	0.94
NT2RP5003506	F-NT2RP5003506	0.94
NT2RP5003512	F-NT2RP5003512	0.42
NT2RP5003522	F-NT2RP5003522	0.94
NT2RP5003524	F-NT2RP5003524	0.58
NT2RP5003534	F-NT2RP5003534	0.32

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OVARC1000001	F-OVARC1000001	0.74
OVARC1000004	F-OVARC1000004	0.90
OVARC1000006	F-OVARC1000006	0.94
OVARC1000013	F-OVARC1000013	0.48
OVARC1000014	F-OVARC1000014	0.69
OVARC1000035	F-OVARC1000035	0.59
OVARC1000060	F-OVARC1000060	0.76
OVARC1000087	F-OVARC1000087	0.31
OVARC1000091	F-OVARC1000091	0.88
OVARC1000106	F-OVARC1000106	0.88
OVARC1000109	F-OVARC1000109	0.94
OVARC1000113	F-OVARC1000113	0.40
OVARC1000114	F-OVARC1000114	0.53
OVARC1000139	F-OVARC1000139	0.88
OVARC1000148	F-OVARC1000148	0.94
OVARC1000151	F-OVARC1000151	0.34
OVARC1000168	F-OVARC1000168	0.56
OVARC1000209	F-OVARC1000209	0.94
OVARC1000212	F-OVARC1000212	0.87
OVARC1000241	F-OVARC1000241	0.59
OVARC1000288	F-OVARC1000288	0.87
OVARC1000304	F-OVARC1000304	0.94
OVARC1000309	F-OVARC1000309	0.76
OVARC1000321	F-OVARC1000321	0.90
OVARC1000326	F-OVARC1000326	0.46
OVARC1000335	F-OVARC1000335	0.55
OVARC1000347	F-OVARC1000347	0.43
OVARC1000384	F-OVARC1000384	0.90
OVARC1000408	F-OVARC1000408	0.42
OVARC1000411	F-OVARC1000411	0.65
OVARC1000420	F-OVARC1000420	0.84
OVARC1000437	F-OVARC1000437	0.94
OVARC1000440	F-OVARC1000440	0.94
OVARC1000442	F-OVARC1000442	0.94
OVARC1000443	F-OVARC1000443	0.74
OVARC1000461	F-OVARC1000461	0.89
OVARC1000465	F-OVARC1000465	0.75
OVARC1000466	F-OVARC1000466	0.94
OVARC1000473	F-OVARC1000473	0.31
OVARC1000479	F-OVARC1000479	0.42
OVARC1000520	F-OVARC1000520	0.94
OVARC1000556	F-OVARC1000556	0.94
OVARC1000557	F-OVARC1000557	0.72
OVARC1000564	F-OVARC1000564	0.94
OVARC1000576	F-OVARC1000576	0.40
OVARC1000588	F-OVARC1000588	0.45

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OVARC1000605	F-OVARC1000605	0.58
OVARC1000622	F-OVARC1000622	0.80
OVARC1000640	F-OVARC1000640	0.35
OVARC1000649	F-OVARC1000649	0.94
OVARC1000661	F-OVARC1000661	0.87
OVARC1000681	F-OVARC1000681	0.84
OVARC1000682	F-OVARC1000682	0.38
OVARC1000689	F-OVARC1000689	0.36
OVARC1000703	F-OVARC1000703	0.92
OVARC1000722	F-OVARC1000722	0.94
OVARC1000730	F-OVARC1000730	0.90
OVARC1000746	F-OVARC1000746	0.42
OVARC1000771	F-OVARC1000771	0.94
OVARC1000781	F-OVARC1000781	0.80
OVARC1000787	F-OVARC1000787	0.41
OVARC1000800	F-OVARC1000800	0.85
OVARC1000834	F-OVARC1000834	0.62
OVARC1000846	F-OVARC1000846	0.49
OVARC1000850	F-OVARC1000850	0.94
OVARC1000862	F-OVARC1000862	0.54
OVARC1000876	F-OVARC1000876	0.74
OVARC1000883	F-OVARC1000883	0.55
OVARC1000885	F-OVARC1000885	0.94
OVARC1000886	F-OVARC1000886	0.61
OVARC1000890	F-OVARC1000890	0.45
OVARC1000912	F-OVARC1000912	0.63
OVARC1000915	F-OVARC1000915	0.31
OVARC1000924	F-OVARC1000924	0.82
OVARC1000945	F-OVARC1000945	0.74
OVARC1000959	F-OVARC1000959	0.33
OVARC1000964	F-OVARC1000964	0.60
OVARC1000984	F-OVARC1000984	0.59
OVARC1000996	F-OVARC1000996	0.83
OVARC1000999	F-OVARC1000999	0.94
OVARC1001004	F-OVARC1001004	0.69
OVARC1001010	F-OVARC1001010	0.51
OVARC1001032	F-OVARC1001032	0.32
OVARC1001034	F-OVARC1001034	0.78
OVARC1001038	F-OVARC1001038	0.93
OVARC1001040	F-OVARC1001040	0.68
OVARC1001044	F-OVARC1001044	0.66
OVARC1001055	F-OVARC1001055	0.76
OVARC1001065	F-OVARC1001065	0.31
OVARC1001068	F-OVARC1001068	0.63
OVARC1001074	F-OVARC1001074	0.82
OVARC1001092	F-OVARC1001092	0.50

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OVARC1001107	F-OVARC1001107	0.65
OVARC1001113	F-OVARC1001113	0.86
OVARC1001154	F-OVARC1001154	0.43
OVARC1001161	F-OVARC1001161	0.75
OVARC1001162	F-OVARC1001162	0.61
OVARC1001167	F-OVARC1001167	0.31
OVARC1001170	F-OVARC1001170	0.46
OVARC1001171	F-OVARC1001171	0.78
OVARC1001173	F-OVARC1001173	0.71
OVARC1001176	F-OVARC1001176	0.83
OVARC1001180	F-OVARC1001180	0.53
OVARC1001188	F-OVARC1001188	0.42
OVARC1001200	F-OVARC1001200	0.94
OVARC1001232	F-OVARC1001232	0.90
OVARC1001243	F-OVARC1001243	0.59
OVARC1001244	F-OVARC1001244	0.79
OVARC1001270	F-OVARC1001270	0.48
OVARC1001271	F-OVARC1001271	0.67
OVARC1001296	F-OVARC1001296	0.60
OVARC1001306	F-OVARC1001306	0.44
OVARC1001329	F-OVARC1001329	0.91
OVARC1001341	F-OVARC1001341	0.82
OVARC1001344	F-OVARC1001344	0.94
OVARC1001360	F-OVARC1001360	0.94
OVARC1001369	F-OVARC1001369	0.36
OVARC1001372	F-OVARC1001372	0.63
OVARC1001376	F-OVARC1001376	0.81
OVARC1001381	F-OVARC1001381	0.78
OVARC1001391	F-OVARC1001391	0.33
OVARC1001399	F-OVARC1001399	0.67
OVARC1001417	F-OVARC1001417	0.94
OVARC1001419	F-OVARC1001419	0.34
OVARC1001425	F-OVARC1001425	0.73
OVARC1001436	F-OVARC1001436	0.59
OVARC1001453	F-OVARC1001453	0.45
OVARC1001476	F-OVARC1001476	0.85
OVARC1001489	F-OVARC1001489	0.35
OVARC1001496	F-OVARC1001496	0.90
OVARC1001506	F-OVARC1001506	0.59
OVARC1001525	F-OVARC1001525	0.87
OVARC1001555	F-OVARC1001555	0.67
OVARC1001577	F-OVARC1001577	0.94
OVARC1001610	F-OVARC1001610	0.38
OVARC1001611	F-OVARC1001611	0.34
OVARC1001702	F-OVARC1001702	0.88
OVARC1001703	F-OVARC1001703	0.76

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OVARC1001711	F-OVARC1001711	0.82
OVARC1001713	F-OVARC1001713	0.82
OVARC1001731	F-OVARC1001731	0.94
OVARC1001762	F-OVARC1001762	0.59
OVARC1001766	F-OVARC1001766	0.94
OVARC1001767	F-OVARC1001767	0.70
OVARC1001768	F-OVARC1001768	0.32
OVARC1001791	F-OVARC1001791	0.74
OVARC1001802	F-OVARC1001802	0.76
OVARC1001809	F-OVARC1001809	0.63
OVARC1001820	F-OVARC1001820	0.94
OVARC1001828	F-OVARC1001828	0.78
OVARC1001861	F-OVARC1001861	0.94
OVARC1001873	F-OVARC1001873	0.31
OVARC1001879	F-OVARC1001879	0.94
OVARC1001880	F-OVARC1001880	0.46
OVARC1001916	F-OVARC1001916	0.82
OVARC1001942	F-OVARC1001942	0.72
OVARC1001943	F-OVARC1001943	0.49
OVARC1001949	F-OVARC1001949	0.46
OVARC1001950	F-OVARC1001950	0.94
OVARC1001987	F-OVARC1001987	0.91
OVARC1002050	F-OVARC1002050	0.85
OVARC1002082	F-OVARC1002082	0.94
OVARC1002107	F-OVARC1002107	0.33
OVARC1002112	F-OVARC1002112	0.94
OVARC1002127	F-OVARC1002127	0.80
OVARC1002138	F-OVARC1002138	0.46
OVARC1002156	F-OVARC1002156	0.43
OVARC1002158	F-OVARC1002158	0.94
OVARC1002165	F-OVARC1002165	0.88
OVARC1002182	F-OVARC1002182	0.94
PLACE1000004	F-PLACE1000004	0.43
PLACE1000005	F-PLACE1000005	0.37
PLACE1000007	F-PLACE1000007	0.72
PLACE1000014	F-PLACE1000014	0.38
PLACE1000048	F-PLACE1000048	0.36
PLACE1000050	F-PLACE1000050	0.94
PLACE1000061	F-PLACE1000061	0.56
PLACE1000066	F-PLACE1000066	0.94
PLACE1000081	F-PLACE1000081	0.37
PLACE1000133	F-PLACE1000133	0.53
PLACE1000142	F-PLACE1000142	0.94
PLACE1000184	F-PLACE1000184	0.73
PLACE1000185	F-PLACE1000185	0.86
PLACE1000213	F-PLACE1000213	0.34

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PLACE1000236	F-PLACE1000236	0.76
PLACE1000246	F-PLACE1000246	0.91
PLACE1000308	F-PLACE1000308	0.40
PLACE1000347	F-PLACE1000347	0.48
PLACE1000374	F-PLACE1000374	0.58
PLACE1000380	F-PLACE1000380	0.94
PLACE1000383	F-PLACE1000383	0.39
PLACE1000401	F-PLACE1000401	0.94
PLACE1000406	F-PLACE1000406	0.94
PLACE1000420	F-PLACE1000420	0.82
PLACE1000435	F-PLACE1000435	0.32
PLACE1000444	F-PLACE1000444	0.41
PLACE1000453	F-PLACE1000453	0.76
PLACE1000492	F-PLACE1000492	0.65
PLACE1000547	F-PLACE1000547	0.94
PLACE1000562	F-PLACE1000562	0.94
PLACE1000564	F-PLACE1000564	0.45
PLACE1000588	F-PLACE1000588	0.67
PLACE1000596	F-PLACE1000596	0.60
PLACE1000610	F-PLACE1000610	0.94
PLACE1000611	F-PLACE1000611	0.48
PLACE1000636	F-PLACE1000636	0.92
PLACE1000653	F-PLACE1000653	0.57
PLACE1000656	F-PLACE1000656	0.94
PLACE1000706	F-PLACE1000706	0.94
PLACE1000712	F-PLACE1000712	0.78
PLACE1000716	F-PLACE1000716	0.94
PLACE1000748	F-PLACE1000748	0.52
PLACE1000755	F-PLACE1000755	0.87
PLACE1000769	F-PLACE1000769	0.94
PLACE1000785	F-PLACE1000785	0.33
PLACE1000786	F-PLACE1000786	0.88
PLACE1000793	F-PLACE1000793	0.79
PLACE1000798	F-PLACE1000798	0.59
PLACE1000849	F-PLACE1000849	0.64
PLACE1000856	F-PLACE1000856	0.40
PLACE1000863	F-PLACE1000863	0.94
PLACE1000909	F-PLACE1000909	0.94
PLACE1000948	F-PLACE1000948	0.92
PLACE1000972	F-PLACE1000972	0.73
PLACE1000977	F-PLACE1000977	0.72
PLACE1000987	F-PLACE1000987	0.93
PLACE1001000	F-PLACE1001000	0.37
PLACE1001010	F-PLACE1001010	0.50
PLACE1001024	F-PLACE1001024	0.94
PLACE1001036	F-PLACE1001036	0.51

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PLACE1001054	F-PLACE1001054	0.88
PLACE1001062	F-PLACE1001062	0.57
PLACE1001092	F-PLACE1001092	0.94
PLACE1001104	F-PLACE1001104	0.38
PLACE1001168	F-PLACE1001168	0.41
PLACE1001171	F-PLACE1001171	0.36
PLACE1001185	F-PLACE1001185	0.93
PLACE1001238	F-PLACE1001238	0.87
PLACE1001241	F-PLACE1001241	0.67
PLACE1001257	F-PLACE1001257	0.40
PLACE1001280	F-PLACE1001280	0.70
PLACE1001294	F-PLACE1001294	0.49
PLACE1001304	F-PLACE1001304	0.94
PLACE1001311	F-PLACE1001311	0.53
PLACE1001351	F-PLACE1001351	0.86
PLACE1001366	F-PLACE1001366	0.39
PLACE1001383	F-PLACE1001383	0.94
PLACE1001387	F-PLACE1001387	0.34
PLACE1001399	F-PLACE1001399	0.38
PLACE1001412	F-PLACE1001412	0.94
PLACE1001456	F-PLACE1001456	0.42
PLACE1001484	F-PLACE1001484	0.88
PLACE1001503	F-PLACE1001503	0.85
PLACE1001545	F-PLACE1001545	0.92
PLACE1001551	F-PLACE1001551	0.39
PLACE1001570	F-PLACE1001570	0.40
PLACE1001602	F-PLACE1001602	0.60
PLACE1001608	F-PLACE1001608	0.40
PLACE1001610	F-PLACE1001610	0.43
PLACE1001632	F-PLACE1001632	0.48
PLACE1001634	F-PLACE1001634	0.60
PLACE1001692	F-PLACE1001692	0.74
PLACE1001729	F-PLACE1001729	0.69
PLACE1001739	F-PLACE1001739	0.49
PLACE1001740	F-PLACE1001740	0.50
PLACE1001761	F-PLACE1001761	0.71
PLACE1001771	F-PLACE1001771	0.39
PLACE1001781	F-PLACE1001781	0.57
PLACE1001810	F-PLACE1001810	0.57
PLACE1001817	F-PLACE1001817	0.91
PLACE1001844	F-PLACE1001844	0.34
PLACE1001869	F-PLACE1001869	0.34
PLACE1001912	F-PLACE1001912	0.82
PLACE1001920	F-PLACE1001920	0.85
PLACE1001928	F-PLACE1001928	0.60
PLACE1001983	F-PLACE1001983	0.39

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PLACE1001989	F-PLACE1001989	0.74
PLACE1002004	F-PLACE1002004	0.70
PLACE1002046	F-PLACE1002046	0.81
PLACE1002072	F-PLACE1002072	0.94
PLACE1002073	F-PLACE1002073	0.70
PLACE1002090	F-PLACE1002090	0.64
PLACE1002115	F-PLACE1002115	0.60
PLACE1002119	F-PLACE1002119	0.71
PLACE1002140	F-PLACE1002140	0.94
PLACE1002163	F-PLACE1002163	0.56
PLACE1002170	F-PLACE1002170	0.60
PLACE1002171	F-PLACE1002171	0.72
PLACE1002213	F-PLACE1002213	0.35
PLACE1002342	F-PLACE1002342	0.40
PLACE1002395	F-PLACE1002395	0.87
PLACE1002433	F-PLACE1002433	0.73
PLACE1002437	F-PLACE1002437	0.46
PLACE1002438	F-PLACE1002438	0.41
PLACE1002450	F-PLACE1002450	0.48
PLACE1002465	F-PLACE1002465	0.34
PLACE1002474	F-PLACE1002474	0.89
PLACE1002499	F-PLACE1002499	0.94
PLACE1002529	F-PLACE1002529	0.45
PLACE1002532	F-PLACE1002532	0.76
PLACE1002571	F-PLACE1002571	0.40
PLACE1002625	F-PLACE1002625	0.36
PLACE1002655	F-PLACE1002655	0.41
PLACE1002665	F-PLACE1002665	0.80
PLACE1002685	F-PLACE1002685	0.31
PLACE1002714	F-PLACE1002714	0.90
PLACE1002722	F-PLACE1002722	0.43
PLACE1002775	F-PLACE1002775	0.94
PLACE1002794	F-PLACE1002794	0.90
PLACE1002811	F-PLACE1002811	0.88
PLACE1002815	F-PLACE1002815	0.40
PLACE1002816	F-PLACE1002816	0.73
PLACE1002834	F-PLACE1002834	0.41
PLACE1002839	F-PLACE1002839	0.73
PLACE1002851	F-PLACE1002851	0.90
PLACE1002908	F-PLACE1002908	0.94
PLACE1002941	F-PLACE1002941	0.33
PLACE1002991	F-PLACE1002991	0.39
PLACE1002993	F-PLACE1002993	0.94
PLACE1002996	F-PLACE1002996	0.40
PLACE1003025	F-PLACE1003025	0.77
PLACE1003027	F-PLACE1003027	0.54

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PLACE1003044	F-PLACE1003044	0.71
PLACE1003045	F-PLACE1003045	0.89
PLACE1003092	F-PLACE1003092	0.59
PLACE1003100	F-PLACE1003100	0.38
PLACE1003108	F-PLACE1003108	0.94
PLACE1003136	F-PLACE1003136	0.87
PLACE1003145	F-PLACE1003145	0.94
PLACE1003174	F-PLACE1003174	0.46
PLACE1003176	F-PLACE1003176	0.48
PLACE1003190	F-PLACE1003190	0.57
PLACE1003200	F-PLACE1003200	0.47
PLACE1003249	F-PLACE1003249	0.33
PLACE1003256	F-PLACE1003256	0.57
PLACE1003296	F-PLACE1003296	0.41
PLACE1003302	F-PLACE1003302	0.94
PLACE1003334	F-PLACE1003334	0.78
PLACE1003342	F-PLACE1003342	0.34
PLACE1003353	F-PLACE1003353	0.71
PLACE1003366	F-PLACE1003366	0.66
PLACE1003369	F-PLACE1003369	0.91
PLACE1003383	F-PLACE1003383	0.70
PLACE1003394	F-PLACE1003394	0.94
PLACE1003454	F-PLACE1003454	0.94
PLACE1003493	F-PLACE1003493	0.93
PLACE1003537	F-PLACE1003537	0.94
PLACE1003553	F-PLACE1003553	0.34
PLACE1003592	F-PLACE1003592	0.33
PLACE1003596	F-PLACE1003596	0.89
PLACE1003602	F-PLACE1003602	0.94
PLACE1003605	F-PLACE1003605	0.94
PLACE1003611	F-PLACE1003611	0.80
PLACE1003625	F-PLACE1003625	0.39
PLACE1003669	F-PLACE1003669	0.79
PLACE1003704	F-PLACE1003704	0.43
PLACE1003709	F-PLACE1003709	0.90
PLACE1003711	F-PLACE1003711	0.74
PLACE1003723	F-PLACE1003723	0.63
PLACE1003738	F-PLACE1003738	0.91
PLACE1003762	F-PLACE1003762	0.94
PLACE1003771	F-PLACE1003771	0.56
PLACE1003783	F-PLACE1003783	0.39
PLACE1003784	F-PLACE1003784	0.61
PLACE1003795	F-PLACE1003795	0.32
PLACE1003870	F-PLACE1003870	0.94
PLACE1003885	F-PLACE1003885	0.94
PLACE1003886	F-PLACE1003886	0.94

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PLACE1003888	F-PLACE1003888	0.36
PLACE1003892	F-PLACE1003892	0.92
PLACE1003903	F-PLACE1003903	0.68
PLACE1003915	F-PLACE1003915	0.54
PLACE1003923	F-PLACE1003923	0.52
PLACE1003936	F-PLACE1003936	0.67
PLACE1003968	F-PLACE1003968	0.59
PLACE1004103	F-PLACE1004103	0.94
PLACE1004104	F-PLACE1004104	0.44
PLACE1004114	F-PLACE1004114	0.91
PLACE1004128	F-PLACE1004128	0.72
PLACE1004149	F-PLACE1004149	0.41
PLACE1004156	F-PLACE1004156	0.50
PLACE1004161	F-PLACE1004161	0.77
PLACE1004183	F-PLACE1004183	0.62
PLACE1004197	F-PLACE1004197	0.39
PLACE1004203	F-PLACE1004203	0.94
PLACE1004258	F-PLACE1004258	0.46
PLACE1004270	F-PLACE1004270	0.65
PLACE1004277	F-PLACE1004277	0.86
PLACE1004289	F-PLACE1004289	0.79
PLACE1004302	F-PLACE1004302	0.57
PLACE1004316	F-PLACE1004316	0.64
PLACE1004358	F-PLACE1004358	0.85
PLACE1004376	F-PLACE1004376	0.64
PLACE1004388	F-PLACE1004388	0.94
PLACE1004405	F-PLACE1004405	0.82
PLACE1004428	F-PLACE1004428	0.68
PLACE1004437	F-PLACE1004437	0.94
PLACE1004451	F-PLACE1004451	0.39
PLACE1004460	F-PLACE1004460	0.92
PLACE1004473	F-PLACE1004473	0.94
PLACE1004510	F-PLACE1004510	0.94
PLACE1004516	F-PLACE1004516	0.58
PLACE1004548	F-PLACE1004548	0.59
PLACE1004550	F-PLACE1004550	0.94
PLACE1004564	F-PLACE1004564	0.53
PLACE1004629	F-PLACE1004629	0.34
PLACE1004645	F-PLACE1004645	0.59
PLACE1004646	F-PLACE1004646	0.35
PLACE1004664	F-PLACE1004664	0.31
PLACE1004672	F-PLACE1004672	0.83
PLACE1004674	F-PLACE1004674	0.90
PLACE1004686	F-PLACE1004686	0.31
PLACE1004691	F-PLACE1004691	0.89
PLACE1004722	F-PLACE1004722	0.48

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PLACE1004736	F-PLACE1004736	0. 80
PLACE1004740	F-PLACE1004740	0. 34
PLACE1004743	F-PLACE1004743	0. 70
PLACE1004751	F-PLACE1004751	0. 49
PLACE1004777	F-PLACE1004777	0. 72
PLACE1004804	F-PLACE1004804	0. 46
PLACE1004814	F-PLACE1004814	0. 70
PLACE1004824	F-PLACE1004824	0. 63
PLACE1004868	F-PLACE1004868	0. 94
PLACE1004885	F-PLACE1004885	0. 63
PLACE1004902	F-PLACE1004902	0. 56
PLACE1004918	F-PLACE1004918	0. 85
PLACE1004930	F-PLACE1004930	0. 83
PLACE1004937	F-PLACE1004937	0. 46
PLACE1004969	F-PLACE1004969	0. 62
PLACE1004982	F-PLACE1004982	0. 61
PLACE1005026	F-PLACE1005026	0. 81
PLACE1005027	F-PLACE1005027	0. 91
PLACE1005046	F-PLACE1005046	0. 31
PLACE1005055	F-PLACE1005055	0. 57
PLACE1005066	F-PLACE1005066	0. 68
PLACE1005101	F-PLACE1005101	0. 94
PLACE1005102	F-PLACE1005102	0. 94
PLACE1005181	F-PLACE1005181	0. 94
PLACE1005187	F-PLACE1005187	0. 94
PLACE1005206	F-PLACE1005206	0. 67
PLACE1005232	F-PLACE1005232	0. 72
PLACE1005243	F-PLACE1005243	0. 81
PLACE1005261	F-PLACE1005261	0. 75
PLACE1005266	F-PLACE1005266	0. 55
PLACE1005277	F-PLACE1005277	0. 43
PLACE1005287	F-PLACE1005287	0. 77
PLACE1005305	F-PLACE1005305	0. 94
PLACE1005308	F-PLACE1005308	0. 46
PLACE1005313	F-PLACE1005313	0. 94
PLACE1005327	F-PLACE1005327	0. 82
PLACE1005331	F-PLACE1005331	0. 94
PLACE1005335	F-PLACE1005335	0. 94
PLACE1005373	F-PLACE1005373	0. 71
PLACE1005374	F-PLACE1005374	0. 82
PLACE1005480	F-PLACE1005480	0. 43
PLACE1005481	F-PLACE1005481	0. 42
PLACE1005494	F-PLACE1005494	0. 34
PLACE1005530	F-PLACE1005530	0. 94
PLACE1005550	F-PLACE1005550	0. 86
PLACE1005554	F-PLACE1005554	0. 34

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PLACE1005557	F-PLACE1005557	0.80
PLACE1005595	F-PLACE1005595	0.69
PLACE1005603	F-PLACE1005603	0.92
PLACE1005623	F-PLACE1005623	0.68
PLACE1005630	F-PLACE1005630	0.58
PLACE1005646	F-PLACE1005646	0.31
PLACE1005656	F-PLACE1005656	0.85
PLACE1005698	F-PLACE1005698	0.91
PLACE1005727	F-PLACE1005727	0.94
PLACE1005739	F-PLACE1005739	0.87
PLACE1005755	F-PLACE1005755	0.32
PLACE1005763	F-PLACE1005763	0.74
PLACE1005799	F-PLACE1005799	0.47
PLACE1005803	F-PLACE1005803	0.88
PLACE1005804	F-PLACE1005804	0.36
PLACE1005813	F-PLACE1005813	0.76
PLACE1005828	F-PLACE1005828	0.43
PLACE1005834	F-PLACE1005834	0.89
PLACE1005851	F-PLACE1005851	0.39
PLACE1005876	F-PLACE1005876	0.51
PLACE1005890	F-PLACE1005890	0.81
PLACE1005921	F-PLACE1005921	0.90
PLACE1005923	F-PLACE1005923	0.70
PLACE1005925	F-PLACE1005925	0.55
PLACE1005934	F-PLACE1005934	0.94
PLACE1005936	F-PLACE1005936	0.41
PLACE1005951	F-PLACE1005951	0.34
PLACE1005953	F-PLACE1005953	0.31
PLACE1005955	F-PLACE1005955	0.89
PLACE1005966	F-PLACE1005966	0.73
PLACE1005990	F-PLACE1005990	0.37
PLACE1006011	F-PLACE1006011	0.94
PLACE1006037	F-PLACE1006037	0.65
PLACE1006040	F-PLACE1006040	0.94
PLACE1006119	F-PLACE1006119	0.52
PLACE1006139	F-PLACE1006139	0.94
PLACE1006157	F-PLACE1006157	0.34
PLACE1006159	F-PLACE1006159	0.50
PLACE1006167	F-PLACE1006167	0.94
PLACE1006170	F-PLACE1006170	0.94
PLACE1006195	F-PLACE1006195	0.31
PLACE1006196	F-PLACE1006196	0.84
PLACE1006225	F-PLACE1006225	0.87
PLACE1006236	F-PLACE1006236	0.92
PLACE1006239	F-PLACE1006239	0.53
PLACE1006246	F-PLACE1006246	0.44

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PLACE1006248	F-PLACE1006248	0.49
PLACE1006325	F-PLACE1006325	0.74
PLACE1006335	F-PLACE1006335	0.82
PLACE1006357	F-PLACE1006357	0.33
PLACE1006385	F-PLACE1006385	0.54
PLACE1006412	F-PLACE1006412	0.79
PLACE1006414	F-PLACE1006414	0.52
PLACE1006438	F-PLACE1006438	0.94
PLACE1006445	F-PLACE1006445	0.37
PLACE1006469	F-PLACE1006469	0.85
PLACE1006482	F-PLACE1006482	0.94
PLACE1006488	F-PLACE1006488	0.94
PLACE1006492	F-PLACE1006492	0.32
PLACE1006531	F-PLACE1006531	0.45
PLACE1006552	F-PLACE1006552	0.42
PLACE1006598	F-PLACE1006598	0.33
PLACE1006615	F-PLACE1006615	0.89
PLACE1006626	F-PLACE1006626	0.69
PLACE1006673	F-PLACE1006673	0.61
PLACE1006678	F-PLACE1006678	0.53
PLACE1006704	F-PLACE1006704	0.47
PLACE1006731	F-PLACE1006731	0.72
PLACE1006782	F-PLACE1006782	0.68
PLACE1006819	F-PLACE1006819	0.57
PLACE1006829	F-PLACE1006829	0.47
PLACE1006883	F-PLACE1006883	0.88
PLACE1006901	F-PLACE1006901	0.43
PLACE1006917	F-PLACE1006917	0.56
PLACE1006932	F-PLACE1006932	0.45
PLACE1006935	F-PLACE1006935	0.58
PLACE1006956	F-PLACE1006956	0.77
PLACE1006958	F-PLACE1006958	0.75
PLACE1006961	F-PLACE1006961	0.34
PLACE1006962	F-PLACE1006962	0.94
PLACE1006966	F-PLACE1006966	0.56
PLACE1006989	F-PLACE1006989	0.47
PLACE1007014	F-PLACE1007014	0.94
PLACE1007021	F-PLACE1007021	0.74
PLACE1007053	F-PLACE1007053	0.73
PLACE1007068	F-PLACE1007068	0.43
PLACE1007105	F-PLACE1007105	0.88
PLACE1007112	F-PLACE1007112	0.82
PLACE1007178	F-PLACE1007178	0.91
PLACE1007226	F-PLACE1007226	0.79
PLACE1007238	F-PLACE1007238	0.94
PLACE1007239	F-PLACE1007239	0.94

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PLACE1007242	F-PLACE1007242	0.48
PLACE1007243	F-PLACE1007243	0.77
PLACE1007257	F-PLACE1007257	0.54
PLACE1007274	F-PLACE1007274	0.94
PLACE1007282	F-PLACE1007282	0.94
PLACE1007301	F-PLACE1007301	0.34
PLACE1007317	F-PLACE1007317	0.43
PLACE1007342	F-PLACE1007342	0.72
PLACE1007346	F-PLACE1007346	0.92
PLACE1007367	F-PLACE1007367	0.43
PLACE1007375	F-PLACE1007375	0.85
PLACE1007386	F-PLACE1007386	0.58
PLACE1007402	F-PLACE1007402	0.74
PLACE1007409	F-PLACE1007409	0.39
PLACE1007416	F-PLACE1007416	0.80
PLACE1007450	F-PLACE1007450	0.41
PLACE1007452	F-PLACE1007452	0.68
PLACE1007454	F-PLACE1007454	0.39
PLACE1007460	F-PLACE1007460	0.58
PLACE1007484	F-PLACE1007484	0.94
PLACE1007488	F-PLACE1007488	0.50
PLACE1007507	F-PLACE1007507	0.44
PLACE1007511	F-PLACE1007511	0.86
PLACE1007524	F-PLACE1007524	0.66
PLACE1007537	F-PLACE1007537	0.93
PLACE1007544	F-PLACE1007544	0.94
PLACE1007547	F-PLACE1007547	0.65
PLACE1007583	F-PLACE1007583	0.87
PLACE1007598	F-PLACE1007598	0.39
PLACE1007618	F-PLACE1007618	0.62
PLACE1007621	F-PLACE1007621	0.63
PLACE1007632	F-PLACE1007632	0.75
PLACE1007645	F-PLACE1007645	0.94
PLACE1007649	F-PLACE1007649	0.56
PLACE1007688	F-PLACE1007688	0.94
PLACE1007690	F-PLACE1007690	0.44
PLACE1007697	F-PLACE1007697	0.93
PLACE1007705	F-PLACE1007705	0.61
PLACE1007706	F-PLACE1007706	0.47
PLACE1007725	F-PLACE1007725	0.61
PLACE1007729	F-PLACE1007729	0.53
PLACE1007730	F-PLACE1007730	0.31
PLACE1007746	F-PLACE1007746	0.81
PLACE1007791	F-PLACE1007791	0.46
PLACE1007810	F-PLACE1007810	0.73
PLACE1007843	F-PLACE1007843	0.31

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PLACE1007846	F-PLACE1007846	0.38
PLACE1007858	F-PLACE1007858	0.79
PLACE1007897	F-PLACE1007897	0.94
PLACE1007908	F-PLACE1007908	0.94
PLACE1007946	F-PLACE1007946	0.52
PLACE1007954	F-PLACE1007954	0.43
PLACE1007955	F-PLACE1007955	0.41
PLACE1007958	F-PLACE1007958	0.37
PLACE1007969	F-PLACE1007969	0.87
PLACE1007990	F-PLACE1007990	0.94
PLACE1008000	F-PLACE1008000	0.94
PLACE1008002	F-PLACE1008002	0.93
PLACE1008044	F-PLACE1008044	0.72
PLACE1008095	F-PLACE1008095	0.94
PLACE1008122	F-PLACE1008122	0.94
PLACE1008129	F-PLACE1008129	0.80
PLACE1008132	F-PLACE1008132	0.37
PLACE1008177	F-PLACE1008177	0.74
PLACE1008198	F-PLACE1008198	0.94
PLACE1008209	F-PLACE1008209	0.54
PLACE1008273	F-PLACE1008273	0.94
PLACE1008275	F-PLACE1008275	0.82
PLACE1008280	F-PLACE1008280	0.34
PLACE1008309	F-PLACE1008309	0.90
PLACE1008329	F-PLACE1008329	0.38
PLACE1008356	F-PLACE1008356	0.93
PLACE1008368	F-PLACE1008368	0.43
PLACE1008398	F-PLACE1008398	0.78
PLACE1008401	F-PLACE1008401	0.81
PLACE1008402	F-PLACE1008402	0.88
PLACE1008429	F-PLACE1008429	0.39
PLACE1008457	F-PLACE1008457	0.77
PLACE1008465	F-PLACE1008465	0.94
PLACE1008488	F-PLACE1008488	0.42
PLACE1008524	F-PLACE1008524	0.41
PLACE1008531	F-PLACE1008531	0.94
PLACE1008532	F-PLACE1008532	0.61
PLACE1008533	F-PLACE1008533	0.45
PLACE1008568	F-PLACE1008568	0.65
PLACE1008603	F-PLACE1008603	0.42
PLACE1008626	F-PLACE1008626	0.94
PLACE1008627	F-PLACE1008627	0.72
PLACE1008629	F-PLACE1008629	0.33
PLACE1008650	F-PLACE1008650	0.79
PLACE1008693	F-PLACE1008693	0.32
PLACE1008696	F-PLACE1008696	0.39

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PLACE1008790	F-PLACE1008790	0.81
PLACE1008808	F-PLACE1008808	0.51
PLACE1008813	F-PLACE1008813	0.36
PLACE1008854	F-PLACE1008854	0.81
PLACE1008867	F-PLACE1008867	0.34
PLACE1008887	F-PLACE1008887	0.49
PLACE1008902	F-PLACE1008902	0.91
PLACE1008925	F-PLACE1008925	0.94
PLACE1008934	F-PLACE1008934	0.70
PLACE1009027	F-PLACE1009027	0.32
PLACE1009045	F-PLACE1009045	0.42
PLACE1009060	F-PLACE1009060	0.69
PLACE1009090	F-PLACE1009090	0.46
PLACE1009091	F-PLACE1009091	0.90
PLACE1009094	F-PLACE1009094	0.44
PLACE1009099	F-PLACE1009099	0.56
PLACE1009110	F-PLACE1009110	0.84
PLACE1009111	F-PLACE1009111	0.80
PLACE1009113	F-PLACE1009113	0.88
PLACE1009130	F-PLACE1009130	0.60
PLACE1009158	F-PLACE1009158	0.41
PLACE1009166	F-PLACE1009166	0.94
PLACE1009174	F-PLACE1009174	0.38
PLACE1009186	F-PLACE1009186	0.59
PLACE1009190	F-PLACE1009190	0.66
PLACE1009230	F-PLACE1009230	0.87
PLACE1009298	F-PLACE1009298	0.41
PLACE1009319	F-PLACE1009319	0.53
PLACE1009328	F-PLACE1009328	0.66
PLACE1009335	F-PLACE1009335	0.47
PLACE1009338	F-PLACE1009338	0.70
PLACE1009368	F-PLACE1009368	0.94
PLACE1009375	F-PLACE1009375	0.76
PLACE1009388	F-PLACE1009388	0.46
PLACE1009404	F-PLACE1009404	0.72
PLACE1009434	F-PLACE1009434	0.50
PLACE1009443	F-PLACE1009443	0.90
PLACE1009444	F-PLACE1009444	0.33
PLACE1009459	F-PLACE1009459	0.94
PLACE1009468	F-PLACE1009468	0.88
PLACE1009476	F-PLACE1009476	0.84
PLACE1009524	F-PLACE1009524	0.88
PLACE1009542	F-PLACE1009542	0.55
PLACE1009571	F-PLACE1009571	0.61
PLACE1009581	F-PLACE1009581	0.94
PLACE1009596	F-PLACE1009596	0.44

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PLACE1009607	F-PLACE1009607	0.47
PLACE1009622	F-PLACE1009622	0.65
PLACE1009659	F-PLACE1009659	0.36
PLACE1009665	F-PLACE1009665	0.43
PLACE1009670	F-PLACE1009670	0.33
PLACE1009708	F-PLACE1009708	0.80
PLACE1009721	F-PLACE1009721	0.81
PLACE1009731	F-PLACE1009731	0.47
PLACE1009763	F-PLACE1009763	0.94
PLACE1009794	F-PLACE1009794	0.33
PLACE1009798	F-PLACE1009798	0.34
PLACE1009845	F-PLACE1009845	0.66
PLACE1009861	F-PLACE1009861	0.72
PLACE1009886	F-PLACE1009886	0.63
PLACE1009908	F-PLACE1009908	0.92
PLACE1009921	F-PLACE1009921	0.70
PLACE1009971	F-PLACE1009971	0.40
PLACE1009992	F-PLACE1009992	0.89
PLACE1009995	F-PLACE1009995	0.88
PLACE1009997	F-PLACE1009997	0.41
PLACE1010023	F-PLACE1010023	0.90
PLACE1010031	F-PLACE1010031	0.71
PLACE1010053	F-PLACE1010053	0.51
PLACE1010074	F-PLACE1010074	0.75
PLACE1010076	F-PLACE1010076	0.53
PLACE1010096	F-PLACE1010096	0.44
PLACE1010102	F-PLACE1010102	0.77
PLACE1010105	F-PLACE1010105	0.58
PLACE1010106	F-PLACE1010106	0.39
PLACE1010134	F-PLACE1010134	0.85
PLACE1010148	F-PLACE1010148	0.32
PLACE1010152	F-PLACE1010152	0.94
PLACE1010194	F-PLACE1010194	0.94
PLACE1010202	F-PLACE1010202	0.33
PLACE1010261	F-PLACE1010261	0.36
PLACE1010274	F-PLACE1010274	0.94
PLACE1010293	F-PLACE1010293	0.55
PLACE1010310	F-PLACE1010310	0.41
PLACE1010321	F-PLACE1010321	0.40
PLACE1010324	F-PLACE1010324	0.40
PLACE1010329	F-PLACE1010329	0.36
PLACE1010362	F-PLACE1010362	0.34
PLACE1010364	F-PLACE1010364	0.37
PLACE1010383	F-PLACE1010383	0.94
PLACE1010401	F-PLACE1010401	0.53
PLACE1010481	F-PLACE1010481	0.74

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PLACE1010491	F-PLACE1010491	0.31
PLACE1010492	F-PLACE1010492	0.39
PLACE1010522	F-PLACE1010522	0.92
PLACE1010529	F-PLACE1010529	0.65
PLACE1010547	F-PLACE1010547	0.82
PLACE1010580	F-PLACE1010580	0.72
PLACE1010599	F-PLACE1010599	0.83
PLACE1010616	F-PLACE1010616	0.54
PLACE1010622	F-PLACE1010622	0.92
PLACE1010629	F-PLACE1010629	0.94
PLACE1010630	F-PLACE1010630	0.37
PLACE1010661	F-PLACE1010661	0.56
PLACE1010714	F-PLACE1010714	0.68
PLACE1010720	F-PLACE1010720	0.90
PLACE1010743	F-PLACE1010743	0.75
PLACE1010761	F-PLACE1010761	0.69
PLACE1010771	F-PLACE1010771	0.94
PLACE1010786	F-PLACE1010786	0.80
PLACE1010800	F-PLACE1010800	0.41
PLACE1010811	F-PLACE1010811	0.94
PLACE1010833	F-PLACE1010833	0.94
PLACE1010856	F-PLACE1010856	0.37
PLACE1010857	F-PLACE1010857	0.54
PLACE1010870	F-PLACE1010870	0.50
PLACE1010877	F-PLACE1010877	0.77
PLACE1010900	F-PLACE1010900	0.70
PLACE1010917	F-PLACE1010917	0.94
PLACE1010925	F-PLACE1010925	0.79
PLACE1010926	F-PLACE1010926	0.94
PLACE1010942	F-PLACE1010942	0.36
PLACE1010944	F-PLACE1010944	0.61
PLACE1010954	F-PLACE1010954	0.83
PLACE1010960	F-PLACE1010960	0.38
PLACE1010965	F-PLACE1010965	0.68
PLACE1011026	F-PLACE1011026	0.38
PLACE1011041	F-PLACE1011041	0.94
PLACE1011046	F-PLACE1011046	0.85
PLACE1011054	F-PLACE1011054	0.65
PLACE1011056	F-PLACE1011056	0.82
PLACE1011090	F-PLACE1011090	0.94
PLACE1011114	F-PLACE1011114	0.94
PLACE1011160	F-PLACE1011160	0.62
PLACE1011214	F-PLACE1011214	0.40
PLACE1011219	F-PLACE1011219	0.48
PLACE1011221	F-PLACE1011221	0.94
PLACE1011229	F-PLACE1011229	0.46

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PLACE1011263	F-PLACE1011263	0.94
PLACE1011273	F-PLACE1011273	0.32
PLACE1011291	F-PLACE1011291	0.55
PLACE1011310	F-PLACE1011310	0.74
PLACE1011325	F-PLACE1011325	0.39
PLACE1011332	F-PLACE1011332	0.74
PLACE1011371	F-PLACE1011371	0.32
PLACE1011399	F-PLACE1011399	0.89
PLACE1011433	F-PLACE1011433	0.33
PLACE1011472	F-PLACE1011472	0.59
PLACE1011477	F-PLACE1011477	0.80
PLACE1011563	F-PLACE1011563	0.83
PLACE1011586	F-PLACE1011586	0.82
PLACE1011635	F-PLACE1011635	0.62
PLACE1011646	F-PLACE1011646	0.37
PLACE1011664	F-PLACE1011664	0.65
PLACE1011675	F-PLACE1011675	0.89
PLACE1011682	F-PLACE1011682	0.81
PLACE1011725	F-PLACE1011725	0.86
PLACE1011783	F-PLACE1011783	0.78
PLACE1011858	F-PLACE1011858	0.76
PLACE1011875	F-PLACE1011875	0.49
PLACE1011891	F-PLACE1011891	0.34
PLACE1011896	F-PLACE1011896	0.34
PLACE1011922	F-PLACE1011922	0.46
PLACE1011923	F-PLACE1011923	0.74
PLACE1011982	F-PLACE1011982	0.71
PLACE1012031	F-PLACE1012031	0.80
PLACE2000006	F-PLACE2000006	0.61
PLACE2000007	F-PLACE2000007	0.37
PLACE2000014	F-PLACE2000014	0.67
PLACE2000015	F-PLACE2000015	0.53
PLACE2000021	F-PLACE2000021	0.36
PLACE2000030	F-PLACE2000030	0.83
PLACE2000033	F-PLACE2000033	0.44
PLACE2000034	F-PLACE2000034	0.88
PLACE2000039	F-PLACE2000039	0.67
PLACE2000047	F-PLACE2000047	0.84
PLACE2000050	F-PLACE2000050	0.41
PLACE2000062	F-PLACE2000062	0.94
PLACE2000072	F-PLACE2000072	0.86
PLACE2000097	F-PLACE2000097	0.94
PLACE2000100	F-PLACE2000100	0.75
PLACE2000111	F-PLACE2000111	0.62
PLACE2000124	F-PLACE2000124	0.77
PLACE2000164	F-PLACE2000164	0.57

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PLACE2000170	F-PLACE2000170	0.60
PLACE2000172	F-PLACE2000172	0.55
PLACE2000223	F-PLACE2000223	0.54
PLACE2000235	F-PLACE2000235	0.94
PLACE2000246	F-PLACE2000246	0.94
PLACE2000274	F-PLACE2000274	0.82
PLACE2000302	F-PLACE2000302	0.92
PLACE2000341	F-PLACE2000341	0.58
PLACE2000359	F-PLACE2000359	0.33
PLACE2000371	F-PLACE2000371	0.71
PLACE2000373	F-PLACE2000373	0.65
PLACE2000399	F-PLACE2000399	0.41
PLACE2000404	F-PLACE2000404	0.94
PLACE2000411	F-PLACE2000411	0.90
PLACE2000427	F-PLACE2000427	0.60
PLACE2000433	F-PLACE2000433	0.61
PLACE2000438	F-PLACE2000438	0.56
PLACE2000458	F-PLACE2000458	0.82
PLACE3000009	F-PLACE3000009	0.56
PLACE3000020	F-PLACE3000020	0.94
PLACE3000029	F-PLACE3000029	0.94
PLACE3000059	F-PLACE3000059	0.51
PLACE3000070	F-PLACE3000070	0.67
PLACE3000103	F-PLACE3000103	0.34
PLACE3000121	F-PLACE3000121	0.32
PLACE3000142	F-PLACE3000142	0.67
PLACE3000145	F-PLACE3000145	0.84
PLACE3000147	F-PLACE3000147	0.57
PLACE3000148	F-PLACE3000148	0.94
PLACE3000155	F-PLACE3000155	0.42
PLACE3000156	F-PLACE3000156	0.40
PLACE3000157	F-PLACE3000157	0.75
PLACE3000160	F-PLACE3000160	0.44
PLACE3000194	F-PLACE3000194	0.37
PLACE3000197	F-PLACE3000197	0.37
PLACE3000221	F-PLACE3000221	0.49
PLACE3000226	F-PLACE3000226	0.39
PLACE3000242	F-PLACE3000242	0.94
PLACE3000244	F-PLACE3000244	0.56
PLACE3000254	F-PLACE3000254	0.60
PLACE3000304	F-PLACE3000304	0.42
PLACE3000310	F-PLACE3000310	0.71
PLACE3000320	F-PLACE3000320	0.37
PLACE3000322	F-PLACE3000322	0.46
PLACE3000331	F-PLACE3000331	0.31
PLACE3000339	F-PLACE3000339	0.45

BNSDOCID: <EP___1074617A2_I_>

PLACE3000350	F-PLACE3000350	0.52
PLACE3000352	F-PLACE3000352	0.65
PLACE3000353	F-PLACE3000353	0.71
PLACE3000363	F-PLACE3000363	0.45
PLACE3000405	F-PLACE3000405	0.52
PLACE3000413	F-PLACE3000413	0.85
PLACE3000416	F-PLACE3000416	0.94
PLACE3000425	F-PLACE3000425	0.40
PLACE3000455	F-PLACE3000455	0.45
PLACE3000477	F-PLACE3000477	0.79
PLACE4000009	F-PLACE4000009	0.74
PLACE4000014	F-PLACE4000014	0.46
PLACE4000034	F-PLACE4000034	0.89
PLACE4000049	F-PLACE4000049	0.68
PLACE4000052	F-PLACE4000052	0.80
PLACE4000063	F-PLACE4000063	0.69
PLACE4000089	F-PLACE4000089	0.44
PLACE4000106	F-PLACE4000106	0.34
PLACE4000128	F-PLACE4000128	0.89
PLACE4000129	F-PLACE4000129	0.61
PLACE4000131	F-PLACE4000131	0.55
PLACE4000147	F-PLACE4000147	0.94
PLACE4000156	F-PLACE4000156	0.37
PLACE4000192	F-PLACE4000192	0.88
PLACE4000211	F-PLACE4000211	0.64
PLACE4000222	F-PLACE4000222	0.40
PLACE4000230	F-PLACE4000230	0.49
PLACE4000259	F-PLACE4000259	0.84
PLACE4000261	F-PLACE4000261	0.42
PLACE4000269	F-PLACE4000269	0.60
PLACE4000270	F-PLACE4000270	0.61
PLACE4000300	F-PLACE4000300	0.85
PLACE4000323	F-PLACE4000323	0.76
PLACE4000326	F-PLACE4000326	0.86
PLACE4000369	F-PLACE4000369	0.87
PLACE4000387	F-PLACE4000387	0.41
PLACE4000392	F-PLACE4000392	0.39
PLACE4000431	F-PLACE4000431	0.88
PLACE4000445	F-PLACE4000445	0.40
PLACE4000450	F-PLACE4000450	0.89
PLACE4000465	F-PLACE4000465	0.38
PLACE4000487	F-PLACE4000487	0.44
PLACE4000489	F-PLACE4000489	0.51
PLACE4000521	F-PLACE4000521	0.38
PLACE4000522	F-PLACE4000522	0.33
PLACE4000558	F-PLACE4000558	0.44

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PLACE4000581	F-PLACE4000581	0.59
PLACE4000590	F-PLACE4000590	0.38
PLACE4000593	F-PLACE4000593	0.33
PLACE4000612	F-PLACE4000612	0.37
PLACE4000638	F-PLACE4000638	0.38
PLACE4000650	F-PLACE4000650	0.59
PLACE4000654	F-PLACE4000654	0.57
PLACE4000670	F-PLACE4000670	0.71
SKNMC1000011	F-SKNMC1000011	0.94
SKNMC1000013	F-SKNMC1000013	0.66
SKNMC1000046	F-SKNMC1000046	0.72
SKNMC1000050	F-SKNMC1000050	0.47
SKNMC1000091	F-SKNMC1000091	0.68
THYR01000017	F-THYR01000017	0.93
THYR01000034	F-THYR01000034	0.48
THYR01000040	F-THYR01000040	0.32
THYR01000070	F-THYR01000070	0.75
THYR01000072	F-THYR01000072	0.94
THYR01000107	F-THYR01000107	0.94
THYR01000121	F-THYR01000121	0.46
THYR01000124	F-THYR01000124	0.37
THYR01000163	F-THYR01000163	0.45
THYR01000173	F-THYR01000173	0.94
THYR01000197	F-THYR01000197	0.78
THYR01000199	F-THYR01000199	0.55
THYR01000206	F-THYR01000206	0.59
THYR01000242	F-THYR01000242	0.69
THYR01000253	F-THYR01000253	0.48
THYR01000270	F-THYR01000270	0.85
THYR01000288	F-THYR01000288	0.31
THYR01000320	F-THYR01000320	0.94
THYR01000327	F-THYR01000327	0.44
THYR01000343	F-THYR01000343	0.82
THYR01000358	F-THYR01000358	0.89
THYR01000368	F-THYR01000368	0.94
THYR01000381	F-THYR01000381	0.64
THYR01000387	F-THYR01000387	0.57
THYR01000394	F-THYR01000394	0.94
THYR01000395	F-THYR01000395	0.91
THYR01000401	F-THYR01000401	0.73
THYR01000488	F-THYR01000488	0.94
THYR01000501	F-THYR01000501	0.74
THYR01000502	F-THYR01000502	0.64
THYR01000505	F-THYR01000505	0.47
THYR01000569	F-THYR01000569	0.76
THYR01000570	F-THYR01000570	0.79

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THYR01000585	F-THYR01000585	0.60
THYR01000605	F-THYR01000605	0.79
THYR01000637	F-THYR01000637	0.80
THYR01000662	F-THYR01000662	0.77
THYR01000666	F-THYR01000666	0.47
THYR01000676	F-THYR01000676	0.94
THYR01000684	F-THYR01000684	0.72
THYR01000712	F-THYR01000712	0.94
THYR01000715	F-THYR01000715	0.94
THYR01000734	F-THYR01000734	0.44
THYR01000756	F-THYR01000756	0.94
THYR01000777	F-THYR01000777	0.73
THYR01000783	F-THYR01000783	0.74
THYR01000787	F-THYR01000787	0.67
THYR01000829	F-THYR01000829	0.43
THYR01000855	F-THYR01000855	0.91
THYR01000916	F-THYR01000916	0.64
THYR01000926	F-THYR01000926	0.39
THYR01000934	F-THYR01000934	0.94
THYR01000951	F-THYR01000951	0.94
THYR01000952	F-THYR01000952	0.67
THYR01000983	F-THYR01000983	0.87
THYR01000984	F-THYR01000984	0.94
THYR01000988	F-THYR01000988	0.37
THYR01001033	F-THYR01001033	0.74
THYR01001100	F-THYR01001100	0.74
THYR01001120	F-THYR01001120	0.87
THYR01001134	F-THYR01001134	0.93
THYR01001142	F-THYR01001142	0.61
THYR01001173	F-THYR01001173	0.50
THYR01001189	F-THYR01001189	0.40
THYR01001204	F-THYR01001204	0.94
THYR01001213	F-THYR01001213	0.94
THYR01001271	F-THYR01001271	0.93
THYR01001287	F-THYR01001287	0.32
THYR01001313	F-THYR01001313	0.53
THYR01001320	F-THYR01001320	0.68
THYR01001347	F-THYR01001347	0.68
THYR01001363	F-THYR01001363	0.39
THYR01001374	F-THYR01001374	0.94
THYR01001403	F-THYR01001403	0.49
THYR01001405	F-THYR01001405	0.90
THYR01001406	F-THYR01001406	0.67
THYR01001458	F-THYR01001458	0.94
THYR01001487	F-THYR01001487	0.63
THYR01001537	F-THYR01001537	0.94

BNSDOCID: <EP___1074617A2_I_>

THYR01001584	F-THYR01001584	0.77
THYR01001602	F-THYR01001602	0.64
THYR01001605	F-THYR01001605	0.52
THYR01001637	F-THYR01001637	0.68
THYR01001656	F-THYR01001656	0.82
THYR01001661	F-THYR01001661	0.94
THYR01001671	F-THYR01001671	0.94
THYR01001703	F-THYR01001703	0.87
THYR01001721	F-THYR01001721	0.38
THYR01001738	F-THYR01001738	0.51
THYR01001793	F-THYR01001793	0.84
THYR01001809	F-THYR01001809	0.73
THYR01001828	F-THYR01001828	0.88
THYR01001854	F-THYR01001854	0.47
VESEN1000122	F-VESEN1000122	0.36
Y79AA1000013	F-Y79AA1000013	0.94
Y79AA1000037	F-Y79AA1000037	0.94
Y79AA1000059	F-Y79AA1000059	0.94
Y79AA1000131	F-Y79AA1000131	0.56
Y79AA1000181	F-Y79AA1000181	0.59
Y79AA1000202	F-Y79AA1000202	0.45
Y79AA1000214	F-Y79AA1000214	0.93
Y79AA1000230	F-Y79AA1000230	0.94
Y79AA1000231	F-Y79AA1000231	0.36
Y79AA1000258	F-Y79AA1000258	0.36
Y79AA1000268	F-Y79AA1000268	0.92
Y79AA1000313	F-Y79AA1000313	0.91
Y79AA1000328	F-Y79AA1000328	0.94
Y79AA1000342	F-Y79AA1000342	0.83
Y79AA1000349	F-Y79AA1000349	0.50
Y79AA1000355	F-Y79AA1000355	0.94
Y79AA1000368	F-Y79AA1000368	0.91
Y79AA1000420	F-Y79AA1000420	0.94
Y79AA1000469	F-Y79AA1000469	0.51
Y79AA1000480	F-Y79AA1000480	0.94
Y79AA1000539	F-Y79AA1000539	0.74
Y79AA1000540	F-Y79AA1000540	0.94
Y79AA1000560	F-Y79AA1000560	0.93
Y79AA1000574	F-Y79AA1000574	0.87
Y79AA1000589	F-Y79AA1000589	0.94
Y79AA1000627	F-Y79AA1000627	0.55
Y79AA1000705	F-Y79AA1000705	0.76
Y79AA1000734	F-Y79AA1000734	0.60
Y79AA1000748	F-Y79AA1000748	0.45
Y79AA1000752	F-Y79AA1000752	0.94
Y79AA1000774	F-Y79AA1000774	0.38

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Y79AA1000782	F-Y79AA1000782	0.47
Y79AA1000784	F-Y79AA1000784	0.93
Y79AA1000794	F-Y79AA1000794	0.67
Y79AA1000800	F-Y79AA1000800	0.94
Y79AA1000824	F-Y79AA1000824	0.90
Y79AA1000827	F-Y79AA1000827	0.94
Y79AA1000833	F-Y79AA1000833	0.34
Y79AA1000850	F-Y79AA1000850	0.92
Y79AA1000962	F-Y79AA1000962	0.69
Y79AA1000966	F-Y79AA1000966	0.64
Y79AA1000968	F-Y79AA1000968	0.64
Y79AA1000976	F-Y79AA1000976	0.66
Y79AA1000985	F-Y79AA1000985	0.66
Y79AA1001023	F-Y79AA1001023	0.33
Y79AA1001041	F-Y79AA1001041	0.90
Y79AA1001048	F-Y79AA1001048	0.81
Y79AA1001068	F-Y79AA1001068	0.64
Y79AA1001077	F-Y79AA1001077	0.78
Y79AA1001078	F-Y79AA1001078	0.92
Y79AA1001105	F-Y79AA1001105	0.70
Y79AA1001145	F-Y79AA1001145	0.46
Y79AA1001177	F-Y79AA1001177	0.74
Y79AA1001185	F-Y79AA1001185	0.74
Y79AA1001211	F-Y79AA1001211	0.94
Y79AA1001216	F-Y79AA1001216	0.61
Y79AA1001228	F-Y79AA1001228	0.56
Y79AA1001233	F-Y79AA1001233	0.83
Y79AA1001236	F-Y79AA1001236	0.32
Y79AA1001281	F-Y79AA1001281	0.51
Y79AA1001299	F-Y79AA1001299	0.94
Y79AA1001312	F-Y79AA1001312	0.53
Y79AA1001323	F-Y79AA1001323	0.76
Y79AA1001391	F-Y79AA1001391	0.83
Y79AA1001394	F-Y79AA1001394	0.94
Y79AA1001402	F-Y79AA1001402	0.90
Y79AA1001493	F-Y79AA1001493	0.94
Y79AA1001511	F-Y79AA1001511	0.47
Y79AA1001533	F-Y79AA1001533	0.92
Y79AA1001541	F-Y79AA1001541	0.32
Y79AA1001548	F-Y79AA1001548	0.50
Y79AA1001555	F-Y79AA1001555	0.92
Y79AA1001581	F-Y79AA1001581	0.94
Y79AA1001585	F-Y79AA1001585	0.80
Y79AA1001603	F-Y79AA1001603	0.94
Y79AA1001613	F-Y79AA1001613	0.94
Y79AA1001647	F-Y79AA1001647	0.49

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Y79AA1001665	F-Y79AA1001665	0.78
Y79AA1001679	F-Y79AA1001679	0.94
Y79AA1001696	F-Y79AA1001696	0.60
Y79AA1001705	F-Y79AA1001705	0.67
Y79AA1001711	F-Y79AA1001711	0.59
Y79AA1001781	F-Y79AA1001781	0.74
Y79AA1001805	F-Y79AA1001805	0.79
Y79AA1001827	F-Y79AA1001827	0.84
Y79AA1001846	F-Y79AA1001846	0.34
Y79AA1001866	F-Y79AA1001866	0.75
Y79AA1001874	F-Y79AA1001874	0.59
Y79AA1001923	F-Y79AA1001923	0.32
Y79AA1001963	F-Y79AA1001963	0.51
Y79AA1002027	F-Y79AA1002027	0.39
Y79AA1002083	F-Y79AA1002083	0.65
Y79AA1002089	F-Y79AA1002089	0.94
Y79AA1002093	F-Y79AA1002093	0.89
Y79AA1002115	F-Y79AA1002115	0.31
Y79AA1002125	F-Y79AA1002125	0.76
Y79AA1002139	F-Y79AA1002139	0.32
Y79AA1002204	F-Y79AA1002204	0.94
Y79AA1002208	F-Y79AA1002208	0.76
Y79AA1002209	F-Y79AA1002209	0.91
Y79AA1002210	F-Y79AA1002210	0.60
Y79AA1002229	F-Y79AA1002229	0.76
Y79AA1002234	F-Y79AA1002234	0.94
Y79AA1002246	F-Y79AA1002246	0.65
Y79AA1002258	F-Y79AA1002258	0.79
Y79AA1002298	F-Y79AA1002298	0.83
Y79AA1002307	F-Y79AA1002307	0.52
Y79AA1002311	F-Y79AA1002311	0.92
Y79AA1002351	F-Y79AA1002351	0.85
Y79AA1002361	F-Y79AA1002361	0.90
Y79AA1002399	F-Y79AA1002399	0.94
Y79AA1002407	F-Y79AA1002407	0.83
Y79AA1002416	F-Y79AA1002416	0.77
Y79AA1002431	F-Y79AA1002431	0.61
Y79AA1002433	F-Y79AA1002433	0.81
Y79AA1002472	F-Y79AA1002472	0.39
Y79AA1002482	F-Y79AA1002482	0.88
Y79AA1002487	F-Y79AA1002487	0.87

BNSDOCID: <EP___1074617A2_I_>

Table 10

Selected clones having the maximal ATGpr1 score of not more than 0.3 (1857 clones including the 9 clones whose 5'-end sequence does not contain the ATG codon. Blank of the maximal ATGpr1 score indicates that clones whose 5'-end sequence does not contain the ATG codon).

BNSDOCID: <EP___1074617A2_I_>

clone name	name of sequence	maximal ATGpr1 score
HEMBA1000042	F-HEMBA1000042	0.08
HEMBA1000111	F-HEMBA1000111	0.1
HEMBA1000180	F-HEMBA1000180	0.09
HEMBA1000213	F-HEMBA1000213	0.21
HEMBA1000243	F-HEMBA1000243	0.1
HEMBA1000251	F-HEMBA1000251	0.08
HEMBA1000264	F-HEMBA1000264	0.08
HEMBA1000280	F-HEMBA1000280	0.13
HEMBA1000282	F-HEMBA1000282	0.1
HEMBA1000333	F-HEMBA1000333	0.17
HEMBA1000338	F-HEMBA1000338	0.16
HEMBA1000351	F-HEMBA1000351	0.17
HEMBA1000355	F-HEMBA1000355	0.11
HEMBA1000357	F-HEMBA1000357	0.08
HEMBA1000366	F-HEMBA1000366	0.11
HEMBA1000376	F-HEMBA1000376	0.1
HEMBA1000390	F-HEMBA1000390	0.11
HEMBA1000411	F-HEMBA1000411	0.07
HEMBA1000418	F-HEMBA1000418	0.06
HEMBA1000422	F-HEMBA1000422	0.07
HEMBA1000428	F-HEMBA1000428	0.08
HEMBA1000434	F-HEMBA1000434	0.11
HEMBA1000442	F-HEMBA1000442	0.1
HEMBA1000459	F-HEMBA1000459	0.08
HEMBA1000464	F-HEMBA1000464	0.12
HEMBA1000469	F-HEMBA1000469	0.07
HEMBA1000504	F-HEMBA1000504	0.1
HEMBA1000518	F-HEMBA1000518	0.23
HEMBA1000519	F-HEMBA1000519	0.3
HEMBA1000540	F-HEMBA1000540	0.06
HEMBA1000545	F-HEMBA1000545	0.18
HEMBA1000557	F-HEMBA1000557	0.19
HEMBA1000563	F-HEMBA1000563	0.17
HEMBA1000569	F-HEMBA1000569	0.12
HEMBA1000575	F-HEMBA1000575	0.14
HEMBA1000604	F-HEMBA1000604	0.1
HEMBA1000622	F-HEMBA1000622	0.08
HEMBA1000655	F-HEMBA1000655	0.19
HEMBA1000662	F-HEMBA1000662	0.15
HEMBA1000673	F-HEMBA1000673	0.08
HEMBA1000702	F-HEMBA1000702	0.12

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HEMBA1000705	F-HEMBA1000705	0.06
HEMBA1000722	F-HEMBA1000722	0.17
HEMBA1000726	F-HEMBA1000726	0.08
HEMBA1000747	F-HEMBA1000747	0.06
HEMBA1000749	F-HEMBA1000749	0.09
HEMBA1000769	F-HEMBA1000769	0.19
HEMBA1000773	F-HEMBA1000773	0.08
HEMBA1000774	F-HEMBA1000774	0.17
HEMBA1000791	F-HEMBA1000791	0.08
HEMBA1000822	F-HEMBA1000822	0.19
HEMBA1000827	F-HEMBA1000827	0.09
HEMBA1000843	F-HEMBA1000843	0.12
HEMBA1000852	F-HEMBA1000852	0.16
HEMBA1000870	F-HEMBA1000870	0.14
HEMBA1000876	F-HEMBA1000876	0.15
HEMBA1000908	F-HEMBA1000908	0.17
HEMBA1000934	F-HEMBA1000934	0.2
HEMBA1000943	F-HEMBA1000943	0.08
HEMBA1000960	F-HEMBA1000960	0.09
HEMBA1000972	F-HEMBA1000972	0.12
HEMBA1000974	F-HEMBA1000974	0.08
HEMBA1000985	F-HEMBA1000985	0.06
HEMBA1000991	F-HEMBA1000991	0.23
HEMBA1001007	F-HEMBA1001007	0.06
HEMBA1001017	F-HEMBA1001017	0.06
HEMBA1001019	F-HEMBA1001019	0.08
HEMBA1001020	F-HEMBA1001020	0.15
HEMBA1001024	F-HEMBA1001024	0.1
HEMBA1001026	F-HEMBA1001026	0.13
HEMBA1001051	F-HEMBA1001051	0.27
HEMBA1001060	F-HEMBA1001060	0.11
HEMBA1001071	F-HEMBA1001071	0.1
HEMBA1001077	F-HEMBA1001077	0.07
HEMBA1001094	F-HEMBA1001094	0.07
HEMBA1001099	F-HEMBA1001099	0.08
HEMBA1001121	F-HEMBA1001121	0.25
HEMBA1001123	F-HEMBA1001123	0.05
HEMBA1001172	F-HEMBA1001172	0.08
HEMBA1001208	F-HEMBA1001208	0.11
HEMBA1001226	F-HEMBA1001226	0.27
HEMBA1001265	F-HEMBA1001265	0.06
HEMBA1001294	F-HEMBA1001294	0.12
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HEMBA1001323	F-HEMBA1001323	0.07
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HEMBA1001383	F-HEMBA1001383	0.11
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HEMBA1002321	F-HEMBA1002321	0. 07
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HEMBA1002748	F-HEMBA1002748	0.17
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HEMBA1002826	F-HEMBA1002826	0.1
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HEMBA1002924	F-HEMBA1002924	0.12
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HEMBA1002968	F-HEMBA1002968	0.12
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HEMBA1003037	F-HEMBA1003037	0.11
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HEMBA1003083	F-HEMBA1003083	0.18
HEMBA1003086	F-HEMBA1003086	0.06
HEMBA1003098	F-HEMBA1003098	0.09
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HEMBA1003276	F-HEMBA1003276	0.12
HEMBA1003278	F-HEMBA1003278	0.09
HEMBA1003296	F-HEMBA1003296	0.07
HEMBA1003304	F-HEMBA1003304	0.09
HEMBA1003309	F-HEMBA1003309	0.07
HEMBA1003314	F-HEMBA1003314	0.21
HEMBA1003328	F-HEMBA1003328	0.13
HEMBA1003330	F-HEMBA1003330	0.08
HEMBA1003348	F-HEMBA1003348	0.17
HEMBA1003373	F-HEMBA1003373	0.21

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HEMBA1003531	F-HEMBA1003531	0.2
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HEMBA1003773	F-HEMBA1003773	0.11
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HEMBA1003885	F-HEMBA1003885	0.09
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HEMBA1003939	F-HEMBA1003939	0.12
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HEMBA1003950	F-HEMBA1003950	0.09
HEMBA1003958	F-HEMBA1003958	0.07
HEMBA1003976	F-HEMBA1003976	0.28
HEMBA1003987	F-HEMBA1003987	0.24
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HEMBA1004042	F-HEMBA1004042	0.09
HEMBA1004045	F-HEMBA1004045	0.09
HEMBA1004049	F-HEMBA1004049	0.09
HEMBA1004132	F-HEMBA1004132	0.08
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HEMBA1004164	F-HEMBA1004164	0.08
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HEMBA1004272	F-HEMBA1004272	0.09
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HEMBA1004306	F-HEMBA1004306	0.07
HEMBA1004312	F-HEMBA1004312	0.26
HEMBA1004323	F-HEMBA1004323	0.13
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HEMBA1004354	F-HEMBA1004354	0.1
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HEMBA1004366	F-HEMBA1004366	0.14
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HEMBA1004396	F-HEMBA1004396	0.05
HEMBA1004405	F-HEMBA1004405	0.17
HEMBA1004429	F-HEMBA1004429	0.22
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HEMBA1004538	F-HEMBA1004538	0.15
HEMBA1004577	F-HEMBA1004577	0.17
HEMBA1004586	F-HEMBA1004586	0.06
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HEMBA1004670	F-HEMBA1004670	0.15
HEMBA1004672	F-HEMBA1004672	0.14
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HEMBA1004733	F-HEMBA1004733	0.12
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HEMBA1004770	F-HEMBA1004770	0.15
HEMBA1004778	F-HEMBA1004778	0.14
HEMBA1004803	F-HEMBA1004803	0.13
HEMBA1004807	F-HEMBA1004807	0.18
HEMBA1004816	F-HEMBA1004816	0.06
HEMBA1004820	F-HEMBA1004820	0.11
HEMBA1004865	F-HEMBA1004865	0.17
HEMBA1004880	F-HEMBA1004880	0.28
HEMBA1004900	F-HEMBA1004900	0.11
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HEMBA1004956	F-HEMBA1004956	0.05
HEMBA1004960	F-HEMBA1004960	0.21
HEMBA1004978	F-HEMBA1004978	0.1
HEMBA1004983	F-HEMBA1004983	0.28

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HEMBA1005008	F-HEMBA1005008	0. 07
HEMBA1005039	F-HEMBA1005039	0. 08
HEMBA1005062	F-HEMBA1005062	0. 11
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HEMBA1005241	F-HEMBA1005241	0. 14
HEMBA1005251	F-HEMBA1005251	0. 29
HEMBA1005274	F-HEMBA1005274	0. 06
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HEMBA1005304	F-HEMBA1005304	0. 09
HEMBA1005311	F-HEMBA1005311	0. 2
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HEMBA1005318	F-HEMBA1005318	0. 08
HEMBA1005353	F-HEMBA1005353	0. 12
HEMBA1005359	F-HEMBA1005359	0. 15
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HEMBA1005443	F-HEMBA1005443	0. 17
HEMBA1005447	F-HEMBA1005447	0. 25
HEMBA1005497	F-HEMBA1005497	0. 09
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HEMBA1005588	F-HEMBA1005588	0. 25
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HEMBA1005606	F-HEMBA1005606	0. 16
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HEMBA1005627	F-HEMBA1005627	0. 11
HEMBA1005631	F-HEMBA1005631	0. 07
HEMBA1005632	F-HEMBA1005632	0. 07
HEMBA1005634	F-HEMBA1005634	0. 07
HEMBA1005670	F-HEMBA1005670	0. 11

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HEMBA1005705	F-HEMBA1005705	0.08
HEMBA1005717	F-HEMBA1005717	0.17
HEMBA1005765	F-HEMBA1005765	0.08
HEMBA1005780	F-HEMBA1005780	0.16
HEMBA1005829	F-HEMBA1005829	0.09
HEMBA1005853	F-HEMBA1005853	0.06
HEMBA1005894	F-HEMBA1005894	0.16
HEMBA1005909	F-HEMBA1005909	0.13
HEMBA1005911	F-HEMBA1005911	0.22
HEMBA1005921	F-HEMBA1005921	0.1
HEMBA1005931	F-HEMBA1005931	0.16
HEMBA1005934	F-HEMBA1005934	0.1
HEMBA1005962	F-HEMBA1005962	0.07
HEMBA1005999	F-HEMBA1005999	0.14
HEMBA1006002	F-HEMBA1006002	0.09
HEMBA1006005	F-HEMBA1006005	0.2
HEMBA1006036	F-HEMBA1006036	0.24
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HEMBA1006090	F-HEMBA1006090	0.09
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HEMBA1006142	F-HEMBA1006142	0.13
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HEMBA1006253	F-HEMBA1006253	0.29
HEMBA1006259	F-HEMBA1006259	0.11
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HEMBA1006328	F-HEMBA1006328	0.06
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HEMBA1006359	F-HEMBA1006359	0.22
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HEMBA1006416	F-HEMBA1006416	0.25
HEMBA1006419	F-HEMBA1006419	0.08
HEMBA1006421	F-HEMBA1006421	0.26
HEMBA1006426	F-HEMBA1006426	0.17
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HEMBA1006446	F-HEMBA1006446	0.11
HEMBA1006461	F-HEMBA1006461	0.15
HEMBA1006471	F-HEMBA1006471	0.06
HEMBA1006486	F-HEMBA1006486	0.11
HEMBA1006489	F-HEMBA1006489	0.09
HEMBA1006540	F-HEMBA1006540	0.23
HEMBA1006546	F-HEMBA1006546	0.07
HEMBA1006562	F-HEMBA1006562	0.12

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HEMBA1006595	F-HEMBA1006595	0.08
HEMBA1006597	F-HEMBA1006597	0.17
HEMBA1006617	F-HEMBA1006617	0.07
HEMBA1006635	F-HEMBA1006635	0.07
HEMBA1006639	F-HEMBA1006639	0.25
HEMBA1006648	F-HEMBA1006648	0.24
HEMBA1006653	F-HEMBA1006653	0.09
HEMBA1006665	F-HEMBA1006665	0.17
HEMBA1006676	F-HEMBA1006676	0.17
HEMBA1006695	F-HEMBA1006695	0.1
HEMBA1006696	F-HEMBA1006696	0.05
HEMBA1006744	F-HEMBA1006744	0.12
HEMBA1006779	F-HEMBA1006779	0.07
HEMBA1006780	F-HEMBA1006780	0.23
HEMBA1006821	F-HEMBA1006821	0.08
HEMBA1006824	F-HEMBA1006824	0.09
HEMBA1006849	F-HEMBA1006849	0.05
HEMBA1006865	F-HEMBA1006865	0.1
HEMBA1006921	F-HEMBA1006921	0.22
HEMBA1006929	F-HEMBA1006929	0.15
HEMBA1006938	F-HEMBA1006938	0.07
HEMBA1006949	F-HEMBA1006949	0.27
HEMBA1007017	F-HEMBA1007017	0.07
HEMBA1007045	F-HEMBA1007045	0.14
HEMBA1007051	F-HEMBA1007051	0.19
HEMBA1007073	F-HEMBA1007073	0.22
HEMBA1007078	F-HEMBA1007078	0.12
HEMBA1007113	F-HEMBA1007113	0.12
HEMBA1007129	F-HEMBA1007129	0.18
HEMBA1007147	F-HEMBA1007147	0.08
HEMBA1007206	F-HEMBA1007206	0.11
HEMBA1007256	F-HEMBA1007256	0.13
HEMBA1007273	F-HEMBA1007273	0.05
HEMBA1007279	F-HEMBA1007279	0.09
HEMBA1007288	F-HEMBA1007288	0.06
HEMBA1007322	F-HEMBA1007322	0.12
HEMBA1007327	F-HEMBA1007327	0.12
HEMBA1007341	F-HEMBA1007341	0.1
HEMBA1007347	F-HEMBA1007347	0.14
HEMBB1000005	F-HEMBB1000005	0.13
HEMBB1000039	F-HEMBB1000039	0.07
HEMBB1000044	F-HEMBB1000044	0.08
HEMBB1000050	F-HEMBB1000050	0.07
HEMBB1000054	F-HEMBB1000054	0.12
HEMBB1000055	F-HEMBB1000055	0.2

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HEMBB1000089	F-HEMBB1000089	0.09
HEMBB1000099	F-HEMBB1000099	0.17
HEMBB1000113	F-HEMBB1000113	0.12
HEMBB1000141	F-HEMBB1000141	0.13
HEMBB1000144	F-HEMBB1000144	0.2
HEMBB1000218	F-HEMBB1000218	0.07
HEMBB1000250	F-HEMBB1000250	0.26
HEMBB1000258	F-HEMBB1000258	0.15
HEMBB1000264	F-HEMBB1000264	0.08
HEMBB1000272	F-HEMBB1000272	0.11
HEMBB1000274	F-HEMBB1000274	0.12
HEMBB1000284	F-HEMBB1000284	0.1
HEMBB1000307	F-HEMBB1000307	0.11
HEMBB1000312	F-HEMBB1000312	0.07
HEMBB1000317	F-HEMBB1000317	0.27
HEMBB1000318	F-HEMBB1000318	0.11
HEMBB1000335	F-HEMBB1000335	0.15
HEMBB1000336	F-HEMBB1000336	0.28
HEMBB1000337	F-HEMBB1000337	0.25
HEMBB1000341	F-HEMBB1000341	0.24
HEMBB1000343	F-HEMBB1000343	0.07
HEMBB1000354	F-HEMBB1000354	0.15
HEMBB1000369	F-HEMBB1000369	0.08
HEMBB1000374	F-HEMBB1000374	0.3
HEMBB1000376	F-HEMBB1000376	0.12
HEMBB1000399	F-HEMBB1000399	0.08
HEMBB1000402	F-HEMBB1000402	0.29
HEMBB1000404	F-HEMBB1000404	0.29
HEMBB1000420	F-HEMBB1000420	0.11
HEMBB1000434	F-HEMBB1000434	0.05
HEMBB1000441	F-HEMBB1000441	0.12
HEMBB1000455	F-HEMBB1000455	0.05
HEMBB1000472	F-HEMBB1000472	0.05
HEMBB1000480	F-HEMBB1000480	0.13
HEMBB1000487	F-HEMBB1000487	0.09
HEMBB1000490	F-HEMBB1000490	0.06
HEMBB1000491	F-HEMBB1000491	0.16
HEMBB1000493	F-HEMBB1000493	0.15
HEMBB1000518	F-HEMBB1000518	0.05
HEMBB1000523	F-HEMBB1000523	0.07
HEMBB1000530	F-HEMBB1000530	0.14
HEMBB1000554	F-HEMBB1000554	0.23
HEMBB1000564	F-HEMBB1000564	0.09
HEMBB1000573	F-HEMBB1000573	0.1
HEMBB1000575	F-HEMBB1000575	0.08

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HEMBB1000586	F-HEMBB1000586	0.12
HEMBB1000598	F-HEMBB1000598	0.12
HEMBB1000637	F-HEMBB1000637	0.19
HEMBB1000638	F-HEMBB1000638	0.07
HEMBB1000643	F-HEMBB1000643	0.07
HEMBB1000649	F-HEMBB1000649	0.13
HEMBB1000652	F-HEMBB1000652	0.2
HEMBB1000665	F-HEMBB1000665	0.07
HEMBB1000684	F-HEMBB1000684	0.06
HEMBB1000709	F-HEMBB1000709	0.09
HEMBB1000726	F-HEMBB1000726	0.07
HEMBB1000738	F-HEMBB1000738	0.19
HEMBB1000749	F-HEMBB1000749	0.14
HEMBB1000770	F-HEMBB1000770	0.09
HEMBB1000790	F-HEMBB1000790	0.23
HEMBB1000794	F-HEMBB1000794	0.09
HEMBB1000821	F-HEMBB1000821	0.1
HEMBB1000822	F-HEMBB1000822	0.18
HEMBB1000827	F-HEMBB1000827	0.1
HEMBB1000831	F-HEMBB1000831	0.2
HEMBB1000840	F-HEMBB1000840	0.09
HEMBB1000876	F-HEMBB1000876	0.12
HEMBB1000883	F-HEMBB1000883	0.13
HEMBB1000888	F-HEMBB1000888	0.1
HEMBB1000890	F-HEMBB1000890	0.09
HEMBB1000893	F-HEMBB1000893	0.1
HEMBB1000910	F-HEMBB1000910	0.06
HEMBB1000913	F-HEMBB1000913	0.09
HEMBB1000915	F-HEMBB1000915	0.12
HEMBB1000917	F-HEMBB1000917	0.15
HEMBB1000959	F-HEMBB1000959	0.08
HEMBB1000981	F-HEMBB1000981	0.09
HEMBB1000996	F-HEMBB1000996	0.1
HEMBB1001004	F-HEMBB1001004	0.08
HEMBB1001008	F-HEMBB1001008	0.25
HEMBB1001037	F-HEMBB1001037	0.14
HEMBB1001047	F-HEMBB1001047	0.14
HEMBB1001051	F-HEMBB1001051	0.13
HEMBB1001060	F-HEMBB1001060	0.16
HEMBB1001063	F-HEMBB1001063	0.1
HEMBB1001102	F-HEMBB1001102	0.19
HEMBB1001114	F-HEMBB1001114	0.08
HEMBB1001119	F-HEMBB1001119	0.13
HEMBB1001133	F-HEMBB1001133	0.06
HEMBB1001142	F-HEMBB1001142	0.17
HEMBB1001177	F-HEMBB1001177	0.2

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HEMBB1001208	F-HEMBB1001208	0. 12
HEMBB1001209	F-HEMBB1001209	0. 11
HEMBB1001218	F-HEMBB1001218	0. 1
HEMBB1001221	F-HEMBB1001221	0. 1
HEMBB1001249	F-HEMBB1001249	0. 12
HEMBB1001253	F-HEMBB1001253	0. 13
HEMBB1001254	F-HEMBB1001254	0. 13
HEMBB1001267	F-HEMBB1001267	0. 09
HEMBB1001271	F-HEMBB1001271	0. 16
HEMBB1001282	F-HEMBB1001282	0. 14
HEMBB1001302	F-HEMBB1001302	0. 18
HEMBB1001304	F-HEMBB1001304	0. 17
HEMBB1001315	F-HEMBB1001315	0. 18
HEMBB1001317	F-HEMBB1001317	0. 12
HEMBB1001326	F-HEMBB1001326	0. 09
HEMBB1001335	F-HEMBB1001335	0. 08
HEMBB1001337	F-HEMBB1001337	0. 12
HEMBB1001348	F-HEMBB1001348	0. 11
HEMBB1001356	F-HEMBB1001356	0. 1
HEMBB1001366	F-HEMBB1001366	0. 16
HEMBB1001367	F-HEMBB1001367	0. 11
HEMBB1001380	F-HEMBB1001380	0. 07
HEMBB1001424	F-HEMBB1001424	0. 05
HEMBB1001436	F-HEMBB1001436	0. 14
HEMBB1001443	F-HEMBB1001443	0. 28
HEMBB1001454	F-HEMBB1001454	
HEMBB1001458	F-HEMBB1001458	0. 11
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HEMBB1001464	F-HEMBB1001464	0. 06
HEMBB1001500	F-HEMBB1001500	0. 11
HEMBB1001521	F-HEMBB1001521	0. 13
HEMBB1001527	F-HEMBB1001527	0. 13
HEMBB1001535	F-HEMBB1001535	0. 11
HEMBB1001536	F-HEMBB1001536	0. 08
HEMBB1001537	F-HEMBB1001537	0. 11
HEMBB1001555	F-HEMBB1001555	0. 08
HEMBB1001565	F-HEMBB1001565	0. 1
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HEMBB1001588	F-HEMBB1001588	0. 06
HEMBB1001618	F-HEMBB1001618	0. 09
HEMBB1001619	F-HEMBB1001619	0. 12
HEMBB1001630	F-HEMBB1001630	0. 12
HEMBB1001637	F-HEMBB1001637	0. 08
HEMBB1001641	F-HEMBB1001641	0. 09
HEMBB1001704	F-HEMBB1001704	0. 09
HEMBB1001706	F-HEMBB1001706	0. 11

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HEMBB1001735	F-HEMBB1001735	0.21
HEMBB1001747	F-HEMBB1001747	0.07
HEMBB1001749	F-HEMBB1001749	0.13
HEMBB1001753	F-HEMBB1001753	0.08
HEMBB1001756	F-HEMBB1001756	0.11
HEMBB1001762	F-HEMBB1001762	0.11
HEMBB1001797	F-HEMBB1001797	0.13
HEMBB1001802	F-HEMBB1001802	0.06
HEMBB1001836	F-HEMBB1001836	0.15
HEMBB1001850	F-HEMBB1001850	0.06
HEMBB1001863	F-HEMBB1001863	0.09
HEMBB1001867	F-HEMBB1001867	0.11
HEMBB1001868	F-HEMBB1001868	0.24
HEMBB1001875	F-HEMBB1001875	0.05
HEMBB1001880	F-HEMBB1001880	0.08
HEMBB1001899	F-HEMBB1001899	0.16
HEMBB1001911	F-HEMBB1001911	0.22
HEMBB1001921	F-HEMBB1001921	0.07
HEMBB1001922	F-HEMBB1001922	0.11
HEMBB1001925	F-HEMBB1001925	0.19
HEMBB1001930	F-HEMBB1001930	0.1
HEMBB1001944	F-HEMBB1001944	0.14
HEMBB1001952	F-HEMBB1001952	0.08
HEMBB1001953	F-HEMBB1001953	0.15
HEMBB1001967	F-HEMBB1001967	0.08
HEMBB1001973	F-HEMBB1001973	0.09
HEMBB1001983	F-HEMBB1001983	0.1
HEMBB1001988	F-HEMBB1001988	0.15
HEMBB1001996	F-HEMBB1001996	0.19
HEMBB1001997	F-HEMBB1001997	0.08
HEMBB1002002	F-HEMBB1002002	0.21
HEMBB1002005	F-HEMBB1002005	0.18
HEMBB1002009	F-HEMBB1002009	0.09
HEMBB1002015	F-HEMBB1002015	0.26
HEMBB1002042	F-HEMBB1002042	0.11
HEMBB1002043	F-HEMBB1002043	0.09
HEMBB1002045	F-HEMBB1002045	0.26
HEMBB1002049	F-HEMBB1002049	0.12
HEMBB1002069	F-HEMBB1002069	0.12
HEMBB1002092	F-HEMBB1002092	0.16
HEMBB1002094	F-HEMBB1002094	0.11
HEMBB1002115	F-HEMBB1002115	0.09
HEMBB1002139	F-HEMBB1002139	0.13
HEMBB1002189	F-HEMBB1002189	0.06
HEMBB1002190	F-HEMBB1002190	0.18

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HEMBB1002232	F-HEMBB1002232	0. 09
HEMBB1002247	F-HEMBB1002247	0. 17
HEMBB1002254	F-HEMBB1002254	0. 05
HEMBB1002255	F-HEMBB1002255	0. 11
HEMBB1002266	F-HEMBB1002266	0. 28
HEMBB1002280	F-HEMBB1002280	0. 07
HEMBB1002306	F-HEMBB1002306	0. 06
HEMBB1002364	F-HEMBB1002364	0. 05
HEMBB1002371	F-HEMBB1002371	0. 12
HEMBB1002381	F-HEMBB1002381	0. 09
HEMBB1002387	F-HEMBB1002387	0. 17
HEMBB1002425	F-HEMBB1002425	0. 08
HEMBB1002453	F-HEMBB1002453	0. 12
HEMBB1002458	F-HEMBB1002458	0. 09
HEMBB1002477	F-HEMBB1002477	0. 17
HEMBB1002509	F-HEMBB1002509	0. 06
HEMBB1002520	F-HEMBB1002520	0. 08
HEMBB1002522	F-HEMBB1002522	0. 21
HEMBB1002531	F-HEMBB1002531	0. 1
HEMBB1002534	F-HEMBB1002534	0. 09
HEMBB1002556	F-HEMBB1002556	0. 1
HEMBB1002579	F-HEMBB1002579	0. 13
HEMBB1002582	F-HEMBB1002582	0. 17
HEMBB1002590	F-HEMBB1002590	0. 08
HEMBB1002596	F-HEMBB1002596	0. 15
HEMBB1002601	F-HEMBB1002601	0. 1
HEMBB1002603	F-HEMBB1002603	0. 12
HEMBB1002610	F-HEMBB1002610	0. 1
HEMBB1002613	F-HEMBB1002613	0. 09
HEMBB1002617	F-HEMBB1002617	0. 12
HEMBB1002623	F-HEMBB1002623	0. 14
HEMBB1002635	F-HEMBB1002635	0. 08
HEMBB1002664	F-HEMBB1002664	0. 06
HEMBB1002677	F-HEMBB1002677	0. 07
HEMBB1002683	F-HEMBB1002683	0. 06
HEMBB1002686	F-HEMBB1002686	0. 12
HEMBB1002699	F-HEMBB1002699	0. 15
HEMBB1002702	F-HEMBB1002702	0. 16
HEMBB1002712	F-HEMBB1002712	0. 07
MAMMA1000009	F-MAMMA1000009	0. 11
MAMMA1000043	F-MAMMA1000043	0. 19
MAMMA1000045	F-MAMMA1000045	0. 08
MAMMA1000092	F-MAMMA1000092	0. 11
MAMMA1000103	F-MAMMA1000103	0. 09
MAMMA1000117	F-MAMMA1000117	0. 2
MAMMA1000129	F-MAMMA1000129	0. 17

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MAMMA1000133	F-MAMMA1000133	0. 1
MAMMA1000134	F-MAMMA1000134	0. 05
MAMMA1000155	F-MAMMA1000155	0. 12
MAMMA1000175	F-MAMMA1000175	0. 07
MAMMA1000198	F-MAMMA1000198	0. 2
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MAMMA1000227	F-MAMMA1000227	0. 08
MAMMA1000241	F-MAMMA1000241	0. 16
MAMMA1000254	F-MAMMA1000254	0. 08
MAMMA1000264	F-MAMMA1000264	0. 1
MAMMA1000266	F-MAMMA1000266	0. 18
MAMMA1000270	F-MAMMA1000270	0. 1
MAMMA1000287	F-MAMMA1000287	0. 1
MAMMA1000302	F-MAMMA1000302	0. 07
MAMMA1000307	F-MAMMA1000307	0. 26
MAMMA1000331	F-MAMMA1000331	0. 18
MAMMA1000340	F-MAMMA1000340	0. 2
MAMMA1000348	F-MAMMA1000348	0. 09
MAMMA1000356	F-MAMMA1000356	0. 15
MAMMA1000360	F-MAMMA1000360	0. 09
MAMMA1000385	F-MAMMA1000385	0. 08
MAMMA1000402	F-MAMMA1000402	0. 11
MAMMA1000413	F-MAMMA1000413	0. 1
MAMMA1000414	F-MAMMA1000414	0. 1
MAMMA1000423	F-MAMMA1000423	0. 06
MAMMA1000424	F-MAMMA1000424	0. 1
MAMMA1000431	F-MAMMA1000431	0. 28
MAMMA1000444	F-MAMMA1000444	0. 07
MAMMA1000446	F-MAMMA1000446	0. 08
MAMMA1000478	F-MAMMA1000478	0. 1
MAMMA1000483	F-MAMMA1000483	0. 07
MAMMA1000500	F-MAMMA1000500	0. 16
MAMMA1000501	F-MAMMA1000501	0. 05
MAMMA1000516	F-MAMMA1000516	0. 06
MAMMA1000522	F-MAMMA1000522	0. 21
MAMMA1000559	F-MAMMA1000559	0. 12
MAMMA1000565	F-MAMMA1000565	0. 09
MAMMA1000576	F-MAMMA1000576	0. 14
MAMMA1000585	F-MAMMA1000585	0. 07
MAMMA1000594	F-MAMMA1000594	0. 17
MAMMA1000597	F-MAMMA1000597	0. 1
MAMMA1000605	F-MAMMA1000605	0. 09
MAMMA1000616	F-MAMMA1000616	0. 08
MAMMA1000621	F-MAMMA1000621	0. 07
MAMMA1000643	F-MAMMA1000643	0. 1
MAMMA1000669	F-MAMMA1000669	0. 11

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MAMMA1000696	F-MAMMA1000696	0.08
MAMMA1000707	F-MAMMA1000707	0.07
MAMMA1000714	F-MAMMA1000714	0.18
MAMMA1000718	F-MAMMA1000718	0.06
MAMMA1000720	F-MAMMA1000720	0.15
MAMMA1000723	F-MAMMA1000723	0.14
MAMMA1000732	F-MAMMA1000732	0.06
MAMMA1000733	F-MAMMA1000733	0.1
MAMMA1000744	F-MAMMA1000744	0.15
MAMMA1000752	F-MAMMA1000752	0.12
MAMMA1000761	F-MAMMA1000761	0.24
MAMMA1000775	F-MAMMA1000775	0.24
MAMMA1000778	F-MAMMA1000778	0.09
MAMMA1000782	F-MAMMA1000782	0.1
MAMMA1000798	F-MAMMA1000798	0.16
MAMMA1000802	F-MAMMA1000802	0.11
MAMMA1000839	F-MAMMA1000839	0.09
MAMMA1000845	F-MAMMA1000845	0.1
MAMMA1000851	F-MAMMA1000851	0.08
MAMMA1000855	F-MAMMA1000855	0.23
MAMMA1000862	F-MAMMA1000862	0.12
MAMMA1000863	F-MAMMA1000863	0.16
MAMMA1000867	F-MAMMA1000867	0.25
MAMMA1000876	F-MAMMA1000876	0.14
MAMMA1000877	F-MAMMA1000877	0.07
MAMMA1000880	F-MAMMA1000880	0.13
MAMMA1000883	F-MAMMA1000883	0.3
MAMMA1000905	F-MAMMA1000905	0.08
MAMMA1000931	F-MAMMA1000931	0.18
MAMMA1000940	F-MAMMA1000940	0.21
MAMMA1000941	F-MAMMA1000941	0.13
MAMMA1000942	F-MAMMA1000942	0.08
MAMMA1000943	F-MAMMA1000943	0.09
MAMMA1000957	F-MAMMA1000957	0.13
MAMMA1000962	F-MAMMA1000962	0.06
MAMMA1000975	F-MAMMA1000975	0.26
MAMMA1000987	F-MAMMA1000987	0.08
MAMMA1000998	F-MAMMA1000998	0.08
MAMMA1001003	F-MAMMA1001003	0.15
MAMMA1001024	F-MAMMA1001024	0.08
MAMMA1001030	F-MAMMA1001030	0.2
MAMMA1001035	F-MAMMA1001035	0.08
MAMMA1001038	F-MAMMA1001038	0.15
MAMMA1001050	F-MAMMA1001050	0.06
MAMMA1001067	F-MAMMA1001067	0.08
MAMMA1001074	F-MAMMA1001074	0.09

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MAMMA1001133	F-MAMMA1001133	0. 11
MAMMA1001145	F-MAMMA1001145	0. 05
MAMMA1001161	F-MAMMA1001161	0. 11
MAMMA1001162	F-MAMMA1001162	0. 11
MAMMA1001186	F-MAMMA1001186	0. 09
MAMMA1001191	F-MAMMA1001191	0. 08
MAMMA1001203	F-MAMMA1001203	0. 08
MAMMA1001206	F-MAMMA1001206	0. 09
MAMMA1001220	F-MAMMA1001220	0. 1
MAMMA1001243	F-MAMMA1001243	0. 14
MAMMA1001249	F-MAMMA1001249	0. 13
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MAMMA1001268	F-MAMMA1001268	0. 26
MAMMA1001274	F-MAMMA1001274	0. 13
MAMMA1001280	F-MAMMA1001280	0. 1
MAMMA1001298	F-MAMMA1001298	0. 07
MAMMA1001322	F-MAMMA1001322	0. 18
MAMMA1001324	F-MAMMA1001324	0. 25
MAMMA1001330	F-MAMMA1001330	0. 13
MAMMA1001341	F-MAMMA1001341	0. 16
MAMMA1001383	F-MAMMA1001383	0. 05
MAMMA1001397	F-MAMMA1001397	0. 22
MAMMA1001408	F-MAMMA1001408	0. 06
MAMMA1001420	F-MAMMA1001420	0. 1
MAMMA1001435	F-MAMMA1001435	0. 07
MAMMA1001442	F-MAMMA1001442	0. 13
MAMMA1001446	F-MAMMA1001446	0. 08
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MAMMA1001501	F-MAMMA1001501	0. 12
MAMMA1001502	F-MAMMA1001502	0. 09
MAMMA1001547	F-MAMMA1001547	0. 22
MAMMA1001575	F-MAMMA1001575	0. 08
MAMMA1001590	F-MAMMA1001590	0. 14
MAMMA1001606	F-MAMMA1001606	0. 13
MAMMA1001663	F-MAMMA1001663	0. 11
MAMMA1001670	F-MAMMA1001670	0. 2
MAMMA1001671	F-MAMMA1001671	0. 13
MAMMA1001679	F-MAMMA1001679	0. 13
MAMMA1001683	F-MAMMA1001683	0. 16
MAMMA1001686	F-MAMMA1001686	0. 09
MAMMA1001711	F-MAMMA1001711	0. 11
MAMMA1001715	F-MAMMA1001715	0. 11
MAMMA1001740	F-MAMMA1001740	0. 1
MAMMA1001745	F-MAMMA1001745	0. 09

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MAMMA1001760	F-MAMMA1001760	0. 16
MAMMA1001769	F-MAMMA1001769	0. 09
MAMMA1001788	F-MAMMA1001788	0. 1
MAMMA1001806	F-MAMMA1001806	0. 06
MAMMA1001815	F-MAMMA1001815	0. 1
MAMMA1001818	F-MAMMA1001818	0. 1
MAMMA1001820	F-MAMMA1001820	0. 27
MAMMA1001836	F-MAMMA1001836	0. 05
MAMMA1001854	F-MAMMA1001854	0. 17
MAMMA1001878	F-MAMMA1001878	0. 13
MAMMA1001880	F-MAMMA1001880	0. 15
MAMMA1001890	F-MAMMA1001890	0. 05
MAMMA1001907	F-MAMMA1001907	0. 1
MAMMA1001908	F-MAMMA1001908	0. 3
MAMMA1001931	F-MAMMA1001931	0. 14
MAMMA1001963	F-MAMMA1001963	0. 08
MAMMA1001992	F-MAMMA1001992	0. 12
MAMMA1002032	F-MAMMA1002032	0. 08
MAMMA1002056	F-MAMMA1002056	0. 09
MAMMA1002058	F-MAMMA1002058	0. 16
MAMMA1002078	F-MAMMA1002078	0. 28
MAMMA1002082	F-MAMMA1002082	0. 08
MAMMA1002084	F-MAMMA1002084	0. 24
MAMMA1002093	F-MAMMA1002093	0. 12
MAMMA1002108	F-MAMMA1002108	0. 05
MAMMA1002118	F-MAMMA1002118	0. 1
MAMMA1002125	F-MAMMA1002125	0. 09
MAMMA1002132	F-MAMMA1002132	0. 11
MAMMA1002140	F-MAMMA1002140	0. 11
MAMMA1002145	F-MAMMA1002145	0. 11
MAMMA1002155	F-MAMMA1002155	0. 1
MAMMA1002158	F-MAMMA1002158	0. 11
MAMMA1002215	F-MAMMA1002215	0. 05
MAMMA1002230	F-MAMMA1002230	0. 07
MAMMA1002250	F-MAMMA1002250	0. 2
MAMMA1002267	F-MAMMA1002267	0. 08
MAMMA1002282	F-MAMMA1002282	0. 05
MAMMA1002293	F-MAMMA1002293	0. 09
MAMMA1002298	F-MAMMA1002298	0. 09
MAMMA1002299	F-MAMMA1002299	0. 16
MAMMA1002310	F-MAMMA1002310	0. 16
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MAMMA1002322	F-MAMMA1002322	0. 07
MAMMA1002332	F-MAMMA1002332	0. 08
MAMMA1002339	F-MAMMA1002339	0. 09
MAMMA1002347	F-MAMMA1002347	0. 06

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MAMMA1002352	F-MAMMA1002352	0.08
MAMMA1002359	F-MAMMA1002359	0.13
MAMMA1002360	F-MAMMA1002360	0.17
MAMMA1002361	F-MAMMA1002361	0.13
MAMMA1002392	F-MAMMA1002392	0.16
MAMMA1002411	F-MAMMA1002411	0.28
MAMMA1002417	F-MAMMA1002417	0.19
MAMMA1002428	F-MAMMA1002428	0.07
MAMMA1002446	F-MAMMA1002446	0.17
MAMMA1002475	F-MAMMA1002475	0.17
MAMMA1002480	F-MAMMA1002480	0.07
MAMMA1002494	F-MAMMA1002494	0.17
MAMMA1002498	F-MAMMA1002498	0.28
MAMMA1002545	F-MAMMA1002545	0.12
MAMMA1002556	F-MAMMA1002556	0.06
MAMMA1002566	F-MAMMA1002566	0.13
MAMMA1002571	F-MAMMA1002571	0.29
MAMMA1002573	F-MAMMA1002573	0.29
MAMMA1002597	F-MAMMA1002597	0.1
MAMMA1002603	F-MAMMA1002603	0.1
MAMMA1002612	F-MAMMA1002612	0.14
MAMMA1002618	F-MAMMA1002618	0.11
MAMMA1002622	F-MAMMA1002622	0.24
MAMMA1002623	F-MAMMA1002623	0.1
MAMMA1002625	F-MAMMA1002625	0.11
MAMMA1002629	F-MAMMA1002629	0.05
MAMMA1002636	F-MAMMA1002636	0.12
MAMMA1002646	F-MAMMA1002646	0.05
MAMMA1002662	F-MAMMA1002662	0.09
MAMMA1002698	F-MAMMA1002698	0.08
MAMMA1002701	F-MAMMA1002701	0.11
MAMMA1002708	F-MAMMA1002708	0.09
MAMMA1002721	F-MAMMA1002721	0.06
MAMMA1002727	F-MAMMA1002727	0.15
MAMMA1002728	F-MAMMA1002728	0.12
MAMMA1002744	F-MAMMA1002744	0.08
MAMMA1002746	F-MAMMA1002746	0.09
MAMMA1002748	F-MAMMA1002748	0.1
MAMMA1002754	F-MAMMA1002754	0.07
MAMMA1002758	F-MAMMA1002758	0.29
MAMMA1002764	F-MAMMA1002764	0.2
MAMMA1002765	F-MAMMA1002765	0.29
MAMMA1002780	F-MAMMA1002780	0.12
MAMMA1002820	F-MAMMA1002820	0.3
MAMMA1002830	F-MAMMA1002830	0.16
MAMMA1002833	F-MAMMA1002833	0.14

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MAMMA1002835	F-MAMMA1002835	0. 13
MAMMA1002838	F-MAMMA1002838	0. 09
MAMMA1002844	F-MAMMA1002844	0. 27
MAMMA1002858	F-MAMMA1002858	0. 29
MAMMA1002871	F-MAMMA1002871	0. 11
MAMMA1002880	F-MAMMA1002880	0. 11
MAMMA1002887	F-MAMMA1002887	0. 09
MAMMA1002892	F-MAMMA1002892	0. 17
MAMMA1002908	F-MAMMA1002908	0. 11
MAMMA1002909	F-MAMMA1002909	0. 22
MAMMA1002930	F-MAMMA1002930	0. 2
MAMMA1002941	F-MAMMA1002941	0. 23
MAMMA1002970	F-MAMMA1002970	0. 06
MAMMA1002972	F-MAMMA1002972	0. 08
MAMMA1002973	F-MAMMA1002973	0. 1
MAMMA1002982	F-MAMMA1002982	0. 1
MAMMA1003003	F-MAMMA1003003	0. 2
MAMMA1003004	F-MAMMA1003004	0. 14
MAMMA1003007	F-MAMMA1003007	0. 09
MAMMA1003019	F-MAMMA1003019	0. 12
MAMMA1003026	F-MAMMA1003026	0. 26
MAMMA1003031	F-MAMMA1003031	0. 18
MAMMA1003039	F-MAMMA1003039	0. 09
MAMMA1003040	F-MAMMA1003040	0. 07
MAMMA1003055	F-MAMMA1003055	0. 08
MAMMA1003089	F-MAMMA1003089	0. 14
MAMMA1003140	F-MAMMA1003140	0. 19
NT2RM2000609	F-NT2RM2000609	0. 26
NT2RM4000046	F-NT2RM4000046	0. 1
NT2RM4000085	F-NT2RM4000085	0. 23
NT2RM4000086	F-NT2RM4000086	0. 28
NT2RM4000200	F-NT2RM4000200	0. 16
NT2RM4000244	F-NT2RM4000244	0. 07
NT2RM4000265	F-NT2RM4000265	0. 18
NT2RM4000327	F-NT2RM4000327	0. 06
NT2RM4000366	F-NT2RM4000366	0. 28
NT2RM4000368	F-NT2RM4000368	0. 11
NT2RM4000414	F-NT2RM4000414	0. 19
NT2RM4000425	F-NT2RM4000425	0. 22
NT2RM4000532	F-NT2RM4000532	0. 14
NT2RM4000779	F-NT2RM4000779	0. 13
NT2RM4000855	F-NT2RM4000855	0. 13
NT2RM4000979	F-NT2RM4000979	0. 22
NT2RM4001016	F-NT2RM4001016	0. 2
NT2RM4001160	F-NT2RM4001160	0. 1
NT2RM4001313	F-NT2RM4001313	0. 26

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NT2RM4001414	F-NT2RM4001414	0.23
NT2RM4001437	F-NT2RM4001437	0.12
NT2RM4001519	F-NT2RM4001519	0.07
NT2RM4001557	F-NT2RM4001557	0.3
NT2RM4001605	F-NT2RM4001605	0.22
NT2RM4001754	F-NT2RM4001754	0.26
NT2RM4001776	F-NT2RM4001776	0.18
NT2RM4001810	F-NT2RM4001810	0.22
NT2RM4001856	F-NT2RM4001856	0.11
NT2RM4001858	F-NT2RM4001858	0.14
NT2RM4001930	F-NT2RM4001930	0.3
NT2RM4001953	F-NT2RM4001953	0.09
NT2RM4001984	F-NT2RM4001984	0.09
NT2RM4002067	F-NT2RM4002067	0.08
NT2RM4002278	F-NT2RM4002278	0.07
NT2RM4002281	F-NT2RM4002281	0.07
NT2RM4002287	F-NT2RM4002287	0.27
NT2RM4002383	F-NT2RM4002383	0.08
NT2RM4002390	F-NT2RM4002390	0.18
NT2RM4002438	F-NT2RM4002438	0.23
NT2RM4002479	F-NT2RM4002479	0.27
NT2RM4002499	F-NT2RM4002499	0.08
NT2RM4002504	F-NT2RM4002504	0.08
NT2RM4002532	F-NT2RM4002532	0.15
NT2RM4002567	F-NT2RM4002567	0.28
NT2RP2000027	F-NT2RP2000027	0.07
NT2RP2000076	F-NT2RP2000076	0.16
NT2RP2000077	F-NT2RP2000077	0.2
NT2RP2000098	F-NT2RP2000098	0.23
NT2RP2000108	F-NT2RP2000108	0.07
NT2RP2000183	F-NT2RP2000183	0.12
NT2RP2000257	F-NT2RP2000257	0.27
NT2RP2000258	F-NT2RP2000258	0.19
NT2RP2000270	F-NT2RP2000270	0.06
NT2RP2000289	F-NT2RP2000289	0.06
NT2RP2000327	F-NT2RP2000327	0.08
NT2RP2000337	F-NT2RP2000337	0.14
NT2RP2000420	F-NT2RP2000420	0.2
NT2RP2000459	F-NT2RP2000459	0.12
NT2RP2000498	F-NT2RP2000498	0.05
NT2RP2000523	F-NT2RP2000523	0.14
NT2RP2000603	F-NT2RP2000603	0.22
NT2RP2000644	F-NT2RP2000644	0.05
NT2RP2000678	F-NT2RP2000678	0.11
NT2RP2000715	F-NT2RP2000715	0.21
NT2RP2000731	F-NT2RP2000731	0.09

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NT2RP2000758	F-NT2RP2000758	0.2
NT2RP2000842	F-NT2RP2000842	0.14
NT2RP2000970	F-NT2RP2000970	0.12
NT2RP2000987	F-NT2RP2000987	0.07
NT2RP2001149	F-NT2RP2001149	0.08
NT2RP2001196	F-NT2RP2001196	0.27
NT2RP2001226	F-NT2RP2001226	0.18
NT2RP2001277	F-NT2RP2001277	0.09
NT2RP2001290	F-NT2RP2001290	0.1
NT2RP2001295	F-NT2RP2001295	0.13
NT2RP2001312	F-NT2RP2001312	0.15
NT2RP2001347	F-NT2RP2001347	0.11
NT2RP2001423	F-NT2RP2001423	0.06
NT2RP2001445	F-NT2RP2001445	0.11
NT2RP2001449	F-NT2RP2001449	0.15
NT2RP2001467	F-NT2RP2001467	0.21
NT2RP2001506	F-NT2RP2001506	0.06
NT2RP2001526	F-NT2RP2001526	0.1
NT2RP2001569	F-NT2RP2001569	0.09
NT2RP2001663	F-NT2RP2001663	0.08
NT2RP2001677	F-NT2RP2001677	0.14
NT2RP2001678	F-NT2RP2001678	0.17
NT2RP2001699	F-NT2RP2001699	0.05
NT2RP2001720	F-NT2RP2001720	0.08
NT2RP2001740	F-NT2RP2001740	0.23
NT2RP2001762	F-NT2RP2001762	0.11
NT2RP2001813	F-NT2RP2001813	0.19
NT2RP2001869	F-NT2RP2001869	0.22
NT2RP2001926	F-NT2RP2001926	0.07
NT2RP2001936	F-NT2RP2001936	0.08
NT2RP2001943	F-NT2RP2001943	0.27
NT2RP2002032	F-NT2RP2002032	0.23
NT2RP2002041	F-NT2RP2002041	0.1
NT2RP2002047	F-NT2RP2002047	0.12
NT2RP2002066	F-NT2RP2002066	0.25
NT2RP2002070	F-NT2RP2002070	0.07
NT2RP2002105	F-NT2RP2002105	0.13
NT2RP2002124	F-NT2RP2002124	0.13
NT2RP2002137	F-NT2RP2002137	0.07
NT2RP2002172	F-NT2RP2002172	0.21
NT2RP2002192	F-NT2RP2002192	0.05
NT2RP2002219	F-NT2RP2002219	0.13
NT2RP2002256	F-NT2RP2002256	0.17
NT2RP2002259	F-NT2RP2002259	0.28
NT2RP2002316	F-NT2RP2002316	0.15
NT2RP2002394	F-NT2RP2002394	0.16

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NT2RP2002439	F-NT2RP2002439	0.07
NT2RP2002457	F-NT2RP2002457	0.11
NT2RP2002475	F-NT2RP2002475	0.14
NT2RP2002504	F-NT2RP2002504	0.21
NT2RP2002546	F-NT2RP2002546	0.17
NT2RP2002591	F-NT2RP2002591	0.15
NT2RP2002606	F-NT2RP2002606	0.11
NT2RP2002643	F-NT2RP2002643	0.26
NT2RP2002727	F-NT2RP2002727	0.26
NT2RP2002736	F-NT2RP2002736	0.12
NT2RP2002740	F-NT2RP2002740	0.16
NT2RP2002741	F-NT2RP2002741	0.11
NT2RP2002750	F-NT2RP2002750	0.14
NT2RP2002752	F-NT2RP2002752	0.1
NT2RP2002753	F-NT2RP2002753	0.09
NT2RP2002778	F-NT2RP2002778	0.13
NT2RP2002839	F-NT2RP2002839	
NT2RP2002857	F-NT2RP2002857	0.21
NT2RP2002987	F-NT2RP2002987	0.08
NT2RP2003000	F-NT2RP2003000	0.24
NT2RP2003073	F-NT2RP2003073	0.08
NT2RP2003129	F-NT2RP2003129	0.07
NT2RP2003161	F-NT2RP2003161	0.05
NT2RP2003164	F-NT2RP2003164	0.09
NT2RP2003206	F-NT2RP2003206	0.22
NT2RP2003230	F-NT2RP2003230	0.08
NT2RP2003237	F-NT2RP2003237	0.24
NT2RP2003339	F-NT2RP2003339	0.1
NT2RP2003394	F-NT2RP2003394	0.07
NT2RP2003456	F-NT2RP2003456	0.08
NT2RP2003499	F-NT2RP2003499	0.08
NT2RP2003517	F-NT2RP2003517	0.29
NT2RP2003522	F-NT2RP2003522	0.22
NT2RP2003559	F-NT2RP2003559	0.12
NT2RP2003668	F-NT2RP2003668	0.08
NT2RP2003704	F-NT2RP2003704	0.09
NT2RP2003706	F-NT2RP2003706	0.28
NT2RP2003727	F-NT2RP2003727	0.17
NT2RP2003770	F-NT2RP2003770	0.09
NT2RP2003859	F-NT2RP2003859	0.18
NT2RP2003871	F-NT2RP2003871	0.23
NT2RP2003885	F-NT2RP2003885	0.24
NT2RP2003912	F-NT2RP2003912	0.26
NT2RP2003968	F-NT2RP2003968	0.2
NT2RP2003988	F-NT2RP2003988	0.09
NT2RP2004014	F-NT2RP2004014	0.07

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NT2RP2004142	F-NT2RP2004142	0.14
NT2RP2004170	F-NT2RP2004170	0.09
NT2RP2004172	F-NT2RP2004172	0.15
NT2RP2004207	F-NT2RP2004207	0.11
NT2RP2004232	F-NT2RP2004232	0.17
NT2RP2004270	F-NT2RP2004270	0.29
NT2RP2004300	F-NT2RP2004300	0.11
NT2RP2004321	F-NT2RP2004321	0.13
NT2RP2004339	F-NT2RP2004339	0.14
NT2RP2004347	F-NT2RP2004347	0.14
NT2RP2004396	F-NT2RP2004396	0.29
NT2RP2004400	F-NT2RP2004400	0.06
NT2RP2004412	F-NT2RP2004412	0.24
NT2RP2004425	F-NT2RP2004425	0.13
NT2RP2004490	F-NT2RP2004490	0.13
NT2RP2004512	F-NT2RP2004512	0.1
NT2RP2004523	F-NT2RP2004523	0.15
NT2RP2004580	F-NT2RP2004580	0.12
NT2RP2004587	F-NT2RP2004587	0.08
NT2RP2004675	F-NT2RP2004675	0.14
NT2RP2004681	F-NT2RP2004681	0.17
NT2RP2004709	F-NT2RP2004709	0.08
NT2RP2004736	F-NT2RP2004736	0.13
NT2RP2004767	F-NT2RP2004767	0.21
NT2RP2004775	F-NT2RP2004775	0.17
NT2RP2004961	F-NT2RP2004961	0.21
NT2RP2004962	F-NT2RP2004962	0.24
NT2RP2004967	F-NT2RP2004967	0.05
NT2RP2004982	F-NT2RP2004982	0.11
NT2RP2005020	F-NT2RP2005020	0.16
NT2RP2005031	F-NT2RP2005031	0.07
NT2RP2005108	F-NT2RP2005108	0.11
NT2RP2005254	F-NT2RP2005254	0.16
NT2RP2005289	F-NT2RP2005289	0.22
NT2RP2005293	F-NT2RP2005293	0.08
NT2RP2005325	F-NT2RP2005325	
NT2RP2005336	F-NT2RP2005336	0.27
NT2RP2005344	F-NT2RP2005344	0.24
NT2RP2005354	F-NT2RP2005354	0.08
NT2RP2005360	F-NT2RP2005360	0.12
NT2RP2005407	F-NT2RP2005407	0.28
NT2RP2005476	F-NT2RP2005476	0.14
NT2RP2005491	F-NT2RP2005491	0.18
NT2RP2005501	F-NT2RP2005501	0.1
NT2RP2005531	F-NT2RP2005531	0.29
NT2RP2005581	F-NT2RP2005581	0.07

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NT2RP2005645	F-NT2RP2005645	0.13
NT2RP2005651	F-NT2RP2005651	0.06
NT2RP2005694	F-NT2RP2005694	0.3
NT2RP2005701	F-NT2RP2005701	0.11
NT2RP2005719	F-NT2RP2005719	0.06
NT2RP2005726	F-NT2RP2005726	0.29
NT2RP2005741	F-NT2RP2005741	0.22
NT2RP2005753	F-NT2RP2005753	0.16
NT2RP2005815	F-NT2RP2005815	0.18
NT2RP2005841	F-NT2RP2005841	0.05
NT2RP2005857	F-NT2RP2005857	0.28
NT2RP2005908	F-NT2RP2005908	0.05
NT2RP2005942	F-NT2RP2005942	0.26
NT2RP2005980	F-NT2RP2005980	0.1
NT2RP2006098	F-NT2RP2006098	0.06
NT2RP2006103	F-NT2RP2006103	0.07
NT2RP2006166	F-NT2RP2006166	0.27
NT2RP2006184	F-NT2RP2006184	0.23
NT2RP2006258	F-NT2RP2006258	0.12
NT2RP2006261	F-NT2RP2006261	0.16
NT2RP2006320	F-NT2RP2006320	0.16
NT2RP2006321	F-NT2RP2006321	0.15
NT2RP2006323	F-NT2RP2006323	
NT2RP2006393	F-NT2RP2006393	0.07
NT2RP2006454	F-NT2RP2006454	0.11
NT2RP2006467	F-NT2RP2006467	0.24
NT2RP2006534	F-NT2RP2006534	0.14
NT2RP2006554	F-NT2RP2006554	0.16
NT2RP2006598	F-NT2RP2006598	0.08
NT2RP3000055	F-NT2RP3000055	0.14
NT2RP3000109	F-NT2RP3000109	0.18
NT2RP3000186	F-NT2RP3000186	0.06
NT2RP3000233	F-NT2RP3000233	0.29
NT2RP3000235	F-NT2RP3000235	0.09
NT2RP3000247	F-NT2RP3000247	0.19
NT2RP3000341	F-NT2RP3000341	0.16
NT2RP3000418	F-NT2RP3000418	0.15
NT2RP3000433	F-NT2RP3000433	0.11
NT2RP3000441	F-NT2RP3000441	0.2
NT2RP3000449	F-NT2RP3000449	0.16
NT2RP3000451	F-NT2RP3000451	0.14
NT2RP3000512	F-NT2RP3000512	0.08
NT2RP3000542	F-NT2RP3000542	0.1
NT2RP3000561	F-NT2RP3000561	0.1
NT2RP3000578	F-NT2RP3000578	0.3
NT2RP3000582	F-NT2RP3000582	0.08

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NT2RP3000584	F-NT2RP3000584	0.07
NT2RP3000622	F-NT2RP3000622	0.17
NT2RP3000628	F-NT2RP3000628	0.08
NT2RP3000685	F-NT2RP3000685	0.17
NT2RP3000736	F-NT2RP3000736	0.26
NT2RP3000742	F-NT2RP3000742	0.22
NT2RP3000815	F-NT2RP3000815	0.06
NT2RP3000865	F-NT2RP3000865	0.13
NT2RP3000875	F-NT2RP3000875	0.16
NT2RP3000904	F-NT2RP3000904	0.13
NT2RP3001007	F-NT2RP3001007	0.1
NT2RP3001115	F-NT2RP3001115	0.1
NT2RP3001232	F-NT2RP3001232	0.09
NT2RP3001245	F-NT2RP3001245	0.09
NT2RP3001281	F-NT2RP3001281	0.29
NT2RP3001318	F-NT2RP3001318	0.12
NT2RP3001339	F-NT2RP3001339	0.27
NT2RP3001340	F-NT2RP3001340	0.11
NT2RP3001374	F-NT2RP3001374	0.21
NT2RP3001383	F-NT2RP3001383	0.09
NT2RP3001432	F-NT2RP3001432	0.29
NT2RP3001459	F-NT2RP3001459	0.16
NT2RP3001527	F-NT2RP3001527	0.3
NT2RP3001580	F-NT2RP3001580	0.23
NT2RP3001589	F-NT2RP3001589	0.12
NT2RP3001607	F-NT2RP3001607	0.12
NT2RP3001634	F-NT2RP3001634	0.15
NT2RP3001752	F-NT2RP3001752	0.09
NT2RP3001782	F-NT2RP3001782	0.21
NT2RP3001898	F-NT2RP3001898	0.07
NT2RP3001926	F-NT2RP3001926	0.05
NT2RP3001989	F-NT2RP3001989	0.14
NT2RP3002002	F-NT2RP3002002	0.18
NT2RP3002004	F-NT2RP3002004	0.11
NT2RP3002056	F-NT2RP3002056	0.16
NT2RP3002057	F-NT2RP3002057	0.08
NT2RP3002166	F-NT2RP3002166	0.15
NT2RP3002173	F-NT2RP3002173	0.28
NT2RP3002352	F-NT2RP3002352	0.19
NT2RP3002687	F-NT2RP3002687	0.12
NT2RP3002713	F-NT2RP3002713	0.1
NT2RP3002770	F-NT2RP3002770	0.23
NT2RP3002799	F-NT2RP3002799	0.17
NT2RP3002810	F-NT2RP3002810	0.2
NT2RP3002955	F-NT2RP3002955	0.17
NT2RP3002978	F-NT2RP3002978	0.06

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NT2RP3003032	F-NT2RP3003032	0. 1
NT2RP3003059	F-NT2RP3003059	0. 11
NT2RP3003121	F-NT2RP3003121	0. 23
NT2RP3003133	F-NT2RP3003133	0. 21
NT2RP3003138	F-NT2RP3003138	0. 29
NT2RP3003264	F-NT2RP3003264	0. 15
NT2RP3003346	F-NT2RP3003346	0. 16
NT2RP3003384	F-NT2RP3003384	0. 12
NT2RP3003403	F-NT2RP3003403	0. 26
NT2RP3003433	F-NT2RP3003433	0. 22
NT2RP3003464	F-NT2RP3003464	0. 28
NT2RP3003500	F-NT2RP3003500	0. 2
NT2RP3003572	F-NT2RP3003572	0. 29
NT2RP3003576	F-NT2RP3003576	0. 16
NT2RP3003625	F-NT2RP3003625	0. 29
NT2RP3003665	F-NT2RP3003665	0. 15
NT2RP3003746	F-NT2RP3003746	0. 07
NT2RP3003799	F-NT2RP3003799	0. 13
NT2RP3003800	F-NT2RP3003800	0. 28
NT2RP3003819	F-NT2RP3003819	0. 19
NT2RP3003828	F-NT2RP3003828	0. 12
NT2RP3003842	F-NT2RP3003842	0. 11
NT2RP3003989	F-NT2RP3003989	0. 1
NT2RP3004016	F-NT2RP3004016	0. 09
NT2RP3004070	F-NT2RP3004070	0. 11
NT2RP3004095	F-NT2RP3004095	0. 1
NT2RP3004110	F-NT2RP3004110	0. 07
NT2RP3004145	F-NT2RP3004145	0. 15
NT2RP3004148	F-NT2RP3004148	0. 14
NT2RP3004215	F-NT2RP3004215	0. 16
NT2RP3004334	F-NT2RP3004334	0. 1
NT2RP3004349	F-NT2RP3004349	0. 09
NT2RP3004399	F-NT2RP3004399	0. 16
NT2RP3004470	F-NT2RP3004470	0. 23
NT2RP3004475	F-NT2RP3004475	0. 26
NT2RP3004503	F-NT2RP3004503	0. 12
NT2RP3004527	F-NT2RP3004527	0. 06
NT2RP4000023	F-NT2RP4000023	0. 13
NT2RP4000035	F-NT2RP4000035	0. 17
NT2RP4000049	F-NT2RP4000049	0. 1
NT2RP4000078	F-NT2RP4000078	0. 28
NT2RP4000102	F-NT2RP4000102	0. 15
NT2RP4000167	F-NT2RP4000167	0. 19
NT2RP4000214	F-NT2RP4000214	0. 12
NT2RP4000218	F-NT2RP4000218	0. 17
NT2RP4000321	F-NT2RP4000321	0. 18

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NT2RP4000424	F-NT2RP4000424	0.22
NT2RP4000515	F-NT2RP4000515	0.13
NT2RP4000517	F-NT2RP4000517	0.1
NT2RP4000519	F-NT2RP4000519	0.26
NT2RP4000915	F-NT2RP4000915	0.19
NT2RP4000996	F-NT2RP4000996	0.05
NT2RP4001407	F-NT2RP4001407	0.2
NT2RP4001889	F-NT2RP4001889	0.09
NT2RP4002075	F-NT2RP4002075	0.19
NT2RP4002905	F-NT2RP4002905	0.15
OVARC1000017	F-OVARC1000017	0.12
OVARC1000058	F-OVARC1000058	0.2
OVARC1000068	F-OVARC1000068	0.14
OVARC1000071	F-OVARC1000071	0.15
OVARC1000085	F-OVARC1000085	0.16
OVARC1000092	F-OVARC1000092	0.26
OVARC1000133	F-OVARC1000133	0.14
OVARC1000145	F-OVARC1000145	0.15
OVARC1000191	F-OVARC1000191	0.07
OVARC1000198	F-OVARC1000198	0.23
OVARC1000240	F-OVARC1000240	0.11
OVARC1000302	F-OVARC1000302	0.08
OVARC1000414	F-OVARC1000414	0.12
OVARC1000427	F-OVARC1000427	0.1
OVARC1000431	F-OVARC1000431	0.06
OVARC1000486	F-OVARC1000486	0.08
OVARC1000496	F-OVARC1000496	0.13
OVARC1000526	F-OVARC1000526	0.09
OVARC1000533	F-OVARC1000533	0.11
OVARC1000543	F-OVARC1000543	0.2
OVARC1000573	F-OVARC1000573	0.09
OVARC1000578	F-OVARC1000578	0.13
OVARC1000678	F-OVARC1000678	0.17
OVARC1000679	F-OVARC1000679	0.23
OVARC1000700	F-OVARC1000700	0.28
OVARC1000769	F-OVARC1000769	0.05
OVARC1000802	F-OVARC1000802	0.06
OVARC1000891	F-OVARC1000891	0.08
OVARC1000897	F-OVARC1000897	0.11
OVARC1000936	F-OVARC1000936	0.14
OVARC1000937	F-OVARC1000937	0.29
OVARC1000948	F-OVARC1000948	0.14
OVARC1000960	F-OVARC1000960	0.07
OVARC1000971	F-OVARC1000971	0.11
OVARC1001000	F-OVARC1001000	0.06
OVARC1001011	F-OVARC1001011	0.15

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OVARC1001051	F-OVARC1001051	0. 16
OVARC1001062	F-OVARC1001062	0. 09
OVARC1001072	F-OVARC1001072	0. 11
OVARC1001085	F-OVARC1001085	0. 12
OVARC1001117	F-OVARC1001117	0. 21
OVARC1001118	F-OVARC1001118	0. 08
OVARC1001129	F-OVARC1001129	0. 28
OVARC1001169	F-OVARC1001169	0. 12
OVARC1001240	F-OVARC1001240	0. 09
OVARC1001261	F-OVARC1001261	0. 1
OVARC1001268	F-OVARC1001268	0. 05
OVARC1001282	F-OVARC1001282	0. 09
OVARC1001330	F-OVARC1001330	0. 08
OVARC1001339	F-OVARC1001339	0. 15
OVARC1001342	F-OVARC1001342	0. 16
OVARC1001357	F-OVARC1001357	0. 06
OVARC1001442	F-OVARC1001442	0. 15
OVARC1001480	F-OVARC1001480	0. 23
OVARC1001542	F-OVARC1001542	0. 13
OVARC1001547	F-OVARC1001547	0. 12
OVARC1001600	F-OVARC1001600	0. 13
OVARC1001615	F-OVARC1001615	0. 11
OVARC1001668	F-OVARC1001668	0. 05
OVARC1001726	F-OVARC1001726	0. 18
OVARC1001745	F-OVARC1001745	0. 22
OVARC1001795	F-OVARC1001795	0. 28
OVARC1001805	F-OVARC1001805	0. 16
OVARC1001812	F-OVARC1001812	0. 05
OVARC1001813	F-OVARC1001813	0. 11
OVARC1001846	F-OVARC1001846	0. 13
OVARC1001883	F-OVARC1001883	0. 05
OVARC1001900	F-OVARC1001900	0. 28
OVARC1001901	F-OVARC1001901	0. 09
OVARC1001911	F-OVARC1001911	0. 06
OVARC1001928	F-OVARC1001928	0. 1
OVARC1001989	F-OVARC1001989	0. 07
OVARC1002044	F-OVARC1002044	0. 06
OVARC1002066	F-OVARC1002066	0. 08
OVARC1002143	F-OVARC1002143	0. 27
PLACE1000031	F-PLACE1000031	0. 09
PLACE1000040	F-PLACE1000040	0. 15
PLACE1000078	F-PLACE1000078	0. 12
PLACE1000094	F-PLACE1000094	0. 16
PLACE1000214	F-PLACE1000214	0. 15
PLACE1000292	F-PLACE1000292	0. 05
PLACE1000332	F-PLACE1000332	0. 1

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PLACE1000421	F-PLACE1000421	0.14
PLACE1000424	F-PLACE1000424	0.08
PLACE1000481	F-PLACE1000481	0.12
PLACE1000540	F-PLACE1000540	0.11
PLACE1000583	F-PLACE1000583	0.1
PLACE1000599	F-PLACE1000599	0.22
PLACE1000749	F-PLACE1000749	0.2
PLACE1000841	F-PLACE1000841	0.09
PLACE1000931	F-PLACE1000931	0.22
PLACE1000979	F-PLACE1000979	0.16
PLACE1001007	F-PLACE1001007	0.19
PLACE1001015	F-PLACE1001015	0.25
PLACE1001076	F-PLACE1001076	0.08
PLACE1001088	F-PLACE1001088	0.18
PLACE1001118	F-PLACE1001118	0.24
PLACE1001136	F-PLACE1001136	0.12
PLACE1001272	F-PLACE1001272	0.07
PLACE1001279	F-PLACE1001279	0.08
PLACE1001323	F-PLACE1001323	0.18
PLACE1001377	F-PLACE1001377	0.16
PLACE1001384	F-PLACE1001384	0.06
PLACE1001395	F-PLACE1001395	0.08
PLACE1001414	F-PLACE1001414	0.11
PLACE1001440	F-PLACE1001440	0.14
PLACE1001468	F-PLACE1001468	0.05
PLACE1001502	F-PLACE1001502	0.06
PLACE1001517	F-PLACE1001517	0.09
PLACE1001534	F-PLACE1001534	0.08
PLACE1001603	F-PLACE1001603	0.08
PLACE1001611	F-PLACE1001611	0.25
PLACE1001640	F-PLACE1001640	0.09
PLACE1001672	F-PLACE1001672	0.11
PLACE1001691	F-PLACE1001691	0.11
PLACE1001705	F-PLACE1001705	0.1
PLACE1001716	F-PLACE1001716	0.15
PLACE1001720	F-PLACE1001720	0.18
PLACE1001745	F-PLACE1001745	0.09
PLACE1001746	F-PLACE1001746	0.12
PLACE1001748	F-PLACE1001748	0.08
PLACE1001756	F-PLACE1001756	0.17
PLACE1001799	F-PLACE1001799	0.14
PLACE1001821	F-PLACE1001821	0.09
PLACE1001845	F-PLACE1001845	0.08
PLACE1001897	F-PLACE1001897	0.15
PLACE1002052	F-PLACE1002052	0.13
PLACE1002066	F-PLACE1002066	0.07

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PLACE1002150	F-PLACE1002150	0.08
PLACE1002157	F-PLACE1002157	0.15
PLACE1002205	F-PLACE1002205	0.13
PLACE1002227	F-PLACE1002227	0.12
PLACE1002256	F-PLACE1002256	0.11
PLACE1002259	F-PLACE1002259	0.09
PLACE1002319	F-PLACE1002319	0.27
PLACE1002399	F-PLACE1002399	0.08
PLACE1002477	F-PLACE1002477	0.17
PLACE1002493	F-PLACE1002493	0.09
PLACE1002500	F-PLACE1002500	0.25
PLACE1002514	F-PLACE1002514	0.06
PLACE1002537	F-PLACE1002537	0.17
PLACE1002578	F-PLACE1002578	0.11
PLACE1002583	F-PLACE1002583	0.25
PLACE1002591	F-PLACE1002591	0.28
PLACE1002598	F-PLACE1002598	0.29
PLACE1002604	F-PLACE1002604	0.15
PLACE1002768	F-PLACE1002768	0.11
PLACE1002772	F-PLACE1002772	0.15
PLACE1002782	F-PLACE1002782	0.16
PLACE1002853	F-PLACE1002853	0.16
PLACE1002881	F-PLACE1002881	0.09
PLACE1002962	F-PLACE1002962	0.13
PLACE1002968	F-PLACE1002968	0.23
PLACE1003153	F-PLACE1003153	0.07
PLACE1003205	F-PLACE1003205	0.2
PLACE1003238	F-PLACE1003238	0.22
PLACE1003258	F-PLACE1003258	0.17
PLACE1003343	F-PLACE1003343	0.07
PLACE1003361	F-PLACE1003361	0.19
PLACE1003373	F-PLACE1003373	0.08
PLACE1003375	F-PLACE1003375	0.26
PLACE1003401	F-PLACE1003401	0.11
PLACE1003420	F-PLACE1003420	0.22
PLACE1003478	F-PLACE1003478	0.14
PLACE1003516	F-PLACE1003516	0.17
PLACE1003519	F-PLACE1003519	0.14
PLACE1003521	F-PLACE1003521	0.17
PLACE1003528	F-PLACE1003528	0.16
PLACE1003566	F-PLACE1003566	0.16
PLACE1003575	F-PLACE1003575	0.06
PLACE1003583	F-PLACE1003583	0.08
PLACE1003584	F-PLACE1003584	0.1
PLACE1003593	F-PLACE1003593	0.15
PLACE1003618	F-PLACE1003618	0.25

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PLACE1003638	F-PLACE1003638	0.06
PLACE1003760	F-PLACE1003760	0.12
PLACE1003768	F-PLACE1003768	0.13
PLACE1003833	F-PLACE1003833	0.06
PLACE1003850	F-PLACE1003850	0.07
PLACE1003858	F-PLACE1003858	0.07
PLACE1003864	F-PLACE1003864	0.12
PLACE1003900	F-PLACE1003900	0.11
PLACE1003932	F-PLACE1003932	0.05
PLACE1004118	F-PLACE1004118	0.3
PLACE1004242	F-PLACE1004242	0.05
PLACE1004256	F-PLACE1004256	0.24
PLACE1004257	F-PLACE1004257	0.06
PLACE1004274	F-PLACE1004274	0.25
PLACE1004284	F-PLACE1004284	0.13
PLACE1004336	F-PLACE1004336	0.27
PLACE1004384	F-PLACE1004384	0.17
PLACE1004425	F-PLACE1004425	0.12
PLACE1004467	F-PLACE1004467	0.2
PLACE1004471	F-PLACE1004471	0.12
PLACE1004491	F-PLACE1004491	0.08
PLACE1004506	F-PLACE1004506	
PLACE1004518	F-PLACE1004518	0.14
PLACE1004658	F-PLACE1004658	0.05
PLACE1004681	F-PLACE1004681	0.13
PLACE1004693	F-PLACE1004693	0.11
PLACE1004716	F-PLACE1004716	0.12
PLACE1004773	F-PLACE1004773	0.17
PLACE1004793	F-PLACE1004793	0.21
PLACE1004813	F-PLACE1004813	0.11
PLACE1004815	F-PLACE1004815	0.14
PLACE1004827	F-PLACE1004827	0.15
PLACE1004836	F-PLACE1004836	0.25
PLACE1004838	F-PLACE1004838	0.16
PLACE1004840	F-PLACE1004840	0.06
PLACE1004900	F-PLACE1004900	0.08
PLACE1004913	F-PLACE1004913	0.12
PLACE1004934	F-PLACE1004934	0.17
PLACE1004972	F-PLACE1004972	0.07
PLACE1004979	F-PLACE1004979	0.24
PLACE1004985	F-PLACE1004985	0.05
PLACE1005052	F-PLACE1005052	0.17
PLACE1005077	F-PLACE1005077	0.1
PLACE1005085	F-PLACE1005085	0.13
PLACE1005086	F-PLACE1005086	0.13
PLACE1005108	F-PLACE1005108	0.28

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PLACE1005111	F-PLACE1005111	0.15
PLACE1005128	F-PLACE1005128	0.12
PLACE1005146	F-PLACE1005146	0.07
PLACE1005162	F-PLACE1005162	0.13
PLACE1005176	F-PLACE1005176	0.16
PLACE1005409	F-PLACE1005409	0.09
PLACE1005453	F-PLACE1005453	0.1
PLACE1005467	F-PLACE1005467	0.28
PLACE1005471	F-PLACE1005471	0.06
PLACE1005477	F-PLACE1005477	0.12
PLACE1005502	F-PLACE1005502	0.1
PLACE1005526	F-PLACE1005526	
PLACE1005528	F-PLACE1005528	0.07
PLACE1005574	F-PLACE1005574	0.06
PLACE1005584	F-PLACE1005584	0.24
PLACE1005611	F-PLACE1005611	0.18
PLACE1005639	F-PLACE1005639	0.09
PLACE1005666	F-PLACE1005666	0.07
PLACE1005730	F-PLACE1005730	0.2
PLACE1005802	F-PLACE1005802	0.1
PLACE1005845	F-PLACE1005845	0.09
PLACE1005850	F-PLACE1005850	0.22
PLACE1005884	F-PLACE1005884	0.08
PLACE1005898	F-PLACE1005898	0.12
PLACE1005932	F-PLACE1005932	0.13
PLACE1005968	F-PLACE1005968	0.07
PLACE1006002	F-PLACE1006002	0.08
PLACE1006003	F-PLACE1006003	0.16
PLACE1006017	F-PLACE1006017	0.13
PLACE1006076	F-PLACE1006076	0.11
PLACE1006129	F-PLACE1006129	0.25
PLACE1006143	F-PLACE1006143	0.08
PLACE1006164	F-PLACE1006164	0.05
PLACE1006187	F-PLACE1006187	0.2
PLACE1006205	F-PLACE1006205	0.08
PLACE1006223	F-PLACE1006223	0.05
PLACE1006262	F-PLACE1006262	0.08
PLACE1006288	F-PLACE1006288	0.06
PLACE1006318	F-PLACE1006318	0.12
PLACE1006360	F-PLACE1006360	0.07
PLACE1006368	F-PLACE1006368	0.27
PLACE1006371	F-PLACE1006371	0.14
PLACE1006382	F-PLACE1006382	0.09
PLACE1006470	F-PLACE1006470	0.14
PLACE1006506	F-PLACE1006506	0.24
PLACE1006521	F-PLACE1006521	0.08

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PLACE1006534	F-PLACE1006534	0.06
PLACE1006540	F-PLACE1006540	0.05
PLACE1006617	F-PLACE1006617	0.05
PLACE1006629	F-PLACE1006629	0.2
PLACE1006640	F-PLACE1006640	0.05
PLACE1006754	F-PLACE1006754	0.08
PLACE1006760	F-PLACE1006760	0.05
PLACE1006779	F-PLACE1006779	0.17
PLACE1006792	F-PLACE1006792	0.15
PLACE1006795	F-PLACE1006795	0.1
PLACE1006800	F-PLACE1006800	0.11
PLACE1006805	F-PLACE1006805	0.12
PLACE1006815	F-PLACE1006815	0.14
PLACE1006860	F-PLACE1006860	0.06
PLACE1006867	F-PLACE1006867	0.11
PLACE1006878	F-PLACE1006878	0.23
PLACE1006904	F-PLACE1006904	0.13
PLACE1007045	F-PLACE1007045	0.08
PLACE1007097	F-PLACE1007097	0.13
PLACE1007111	F-PLACE1007111	0.08
PLACE1007132	F-PLACE1007132	0.07
PLACE1007140	F-PLACE1007140	0.16
PLACE1007276	F-PLACE1007276	0.09
PLACE1007286	F-PLACE1007286	0.05
PLACE1007478	F-PLACE1007478	0.19
PLACE1007525	F-PLACE1007525	0.11
PLACE1007557	F-PLACE1007557	0.13
PLACE1007677	F-PLACE1007677	0.08
PLACE1007737	F-PLACE1007737	0.07
PLACE1007743	F-PLACE1007743	0.09
PLACE1007807	F-PLACE1007807	0.09
PLACE1007829	F-PLACE1007829	0.09
PLACE1007852	F-PLACE1007852	0.14
PLACE1007866	F-PLACE1007866	0.07
PLACE1007877	F-PLACE1007877	0.29
PLACE1008045	F-PLACE1008045	0.17
PLACE1008080	F-PLACE1008080	0.05
PLACE1008111	F-PLACE1008111	0.11
PLACE1008181	F-PLACE1008181	0.08
PLACE1008201	F-PLACE1008201	0.12
PLACE1008231	F-PLACE1008231	0.08
PLACE1008244	F-PLACE1008244	0.06
PLACE1008330	F-PLACE1008330	0.13
PLACE1008331	F-PLACE1008331	0.15
PLACE1008369	F-PLACE1008369	0.06
PLACE1008392	F-PLACE1008392	0.09

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PLACE1008405	F-PLACE1008405	0.07
PLACE1008424	F-PLACE1008424	0.06
PLACE1008426	F-PLACE1008426	0.17
PLACE1008437	F-PLACE1008437	0.2
PLACE1008455	F-PLACE1008455	0.07
PLACE1008584	F-PLACE1008584	0.29
PLACE1008621	F-PLACE1008621	0.07
PLACE1008625	F-PLACE1008625	0.12
PLACE1008630	F-PLACE1008630	0.12
PLACE1008643	F-PLACE1008643	0.11
PLACE1008715	F-PLACE1008715	0.2
PLACE1008748	F-PLACE1008748	0.15
PLACE1008757	F-PLACE1008757	0.13
PLACE1008798	F-PLACE1008798	0.14
PLACE1008807	F-PLACE1008807	0.12
PLACE1008851	F-PLACE1008851	0.22
PLACE1008920	F-PLACE1008920	0.1
PLACE1008941	F-PLACE1008941	0.14
PLACE1008947	F-PLACE1008947	0.05
PLACE1009020	F-PLACE1009020	0.14
PLACE1009039	F-PLACE1009039	0.16
PLACE1009048	F-PLACE1009048	0.09
PLACE1009050	F-PLACE1009050	0.09
PLACE1009150	F-PLACE1009150	0.12
PLACE1009155	F-PLACE1009155	0.08
PLACE1009172	F-PLACE1009172	0.07
PLACE1009183	F-PLACE1009183	0.07
PLACE1009200	F-PLACE1009200	0.08
PLACE1009246	F-PLACE1009246	0.08
PLACE1009308	F-PLACE1009308	0.23
PLACE1009398	F-PLACE1009398	0.26
PLACE1009410	F-PLACE1009410	0.15
PLACE1009477	F-PLACE1009477	0.18
PLACE1009493	F-PLACE1009493	0.23
PLACE1009539	F-PLACE1009539	0.11
PLACE1009595	F-PLACE1009595	0.11
PLACE1009613	F-PLACE1009613	0.08
PLACE1009621	F-PLACE1009621	0.19
PLACE1009637	F-PLACE1009637	0.27
PLACE1009639	F-PLACE1009639	0.27
PLACE1009879	F-PLACE1009879	0.07
PLACE1009888	F-PLACE1009888	0.06
PLACE1009924	F-PLACE1009924	0.09
PLACE1009925	F-PLACE1009925	0.21
PLACE1009935	F-PLACE1009935	0.22
PLACE1009947	F-PLACE1009947	0.19

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PLACE1010069	F-PLACE1010069	0.22
PLACE1010083	F-PLACE1010083	0.26
PLACE1010089	F-PLACE1010089	0.13
PLACE1010181	F-PLACE1010181	0.07
PLACE1010231	F-PLACE1010231	0.17
PLACE1010270	F-PLACE1010270	0.08
PLACE1010341	F-PLACE1010341	0.1
PLACE1010562	F-PLACE1010562	0.14
PLACE1010579	F-PLACE1010579	0.15
PLACE1010624	F-PLACE1010624	0.13
PLACE1010628	F-PLACE1010628	0.16
PLACE1010631	F-PLACE1010631	0.23
PLACE1010662	F-PLACE1010662	0.24
PLACE1010702	F-PLACE1010702	0.21
PLACE1010739	F-PLACE1010739	0.13
PLACE1010802	F-PLACE1010802	0.17
PLACE1010891	F-PLACE1010891	0.09
PLACE1010896	F-PLACE1010896	0.22
PLACE1010916	F-PLACE1010916	0.15
PLACE1010947	F-PLACE1010947	0.08
PLACE1011032	F-PLACE1011032	0.17
PLACE1011057	F-PLACE1011057	0.1
PLACE1011109	F-PLACE1011109	0.08
PLACE1011133	F-PLACE1011133	0.08
PLACE1011143	F-PLACE1011143	0.23
PLACE1011165	F-PLACE1011165	0.05
PLACE1011185	F-PLACE1011185	0.17
PLACE1011203	F-PLACE1011203	0.08
PLACE1011296	F-PLACE1011296	0.13
PLACE1011340	F-PLACE1011340	0.05
PLACE1011375	F-PLACE1011375	0.07
PLACE1011419	F-PLACE1011419	0.15
PLACE1011452	F-PLACE1011452	0.13
PLACE1011465	F-PLACE1011465	0.14
PLACE1011492	F-PLACE1011492	0.26
PLACE1011503	F-PLACE1011503	0.14
PLACE1011520	F-PLACE1011520	0.12
PLACE1011567	F-PLACE1011567	0.13
PLACE1011576	F-PLACE1011576	0.29
PLACE1011641	F-PLACE1011641	0.07
PLACE1011643	F-PLACE1011643	0.27
PLACE1011649	F-PLACE1011649	0.17
PLACE1011650	F-PLACE1011650	0.13
PLACE1011719	F-PLACE1011719	0.15
PLACE1011729	F-PLACE1011729	0.23
PLACE1011749	F-PLACE1011749	0.12

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PLACE1011762	F-PLACE1011762	0. 06
PLACE1011778	F-PLACE1011778	0. 07
PLACE1011874	F-PLACE1011874	0. 07
PLACE1011962	F-PLACE1011962	0. 06
PLACE1011964	F-PLACE1011964	0. 13
PLACE1011995	F-PLACE1011995	0. 08
PLACE2000003	F-PLACE2000003	0. 09
PLACE2000011	F-PLACE2000011	0. 12
PLACE2000017	F-PLACE2000017	0. 22
PLACE2000061	F-PLACE2000061	0. 19
PLACE2000103	F-PLACE2000103	0. 16
PLACE2000115	F-PLACE2000115	0. 11
PLACE2000132	F-PLACE2000132	0. 24
PLACE2000136	F-PLACE2000136	0. 09
PLACE2000140	F-PLACE2000140	0. 24
PLACE2000176	F-PLACE2000176	0. 25
PLACE2000187	F-PLACE2000187	0. 16
PLACE2000216	F-PLACE2000216	0. 15
PLACE2000264	F-PLACE2000264	0. 06
PLACE2000305	F-PLACE2000305	0. 05
PLACE2000317	F-PLACE2000317	0. 25
PLACE2000335	F-PLACE2000335	0. 09
PLACE2000342	F-PLACE2000342	0. 07
PLACE2000347	F-PLACE2000347	0. 12
PLACE2000366	F-PLACE2000366	0. 08
PLACE2000379	F-PLACE2000379	0. 24
PLACE2000394	F-PLACE2000394	0. 2
PLACE2000398	F-PLACE2000398	0. 21
PLACE2000419	F-PLACE2000419	0. 05
PLACE2000425	F-PLACE2000425	0. 16
PLACE2000435	F-PLACE2000435	0. 05
PLACE2000450	F-PLACE2000450	0. 12
PLACE2000455	F-PLACE2000455	0. 15
PLACE2000465	F-PLACE2000465	0. 12
PLACE2000477	F-PLACE2000477	0. 3
PLACE3000004	F-PLACE3000004	0. 3
PLACE3000119	F-PLACE3000119	0. 1
PLACE3000124	F-PLACE3000124	0. 11
PLACE3000136	F-PLACE3000136	0. 13
PLACE3000158	F-PLACE3000158	0. 06
PLACE3000169	F-PLACE3000169	0. 13
PLACE3000199	F-PLACE3000199	0. 06
PLACE3000207	F-PLACE3000207	0. 11
PLACE3000208	F-PLACE3000208	0. 07
PLACE3000218	F-PLACE3000218	0. 15
PLACE3000220	F-PLACE3000220	0. 05

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PLACE3000230	F-PLACE3000230	0.23
PLACE3000271	F-PLACE3000271	0.17
PLACE3000276	F-PLACE3000276	0.2
PLACE3000341	F-PLACE3000341	0.08
PLACE3000362	F-PLACE3000362	0.19
PLACE3000365	F-PLACE3000365	0.09
PLACE3000373	F-PLACE3000373	0.22
PLACE3000388	F-PLACE3000388	0.12
PLACE3000399	F-PLACE3000399	0.14
PLACE3000400	F-PLACE3000400	0.08
PLACE3000401	F-PLACE3000401	0.1
PLACE3000402	F-PLACE3000402	0.1
PLACE3000406	F-PLACE3000406	0.17
PLACE3000475	F-PLACE3000475	0.07
PLACE4000093	F-PLACE4000093	0.21
PLACE4000100	F-PLACE4000100	0.19
PLACE4000233	F-PLACE4000233	0.07
PLACE4000247	F-PLACE4000247	0.14
PLACE4000250	F-PLACE4000250	0.17
PLACE4000252	F-PLACE4000252	0.09
PLACE4000320	F-PLACE4000320	0.23
PLACE4000344	F-PLACE4000344	0.21
PLACE4000367	F-PLACE4000367	0.18
PLACE4000379	F-PLACE4000379	0.14
PLACE4000401	F-PLACE4000401	0.13
PLACE4000411	F-PLACE4000411	0.11
PLACE4000494	F-PLACE4000494	0.19
PLACE4000548	F-PLACE4000548	0.27
THYR01000026	F-THYR01000026	0.09
THYR01000035	F-THYR01000035	0.09
THYR01000085	F-THYR01000085	0.13
THYR01000092	F-THYR01000092	0.21
THYR01000111	F-THYR01000111	0.13
THYR01000129	F-THYR01000129	0.11
THYR01000132	F-THYR01000132	0.1
THYR01000156	F-THYR01000156	0.13
THYR01000186	F-THYR01000186	0.12
THYR01000187	F-THYR01000187	0.11
THYR01000190	F-THYR01000190	0.16
THYR01000221	F-THYR01000221	0.08
THYR01000241	F-THYR01000241	0.08
THYR01000279	F-THYR01000279	0.13
THYR01000438	F-THYR01000438	0.06
THYR01000452	F-THYR01000452	0.12
THYR01000471	F-THYR01000471	0.11
THYR01000484	F-THYR01000484	0.24

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THYR01000558	F-THYR01000558	0.09
THYR01000596	F-THYR01000596	0.14
THYR01000602	F-THYR01000602	0.13
THYR01000625	F-THYR01000625	0.2
THYR01000641	F-THYR01000641	0.06
THYR01000658	F-THYR01000658	0.12
THYR01000699	F-THYR01000699	0.09
THYR01000748	F-THYR01000748	0.3
THYR01000793	F-THYR01000793	0.25
THYR01000796	F-THYR01000796	0.11
THYR01000805	F-THYR01000805	0.28
THYR01000815	F-THYR01000815	0.14
THYR01000843	F-THYR01000843	0.13
THYR01000852	F-THYR01000852	0.05
THYR01000865	F-THYR01000865	0.14
THYR01000895	F-THYR01000895	0.12
THYR01000974	F-THYR01000974	0.07
THYR01000975	F-THYR01000975	0.08
THYR01001003	F-THYR01001003	0.11
THYR01001031	F-THYR01001031	0.1
THYR01001062	F-THYR01001062	0.14
THYR01001093	F-THYR01001093	0.13
THYR01001121	F-THYR01001121	0.14
THYR01001133	F-THYR01001133	0.24
THYR01001177	F-THYR01001177	
THYR01001262	F-THYR01001262	0.2
THYR01001290	F-THYR01001290	0.06
THYR01001321	F-THYR01001321	0.09
THYR01001322	F-THYR01001322	0.13
THYR01001365	F-THYR01001365	0.08
THYR01001401	F-THYR01001401	0.21
THYR01001411	F-THYR01001411	0.06
THYR01001426	F-THYR01001426	0.1
THYR01001434	F-THYR01001434	0.15
THYR01001480	F-THYR01001480	0.1
THYR01001534	F-THYR01001534	0.26
THYR01001541	F-THYR01001541	0.22
THYR01001559	F-THYR01001559	0.15
THYR01001570	F-THYR01001570	0.28
THYR01001573	F-THYR01001573	0.05
THYR01001595	F-THYR01001595	0.05
THYR01001617	F-THYR01001617	0.1
THYR01001673	F-THYR01001673	0.07
THYR01001706	F-THYR01001706	0.15
THYR01001745	F-THYR01001745	0.12
THYR01001746	F-THYR01001746	0.1

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THYR01001772	F-THYR01001772	0.08
THYR01001895	F-THYR01001895	0.19
THYR01001907	F-THYR01001907	0.17
Y79AA1000033	F-Y79AA1000033	0.18
Y79AA1000065	F-Y79AA1000065	0.22
Y79AA1000346	F-Y79AA1000346	0.2
Y79AA1000405	F-Y79AA1000405	0.07
Y79AA1000410	F-Y79AA1000410	0.08
Y79AA1000538	F-Y79AA1000538	0.06
Y79AA1000802	F-Y79AA1000802	0.28
Y79AA1000805	F-Y79AA1000805	0.2
Y79AA1000969	F-Y79AA1000969	0.07
Y79AA1001061	F-Y79AA1001061	0.22
Y79AA1001167	F-Y79AA1001167	0.22
Y79AA1001384	F-Y79AA1001384	0.18
Y79AA1001594	F-Y79AA1001594	0.22
Y79AA1001692	F-Y79AA1001692	0.2
Y79AA1001848	F-Y79AA1001848	0.21
Y79AA1001875	F-Y79AA1001875	0.09
Y79AA1002103	F-Y79AA1002103	0.11
Y79AA1002211	F-Y79AA1002211	0.19
Y79AA1002220	F-Y79AA1002220	0.25

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Table 11

574 clones belonging to groups (4), (5), (6), and (7), each having the maximal ATGpr1 score of not more than 0.3 and selected based on the maximal ATGpr2 score, and their maximal ATGpr2 scores

clone name	name of sequence	maximal ATGpr2 score
HEMBA1000180	F-HEMBA1000180	0.37
HEMBA1000251	F-HEMBA1000251	0.14
HEMBA1000280	F-HEMBA1000280	0.33
HEMBA1000282	F-HEMBA1000282	0.36
HEMBA1000333	F-HEMBA1000333	0.59
HEMBA1000351	F-HEMBA1000351	0.36
HEMBA1000357	F-HEMBA1000357	0.39
HEMBA1000376	F-HEMBA1000376	0.53
HEMBA1000469	F-HEMBA1000469	0.32
HEMBA1000504	F-HEMBA1000504	0.34
HEMBA1000519	F-HEMBA1000519	0.72
HEMBA1000545	F-HEMBA1000545	0.32
HEMBA1000557	F-HEMBA1000557	0.35
HEMBA1000575	F-HEMBA1000575	0.34

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HEMBA1000604	F-HEMBA1000604	0.28
HEMBA1000622	F-HEMBA1000622	0.32
HEMBA1000673	F-HEMBA1000673	0.14
HEMBA1000726	F-HEMBA1000726	0.32
HEMBA1000749	F-HEMBA1000749	0.35
HEMBA1000822	F-HEMBA1000822	0.42
HEMBA1000876	F-HEMBA1000876	0.44
HEMBA1000934	F-HEMBA1000934	0.41
HEMBA1000943	F-HEMBA1000943	0.34
HEMBA1000960	F-HEMBA1000960	0.34
HEMBA1000972	F-HEMBA1000972	0.44
HEMBA1001020	F-HEMBA1001020	0.31
HEMBA1001024	F-HEMBA1001024	0.22
HEMBA1001026	F-HEMBA1001026	0.28
HEMBA1001051	F-HEMBA1001051	0.36
HEMBA1001060	F-HEMBA1001060	0.34
HEMBA1001071	F-HEMBA1001071	0.57
HEMBA1001208	F-HEMBA1001208	0.57
HEMBA1001226	F-HEMBA1001226	0.44
HEMBA1001319	F-HEMBA1001319	0.58
HEMBA1001383	F-HEMBA1001383	0.35
HEMBA1001391	F-HEMBA1001391	0.42
HEMBA1001411	F-HEMBA1001411	0.55
HEMBA1001433	F-HEMBA1001433	0.66
HEMBA1001435	F-HEMBA1001435	0.72
HEMBA1001478	F-HEMBA1001478	0.36
HEMBA1001522	F-HEMBA1001522	0.31
HEMBA1001636	F-HEMBA1001636	0.32
HEMBA1001651	F-HEMBA1001651	0.54
HEMBA1001658	F-HEMBA1001658	0.38
HEMBA1001709	F-HEMBA1001709	0.55
HEMBA1001734	F-HEMBA1001734	0.13
HEMBA1001745	F-HEMBA1001745	0.33
HEMBA1001784	F-HEMBA1001784	0.08
HEMBA1001791	F-HEMBA1001791	0.48
HEMBA1001803	F-HEMBA1001803	0.21
HEMBA1001808	F-HEMBA1001808	0.23
HEMBA1001835	F-HEMBA1001835	0.67
HEMBA1001844	F-HEMBA1001844	0.46
HEMBA1001888	F-HEMBA1001888	0.72
HEMBA1001918	F-HEMBA1001918	0.25
HEMBA1001940	F-HEMBA1001940	0.40
HEMBA1001962	F-HEMBA1001962	0.63
HEMBA1002022	F-HEMBA1002022	0.32
HEMBA1002185	F-HEMBA1002185	0.33
HEMBA1002257	F-HEMBA1002257	0.13

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HEMBA1002348	F-HEMBA1002348	0.39
HEMBA1002621	F-HEMBA1002621	0.47
HEMBA1002645	F-HEMBA1002645	0.34
HEMBA1002661	F-HEMBA1002661	0.43
HEMBA1002728	F-HEMBA1002728	0.45
HEMBA1002742	F-HEMBA1002742	0.49
HEMBA1002921	F-HEMBA1002921	0.79
HEMBA1002924	F-HEMBA1002924	0.45
HEMBA1002934	F-HEMBA1002934	0.34
HEMBA1002968	F-HEMBA1002968	0.39
HEMBA1003037	F-HEMBA1003037	0.43
HEMBA1003064	F-HEMBA1003064	0.19
HEMBA1003071	F-HEMBA1003071	0.48
HEMBA1003166	F-HEMBA1003166	0.32
HEMBA1003202	F-HEMBA1003202	0.38
HEMBA1003204	F-HEMBA1003204	0.34
HEMBA1003220	F-HEMBA1003220	0.39
HEMBA1003229	F-HEMBA1003229	0.43
HEMBA1003276	F-HEMBA1003276	0.48
HEMBA1003296	F-HEMBA1003296	0.36
HEMBA1003373	F-HEMBA1003373	0.48
HEMBA1003531	F-HEMBA1003531	0.46
HEMBA1003640	F-HEMBA1003640	0.32
HEMBA1003714	F-HEMBA1003714	0.16
HEMBA1003856	F-HEMBA1003856	0.47
HEMBA1003902	F-HEMBA1003902	0.17
HEMBA1003908	F-HEMBA1003908	0.44
HEMBA1003926	F-HEMBA1003926	0.36
HEMBA1003942	F-HEMBA1003942	0.47
HEMBA1003987	F-HEMBA1003987	0.39
HEMBA1004000	F-HEMBA1004000	0.87
HEMBA1004024	F-HEMBA1004024	0.82
HEMBA1004164	F-HEMBA1004164	0.21
HEMBA1004267	F-HEMBA1004267	0.46
HEMBA1004323	F-HEMBA1004323	0.37
HEMBA1004405	F-HEMBA1004405	0.23
HEMBA1004433	F-HEMBA1004433	0.51
HEMBA1004577	F-HEMBA1004577	0.51
HEMBA1004730	F-HEMBA1004730	0.55
HEMBA1004778	F-HEMBA1004778	0.47
HEMBA1004803	F-HEMBA1004803	0.36
HEMBA1004807	F-HEMBA1004807	0.48
HEMBA1004880	F-HEMBA1004880	0.43
HEMBA1004900	F-HEMBA1004900	0.40
HEMBA1004909	F-HEMBA1004909	0.24
HEMBA1004983	F-HEMBA1004983	0.35

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HEMBA1005123	F-HEMBA1005123	0.35
HEMBA1005232	F-HEMBA1005232	0.09
HEMBA1005241	F-HEMBA1005241	0.34
HEMBA1005311	F-HEMBA1005311	0.37
HEMBA1005318	F-HEMBA1005318	0.59
HEMBA1005353	F-HEMBA1005353	0.34
HEMBA1005374	F-HEMBA1005374	0.38
HEMBA1005447	F-HEMBA1005447	0.34
HEMBA1005508	F-HEMBA1005508	0.14
HEMBA1005577	F-HEMBA1005577	0.22
HEMBA1005588	F-HEMBA1005588	0.54
HEMBA1005593	F-HEMBA1005593	0.44
HEMBA1005606	F-HEMBA1005606	0.38
HEMBA1005679	F-HEMBA1005679	0.87
HEMBA1005894	F-HEMBA1005894	0.46
HEMBA1005911	F-HEMBA1005911	0.56
HEMBA1006036	F-HEMBA1006036	0.87
HEMBA1006124	F-HEMBA1006124	0.35
HEMBA1006253	F-HEMBA1006253	0.35
HEMBA1006259	F-HEMBA1006259	0.54
HEMBA1006364	F-HEMBA1006364	0.55
HEMBA1006380	F-HEMBA1006380	0.48
HEMBA1006426	F-HEMBA1006426	0.54
HEMBA1006461	F-HEMBA1006461	0.20
HEMBA1006562	F-HEMBA1006562	0.72
HEMBA1006597	F-HEMBA1006597	0.64
HEMBA1006639	F-HEMBA1006639	0.55
HEMBA1006653	F-HEMBA1006653	0.34
HEMBA1006695	F-HEMBA1006695	0.16
HEMBA1006696	F-HEMBA1006696	0.37
HEMBA1006744	F-HEMBA1006744	0.33
HEMBA1006824	F-HEMBA1006824	0.37
HEMBA1006949	F-HEMBA1006949	0.78
HEMBA1007078	F-HEMBA1007078	0.44
HEMBA1007129	F-HEMBA1007129	0.55
HEMBA1007147	F-HEMBA1007147	0.41
HEMBA1007206	F-HEMBA1007206	0.46
HEMBA1007279	F-HEMBA1007279	0.45
HEMBA1007327	F-HEMBA1007327	0.71
HEMBB1000005	F-HEMBB1000005	0.35
HEMBB1000054	F-HEMBB1000054	0.18
HEMBB1000055	F-HEMBB1000055	0.87
HEMBB1000144	F-HEMBB1000144	0.47
HEMBB1000258	F-HEMBB1000258	0.87
HEMBB1000318	F-HEMBB1000318	0.34
HEMBB1000335	F-HEMBB1000335	0.48

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HEMBB1000336	F-HEMBB1000336	0. 35
HEMBB1000354	F-HEMBB1000354	0. 47
HEMBB1000374	F-HEMBB1000374	0. 69
HEMBB1000402	F-HEMBB1000402	0. 54
HEMBB1000404	F-HEMBB1000404	0. 47
HEMBB1000480	F-HEMBB1000480	0. 35
HEMBB1000493	F-HEMBB1000493	0. 33
HEMBB1000554	F-HEMBB1000554	0. 46
HEMBB1000573	F-HEMBB1000573	0. 34
HEMBB1000649	F-HEMBB1000649	0. 41
HEMBB1000652	F-HEMBB1000652	0. 46
HEMBB1000709	F-HEMBB1000709	0. 56
HEMBB1000749	F-HEMBB1000749	0. 36
HEMBB1000790	F-HEMBB1000790	0. 58
HEMBB1000827	F-HEMBB1000827	0. 31
HEMBB1000831	F-HEMBB1000831	0. 42
HEMBB1000893	F-HEMBB1000893	0. 36
HEMBB1001004	F-HEMBB1001004	0. 43
HEMBB1001008	F-HEMBB1001008	0. 44
HEMBB1001047	F-HEMBB1001047	0. 47
HEMBB1001119	F-HEMBB1001119	0. 25
HEMBB1001142	F-HEMBB1001142	0. 15
HEMBB1001315	F-HEMBB1001315	0. 72
HEMBB1001317	F-HEMBB1001317	0. 49
HEMBB1001326	F-HEMBB1001326	0. 44
HEMBB1001337	F-HEMBB1001337	0. 18
HEMBB1001367	F-HEMBB1001367	0. 35
HEMBB1001424	F-HEMBB1001424	0. 34
HEMBB1001436	F-HEMBB1001436	0. 34
HEMBB1001458	F-HEMBB1001458	0. 47
HEMBB1001535	F-HEMBB1001535	0. 34
HEMBB1001536	F-HEMBB1001536	0. 22
HEMBB1001565	F-HEMBB1001565	0. 35
HEMBB1001747	F-HEMBB1001747	0. 40
HEMBB1001749	F-HEMBB1001749	0. 39
HEMBB1001797	F-HEMBB1001797	0. 79
HEMBB1001836	F-HEMBB1001836	0. 52
HEMBB1001863	F-HEMBB1001863	0. 38
HEMBB1001868	F-HEMBB1001868	0. 27
HEMBB1001875	F-HEMBB1001875	0. 46
HEMBB1001911	F-HEMBB1001911	0. 87
HEMBB1001922	F-HEMBB1001922	0. 38
HEMBB1001925	F-HEMBB1001925	0. 33
HEMBB1001944	F-HEMBB1001944	0. 35
HEMBB1001983	F-HEMBB1001983	0. 32
HEMBB1001996	F-HEMBB1001996	0. 39

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HEMBB1001997	F-HEMBB1001997	0.36
HEMBB1002045	F-HEMBB1002045	0.20
HEMBB1002092	F-HEMBB1002092	0.31
HEMBB1002247	F-HEMBB1002247	0.53
HEMBB1002266	F-HEMBB1002266	0.34
HEMBB1002387	F-HEMBB1002387	0.32
HEMBB1002425	F-HEMBB1002425	0.31
HEMBB1002458	F-HEMBB1002458	0.44
HEMBB1002522	F-HEMBB1002522	0.56
HEMBB1002534	F-HEMBB1002534	0.43
HEMBB1002579	F-HEMBB1002579	0.21
HEMBB1002582	F-HEMBB1002582	0.48
HEMBB1002596	F-HEMBB1002596	0.42
HEMBB1002617	F-HEMBB1002617	0.47
HEMBB1002702	F-HEMBB1002702	0.31
MAMMA1000043	F-MAMMA1000043	0.45
MAMMA1000092	F-MAMMA1000092	0.39
MAMMA1000129	F-MAMMA1000129	0.47
MAMMA1000175	F-MAMMA1000175	0.18
MAMMA1000198	F-MAMMA1000198	0.46
MAMMA1000221	F-MAMMA1000221	0.43
MAMMA1000307	F-MAMMA1000307	0.35
MAMMA1000331	F-MAMMA1000331	0.41
MAMMA1000356	F-MAMMA1000356	0.41
MAMMA1000360	F-MAMMA1000360	0.33
MAMMA1000402	F-MAMMA1000402	0.35
MAMMA1000414	F-MAMMA1000414	0.32
MAMMA1000444	F-MAMMA1000444	0.13
MAMMA1000500	F-MAMMA1000500	0.36
MAMMA1000522	F-MAMMA1000522	0.46
MAMMA1000576	F-MAMMA1000576	0.58
MAMMA1000594	F-MAMMA1000594	0.69
MAMMA1000597	F-MAMMA1000597	0.35
MAMMA1000720	F-MAMMA1000720	0.43
MAMMA1000761	F-MAMMA1000761	0.13
MAMMA1000775	F-MAMMA1000775	0.35
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MAMMA1000883	F-MAMMA1000883	0.41
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MAMMA1000940	F-MAMMA1000940	0.35
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MAMMA1000943	F-MAMMA1000943	0.23
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MAMMA1001038	F-MAMMA1001038	0. 41
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MAMMA1001745	F-MAMMA1001745	0. 53
MAMMA1001760	F-MAMMA1001760	0. 58
MAMMA1001769	F-MAMMA1001769	0. 33
MAMMA1001815	F-MAMMA1001815	0. 43
MAMMA1001820	F-MAMMA1001820	0. 19
MAMMA1001907	F-MAMMA1001907	0. 38
MAMMA1002056	F-MAMMA1002056	0. 35
MAMMA1002078	F-MAMMA1002078	0. 34
MAMMA1002093	F-MAMMA1002093	0. 55
MAMMA1002125	F-MAMMA1002125	0. 39
MAMMA1002132	F-MAMMA1002132	0. 57
MAMMA1002145	F-MAMMA1002145	0. 78
MAMMA1002250	F-MAMMA1002250	0. 72
MAMMA1002311	F-MAMMA1002311	0. 58
MAMMA1002360	F-MAMMA1002360	0. 19
MAMMA1002411	F-MAMMA1002411	0. 40
MAMMA1002498	F-MAMMA1002498	0. 37
MAMMA1002571	F-MAMMA1002571	0. 32
MAMMA1002701	F-MAMMA1002701	0. 55
MAMMA1002727	F-MAMMA1002727	0. 34
MAMMA1002728	F-MAMMA1002728	0. 55
MAMMA1002746	F-MAMMA1002746	0. 45
MAMMA1002764	F-MAMMA1002764	0. 44
MAMMA1002765	F-MAMMA1002765	0. 40
MAMMA1002820	F-MAMMA1002820	0. 32
MAMMA1002830	F-MAMMA1002830	0. 36
MAMMA1002909	F-MAMMA1002909	0. 64
MAMMA1002941	F-MAMMA1002941	0. 42
MAMMA1002972	F-MAMMA1002972	0. 08
MAMMA1002973	F-MAMMA1002973	0. 35
MAMMA1003004	F-MAMMA1003004	0. 42
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NT2RM4000425	F-NT2RM4000425	0.22
NT2RM4000779	F-NT2RM4000779	0.43
NT2RM4000855	F-NT2RM4000855	0.52
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NT2RM4001313	F-NT2RM4001313	0.38
NT2RM4001437	F-NT2RM4001437	0.53
NT2RM4001754	F-NT2RM4001754	0.35
NT2RM4001856	F-NT2RM4001856	0.27
NT2RM4001953	F-NT2RM4001953	0.59
NT2RM4001984	F-NT2RM4001984	0.35
NT2RM4002390	F-NT2RM4002390	0.24
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NT2RP2000715	F-NT2RP2000715	0.37
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NT2RP2000970	F-NT2RP2000970	0.46
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NT2RP2001226	F-NT2RP2001226	0.44
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NT2RP2001347	F-NT2RP2001347	0.41
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NT2RP2001663	F-NT2RP2001663	0.37
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NT2RP2002475	F-NT2RP2002475	0.09
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NT2RP2002857	F-NT2RP2002857	0.34
NT2RP2003000	F-NT2RP2003000	0.56
NT2RP2003073	F-NT2RP2003073	0.36
NT2RP2003237	F-NT2RP2003237	0.69
NT2RP2003394	F-NT2RP2003394	0.34
NT2RP2003517	F-NT2RP2003517	0.44
NT2RP2003668	F-NT2RP2003668	0.46
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NT2RP2004232	F-NT2RP2004232	0.34
NT2RP2004400	F-NT2RP2004400	0.18
NT2RP2004512	F-NT2RP2004512	0.11
NT2RP2004523	F-NT2RP2004523	0.72
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NT2RP2004736	F-NT2RP2004736	0.70
NT2RP2004767	F-NT2RP2004767	0.54
NT2RP2004775	F-NT2RP2004775	0.53
NT2RP2004961	F-NT2RP2004961	0.49
NT2RP2004962	F-NT2RP2004962	0.87
NT2RP2004982	F-NT2RP2004982	0.32
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NT2RP2005407	F-NT2RP2005407	0.33
NT2RP2005531	F-NT2RP2005531	0.20
NT2RP2005694	F-NT2RP2005694	0.21
NT2RP2005726	F-NT2RP2005726	0.42
NT2RP2005942	F-NT2RP2005942	0.10
NT2RP2006258	F-NT2RP2006258	0.37
NT2RP2006261	F-NT2RP2006261	0.42
NT2RP2006454	F-NT2RP2006454	0.46
NT2RP2006554	F-NT2RP2006554	0.14
NT2RP3000055	F-NT2RP3000055	0.31
NT2RP3000233	F-NT2RP3000233	0.54
NT2RP3000341	F-NT2RP3000341	0.43
NT2RP3000418	F-NT2RP3000418	0.53
NT2RP3000451	F-NT2RP3000451	0.46
NT2RP3000561	F-NT2RP3000561	0.47
NT2RP3000582	F-NT2RP3000582	0.44
NT2RP3001007	F-NT2RP3001007	0.26
NT2RP3001281	F-NT2RP3001281	0.36
NT2RP3001318	F-NT2RP3001318	0.21
NT2RP3001339	F-NT2RP3001339	0.58
NT2RP3001340	F-NT2RP3001340	0.41
NT2RP3001383	F-NT2RP3001383	0.36
NT2RP3001432	F-NT2RP3001432	0.34

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NT2RP3001580	F-NT2RP3001580	0.45
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NT2RP3001898	F-NT2RP3001898	0.19
NT2RP3002004	F-NT2RP3002004	0.36
NT2RP3002173	F-NT2RP3002173	0.39
NT2RP3003133	F-NT2RP3003133	0.35
NT2RP3003264	F-NT2RP3003264	0.13
NT2RP3003346	F-NT2RP3003346	0.72
NT2RP3003403	F-NT2RP3003403	0.45
NT2RP3003433	F-NT2RP3003433	0.24
NT2RP3003576	F-NT2RP3003576	0.35
NT2RP3003625	F-NT2RP3003625	0.43
NT2RP3003665	F-NT2RP3003665	0.32
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NT2RP3003842	F-NT2RP3003842	0.23
NT2RP3004070	F-NT2RP3004070	0.32
NT2RP3004470	F-NT2RP3004470	0.46
NT2RP4000023	F-NT2RP4000023	0.33
NT2RP4000035	F-NT2RP4000035	0.56
NT2RP4000102	F-NT2RP4000102	0.38
NT2RP4000167	F-NT2RP4000167	0.42
NT2RP4000214	F-NT2RP4000214	0.33
NT2RP4000218	F-NT2RP4000218	0.37
NT2RP4000424	F-NT2RP4000424	0.48
NT2RP4000915	F-NT2RP4000915	0.37
NT2RP4002075	F-NT2RP4002075	0.43
OVARC1000017	F-OVARC1000017	0.14
OVARC1000068	F-OVARC1000068	0.17
OVARC1000085	F-OVARC1000085	0.46
OVARC1000092	F-OVARC1000092	0.58
OVARC1000145	F-OVARC1000145	0.53
OVARC1000414	F-OVARC1000414	0.40
OVARC1000486	F-OVARC1000486	0.15
OVARC1000496	F-OVARC1000496	0.36
OVARC1000526	F-OVARC1000526	0.33
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OVARC1001011	F-OVARC1001011	0.42
OVARC1001240	F-OVARC1001240	0.14
OVARC1001600	F-OVARC1001600	0.37
OVARC1001805	F-OVARC1001805	0.51
OVARC1001813	F-OVARC1001813	0.58
OVARC1001846	F-OVARC1001846	0.59
PLACE1000540	F-PLACE1000540	0.35
PLACE1000599	F-PLACE1000599	0.37
PLACE1001088	F-PLACE1001088	0.36

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PLACE1001440	F-PLACE1001440	0. 45
PLACE1001517	F-PLACE1001517	0. 41
PLACE1001672	F-PLACE1001672	0. 35
PLACE1001705	F-PLACE1001705	0. 11
PLACE1001756	F-PLACE1001756	0. 67
PLACE1002157	F-PLACE1002157	0. 68
PLACE1002205	F-PLACE1002205	0. 55
PLACE1002227	F-PLACE1002227	0. 14
PLACE1002259	F-PLACE1002259	0. 47
PLACE1002319	F-PLACE1002319	0. 29
PLACE1002399	F-PLACE1002399	0. 31
PLACE1002477	F-PLACE1002477	0. 35
PLACE1002500	F-PLACE1002500	0. 26
PLACE1002583	F-PLACE1002583	0. 49
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PLACE1002968	F-PLACE1002968	0. 33
PLACE1003238	F-PLACE1003238	0. 46
PLACE1003420	F-PLACE1003420	0. 42
PLACE1003478	F-PLACE1003478	0. 20
PLACE1003566	F-PLACE1003566	0. 35
PLACE1003593	F-PLACE1003593	0. 42
PLACE1003618	F-PLACE1003618	0. 36
PLACE1004274	F-PLACE1004274	0. 41
PLACE1004681	F-PLACE1004681	0. 25
PLACE1004716	F-PLACE1004716	0. 49
PLACE1004773	F-PLACE1004773	0. 31
PLACE1004815	F-PLACE1004815	0. 72
PLACE1004836	F-PLACE1004836	0. 39
PLACE1004913	F-PLACE1004913	0. 44
PLACE1004979	F-PLACE1004979	0. 44
PLACE1005052	F-PLACE1005052	0. 63
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PLACE1005108	F-PLACE1005108	0. 17
PLACE1005128	F-PLACE1005128	0. 40
PLACE1005176	F-PLACE1005176	0. 48
PLACE1005467	F-PLACE1005467	0. 37
PLACE1005639	F-PLACE1005639	0. 33
PLACE1005850	F-PLACE1005850	0. 54
PLACE1005932	F-PLACE1005932	0. 20
PLACE1006003	F-PLACE1006003	0. 71
PLACE1006017	F-PLACE1006017	0. 42
PLACE1006288	F-PLACE1006288	0. 34

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PLACE1006371	F-PLACE1006371	0. 43
PLACE1006506	F-PLACE1006506	0. 28
PLACE1006629	F-PLACE1006629	0. 44
PLACE1006795	F-PLACE1006795	0. 35
PLACE1006904	F-PLACE1006904	0. 20
PLACE1007478	F-PLACE1007478	0. 70
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PLACE1007743	F-PLACE1007743	0. 28
PLACE1007829	F-PLACE1007829	0. 16
PLACE1007877	F-PLACE1007877	0. 16
PLACE1008181	F-PLACE1008181	0. 39
PLACE1008330	F-PLACE1008330	0. 86
PLACE1008584	F-PLACE1008584	0. 61
PLACE1008630	F-PLACE1008630	0. 09
PLACE1008715	F-PLACE1008715	0. 36
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PLACE1009048	F-PLACE1009048	0. 24
PLACE1009493	F-PLACE1009493	0. 35
PLACE1009539	F-PLACE1009539	0. 31
PLACE1009637	F-PLACE1009637	0. 58
PLACE1009925	F-PLACE1009925	0. 17
PLACE1009947	F-PLACE1009947	0. 42
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PLACE1011185	F-PLACE1011185	0. 66
PLACE1011452	F-PLACE1011452	0. 72
PLACE1011465	F-PLACE1011465	0. 51
PLACE1011492	F-PLACE1011492	0. 19
PLACE1011520	F-PLACE1011520	0. 54
PLACE1011567	F-PLACE1011567	0. 51
PLACE1011643	F-PLACE1011643	0. 21
PLACE1011719	F-PLACE1011719	0. 55
PLACE1011749	F-PLACE1011749	0. 24
PLACE2000011	F-PLACE2000011	0. 48
PLACE2000017	F-PLACE2000017	0. 34
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PLACE2000187	F-PLACE2000187	0. 40
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PLACE2000366	F-PLACE2000366	0. 33
PLACE2000394	F-PLACE2000394	0. 54
PLACE2000398	F-PLACE2000398	0. 44
PLACE2000425	F-PLACE2000425	0. 47
PLACE2000450	F-PLACE2000450	0. 53
PLACE2000477	F-PLACE2000477	0. 36
PLACE3000119	F-PLACE3000119	0. 40
PLACE3000207	F-PLACE3000207	0. 32
PLACE3000230	F-PLACE3000230	0. 51
PLACE3000271	F-PLACE3000271	0. 41
PLACE3000373	F-PLACE3000373	0. 37
PLACE3000399	F-PLACE3000399	0. 42
PLACE3000401	F-PLACE3000401	0. 37
PLACE3000406	F-PLACE3000406	0. 46
PLACE4000247	F-PLACE4000247	0. 64
PLACE4000320	F-PLACE4000320	0. 36
PLACE4000344	F-PLACE4000344	0. 31
PLACE4000367	F-PLACE4000367	0. 32
PLACE4000401	F-PLACE4000401	0. 54
PLACE4000548	F-PLACE4000548	0. 26
THYRO1000111	F-THYRO1000111	0. 53
THYRO1000129	F-THYRO1000129	0. 45
THYRO1000187	F-THYRO1000187	0. 46
THYRO1000279	F-THYRO1000279	0. 09
THYRO1000484	F-THYRO1000484	0. 36
THYRO1000596	F-THYRO1000596	0. 47
THYRO1000625	F-THYRO1000625	0. 59
THYRO1000793	F-THYRO1000793	0. 17
THYRO1000815	F-THYRO1000815	0. 58
THYRO1000865	F-THYRO1000865	0. 55
THYRO1001003	F-THYRO1001003	0. 34
THYRO1001031	F-THYRO1001031	0. 43
THYRO1001133	F-THYRO1001133	0. 52
THYRO1001321	F-THYRO1001321	0. 37
THYRO1001401	F-THYRO1001401	0. 36
THYRO1001426	F-THYRO1001426	0. 32
THYRO1001434	F-THYRO1001434	0. 39
THYRO1001559	F-THYRO1001559	0. 45
THYRO1001570	F-THYRO1001570	0. 35
THYRO1001706	F-THYRO1001706	0. 45
THYRO1001746	F-THYRO1001746	0. 43
THYRO1001772	F-THYRO1001772	0. 37

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THYR01001907	F-THYR01001907	0.33
Y79AA1000033	F-Y79AA1000033	0.53
Y79AA1000346	F-Y79AA1000346	0.53
Y79AA1000410	F-Y79AA1000410	0.13
Y79AA1000805	F-Y79AA1000805	0.32
Y79AA1001692	F-Y79AA1001692	0.45
Y79AA1002103	F-Y79AA1002103	0.15
Y79AA1002220	F-Y79AA1002220	0.49

EXAMPLE 13

Full-length sequence analysis and homology search

[0192] Full-length sequence was determined for each selected cDNA clones. The nucleotide sequence determination was performed mainly by the dye-terminator method using custom synthesized DNA primers according to the primer walking procedure (custom synthesized DNA primers were used for sequencing; sequencing reaction was performed with DNA sequencing reagent supplied by PE Biosystems according to the supplier' s manual; and the samples were analyzed in an automatic sequencer made by the same supplier). Sequence determination of some clones was carried out in the same manner but using a Licor DNA sequencer. Overlapping partial nucleotide sequences, which were obtained by the above-described method, were assembled together to determine a full-length nucleotide sequence. Amino acid sequences were then deduced from the determined full-length nucleotide sequences. However, amino acid sequence is not shown for a clone of which coding region was hard to be deduced or of which amino acid sequence has less than 100 amino acid residues. SEQ ID NOs corresponding to the respective clones are indicated in Table 350 and Table 351.

[0193] GenBank, Swiss-Prot and UniGene were searched for the determined nucleotide sequences by BLAST analysis. Matching data of cDNA clone which exhibits higher homology and of which functions are easily predicted based on the nucleotide sequences and the deduced amino acid sequences are selected from the BLAST analysis matching data with P value of 10^{-4} or less. The matching data selected are listed herein. The results of homology search 6, 12, 13, and 14 are indicated in the last part of this specification. However, there are some clones that did not match the criteria for judgment and such matching data of BLAST analysis are not shown herein.

EXAMPLE 14

Novel full-length cDNA clone obtained from a cDNA library prepared by oligo-capping method

[0194] A cDNA clone, NT2RP4002298, was obtained from a cDNA library, NT2RP4 (see Example 1), prepared by oligo-capping method. Analysis of the entire nucleotide sequence of the clone has revealed that the clone encodes a novel protein consisting of 775 amino acids. The ATGpr1 score at the initiation codon of the amino acid sequence is 0.16, and therefore, the fullness ratio is low. However, the sequence can be full-length.

[0195] The full-length nucleotide sequence of NT2RP4002298 is shown in SEQ ID NO: 12370, and the deduced amino acid sequence encoded by the clone NT2RP4002298 is shown in SEQ ID NO: 12371.

EXAMPLE 15

Gene expression analysis with hybridization using high density DNA filter

[0196] Nylon membrane for DNA spotting was prepared according to the following procedure. E. coli was cultured in each well of a 96-well plate (in a LB medium at 37°C for 16 hours). A small aliquot of each culture was suspended in 10 μl of sterile water in a well of a 96-well plate. The plate was heated at 100°C for 10 minutes. Then the boiled samples were analyzed by PCR reaction. PCR was performed in a 20 μl solution by using TaKaRa PCR Amplification Kit (Takara) according to the supplier' s protocol. Primers used for the amplification of an insert cDNA in a plasmid were a pair of sequencing primers, ME761FW (5' tacggaagtgttacttctgc 3' / SEQ ID NO: 13290) and ME1250RV (5' tgtgggaggttttttctcta 3' / SEQ ID NO: 13291), or a pair of primers, M13M4 (5' gttttcccagtcacgac 3' / SEQ ID NO: 13292)

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and M13RV (5' caggaaacagctatgac 3' / SEQ ID NO: 13293). PCR reaction was performed in a thermal cycler, GeneAmp System 9600 (PE Biosystems). The cycling profile consisted of pre-heat at 95°C for 5 mimutes; 10 cycles of denaturation at 95°C for 10 seconds, and annealing/extension at 68°C for 1 minute; 20 cycles of denaturation at 98°C for 20 seconds and annealing/extension at 60°C for 3 minutes; and final extension at 72°C for 10 minutes. After the PCR reaction, the 20 μl reaction solution was loaded onto a 1 % agarose gel and fractionated by electrophoresis. DNA on the gel was stained with ethidium bromide to confirm the amplification of cDNA. When cDNAs were barely amplified by PCR, plasmids containing the corresponding insert cDNAs were prepared by the alkali-extraction method (J. Sambrook, E. F., Fritsh, & T. Maniatis, "Molecular Cloning, A laboratory manual/ 2nd edition, Cold Spring Harbor Laboratory Press, 1989).

[0197] Preparation of DNA array was carried out by the following procedure. An Aliquot of a DNA solution was added in each well of a 384-well plate. DNA was spotted onto a nylon membrane (Boehringer) by using a 384-pin tool of Biomek 2000 Laboratory Automation Sysytem (Beckman-Coulter). Specifically, the 384-well plate containing the DNA was placed under the 384-pin tool. The independent 384 needles were simultaneously dipped into the DNA solution for DNA deposition. The needles were gently pressed onto a nylon membrane and the DNA deposited at the tips of needles was spotted onto the membrane. Denaturation of the spotted DNA and immobilization of the DNA on the nylon membrane were carried out according to usual manners (J. Sambrook, E.F., Fritsh, & T. Maniatis, "Molecular Cloning, A laboratory manual/ 2nd edition, Cold Spring Harbor Laboratory Press, 1989).

[0198] Hybridization probe used was radioisotope-labeled 1st strand cDNA. The 1st strand cDNA synthesis was performed by using Thermoscript(TM) RT-PCR System (GIBCO). Specifically, the 1st strand cDNA was synthesized by using 1.5 μg mRNAs from various human tissues (Clontech), 1 μl aliquots of 50 μM Oligo(dT)20 and 50 μCi [α ^{33}P] dATP according to an attached protocol. Probe purification was carried out by using ProbeQuant(TM) G-50 micro column (Amersham-Pharmacia Biotech) according to an attached protocol. In the next step, 2 units of E. coli RNasH were added to the reaction mixture. The mixture was incubated at room temperature for 10 minutes and then 100 μg of human COT-1 DNA (GIBCO) was added thereto. The mixture was incubated at 97°C for 10 minutes and then was allowed to stand on ice to give hybridization probe.

[0199] Hybridization of the radioisotope-labeled probe to the DNA array was performed in a usual manner (J. Sambrook, E.F., Fritsh, & T. Maniatis, Molecular Cloning, A laboratory manual/ 2nd edition, Cold Spring Harbor Laboratory Press, 1989). The membrane was washed as follows: the nylon membrane was incubated in Washing solution 1 (2 × SSC, 1% SDS) at room temperature (about 26°C) for 20 minutes and this washing was repeated 3 times; then the membrane was washed 3 times by incubating it in Washing solution 2 (0.1 × SSC, 1% SDS) at 65°C for 20 minutes. Autoradiography was performed by using an image plate for BAS2000 (Fuji Photo Film Co.. Ltd.). Specifically, the nylon membrane with probe hybridized thereon was wrapped with a piece of Saran Wrap and brought into tight contact with the image plate on the light-sensitive surface. The membrane with the image plate was placed in an imaging cassette for radioisotope and allowed to stand in dark place for 4 hours. The radioactivity recorded on the image plate was analyzed by using BAS2000 (Fuji Photo Film Co., Ltd.). The activity was subjected to electronic conversion and recorded as an image file of autoradiogram. The signal intensity of each DNA spot was analyzed by using Visage High Density Grid Analysis Systems (Genomic Solutions Inc.). The signal intensity was converted into numerical data. The data were taken by duplicated measurements. The reproducibility was assessed by comparing the signal intensities of the corresponding spots on the duplicated DNA filters that were hybridized to a single DNA probe (Figure 2). The ratio between the corresponding spots falls within a range of 2 or less in 95% of entire spots and the correlation coefficient is r=0.97. Thus the reproducibility is assumed to be satisfactory.

[0200] The detection sensitivity in gene expression analysis was estimated by examining increases in the signal intensity of probe concentration-dependent spot in hybridization using a probe complementary to the DNA spotted on the nylon membrane. DNA used was PLACE1008092 (same as DNA deposited in GenBank under an Accession No. AF107253). The DNA array with DNA of PLACE1008092 was prepared according to the above-mentioned method. The probe used was prepared as follows: mRNA was synthesized in vitro from the clone, PLACE1008092. By using this mRNA as a template, radioisotope-labeled 1st strand cDNA was synthesized in the same manner as described above, and the cDNA was used as the probe. The cDNA PLACE1008092 was inserted into pBluescript SK(-), of which T7 promoter was ligated to the 5' end of the cDNA, to give a plasmid for in vitro synthesis of the mRNA from PLACE1008092. Specifically, the PLACE1008092 insert was cut out from pME18SFL3 carrying the cDNA at a DraIII site thereof by XhoI digestion. The resulting PLACE1008092 fragment was ligated to XhoI-predigested pBluescript SK (-) by using DNA ligation kit ver.2 (Takara). The in-vitro mRNA synthesis from PLACE1008092 inserted in pBluescript SK(-) was carried out by using Ampliscribe(TM) T7 high yield transcription kit (Epicentre technologies). Hybridization and the analysis of signal intensity of each DNA spot were conducted by the same methods as described above. When the probe concentration is 1 × 10^7 μg/ml or less, there was no increase of signal intensity proportional to the probe concentration. Therefore it was assumed to be difficult to compare the signals with one another in the concentration range. Thus the spots with the intensity of 40 or less were indiscriminately taken as low-level signals (Figure 3). Within a concentration of the probe ranging from 1 × 10^7 μg/ml to 0.1 μg/ml, the signal was found to increase in a probe

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concentration-dependent manner. The detection limit w[illegible]en assumed to be 1:100,000 in a ratio of mRNA expression level in a sample.

[0201] Tables 12-168 (also containing clones with d[illegible]escription in Examples) show the expression of each cDNA in human normal tissues (heart, lung, pituitary gland, t[illegible]mus, brain, kidney, liver and spleen). The expression levels are indicated by numerical values of 0-10,000. Gene[illegible]hat were expressed in at least a single tissue are indicated below by the corresponding clone names:

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[0202] Genes that were expressed in all the tissues tested are indicated below by the corresponding clone names:

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[0203] Genes that were expressed at low levels in any of the tissues tested are indicated below by the corresponding clone names:

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[0204] Genes exhibiting characteristic features in the expression thereof were selected by statistical analysis of these data. Two examples are shown below to describe the selection of genes of which expression is varied greatly among tissues. The β' actin gene is used frequently as a control in gene expression analysis. Genes of which expression is varied greatly among tissues as compared that of the β-actin gene were determined as follows. Specifically, sum of squared deviation was calculated in the signal intensity of β-actin observed in each tissue, which was divided by 7 degrees of freedom to determine a variance S_a^2. Next, sum of squared deviation was calculated in the signal intensity of a gene to be compared observed in each tissue, which was divided by 7 degrees of freedom to determine a variance S_b^2. By taking variance ratio F as $F=S_b^2/S_a^2$, genes with a significance level of 5% or more were extracted in the F distribution. Genes extracted are indicated below by the corresponding clone names:
HEMBA1002113, HEMBA1005296, HEMBA1007121, HEMBB1000637, HEMBB1000915, MAMMA1000597, MAMMA1000605, MAMMA1000962, MAMMA1001139, MAMMA1001198, MAMMA1002858, NT2RM2001896, NT2RP2002710, NT2RP2004339, NT2RP2004538, NT2RP3000348, NT2RP3003121, PLACE3000009,

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PLACE3000254, THYRO1000569, Y79AA1000131.

[0205] Gene of OVARC1000037 {heterogeneous nuclear ribonucleoprotein (hnRNP)} which expression is varied little. Genes of which expression is varied greatly among tissues as compared that of the OVARC1000037 gene were determined as follows. Specifically, sum of squared deviation was calculated in the signal intensity of β-actin observed in each tissue, which was divided by 7 degrees of freedom to determine a variance S_a^2. Next, sum of squared deviation was calculated in the signal intensity of a gene to be compared observed in each tissue, which was divided by 7 degrees of freedom to determine a variance S_b^2. By taking variance ratio F as $F=S_b^2/S_a^2$, genes with a significance level of 5% or more were extracted in the F distribution. Genes extracted are indicated below,by the corresponding clone names:

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HEMBA1002160,	HEMBA1001824,	HEMBA1001463,	HEMBA1001533,	HEMBA1001570,
PLACE1001036,	HEMBA1001651,	HEMBA1002381,	HEMBA1002934,	HEMBA1003370,
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HEMBA1003758,	NT2RP2000108,	HEMBA1003838,	NT2RP1000357,	HEMBA1003376,
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NT2RP2001394,	HEMBA1004753,	NT2RP2002621,	HEMBA1005853,	HEMBA1005443,
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[0206] Thus, characteristic features in the expression of a gene are illustrated by comparing and _ statistically analyzing the expression of many genes.

Analysis of disease-associated genes

[0207] Non-enzymic protein glycation reaction is believed to be a cause of a variety of chronic diabetic complications. Accordingly, genes of which expression is elevated or decreased in a glycated protein-specific manner in the endothelial cells are associated with diabetic complications caused by glycated proteins. Vascular endothelial cells are affected with glycated proteins present in blood. Reaction products of non-enzymic protein glycation include amadori compound (glycated protein) as a mildly glycated protein and advanced glycation endproduct as a heavily glycated protein. Hence, a survey was carried out for genes of which expression levels are varied depending on the presence of these glycated proteins in endothelial cells. The mRNAs were extracted from endothelial cells that were cultured in the presence or absence of glycated protein. The mRNAs were converted into radiolabeled first strand cDNAs for preparing probes. The probes were hybridized to the above-mentioned DNA array. Signal of each DNA spot was detected by BAS2000 and analyzed by ArrayGauge (Fuji Photo Film Co., Ltd.).

[0208] Advanced glycation endproduct of bovine serum albumin was prepared as follows: bovine serum albumin (BSA; Sigma) was incubated in a phosphate buffer solution containing 50 mM glucose at 37°C for 8 weeks; and the resulting brownish BSA was dialyzed against a phosphate buffer solution.

[0209] Human normal pulmonary arterial endothelial cells (Cell Applications) were cultured in an Endothelial Cell Growth Medium (Cell Applications). The culture dish (Farcon) with the cells were incubated in a CO_2 incubator (37°C, 5% CO_2, in a humid atmosphere). When the cells were grown to be confluent in the dish, 250 μg/ml of bovine serum albumin (sigma), glycated bovine serum albumin (Sigma) or advanced glycation endproduct of bovine serum albumin was added thereto and the cells were incubated for 33 hours. The mRNA was extracted from the cells by using a FastTack(TM) 2.0 kit (Invitrogen). The labeling of hybridization probe was carried out by using the mRNA according to the same procedure as described above.

[0210] Table 169 shows the expression level of each cDNA in human pulmonary arterial endothelial cells cultured in a medium containing bovine serum albumin (sigma), glycated bovine serum albumin (Sigma) or advanced glycation endproduct of bovine serum albumin. Genes of which expression was detected in the endothelial cell are as follows:

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[0211] Signal ratios of EC_AGE_BSA to EC_BSA and of EC_glycated_BSA to EC_BSA were calculated for each gene. Genes with high signal ratios were selected. In the case of calculating the ratio of signal value of 40 or less to that of more than 40, such signal values were, for convenience, taken as 40 instead of the real values. When the ratio EC_AGE_BSA/EC_BSA is 2 or more, expression of the genes exhibiting such ratio is expected to be elevated due to advanced glycation endproduct of bovine serum albumin. The higher the value is, the higher the gene expression level is. When the ratio EC_AGE_BSA/EC_BSA ranges from 0.5 to 2, expression of the genes exhibiting such ratio is expected to be unaffected due to advanced glycation endproduct of bovine serum albumin. When the ratio EC_AGE_BSA/EC_BSA is less than 0.5, expression of the genes exhibiting such ratio value is expected to be decreased due to advanced glycation endproduct of bovine serum albumin. The lower the value is, the lower the gene expression level is.

[0212] Clone with EC_AGE_BSA/EC_BSA ratio of 2 or higher are as follows: HEMBA1003958, MAMMA1001256, PLACE2000411.

[0213] Clone with EC_AGE_BSA/EC_BSA ratio of 0.5 or less is as follows: MAMMA1001783.
These cDNAs are associated with diabetes.

[0214] When the ratio EC_glycated_BSA/EC_BSA is 2 or more, the expression level of the gene exhibiting such ratio is expected to be elevated due to glycated bovine serum albumin. The higher the value is, the higher the gene expression level is. When the ratio EC_glycated_BSA/EC_BSA ranges from 0.5 to 2, the expression level of the gene exhibiting such ratio is expected to be unaffected with glycated bovine serum albumin. When the ratio EC_glycated_BSA/EC_BSA is less than 0.5, the expression level of a gene exhibiting such ratio is expected to be decreased due to glycated bovine serum albumin. The lower the value is, the lower the gene expression level is.

[0215] Clones with EC_glycated_BSA/EC_BSA ratio of 2 or more are as follows: HEMBA1004850, MAMMA1001256, MAMMA1002132 and PLACE3000119.

[0216] A clone with EC_glycated_BSA/EC_BSA ratio of 0.5 or less is as follows: MAMMA1001783.

[0217] These cDNAs are also associated with diabetes.

Analysis of genes associated with neural cell differentiation

[0218] Genes involved in neural cell differentiation are useful for treating neurological diseases. It is possible that genes with varying expression levels in response to induction of cellular differentiation in neural cells are associated with neurological diseases.

[0219] A survey was performed for genes of which expression levels are varied in response to induction of differentiation (stimulation by retinoic acid (RA)) in cultured cells of a neural strain, NT2.

[0220] The NT2 cells were treated basically according to supplier' s instruction manual. "Undifferentiated NT2 cells" means NT2 cells successively cultured in an Opti-MEM I (GIBCO-BRL; catalog No. 31985) containing 10%(v/v) fetal bovine serum and 1%(v/v) penicillin-streptomycin (GIBCO BRL). "NT2 cells cultured in the presence of retinoic acid" means the cells resulted from transferring undifferentiated NT2 cells into a retinoic acid-containing medium, which consists of D-MEM (GIBCO BRL; catalog No. 11965), 10%(v/v) fetal bovine serum, 1%(v/v) penicillin-streptomycin and 10 μM retinoic acid (GIBCO-BRL), and the subsequent successive culture therein for 5 weeks. "NT2 cells that were cultured in the presence of retinoic acid and then further cultured in the presence of cell-division inhibitor added" means NT2 cells resulted from transferring NT2 cells cultured in the presence of retinoic acid for 5 weeks into a cell-division inhibitor-containing medium, which consisted of D-MEM(GIBCO BRL; catalog No.11965), 10%(v/v) fetal bovine serum, 1%(v/v) penicillin-streptomycin, 10μM retinoic acid, 10 μM FudR (5-fluoro-2' -deoxyuridine: GIBCO BRL), 10 μM Urd (Uridine: GIBCO BRL) and 1 μM araC (Cytosine β-D-Arabinofuranoside: GIBCO BRL), and the subsequence succes-

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sive culture for 2 weeks. Each of the cells were treated with trypsin and then harvested. Total RNAs were extracted from the cells by using S.N.A.P.(TM) Total RNA Isolation kit (Invitrogen(r)). The labeling of probe used for hybridization was carried out by using 10 μg of the total RNA according to the same methods as described above. The data were obtained in triplicate (n=3). The data of signal value representing gene expression level in the cells in the presence of stimulation for inducing differentiation were compared with those in the absence of the stimulation. The comparison was performed by statistical treatment-of two-sample t-test. Clones with significant difference in the signal distribution were selected under the condition of $p<0.05$. In this analysis, clones with the difference can be statistically detected even when the signals were low. Accordingly, clones with signal value of 40 or less were also assessed for the selection.

[0221] Tables 170-349 show the expression level of each cDNA in undifferentiated NT2 cells, NT2 cells cultured in the presence of RA, and NT2 cells that were cultured in the presence of RA and that were further cultured in the presence of cell-division inhibitor added.

[0222] Averaged signal values (M_1, M_2) and sample variances (s_1^2, s_2^2) were calculated for each gene in each of the cells, and then, the pooled sample variances s^2 were obtained from the sample variances of the two types of cells to be compared. The t values were determined according to the following formula: $t=(M1-M2)/s/(1/3+1/3)^{1/2}$. When the determined t-value was greater than a t-value at P, which means the probability of significance level, of 0.05 or 0.01 in the t-distribution table with 4 degrees of freeedom, the difference was judged to be found in the expression level of the gene between the two types of cells at $p<0.05$ or $p<0.01$, respectively. The tables also include the information on an increase (+) or decrease (-) in the expression level of a gene in the treated cells when the level is compared with that of untreated undifferentiated cells.

[0223] Clones of which expression levels increased by RA are as follows:

HEMBA1000005, HEMBA1000042, HEMBA1000046, HEMBA1000076, HEMBA1000111, HEMBA1000141,
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HEMBA1000357, HEMBA1000376, HEMBA1000387, HEMBA1000392, HEMBA1000428, HEMBA1000456,
HEMBA1000459, HEMBA1000469, HEMBA1000504, HEMBA1000508, HEMBA1000519, HEMBA1000540,
HEMBA1000545, HEMBA1000557, HEMBA1000563, HEMBA1000568, HEMBA1000575, HEMBA1000588,
HEMBA1000592, HEMBA1000604, HEMBA1000622, HEMBA1000655, HEMBA1000673, HEMBA1000682,
HEMBA1000726, HEMBA1000727, HEMBA1000749, HEMBA1000769, HEMBA1000774, HEMBA1000791,
HEMBA1000822, HEMBA1000872, HEMBA1000876, HEMBA1000910, HEMBA1000942, HEMBA1000943,
HEMBA1000960, HEMBA1000972, HEMBA1000974, HEMBA1000991, HEMBA1001008, HEMBA1001020,
HEMBA1001043, HEMBA1001051, HEMBA1001060, HEMBA1001071, HEMBA1001077, HEMBA1001085,
HEMBA1001094, HEMBA1001109, HEMBA1001121, HEMBA1001122, HEMBA1001140, HEMBA1001172,
HEMBA1001226, HEMBA1001235, HEMBA1001265, HEMBA1001281, HEMBA1001294, HEMBA1001299,
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HEMBA1002886, HEMBA1002934, HEMBA1002935, HEMBA1002939, HEMBA1002951, HEMBA1002968,
HEMBA1002970, HEMBA1002973, HEMBA1002999, HEMBA1003021, HEMBA1003033, HEMBA1003034,
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HEMBA1003142, HEMBA1003148, HEMBA1003166, HEMBA1003175, HEMBA1003197, HEMBA1003199,
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[0224] Clones of which expression levels decreased by RA are as follows:

HEMBA1000946, HEMBA1003569, HEMBA1005570, HEMBB1000915, NT2RM1000666, NT2RM2000092, NT2RM2000594, NT2RM2001256, NT2RM4001754, NT2RM4001905, NT2RP2001675, NT2RP2002047, NT2RP2005491, NT2RP3000980, NT2RP3002081, NT2RP3004594, NT2RP4001950, NT2RP4002408, OVARC1000431, OVARC1001942, OVARC1001943, PLACE1003190, PLACE1004868, PLACE1005923, PLACE1007257, PLACE1010624, Y79AA1000346.

[0225] Clones of which expression levels increase by RA/inhibitor are as follows:

HEMBA1000046, HEMBA1000307, HEMBA1000434, HEMBA1000504, HEMBA1000588, HEMBA1000682, HEMBA1000726, HEMBA1000943, HEMBA1001071, HEMBA1001094, HEMBA1001122, HEMBA1001323, HEMBA1001361, HEMBA1001455, HEMBA1001709, HEMBA1001746, HEMBA1001869, HEMBA1002084, HEMBA1002583, HEMBA1002628, HEMBA1002801, HEMBA1002937, HEMBA1003096, HEMBA1003142, HEMBA1003229, HEMBA1003276, HEMBA1003309, HEMBA1003463, HEMBA1003597, HEMBA1003617, HEMBA1003725, HEMBA1003803, HEMBA1003879, HEMBA1003989, HEMBA1004000, HEMBA1004015, HEMBA1004024, HEMBA1004049, HEMBA1004056, HEMBA1004199, HEMBA1004248, HEMBA1004356, HEMBA1004554, HEMBA1004666, HEMBA1004725, HEMBA1004770, HEMBA1004803, HEMBA1004923, HEMBA1004934, HEMBA1004954, HEMBA1005039, HEMBA1005075, HEMBA1005113, HEMBA1005219, HEMBA1005232, HEMBA1005251, HEMBA1005304, HEMBA1005367, HEMBA1005372, HEMBA1005403, HEMBA1005410, HEMBA1005411, HEMBA1005548, HEMBA1005581, HEMBA1005631, HEMBA1005666, HEMBA1005755, HEMBA1005780, HEMBA1006067, HEMBA1006130, HEMBA1006364, HEMBA1006485, HEMBA1006559, HEMBA1006579, HEMBA1006754, HEMBB1000059, HEMBB1000575, HEMBB1000709, HEMBB1000822, HEMBB1000848, HEMBB1000852, HEMBB1000913, HEMBB1000985, HEMBB1001117, HEMBB1001210, HEMBB1001317, HEMBB1001394, HEMBB1001443, HEMBB1001668, HEMBB1001695, HEMBB1002049, HEMBB1002254, HEMBB1002266, HEMBB1002371, HEMBB1002502, HEMBB1002614, HEMBB1002617, HEMBB1002692, HEMBB1002697, MAMMA1000241, MAMMA1000424, MAMMA1000616,

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MAMMA1000731, MAMMA1000824, MAMMA1000908, MAMMA1000956, MAMMA1001038, MAMMA1001091, MAMMA1001243, MAMMA1001815, MAMMA1001820, MAMMA1002267, MAMMA1002769, MAMMA1002871, MAMMA1002941, NT2RM1000355, NT2RM1000725, NT2RM1000829, NT2RM1000850, NT2RM1000898, NT2RM2000504, NT2RM2000635, NT2RM2000718, NT2RM2000821, NT2RM2001370, NT2RM2001582, NT2RM2001592, NT2RM2001613, NT2RM2001632, NT2RM2001635, NT2RM2001648, NT2RM2001659, NT2RM2001671, NT2RM2001695, NT2RM2001760, NT2RM2001782, NT2RM2001839, NT2RM2001879, NT2RM2001983, NT2RM4000104, NT2RM4000290, NT2RM4000425, NT2RM4000433, NT2RM4000471, NT2RM4000531, NT2RM4000852, NT2RM4001047, NT2RM4001347, NT2RM4001454, NT2RM4001557, NT2RM4001566, NT2RM4001582, NT2RM4001938, NT2RM4001953, NT2RM4002018, NT2RM4002409, NT2RM4002558, NT2RM4002594, NT2RP1000259, NT2RP1000418, NT2RP1000574, NT2RP1000629, NT2RP1000782, NT2RP1000856, NT2RP1000943, NT2RP1000988, NT2RP1001013, NT2RP1001173, NT2RP1001546, NT2RP2000091, NT2RP2000208, NT2RP2000274, NT2RP2000329, NT2RP2000369, NT2RP2000634, NT2RP2000842, NT2RP2000943, NT2RP2000987, NT2RP2001094, NT2RP2001277, NT2RP2001290, NT2RP2001366, NT2RP2001423, NT2RP2001436, NT2RP2001467, NT2RP2001506, NT2RP2001601, NT2RP2001663, NT2RP2001926, NT2RP2001985, NT2RP2002032, NT2RP2002041, NT2RP2002046, NT2RP2002078, NT2RP2002124, NT2RP2002185, NT2RP2002193, NT2RP2002312, NT2RP2002316, NT2RP2002426, NT2RP2002457, NT2RP2002475, NT2RP2002520, NT2RP2002595, NT2RP2002643, NT2RP2002672, NT2RP2002701, NT2RP2002710, NT2RP2002727, NT2RP2003099, NT2RP2003121, NT2RP2003137, NT2RP2003158, NT2RP2003206, NT2RP2003230, NT2RP2003272, NT2RP2003280, NT2RP2003347, NT2RP2003393, NT2RP2003401, NT2RP2003445, NT2RP2003456, NT2RP2003511, NT2RP2003517, NT2RP2003543, NT2RP2003596, NT2RP2003706, NT2RP2003871, NT2RP2004681, NT2RP2004743, NT2RP2004775, NT2RP2004933, NT2RP2004967, NT2RP2005003, NT2RP2005270, NT2RP2005289, NT2RP2005344, NT2RP2005453, NT2RP2005555, NT2RP2005767, NT2RP2005853, NT2RP2006043; NT2RP2006393, NT2RP2006436, NT2RP2006441, NT2RP2006467, NT2RP2006534, NT2RP2006565, NT2RP3000348, NT2RP3000359, NT2RP3000366, NT2RP3000403, NT2RP3000418, NT2RP3000441, NT2RP3000561, NT2RP3000759, NT2RP3000826, NT2RP3001007, NT2RP3001096, NT2RP3001126, NT2RP3001355, NT2RP3001396, NT2RP3001449, NT2RP3001490, NT2RP3001679, NT2RP3001727, NT2RP3001752, NT2RP3001777, NT2RP3001782, NT2RP3001799, NT2RP3001854, NT2RP3001989, NT2RP3002142, NT2RP3002248, NT2RP3002343, NT2RP3002484, NT2RP3002529, NT2RP3002549, NT2RP3002628, NT2RP3002687, NT2RP3002688, NT2RP3002810, NT2RP3003032, NT2RP3003139, NT2RP3003193, NT2RP3003203, NT2RP3003204, NT2RP3003210, NT2RP3003212, NT2RP3003264, NT2RP3003282, NT2RP3003500, NT2RP3004041, NT2RP3004215, NT2RP4000147, NT2RP4000259, NT2RP4000360, NT2RP4000448, NT2RP4000524, NT2RP4000588, NT2RP4000879, NT2RP4000907, NT2RP4000989, NT2RP4001079, NT2RP4001150, NT2RP4001219, NT2RP4001260, NT2RP4001274, NT2RP4001353, NT2RP4001547, NT2RP4001677, NT2RP4002052, OVARC1000006, OVARC1000092, OVARC1000321, OVARC1000384, OVARC1000408, OVARC1000414, OVARC1000520, OVARC1000526, OVARC1000588, OVARC1000679, OVARC1000682, OVARC1000769, OVARC1000850, OVARC1000862, OVARC1000886, OVARC1000984, OVARC1001000, OVARC1001004, OVARC1001154, OVARC1001170, OVARC1001173, OVARC1001200, OVARC1001268, OVARC1001376, OVARC1001419, OVARC1001425, OVARC1001476, OVARC1001480, OVARC1001542, OVARC1001873, OVARC1001928, OVARC1001987, OVARC1002066, OVARC1002082, OVARC1002112, OVARC1002127, PLACE1000014, PLACE1000048, PLACE1000184, PLACE1000185, PLACE1000246, PLACE1000292, PLACE1000332, PLACE1000347, PLACE1000564, PLACE1000656, PLACE1000712, PLACE1001000, PLACE1001168, PLACE1001185, PLACE1001241, PLACE1001294, PLACE1001311, PLACE1001395, PLACE1001570, PLACE1001608, PLACE1001610, PLACE1001716, PLACE1001746, PLACE1001817, PLACE1001821, PLACE1001844, PLACE1001897, PLACE1002066, PLACE1002119, PLACE1002157, PLACE1002205, PLACE1002256, PLACE1002259, PLACE1002399, PLACE1002438, PLACE1002474, PLACE1002477, PLACE1002500, PLACE1002514, PLACE1002578, PLACE1002815, PLACE1002851, PLACE1002968, PLACE1003108, PLACE1003174, PLACE1003200, PLACE1003238, PLACE1003256, PLACE1003334, PLACE1003342, PLACE1003516, PLACE1003521, PLACE1003537, PLACE1003592, PLACE1003596, PLACE1003723, PLACE1003760, PLACE1003771, PLACE1003783, PLACE1003795, PLACE1003892, PLACE1003968, PLACE1004103, PLACE1004256, PLACE1004405, PLACE1004460, PLACE1004506, PLACE1004629, PLACE1004674, PLACE1004813, PLACE1004979, PLACE1005066, PLACE1005101, PLACE1005102, PLACE1005128, PLACE1005181, PLACE1005287, PLACE1005305, PLACE1005327, PLACE1005477, PLACE1005595, PLACE1005603, PLACE1005666, PLACE1005804, PLACE1005884, PLACE1005934, PLACE1006076, PLACE1006119, PLACE1006159, PLACE1006164, PLACE1006170, PLACE1006382, PLACE1006492, PLACE1006629, PLACE1006704, PLACE1006731, PLACE1006760, PLACE1006779, PLACE1006795, PLACE1006805, PLACE1006962, PLACE1007045,

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[0226] Clones of which expression levels decrease by RA/inhibitor are as follows:

HEMBA1000012, HEMBA1000501, HEMBA1000946, HEMBA1003220, HEMBA1003403, HEMBA1003569, HEMBA1003591, HEMBA1003926, HEMBA1004168, HEMBA1004507, HEMBA1005009, HEMBA1005296, HEMBA1005528, HEMBA1005570, HEMBA1006467, HEMBA1006486, HEMBA1006492, HEMBA1007322, HEMBB1000055, HEMBB1000244, HEMBB1001665, MAMMA1000684, MAMMA1001139, MAMMA1001743, NT2RM1000257, NT2RM1000318, NT2RM1000539, NT2RM1000666, NT2RM2000092, NT2RM2000192, NT2RM2000371, NT2RM2000594, NT2RM4000511, NT2RM4001140, NT2RM4001754, NT2RM4001905, NT2RM4001940, NT2RM4002593, NT2RP1000086, NT2RP1000439, NT2RP1001073, NT2RP2000098, NT2RP2000965, NT2RP2001397, NT2RP2002047, NT2RP2004226, NT2RP2004396, NT2RP2004655, NT2RP2005126, NT2RP2005464, NT2RP2005712, NT2RP2005859, NT2RP2005890, NT2RP3000980, NT2RP3001383, NT2RP3001621, NT2RP3002081, NT2RP3002181, NT2RP3002244, NT2RP3002590, NT2RP3003059, NT2RP3004258, NT2RP3004378, NT2RP3004527, NT2RP3004594, NT2RP4001760, NT2RP4001950, NT2RP4002047, NT2RP4002408, NT2RP5003459, OVARC1000004, OVARC1000035, OVARC1000431, OVARC1001051, OVARC1001129, OVARC1001176, OVARC1001261, OVARC1001342, OVARC1001942, OVARC1001943, PLACE1002171, PLACE1002465, PLACE1003190, PLACE1003375, PLACE1004128, PLACE1005026, PLACE1005876, PLACE1005923, PLACE1007257, PLACE1007375, PLACE1007507, PLACE1008941, PLACE1010624, PLACE1011090, PLACE1011219, THYRO1000270, Y79AA1000346, Y79AA1001541.

[0227] Clones of which expression levels increase in the presence of both RA and RA/inhibitor are as follows:

HEMBA1000046, HEMBA1000307, HEMBA1000504, HEMBA1000588, HEMBA1000682, HEMBA1000726, HEMBA1000943, HEMBA1001071, HEMBA1001094, HEMBA1001122, HEMBA1001323, HEMBA1001361, HEMBA1001455, HEMBA1001869, HEMBA1002084, HEMBA1002583, HEMBA1002628, HEMBA1003096, HEMBA1003142, HEMBA1003276, HEMBA1003309, HEMBA1003463, HEMBA1003597, HEMBA1003617, HEMBA1003725, HEMBA1003803, HEMBA1003879, HEMBA1003989, HEMBA1004000, HEMBA1004015, HEMBA1004024, HEMBA1004049, HEMBA1004056, HEMBA1004199, HEMBA1004248, HEMBA1004356, HEMBA1004666, HEMBA1004770, HEMBA1004803, HEMBA1004923, HEMBA1004934, HEMBA1004954, HEMBA1005039, HEMBA1005075, HEMBA1005113, HEMBA1005219, HEMBA1005232, HEMBA1005251, HEMBA1005304, HEMBA1005367, HEMBA1005410, HEMBA1005411, HEMBA1005548, HEMBA1005581, HEMBA1005631, HEMBA1005666, HEMBA1005780, HEMBA1006485, HEMBA1006559, HEMBA1006579, HEMBA1006754, HEMBB1000059, HEMBB1000575, HEMBB1000709, HEMBB1000848, HEMBB1000985, HEMBB1001117, HEMBB1001210, HEMBB1001394, HEMBB1001668, HEMBB1001695, HEMBB1002049, HEMBB1002254, HEMBB1002266, HEMBB1002371, HEMBB1002614, HEMBB1002617, HEMBB1002697, MAMMA1000241, MAMMA1000424, MAMMA1000616, MAMMA1000731, MAMMA1000824, MAMMA1001038, MAMMA1001243, MAMMA1002769, MAMMA1002871, MAMMA1002941, NT2RM1000725, NT2RM1000829, NT2RM2000504, NT2RM2000635, NT2RM2000821, NT2RM2001582, NT2RM2001592, NT2RM2001632, NT2RM2001648, NT2RM2001671, NT2RM2001695, NT2RM2001879, NT2RM4000290, NT2RM4000425, NT2RM4000471, NT2RM4000531, NT2RM4000852, NT2RM4001047,

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[0228] Clones of which expression levels decrease in the presence of both RA and RA/inhibitor are as follows: HEMBA1000946, HEMBA1003569, HEMBA1005570, NT2RM1000666, NT2RM2000092, NT2RM2000594, NT2RM4001754, NT2RM4001905, NT2RP2002047, NT2RP3000980, NT2RP3002081, NT2RP3004594, NT2RP4001950, NT2RP4002408, OVARC1000431, OVARC1001942, OVARC1001943, PLACE1003190, PLACE1005923, PLACE1007257, PLACE1010624, Y79AA1000346.

[0229] These are neurological disease-associated clones.

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Analysis of rheumatoid arthritis-associated genes

[0230] The onset of rheumatoid arthritis is thought to be involved in the proliferation of synovial cells covering inner surfaces of joint cavity and in inflammatory reaction resulted from the action of cytokines produced by leukocytes infiltrating into the joint synovial tissues (Rheumatism Information Center, http://www.rheuma-net.or.jp/). Recent studies have also revealed that tissue necrosis factor (TNF)-α participates in the onset (Current opinion in immunology 1999, 11, 657-662). When the expression of a gene exhibits responsiveness to the action of TNF on synovial cells, the gene is considered to be involved in rheumatoid arthritis.

[0231] A survey was performed for genes of which expression levels are varied in response to TNF-α in the primary cell culture of synovial tissue. The primary cultured cells of the smooth muscle (Cell Applications) were grown to be confluent in a culture dish, and then, human TNF-α (Boehringer-Mannheim) was added at a final concentration of 10 ng/ml thereto. The culture was further continued for 24 hours.

[0232] Total RNA was extracted from the cells by using S.N.A.P.(TM) Total RNA Isolation kit (Invitrogen). The labeling of probe used for hybridization was carried out by using 10 μg of the total RNA according to the same methods as described above. The data were obtained in triplicate (n=3). The data of signal value representing gene expression level in the cells in the presence of TNF stimulation were compared with those in the absence of the stimulation. The comparison was performed by statistical treatment of two-sample t-test. Clones with significant difference in the signal distribution were selected under the condition of $p<0.05$. In this analysis,
clones with the difference can be statistically detected even when the signals were low.
Accordingly, clones with signal value of 40 or less were also assessed for the selection.
Table 352 shows the expression level of each cDNA in synovial cells cultured in the absence or presence of TNF.

[0233] Averaged signal values (M_1, M_2) and sample variances (s_1^2, s_2^2) for each gene were calculated in each of the cells, and then, the pooled sample variances s^2 were obtained from the sample variances of the two types of cells to be compared. The t-values were determined according to the following formula: $t=(M_1-M_2)/s/(1/3+1/3)^{1/2}$. When the determined t-value was greater than a t-value at P, which means the probability of significance level, of 0.05 or 0.01 in the t-distribution table with 4 degrees of freedom, the difference was judged to be found in the expression level of the gene between the two types of cells at $p<0.05$ or $p<0.01$, respectively.
The tables also include the information of an increase (+) or decrease (-) in the expression level of a gene in the stimulated cells when the level is compared with that of unstimulated cells.

[0234] Clones of which expression levels are elevated by TNF-α are as follows:

HEMBA1000005,	HEMBA1000012,	HEMBA1000020,	HEMBA1000046,	HEMBA1000076,	HEMBA1000111,
HEMBA1000168,	HEMBA1000185,	HEMBA1000201,	HEMBA1000231,	HEMBA1000243,	HEMBA1000280,
HEMBA1000282,	HEMBA1000304,	HEMBA1000307,	HEMBA1000327,	HEMBA1000356,	HEMBA1000376,
HEMBA1000387,	HEMBA1000390,	HEMBA1000418,	HEMBA1000460,	HEMBA1000491,	HEMBA1000501,
HEMBA1000518,	HEMBA1000519,	HEMBA1000520,	HEMBA1000531,	HEMBA1000534,	HEMBA1000542,
HEMBA1000545,	HEMBA1000591,	HEMBA1000592,	HEMBA1000594,	HEMBA1000636,	HEMBA1000655,
HEMBA1000657,	HEMBA1000673,	HEMBA1000682,	HEMBA1000686,	HEMBA1000722,	HEMBA1000726,
HEMBA1000827,	HEMBA1000870,	HEMBA1000918,	HEMBA1000971,	HEMBA1000974,	HEMBA1000986,
HEMBA1001019,	HEMBA1001043,	HEMBA1001051,	HEMBA1001059,	HEMBA1001060,	HEMBA1001071,
HEMBA1001080,	HEMBA1001109,	HEMBA1001140,	HEMBA1001172,	HEMBA1001196,	HEMBA1001213,
HEMBA1001226,	HEMBA1001281,	HEMBA1001299,	HEMBA1001302,	HEMBA1001303,	HEMBA1001323,
HEMBA1001326,	HEMBA1001327,	HEMBA1001330,	HEMBA1001351,	HEMBA1001407,	HEMBA1001411,
HEMBA1001446,	HEMBA1001454,	HEMBA1001569,	HEMBA1001647,	HEMBA1001714,	HEMBA1001800,
HEMBA1001804,	HEMBA1001809,	HEMBA1001888,	HEMBA1001912,	HEMBA1001921,	HEMBA1001967,
HEMBA1002084,	HEMBA1002161,	HEMBA1002166,	HEMBA1002241,	HEMBA1002337,	HEMBA1002363,
HEMBA1002389,	HEMBA1002458,	HEMBA1002460,	HEMBA1002469,	HEMBA1002538,	HEMBA1002542,
HEMBA1002547,	HEMBA1002609,	HEMBA1002624,	HEMBA1002659,	HEMBA1002750,	HEMBA1002770,
HEMBA1002779,	HEMBA1002810,	HEMBA1002816,	HEMBA1002818,	HEMBA1002850,	HEMBA1002863,
HEMBA1003021,	HEMBA1003033,	HEMBA1003078,	HEMBA1003166,	HEMBA1003202,	HEMBA1003204,
HEMBA1003229,	HEMBA1003235,	HEMBA1003276,	HEMBA1003286,	HEMBA1003296,	HEMBA1003370,
HEMBA1003376,	HEMBA1003403,	HEMBA1003418,	HEMBA1003433,	HEMBA1003447,	HEMBA1003560,
HEMBA1003569,	HEMBA1003571,	HEMBA1003591,	HEMBA1003597,	HEMBA1003598,	HEMBA1003621,
HEMBA1003656,	HEMBA1003662,	HEMBA1003680,	HEMBA1003715,	HEMBA1003725,	HEMBA1003729,
HEMBA1003733,	HEMBA1003742,	HEMBA1003773,	HEMBA1003783,	HEMBA1003950,	HEMBA1004012,
HEMBA1004015,	HEMBA1004048,	HEMBA1004074,	HEMBA1004086,	HEMBA1004111,	HEMBA1004131,
HEMBA1004202,	HEMBA1004203,	HEMBA1004207,	HEMBA1004248,	HEMBA1004274,	HEMBA1004321,
HEMBA1004330,	HEMBA1004356,	HEMBA1004366,	HEMBA1004405,	HEMBA1004408,	HEMBA1004429,
HEMBA1004499,	HEMBA1004507,	HEMBA1004509,	HEMBA1004542,	HEMBA1004596,	HEMBA1004604,

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HEMBA1006173, HEMBA1006198, HEMBA1006253, HEMBA1006268, HEMBA1006309, HEMBA1006377,
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HEMBB1000908, HEMBB1000975, HEMBB1000985, HEMBB1001011, HEMBB1001014, HEMBB1001112,
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HEMBB1001915, HEMBB1001973, HEMBB1001983, HEMBB1001990, HEMBB1002190, HEMBB1002193,
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NT2RM4001084, NT2RM4001594, NT2RM4001629, NT2RM4001662, NT2RM4001841, NT2RM4002093,
NT2RM4002109, NT2RM4002145, NT2RM4002189, NT2RM4002194, NT2RM4002226, NT2RP1000170,
NT2RP1000439, NT2RP1000478, NT2RP1000513, NT2RP1000701, NT2RP1000856, NT2RP1001361,
NT2RP2000097, NT2RP2000239, NT2RP2000288, NT2RP2000328, NT2RP2000329, NT2RP2000369,
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OVARC1000106, OVARC1000151, OVARC1000198, OVARC1000431, OVARC1000440, OVARC1000564,
OVARC1000605, OVARC1000679, OVARC1000883, OVARC1000912, OVARC1000960, OVARC1000971,

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[0235] Clones of which expression levels decrease by TNF-α are as follows:

HEMBA1002150, HEMBB1000240, NT2RM2000469, NT2RM2000984, NT2RM2001688, NT2RM4000290, NT2RM4000496, NT2RM4000590, NT2RM4001047, NT2RM4001582, NT2RM4001611, NT2RM4001650, NT2RM4002075, NT2RM4002128, NT2RP1000174, NT2RP1000243, NT2RP1000581, NT2RP1000688, NT2RP1000767, NT2RP1000825, NT2RP1001185, NT2RP1001286, NT2RP1001432, NT2RP1001457, NT2RP2000001, NT2RP2000248, NT2RP2000841, NT2RP2001813, NT2RP2002137, NT2RP2002928, NT2RP2003517, NT2RP2003559, NT2RP2003564, NT2RP2004933, NT2RP2005038, NT2RP2006365, NT2RP3000072, NT2RP3000320, NT2RP3000484, NT2RP3000980, NT2RP3001111, NT2RP3001420, NT2RP3001495, NT2RP3002056, NT2RP3002057, NT2RP3002545, NT2RP3002713, NT2RP3002799, NT2RP3002869, NT2RP3002953, NT2RP3002955, NT2RP3003282, NT2RP3003290, NT2RP3003384, NT2RP3003385, NT2RP3003870, NT2RP3004207, NT2RP3004262, NT2RP3004527, NT2RP4000500, NT2RP4000524, NT2RP4000787, NT2RP4000927, NT2RP4000955, NT2RP4000989, NT2RP4001442, NT2RP4001638, NT2RP4001950, NT2RP4002888, NT2RP5003524, OVARC1001270, PLACE1000246, PLACE1002816.

[0236] These are rheumatoid arthritis-associated clones.

Analysis of ultraviolet radiation damage-associated genes

[0237] It is known that ultraviolet rays give considerably adverse influence on the health. In recent years, there have been significant risks of tissue damage by ultraviolet rays because of destruction of the ozone layer. Thus, ultraviolet radiation has been recognized as a risk factor for skin diseases such as skin cancers (United States Environmental Protection Agency: Ozone Depletion Home Page, http://www.epa.gov/ozone/). Genes of which expression levels are varied in skin epidermal cells exposed to ultraviolet rays are considered to be associated with skin damage caused by ultraviolet radiation.

[0238] After primary cultured skin fibroblast cells were irradiated with ultraviolet ray and were cultured, a survey was performed for genes of which expression levels were varied depending on the irradiation of ultraviolet ray. First, after cultured to be confluent, the primary cultured skin fibroblast cells (Cell Applications) were exposed to 10,000 $\mu J/cm^2$ of 254-nm ultraviolet light.

[0239] Messenger RNAs were, then, extracted by using a FastTrack™ 2.0 mRNA Isolation kit (Invitrogen Co.) from the unexposed cells and from the cells that were exposed to the ultraviolet light and then cultured for 4 or 24 hours. The labeling of the hybridization probe was carried out by using a 1.5 μg of each mRNA in the same manner as described above. The data were obtained in triplicate (n=3). The hybridization signals were compared between the cells exposed to the ultraviolet light and the unexposed cells. The comparison was preformed by statistical treatment with two-sample t-test. Clones with significant differences in the signal distribution were selected under the condition of $p<0.05$. In this analysis, even when the signal is lower than others, the difference in the signal values can be detected statistically. Accordingly, clones with signal value of 40 or lower were also assessed for selection.

[0240] Tables 353-509 show the expression of each cDNA in skin-derived fibroblast cells exposed and unexposed to ultraviolet light.

[0241] Averaged signal values (M_1, M_2) and sample variances (s_1^2, s_2^2) were calculated for each gene in each of the cells, and then, the pooled sample variances s^2 were obtained from the sample variances of the two types of cells to be compared. The t values were determined according to the following formula: $t=(M_1-M_2)/s/(1/3+1/3)^{1/2}$. When the determined t-value was greater than a t-value at P, which means the probability of significance level, of 0.05 or 0.01

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in the t-distribution table with 4 degrees of freedom, the difference was judged to be found in the expression level of the gene between the two types of cells at $p<0.05$ or $p<0.01$, respectively. The tables also include the information of an increase (+) or decrease (-) in the expression level of a gene in the exposed cells in comparison with that of unexposed cells.

[0242] The expression levels of the following clones were elevated 4 or 24 hours after the ultraviolet irradiation:
HEMBA1000542, HEMBA1001808, HEMBA1002177, HEMBA1003314, MAMMA1001874, NT2RM2001100, NT2RP2005732, NT2RP3000592, NT2RP4000657, OVARC1000004, OVARC1001092, OVARC1001342, PLACE1002816, NT2RM4001002, NT2RM4001813, NT2RM4002266, NT2RP2001174, NT2RP2001196, NT2RP2005358, NT2RP3000690, NT2RP3001216, NT2RP3003464, PLACE1006382, THYRO1000070, THYRO1001100, Y79AA1000342.

[0243] The expression levels of the following clones were decreased 4 or 24 hours after the ultraviolet irradiation:
HEMBA1000005, HEMBA1000150, HEMBA1000156, HEMBA1000158, HEMBA1000168, HEMBA1000231, HEMBA1000304, HEMBA1000307, HEMBA1000333, HEMBA1000366, HEMBA1000369, HEMBA1000390, HEMBA1000396, HEMBA1000418, HEMBA1000434, HEMBA1000464, HEMBA1000469, HEMBA1000490, HEMBA1000504, HEMBA1000505, HEMBA1000557, HEMBA1000657, HEMBA1000673, HEMBA1000682, HEMBA1000686, HEMBA1000727, HEMBA1000752, HEMBA1000851, HEMBA1000852, HEMBA1000870, HEMBA1000872, HEMBA1001085, HEMBA1001121, HEMBA1001133, HEMBA1001235, HEMBA1001265, HEMBA1001281, HEMBA1001289, HEMBA1001299, HEMBA1001303, HEMBA1001310, HEMBA1001323, HEMBA1001595, HEMBA1001620, HEMBA1001640, HEMBA1001678, HEMBA1001712, HEMBA1001835, HEMBA1001950, HEMBA1001987, HEMBA1002253, HEMBA1002321, HEMBA1002341, HEMBA1002419, HEMBA1002679, HEMBA1002728, HEMBA1002818, HEMBA1002935, HEMBA1002999, HEMBA1003034, HEMBA1003071, HEMBA1003098, HEMBA1003142, HEMBA1003175, HEMBA1003202, HEMBA1003212, HEMBA1003220, HEMBA1003276, HEMBA1003373, HEMBA1003417, HEMBA1003447, HEMBA1003528, HEMBA1003684, HEMBA1003799, HEMBA1003885, HEMBA1003989, HEMBA1004011, HEMBA1004055, HEMBA1004133, HEMBA1004225, HEMBA1004272, HEMBA1004353, HEMBA1004631, HEMBA1004669, HEMBA1004705, HEMBA1004753, HEMBA1004776, HEMBA1004803, HEMBA1004816, HEMBA1004900, HEMBA1005047, HEMBA1005079, HEMBA1005101, HEMBA1005149, HEMBA1005152, HEMBA1005202, HEMBA1005314, HEMBA1005372, HEMBA1005511, HEMBA1005513, HEMBA1005518, HEMBA1005570, HEMBA1005577, HEMBA1005581, HEMBA1005588, HEMBA1005609, HEMBA1005632, HEMBA1005853, HEMBA1006031, HEMBA1006035, HEMBA1006485, HEMBA1006486, HEMBA1006502, HEMBA1006696, HEMBA1006789, HEMBA1006796, HEMBA1007085, HEMBA1007224, HEMBA1007301, HEMBA1007319, HEMBA1007341, HEMBA1007342, HEMBB1000036, HEMBB1000037, HEMBB1000217, HEMBB1000266, HEMBB1000317, HEMBB1000336, HEMBB1000354, HEMBB1000369, HEMBB1000399, HEMBB1000434, HEMBB1000438, HEMBB1000592, HEMBB1000673, HEMBB1000789, HEMBB1000810, HEMBB1000883, HEMBB1000887, HEMBB1001105, HEMBB1001182, HEMBB1001242, HEMBB1001267, HEMBB1001424, HEMBB1001464, HEMBB1001531, HEMBB1001618, HEMBB1001996, HEMBB1002092, HEMBB1002139, HEMBB1002142, HEMBB1002190, HEMBB1002453, HEMBB1002520, HEMBB1002550, HEMBB1002556, HEMBB1002600, HEMBB1002664, MAMMA1000009, MAMMA1000055, MAMMA1000069, MAMMA1000133, MAMMA1000171, MAMMA1000173, MAMMA1000287, MAMMA1000416, MAMMA1000585, MAMMA1000713, MAMMA1000760, MAMMA1000798, MAMMA1000831, MAMMA1000875, MAMMA1000876, MAMMA1000877, MAMMA1000906, MAMMA1000931, MAMMA1000962, MAMMA1001133, MAMMA1001139, MAMMA1001243, MAMMA1001271, MAMMA1001274, MAMMA1001298, MAMMA1001606, MAMMA1001630, MAMMA1001670, MAMMA1001743, MAMMA1001751, MAMMA1002140, MAMMA1002145, MAMMA1002158, MAMMA1002170, MAMMA1002236, MAMMA1002311, MAMMA1002498, MAMMA1002754, MAMMA1002780, MAMMA1002820, MAMMA1002843, MAMMA1002844, MAMMA1002871, MAMMA1003047, NT2RM1000037, NT2RM1000039, NT2RM1000080, NT2RM1000086, NT2RM1000341, NT2RM1000499, NT2RM1000669, NT2RM1000746, NT2RM1000781, NT2RM1000885, NT2RM1000905, NT2RM1000962, NT2RM2000239, NT2RM2000260, NT2RM2000371, NT2RM2000639, NT2RM2000649, NT2RM2000735, NT2RM2000821, NT2RM2000984, NT2RM2001035, NT2RM2001065, NT2RM2001105, NT2RM2001177, NT2RM2001194, NT2RM2001196, NT2RM2001243, NT2RM2001256, NT2RM2001424, NT2RM2001588, NT2RM2001635, NT2RM2001648, NT2RM2001652, NT2RM2001668, NT2RM2001706, NT2RM2001727, NT2RM2001730, NT2RM2001743, NT2RM2001753, NT2RM2001760, NT2RM2001771, NT2RM2001785, NT2RM2001800, NT2RM2001855, NT2RM2001896, NT2RM2001997, NT2RM2002030, NT2RM2002049, NT2RM2002091, NT2RM2002142, NT2RM2002145, NT2RM2002178, NT2RM2002580, NT2RM4000215, NT2RM4000344, NT2RM4000368, NT2RM4000421, NT2RM4000425, NT2RM4000457, NT2RM4000496, NT2RM4000515, NT2RM4000712, NT2RM4000787, NT2RM4000813, NT2RM4000820, NT2RM4000852, NT2RM4000950, NT2RM4000996, NT2RM4001016, NT2RM4001047, NT2RM4001054, NT2RM4001140, NT2RM4001151, NT2RM4001187, NT2RM4001204, NT2RM4001258, NT2RM4001437, NT2RM4001454, NT2RM4001489, NT2RM4001605,

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[0244] These clones are ultraviolet radiation damage-associated clones.

Table 12

Expression of each cDNA in human tissues (containing clones that are not described in Examples.)

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Clone name	Heart	Lung	P. gland	Thymus	Brain	Kidney	Liver	Spleen
GAPDH(Crl)	38.210	32.670	23.820	13.580	11.230	21.120	24.910	22.440
β actin(Cr2)	279.280	368.870	111.100	117.500	92.880	114.650	82.990	256.790
ADRGL1000005	53.882	23.005	32.749	22.858	26.564	24.940	22.644	27.001
ADRGL1000007	94.778	85.185	160.457	67.191	101.768	62.489	67.150	73.543
ADRGL1000009	11.141	50.520	10.357	7.177	6.013	5.219	14.272	21.225
ADRGL1000011	71.656	24.579	29.358	19.473	24.898	30.747	49.220	22.221
ADRGL1000027	36.238	25.252	20.855	7.328	11.196	14.298	19.658	11.288
ADRGL1000058	66.209	129.497	55.226	49.241	30.219	55.872	67.027	243.436
ADRGL1000069	38.630	23.459	28.991	12.540	27.353	33.633	28.774	20.911
ADRGL1000077	97.465	63.656	448.427	83.412	71.108	53.740	67.906	89.439
ADRGL1000092	89.423	45.692	55.810	26.033	44.148	73.339	96.037	73.091
ADRGL1000099	73.675	24.424	36.128	17.024	25.964	41.391	42.837	29.666
ADRGL1000136	141.745	63.974	77.017	24.777	33.549	58.986	295.009	84.985
ADRGL1000147	394.563	155.829	271.210	92.899	165.627	251.266	253.420	150.294
ADRGL1000159	50.073	25.425	39.296	15.194	16.125	20.040	33.720	23.278
ADRGL1000160	69.386	31.051	59.416	20.154	39.799	27.027	47.169	20.716
ADRGL1000171	57.047	23.011	43.063	23.860	40.581	59.814	117.055	32.630
ADRGL1000181	45.892	18.666	34.476	15.434	34.225	32.962	39.693	16.334
BGGI11000015	153.242	42.337	92.865	41.003	45.168	88.524	85.990	73.392
BGGI11000016	177.367	94.731	119.688	34.159	30.249	98.806	98.783	39.204
BGGI11000017	84.712	32.614	38.131	20.878	18.769	32.340	39.666	20.750
BGGI11000022	52.468	20.452	67.167	12.167	11.158	18.241	19.197	11.937
BGGI11000031	30.008	17.072	40.883	12.585	13.313	15.525	16.757	13.406
BGGI11000042	49.926	36.336	51.176	26.964	43.122	43.770	49.107	38.776
BGGI11000046	31.618	26.472	34.182	31.854	12.650	25.784	18.430	25.385
BNGH41000020	6031.103	2993.496	1444.841	537.162	6973.542	6029.124	8350.527	3649.144
BNGH41000025	91.717	35.026	73.901	27.713	30.765	36.523	37.596	47.074
BNGH41000026	176.757	77.439	98.345	35.807	56.991	91.310	75.797	70.241
BNGH41000027	65.029	56.353	25.896	22.494	12.763	23.748	17.836	23.859
BNGH41000035	148.779	66.776	119.727	56.576	60.996	96.959	72.461	64.458
BNGH41000037	79.500	29.611	43.438	18.317	20.857	36.272	27.525	24.771
BNGH41000042	224.484	110.084	168.448	104.351	102.259	125.323	86.783	122.959
BNGH41000048	56.144	32.253	54.063	14.729	27.312	22.435	29.566	28.937
BNGH41000056	67.258	18.694	30.075	15.602	10.072	20.735	16.100	7.642
BNGH41000087	98.262	46.173	77.657	35.329	40.900	50.029	50.841	45.285
BNGH41000091	50.895	16.985	28.392	10.147	5.469	22.794	10.725	12.410
BNGH41000157	69.043	34.730	40.597	18.088	27.072	22.074	25.410	24.950
BNGH41000169	44.850	21.770	28.655	11.403	25.991	28.509	25.634	25.843
BNGH41000181	17.163	15.689	13.948	3.996	9.287	13.139	15.553	16.575
BNGH41000198	81.510	36.250	60.860	20.585	26.929	35.751	31.695	28.325
BNGH41000219	30.302	25.156	22.187	13.757	11.208	15.235	27.285	35.709
BNGH41000229	252.790	65.948	93.499	51.108	92.555	101.245	96.716	78.266
BNGH41000237	85.757	46.997	55.170	26.780	33.764	47.456	37.007	39.131
BNGH41000238	17.744	36.938	42.360	14.922	35.749	42.848	39.238	13.241
BNGH41000243	45.446	23.667	44.798	20.875	10.516	23.918	22.443	27.033
BNGH41000270	60.889	18.651	29.618	10.724	15.979	12.351	19.152	22.314
BRAWH1000004	43.673	28.539	7.640	11.388	19.198	14.903	32.353	23.777
BRAWH1000018	59.409	17.941	102.270	17.107	709.078	25.732	24.214	24.767
BRAWH1000021	104.772	29.951	51.142	21.042	1169.154	55.762	66.754	27.969
BRAWH1000027	152.205	47.310	67.089	32.199	54.521	70.731	79.670	40.928
BRAWH1000029	106.376	49.221	55.840	40.856	59.552	56.487	64.886	100.132
BRAWH1000040	29.419	16.761	31.101	16.622	30.633	18.200	17.998	15.196
BRAWH1000050	161.264	71.786	118.976	51.863	61.542	97.720	81.271	69.194
BRAWH1000051	74.067	34.341	44.047	20.726	30.434	42.055	53.856	24.624
BRAWH1000060	68.789	22.598	35.012	16.493	19.127	38.662	34.923	28.094
BRAWH1000075	17.318	16.898	36.437	8.901	18.133	17.219	9.321	11.200
BRAWH1000081	43.025	12.998	28.267	7.655	123.677	17.673	15.924	9.844
BRAWH1000084	174.384	42.178	80.534	47.752	152.188	77.111	110.167	102.296
BRAWH1000095	118.239	59.676	64.528	28.174	116.975	53.814	746.700	35.985
BRAWH1000096	146.112	44.967	85.882	27.491	145.013	52.880	52.427	58.678
BRAWH1000097	95.841	72.506	174.954	65.637	64.200	73.707	63.827	63.762
BRAWH1000100	11.943	19.037	18.950	13.536	92.145	16.582	16.646	10.218
BRAWH1000101	134.838	57.232	106.632	40.741	96.396	71.642	88.432	57.336

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Table 13

BRAWH1000104	25.414	18.303	14.825	7.695	38.918	23.970	23.794	11.048
BRAWH1000107	16.949	5.616	12.463	5.518	6.355	5.084	9.107	6.573
BRAWH1000110	615.476	492.704	869.088	383.612	368.156	369.621	277.348	340.450
BRAWH1000111	175.556	68.459	92.209	45.974	64.703	81.723	90.369	57.301
BRAWH1000135	199.303	38.098	72.093	26.809	57.720	91.668	87.016	35.866
BRAWH1000190	56.386	41.640	57.914	22.782	55.671	40.034	35.280	40.134
HEMBA1000005	11.985	23.427	18.882	9.766	12.656	9.959	23.443	21.677
HEMBA1000006	37.398	24.521	24.529	15.587	22.317	13.336	16.038	15.295
HEMBA1000012	81.820	57.193	66.828	26.683	55.423	58.731	85.614	66.259
HEMBA1000020	157.967	64.157	115.635	51.940	77.293	77.321	83.989	74.362
HEMBA1000030	82.882	35.447	66.058	26.464	40.990	60.871	47.058	50.652
HEMBA1000034	47.434	17.878	50.696	5.594	14.005	6.673	24.652	7.134
HEMBA1000042	147.376	94.003	330.908	69.071	76.472	55.477	37.783	60.479
HEMBA1000045	28.478	20.289	20.548	12.445	11.835	22.788	11.196	15.775
HEMBA1000046	85.160	84.475	242.940	57.017	68.488	45.288	37.098	47.486
HEMBA1000047	21.380	18.899	18.166	11.393	11.185	12.292	6.491	12.018
HEMBA1000048	243.559	55.114	84.448	24.247	43.131	99.333	57.041	37.362
HEMBA1000050	22.711	11.876	21.972	7.477	4.096	13.675	10.347	7.770
HEMBA1000053	45.071	26.410	38.158	15.982	30.754	36.740	34.184	24.269
HEMBA1000060	101.197	34.766	50.643	19.938	34.641	54.061	42.309	22.530
HEMBA1000072	240.166	213.938	224.688	163.030	115.246	207.809	112.361	276.098
HEMBA1000073	23.202	9.580	10.815	1.698	6.680	18.155	12.304	14.973
HEMBA1000076	95.997	46.783	177.931	32.617	48.964	50.792	33.947	44.142
HEMBA1000084	66.603	25.710	48.434	18.006	22.553	38.118	40.479	29.683
HEMBA1000087	70.084	17.515	26.544	8.450	17.590	29.220	19.519	22.565
HEMBA1000088	15.474	8.614	19.903	4.775	4.519	11.446	34.905	6.528
HEMBA1000091	80.622	38.604	59.393	23.956	44.939	49.760	33.946	24.614
HEMBA1000111	85.814	95.270	270.642	75.147	54.384	70.071	29.529	55.422
HEMBA1000121	55.476	43.368	146.465	37.419	29.398	30.694	17.702	30.398
HEMBA1000128	37.278	27.165	34.516	13.619	17.702	28.069	12.834	23.965
HEMBA1000129	51.488	19.659	44.907	12.208	27.243	30.959	24.383	26.851
HEMBA1000141	12.961	24.515	32.107	14.353	13.502	11.152	8.907	20.635
HEMBA1000146	29.273	11.479	20.418	8.202	9.575	14.877	10.000	7.817
HEMBA1000150	534.562	326.814	684.147	211.774	218.448	322.246	235.752	256.883
HEMBA1000154	95.272	92.253	101.483	54.276	42.896	75.526	92.689	188.019
HEMBA1000156	50.177	72.591	58.026	31.149	21.865	38.964	27.634	50.220
HEMBA1000158	260.718	63.920	89.680	36.337	44.915	93.421	111.344	53.562
HEMBA1000168	74.416	61.152	62.826	30.512	23.287	34.966	44.005	33.564
HEMBA1000180	28.502	22.412	28.571	11.701	19.230	10.903	11.731	14.102
HEMBA1000185	115.723	50.661	213.994	51.166	43.435	56.261	38.862	44.992
HEMBA1000188	21.302	14.879	16.948	11.392	11.821	10.656	12.501	6.979
HEMBA1000193	14.122	8.318	11.905	7.519	4.736	3.349	8.544	7.842
HEMBA1000194	54.688	49.534	143.817	37.736	20.221	34.328	23.359	56.497
HEMBA1000201	21.062	14.098	8.690	6.237	5.109	5.059	9.317	10.522
HEMBA1000213	22.388	25.532	25.777	8.470	17.320	9.084	8.469	11.766
HEMBA1000216	65.935	51.368	92.680	19.202	33.659	40.971	36.328	34.891
HEMBA1000227	52.577	31.332	34.925	19.503	18.411	21.504	22.590	25.781
HEMBA1000231	114.369	54.299	131.256	38.550	43.246	29.778	24.266	30.410
HEMBA1000237	91.024	91.360	199.338	58.292	93.250	57.000	49.319	59.288
HEMBA1000243	53.456	43.969	117.519	38.431	25.396	32.604	38.910	32.153
HEMBA1000244	173.469	104.733	115.584	33.079	65.527	124.532	90.927	78.610
HEMBA1000251	22.709	12.333	14.367	9.019	16.095	13.221	11.516	11.018
HEMBA1000254	74.060	35.626	130.009	20.848	37.481	24.002	20.553	13.215
HEMBA1000264	29.478	15.248	23.537	9.473	3.863	11.228	13.690	3.797
HEMBA1000269	36.718	13.465	28.932	20.412	9.705	12.833	7.348	24.793
HEMBA1000275	66.201	39.367	84.077	38.846	77.871	49.267	36.211	38.871
HEMBA1000280	33.299	36.073	54.357	24.720	38.017	35.751	21.696	30.785
HEMBA1000282	93.815	121.083	171.037	93.484	123.971	70.384	56.916	92.414
HEMBA1000287	12.439	24.935	29.793	10.840	37.925	9.632	2.866	7.311
HEMBA1000288	45.269	30.009	145.363	25.471	9.769	16.272	9.701	15.510
HEMBA1000290	14.803	5.750	10.615	5.725	2.559	8.602	8.358	9.224
HEMBA1000296	27.085	22.625	21.195	9.790	16.909	12.402	15.289	17.159
HEMBA1000300	98.491	119.119	304.884	73.660	85.595	48.175	43.496	66.547
HEMBA1000302	23.840	15.442	27.722	16.143	13.081	13.879	8.259	12.569

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Table 14

HEMBA1000303	129.286	51.013	88.777	32.513	50.462	82.994	44.818	49.271
HEMBA1000304	112.022	67.470	328.677	54.678	79.305	43.526	38.469	55.762
HEMBA1000307	14.054	22.013	31.964	13.167	15.571	7.974	10.014	8.685
HEMBA1000312	97.082	69.330	183.923	45.322	45.087	52.968	37.741	38.246
HEMBA1000318	16.164	16.264	18.766	11.688	3.620	10.732	8.295	14.675
HEMBA1000327	29.404	59.618	81.147	41.731	85.004	48.526	49.421	46.866
HEMBA1000333	16.964	13.930	14.530	1.872	5.776	1.571	0.392	3.743
HEMBA1000338	121.878	62.572	348.751	55.463	49.114	38.561	30.698	40.644
HEMBA1000343	25.229	29.781	46.395	20.673	5.872	16.551	10.139	14.088
HEMBA1000349	23.061	12.586	31.755	7.020	17.658	11.622	14.807	15.611
HEMBA1000351	92.847	57.338	196.577	41.762	37.094	35.370	27.645	28.615
HEMBA1000355	85.210	38.388	64.299	18.101	33.114	43.511	37.808	26.628
HEMBA1000356	60.438	38.786	62.442	20.784	17.694	38.058	40.431	28.899
HEMBA1000357	84.898	55.990	206.803	54.151	42.793	39.432	26.076	44.579
HEMBA1000366	47.131	42.031	90.450	27.056	20.718	23.499	14.632	23.547
HEMBA1000369	71.428	40.685	54.384	17.613	21.422	34.985	37.622	36.900
HEMBA1000370	16.354	14.949	22.988	7.916	18.390	15.359	13.426	6.647
HEMBA1000376	80.183	75.300	201.705	55.266	66.687	44.612	55.386	56.070
HEMBA1000387	100.497	129.367,	351.196	80.257	104.250	74.007	57.619	79.876
HEMBA1000389	69.142	34.021	71.118	22.346	27.319	47.936	53.026	34.161
HEMBA1000390	19.206	25.788	21.028	12.401	18.372	13.751	16.243	15.036
HEMBA1000392	19.400	22.884	44.179	8.776	11.742	10.594	12.266	12.463
HEMBA1000396	75.409	50.195	81.870	27.979	30.393	31.235	17.771	19.584
HEMBA1000411	35.966	24.397	25.987	10.341	31.398	31.214	50.056	18.580
HEMBA1000418	8.165	10.778	14.987	4.031	12.495	7.913	6.363	2.306
HEMBA1000422	93.699	38.329	85.266	39.826	45.992	44.729	42.886	34.308
HEMBA1000428	51.017	30.690	79.229	26.579	24.840	17.767	18.424	18.608
HEMBA1000434	1.747	3.214	11.346	1.210	1.602	2.927	2.788	2.756
HEMBA1000442	21.750	7.698	16.227	7.252	3.336	17.969	11.723	10.645
HEMBA1000443	67.291	35.910	34.775	26.420	16.860	31.691	47.856	102.287
HEMBA1000448	236.986	69.546	90.283	32.233	34.107	119.377	108.645	60.266
HEMBA1000456	95.368	37.560	63.451	22.640	41.092	65.256	62.972	43.493
HEMBA1000459	28.924	35.333	74.945	20.475	25.324	26.253	13.654	31.317
HEMBA1000460	18.649	27.246	21.973	9.613	15.230	14.091	9.746	16.955
HEMBA1000462	220.184	42.636	96.490	31.332	83.626	109.503	92.971	62.126
HEMBA1000464	34.277	15.137	27.210	10.862	15.595	20.793	16.716	16.539
HEMBA1000468	41.755	41.852	68.356	10.400	23.452	43.909	24.048	22.968
HEMBA1000469	68.229	71.011	256.705	47.636	29.853	34.188	22.568	39.190
HEMBA1000477	185.220	47.546	102.939	26.276	40.188	95.247	52.454	28.109
HEMBA1000481	47.276	37.528	24.407	17.115	24.182	29.826	20.717	25.819
HEMBA1000488	96.226	31.249	71.522	21.667	27.715	44.499	53.708	33.306
HEMBA1000490	29.915	13.747	32.568	14.002	12.056	6.900	11.274	7.559
HEMBA1000491	80.198	22.903	47.786	20.675	32.551	52.682	37.109	28.282
HEMBA1000498	191.186	112.767	454.998	88.614	102.997	82.927	53.205	120.837
HEMBA1000501	57.318	55.923	180.158	44.170	27.291	34.954	18.532	34.117
HEMBA1000504	1.033	5.893	7.152	1.726	0.520	2.245	2.551	1.091
HEMBA1000505	55.746	36.631	48.155	21.562	14.691	34.729	19.508	31.925
HEMBA1000507	204.165	114.530	305.249	86.138	81.505	97.289	230.331	95.150
HEMBA1000508	205.724	105.067	309.791	72.709	70.180	77.388	63.849	45.940
HEMBA1000518	39.157	29.100	31.505	16.650	14.796	15.847	24.729	17.601
HEMBA1000519	166.937	142.676	468.435	148.478	123.978	128.646	85.670	111.078
HEMBA1000520	0.000	0.000	0.000	10.341	10.619	1.488	9.513	9.395
HEMBA1000523	38.708	22.090	40.875	13.852	21.603	32.384	20.478	21.422
HEMBA1000531	21.874	34.044	40.027	12.264	11.034	29.775	20.421	12.540
HEMBA1000534	0.000	0.000	0.000	34.434	48.940	25.365	41.242	72.583
HEMBA1000538	0.000	0.000	0.000	17.833	19.981	17.606	26.698	23.904
HEMBA1000540	21.974	47.343	33.145	42.629	27.059	33.931	16.639	31.893
HEMBA1000542	64.656	33.152	58.093	30.174	35.278	55.508	47.917	47.623
HEMBA1000545	148.870	136.401	48.802	8.499	12.534	7.119	25.484	15.094
HEMBA1000547	14.825	20.199	32.694	7.058	22.359	12.020	13.535	20.227
HEMBA1000551	163.806	171.089	543.876	131.764	115.775	116.646	69.596	152.516
HEMBA1000555	10.531	20.199	25.801	24.488	14.071	15.431	5.986	10.933
HEMBA1000557	80.051	48.396	168.724	37.150	32.863	31.872	22.800	30.926
HEMBA1000561	56.992	22.797	51.047	10.187	16.301	34.904	24.661	22.470

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Table 15

HEMBA1000563	9.473	11.545	18.205	6.139	12.689	10.132	7.939	14.251
HEMBA1000567	41.385	38.483	27.881	32.207	15.544	26.052	15.086	86.601
HEMBA1000568	44.686	33.379	125.524	26.300	22.533	17.402	26.970	18.707
HEMBA1000569	58.184	27.187	41.012	21.787	12.925	36.191	33.944	23.225
HEMBA1000575	155.833	155.759	434.526	92.140	79.143	69.949	59.928	71.189
HEMBA1000588	41.087	26.072	31.610	14.580	18.024	18.458	23.553	13.279
HEMBA1000590	29.693	17.090	23.618	7.069	6.633	16.725	20.068	13.042
HEMBA1000591	106.772	54.874	98.079	34.099	31.776	57.170	48.488	32.766
HEMBA1000592	7.408	10.031	9.435	9.551	8.209	5.142	7.480	10.319
HEMBA1000594	18.401	11.048	22.547	15.327	9.596	12.099	8.751	6.852
HEMBA1000604	96.047	78.462	146.030	49.571	36.099	70.815	41.797	47.748
HEMBA1000607	46.819	15.606	46.037	9.438	19.149	21.038	17.317	25.404
HEMBA1000608	8.985	3.040	6.705	0.000	7.378	4.453	0.000	5.544
HEMBA1000622	45.570	55.746	113.666	40.310	18.167	19.390	15.895	29.149
HEMBA1000634	126.532	49.146	138.073	29.094	95.787	79.662	60.271	71.657
HEMBA1000636	151.899	51.270	126.200	39.161	51.864	62.611	54.056	39.415
HEMBA1000637	33.241	23.587	39.380	18.047	16.265	30.075	28.226	24.559
HEMBA1000655	80.165	70.766	219.283	58.901	61.320	45.821	40.741	62.639
HEMBA1000657	60.961	31.993	41.401	18.008	30.565	35.201	35.611	42.178
HEMBA1000662	8.600	8.490	11.263	5.475	2.201	6.140	1.557	2.504
HEMBA1000664	14.358	5.082	3.637	2.670	3.516	4.913	3.094	3.579
HEMBA1000671	11.588	15.473	26.067	17.940	8.865	7.647	10.779	21.196
HEMBA1000673	73.174	77.410	193.253	46.051	34.388	33.975	25.896	31.646
HEMBA1000675	7.666	12.047	22.123	5.764	42.036	15.788	10.254	15.555
HEMBA1000678	7.453	12.314	21.083	12.174	14.897	12.628	6.969	6.584
HEMBA1000682	118.965	125.696	255.731	86.894	61.443	66.299	49.060	82.939
HEMBA1000686	25.079	17.463	23.126	12.722	10.282	13.835	21.393	18.154
HEMBA1000702	206.683	94.357	266.585	62.386	79.930	90.914	98.397	60.559
HEMBA1000705	25.430	25.862	47.190	13.191	19.599	26.364	25.013	18.833
HEMBA1000713	56.893	25.288	70.751	17.660	24.138	23.311	21.805	21.736
HEMBA1000718	50.149	43.869	128.515	28.289	23.213	18.458	10.003	17.419
HEMBA1000719	37.969	17.467	28.513	12.147	12.768	22.643	14.744	14.432
HEMBA1000722	15.150	9.762	14.699	6.768	11.726	12.080	5.907	9.953
HEMBA1000726	159.817	111.276	463.937	91.448	109.093	58.587	46.517	70.087
HEMBA1000727	22.867	26.803	28.886	21.475	11.199	14.966	8.634	30.401
HEMBA1000732	28.630	11.011	12.790	4.617	3.548	13.325	19.978	13.472
HEMBA1000736	24.568	21.982	21.410	7.431	11.376	41.026	31.698	16.801
HEMBA1000743	0.741	4.467	1.793	1.637	1.227	3.642	4.563	3.368
HEMBA1000745	8.930	7.067	14.546	3.314	10.067	5.403	9.225	6.085
HEMBA1000747	21.442	12.487	25.662	17.081	5.384	10.287	9.865	8.267
HEMBA1000748	22.924	14.885	35.721	12.634	3.045	11.508	4.110	11.756
HEMBA1000749	67.267	50.826	159.211	43.879	20.345	29.613	19.447	31.693
HEMBA1000752	54.929	35.778	162.005	28.209	31.540	25.132	15.650	20.776
HEMBA1000753	120.889	83.878	155.892	48.092	54.307	53.238	38.941	39.331
HEMBA1000757	20.234	22.592	52.608	29.935	23.071	24.503	14.548	43.779
HEMBA1000760	12.599	38.665	19.973	15.800	30.188	14.155	10.570	39.229
HEMBA1000769	114.956	74.924	304.424	66.815	39.365	48.405	39.918	55.931
HEMBA1000773	2.162	5.360	11.883	4.445	0.965	3.158	3.956	2.663
HEMBA1000774	128.563	115.732	330.111	84.461	69.618	59.363	42.656	56.152
HEMBA1000780	6.850	7.130	24.176	6.924	6.903	6.546	6.667	9.576
HEMBA1000783	8.127	5.076	13.701	3.276	8.863	6.241	5.435	4.429
HEMBA1000791	41.433	51.546	108.542	29.633	42.735	44.515	43.187	40.856
HEMBA1000793	108.761	30.885	54.568	18.670	31.512	54.669	45.458	34.788
HEMBA1000802	15.062	11.125	9.052	10.300	11.505	12.950	15.354	16.952
HEMBA1000813	106.763	52.683	69.701	32.507	44.369	65.862	59.842	56.799
HEMBA1000817	19.480	7.070	17.915	4.016	15.239	18.434	11.273	8.079
HEMBA1000822	9.520	10.358	15.760	7.218	8.704	11.185	6.639	4.662
HEMBA1000827	96.001	12.420	24.041	8.305	24.000	6.709	3.488	8.591
HEMBA1000833	53.675	28.970	35.897	14.604	26.383	29.036	20.591	14.341
HEMBA1000835	74.696	67.353	83.737	34.349	42.834	61.145	66.784	52.015
HEMBA1000843	74.227	54.197	92.042	37.825	58.573	98.943	87.569	55.077
HEMBA1000851	23.913	14.070	13.081	6.847	8.634	12.419	19.200	22.286
HEMBA1000852	56.702	54.074	105.085	31.127	34.200	31.843	28.843	30.311
HEMBA1000867	15.548	10.247	11.912	6.256	1.227	12.374	8.518	5.611

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Table 16

HEMBA1000869	19.696	18.785	34.039	15.061	6.930	13.298	14.305	14.712
HEMBA1000870	64.189	38.246	44.665	12.647	23.970	41.195	21.911	17.508
HEMBA1000872	46.848	46.546	86.933	36.087	40.608	42.532	43.479	36.141
HEMBA1000875	35.460	41.166	32.238	11.297	35.077	29.781	19.453	23.540
HEMBA1000876	89.976	56.654	194.869	42.595	57.670	53.567	36.331	40.884
HEMBA1000907	22.959	9.656	10.917	3.599	3.363	5.327	13.032	10.676
HEMBA1000908	45.409	18.456	30.665	12.448	8.174	19.529	24.789	16.299
HEMBA1000910	47.107	13.681	26.933	5.866	7.073	19.938	22.971	11.592
HEMBA1000918	67.437	29.880	114.873	25.206	16.670	25.895	26.769	24.710
HEMBA1000919	44.938	29.704	40.184	22.126	16.008	24.639	23.073	20.233
HEMBA1000934	162.546	35.314	59.012	18.820	30.796	53.492	33.824	20.798
HEMBA1000935	16.284	29.481	71.669	12.587	23.834	13.188	7.830	13.322
HEMBA1000940	44.243	39.296	75.619	25.080	28.113	39.401	25.948	30.168
HEMBA1000942	126.095	96.812	260.912	62.657	49.118	47.891	35.814	49.631
HEMBA1000943	14.419	12.702	14.690	4.792	8.391	11.856	11.039	7.414
HEMBA1000946	15.461	5.506	18.692	9.000	5.772	0.000	19.405	9.939
HEMBA1000960	179.860	151.073	343.747	107.319	85.691	117.093	82.928	94.494
HEMBA1000962	73.195	34.803	60.061	26.562	28.789	47.944	60.067	31.619
HEMBA1000968	14.529	12.486	35.270	18.733	5.213	7.458	7.214	4.624
HEMBA1000971	50.148	19.281	37.515	12.222	19.562	29.874	22.045	23.135
HEMBA1000972	51.100	33.450	188.137	28.972	24.576	23.736	13.731	27.272
HEMBA1000974	5.609	10.649	12.866	2.929	2.603	3.800	6.104	4.964
HEMBA1000975	34.417	19.132	42.499	15.644	4.009	16.478	14.192	14.353
HEMBA1000979	90.061	38.532	99.641	19.754	27.516	38.801	31.347	36.440
HEMBA1000981	35.338	31.281	38.672	19.544	34.385	38.280	24.897	29.059
HEMBA1000983	71.391	34.501	58.683	22.640	32.825	32.384	27.465	31.286
HEMBA1000985	9.290	20.363	22.497	4.058	6.343	9.035	7.852	3.257
HEMBA1000986	128.714	74.713	236.019	56.662	52.957	85.340	63.718	54.892
HEMBA1000991	72.707	55.780	160.717	34.676	32.494	41.317	23.483	37.846
HEMBA1001007	123.690	42.563	69.807	23.525	34.263	47.777	47.496	48.154
HEMBA1001008	124.864	47.842	83.746	18.125	25.490	52.693	30.668	24.961
HEMBA1001009	37.843	29.269	36.715	11.055	17.115	17.937	17.701	22.055
HEMBA1001014	109.049	83.356	233.234	60.123	61.977	94.424	47.095	74.625
HEMBA1001017	50.408	20.212	48.394	16.020	28.537	31.917	27.876	24.283
HEMBA1001019	7.327	7.582	14.865	6.154	10.598	5.643	3.920	7.188
HEMBA1001020	53.067	55.646	115.814	31.640	25.647	24.596	23.146	27.169
HEMBA1001021	115.724	42.415	59.434	28.828	26.181	64.484	64.173	29.614
HEMBA1001022	37.883	25.835	28.969	18.452	20.270	22.790	25.194	20.783
HEMBA1001024	23.524	15.235	16.511	8.023	11.818	13.894	8.606	8.098
HEMBA1001026	21.343	12.515	18.851	6.888	7.288	12.663	8.419	7.418
HEMBA1001043	10.374	11.995	9.892	10.750	19.163	9.299	8.047	8.589
HEMBA1001051	124.869	115.181	387.345	100.376	67.510	61.660	46.295	68.994
HEMBA1001052	38.892	13.860	19.067	12.855	11.445	24.382	15.726	12.323
HEMBA1001059	98.097	41.525	66.565	27.826	26.220	46.725	42.356	36.506
HEMBA1001060	116.857	74.020	161.485	61.750	50.524	52.957	38.575	52.612
HEMBA1001064	32.251	24.026	33.937	14.007	7.907	13.710	17.387	16.720
HEMBA1001071	25.850	16.043	19.924	7.855	3.425	9.530	6.779	24.242
HEMBA1001077	24.689	23.055	64.486	19.413	16.821	16.858	13.165	12.873
HEMBA1001078	33.254	26.761	41.713	26.498	24.531	31.498	25.302	23.636
HEMBA1001080	57.701	23.951	31.254	22.489	24.848	33.265	31.880	26.484
HEMBA1001084	62.698	41.625	171.096	31.438	31.760	24.829	17.487	26.581
HEMBA1001085	159.252	116.909	294.247	77.235	81.384	76.498	59.989	55.574
HEMBA1001088	74.704	42.537	46.695	19.266	25.146	33.498	44.927	26.310
HEMBA1001093	30.048	28.810	72.081	20.831	14.610	11.033	15.558	22.531
HEMBA1001094	5.535	8.779	10.059	3.089	4.628	4.521	4.834	4.468
HEMBA1001099	18.322	24.021	14.814	7.146	13.778	16.055	11.044	10.190
HEMBA1001104	21.919	13.788	35.048	9.637	18.058	24.450	21.559	18.527
HEMBA1001109	186.384	190.240	540.908	155.496	134.630	93.324	78.690	116.187
HEMBA1001114	89.023	252.529	187.547	75.857	35.109	66.259	69.432	341.702
HEMBA1001121	32.820	25.812	89.860	19.710	34.244	18.209	9.519	15.621
HEMBA1001122	3.304	6.213	8.316	4.763	19.120	5.650	4.506	23.059
HEMBA1001123	108.859	55.807	190.789	41.415	39.028	42.683	25.551	30.174
HEMBA1001133	50.744	21.167	36.786	14.764	34.752	26.702	23.524	11.367
HEMBA1001137	38.685	21.659	46.297	21.567	13.174	15.867	11.767	25.508

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Table 17

HEMBA1001140	60.453	66.122	169.353	48.837	60.363	44.403	30.367	43.561
HEMBA1001144	278.126	195.811	643.688	207.291	166.089	101.134	105.337	142.120
HEMBA1001145	58.539	241.368	206.084	46.342	39.316	61.827	91.170	66.852
HEMBA1001158	29.417	28.121	43.877	13.337	24.176	19.965	18.089	28.622
HEMBA1001172	74.727	47.695	213.708	37.115	24.460	26.620	19.178	32.709
HEMBA1001174	6.279	8.617	8.831	7.914	2.574	8.031	3.119	4.980
HEMBA1001175	29.561	34.909	43.568	19.819	34.829	16.588	19.883	17.824
HEMBA1001182	136.762	64.608	105.979	44.066	83.417	86.736	126.297	79.785
HEMBA1001184	16.758	9.703	22.060	9.016	11.018	10.205	6.347	9.176
HEMBA1001192	15.119	10.798	11.626	6.559	5.736	3.435	9.089	11.273
HEMBA1001197	82.571	114.743	110.687	83.431	56.396	68.797	99.959	173.379
HEMBA1001208	40.250	30.964	37.220	19.514	11.451	24.172	27.637	12.469
HEMBA1001213	81.501	37.345	57.618	18.958	24.480	52.160	51.978	31.326
HEMBA1001214	36.798	16.011	20.958	17.612	12.418	20.697	19.108	21.328
HEMBA1001221	14.108	10.456	11.382	7.001	17.058	10.307	7.980	11.111
HEMBA1001225	13.961	14.077	13.384	5.925	5.876	13.456	12.076	5.825
HEMBA1001226	173.501	137.685	444.754	120.060	113.306	75.167	63.960	67.304
HEMBA1001228	115.971	48.677	102.518	36.755	64.214	50.002	60.915	35.178
HEMBA1001229	246.802	111.161	135.886	43.460	94.703	148.387	156.871	115.302
HEMBA1001235	43.880	86.102	81.818	36.769	54.172	65.830	70.065	66.201
HEMBA1001238	67.342	62.561	136.273	36.471	33.652	41.838	26.195	28.747
HEMBA1001242	55.562	43.106	58.593	41.382	47.200	38.498	43.114	44.230
HEMBA1001247	28.768	22.129	16.518	10.576	8.758	17.031	9.651	13.385
HEMBA1001253	58.130	60.415	66.640	18.982	45.992	54.071	95.073	63.393
HEMBA1001257	33.557	18.509	24.256	10.657	12.732	31.261	24.849	9.134
HEMBA1001261	585.214	143.415	243.791	98.186	169.988	310.109	234.388	125.796
HEMBA1001262	27.336	17.339	19.088	5.647	15.678	20.899	11.464	19.889
HEMBA1001265	36.604	28.090	152.221	27.730	49.893	34.423	16.502	26.993
HEMBA1001266	69.367	67.414	170.657	45.898	31.802	39.554	41.287	52.480
HEMBA1001269	69.921	44.649	36.964	34.126	22.232	42.207	49.848	39.719
HEMBA1001272	20.406	15.416	11.514	7.843	8.604	7.893	20.960	13.545
HEMBA1001279	113.597	76.085	147.371	41.113	50.841	58.248	43.344	47.548
HEMBA1001281	45.326	37.551	65.225	44.536	46.787	41.371	32.229	56.625
HEMBA1001286	370.697	150.949	236.623	103.571	123.976	219.461	196.233	117.566
HEMBA1001289	41.041	24.670	40.151	15.175	30.612	27.627	26.637	19.344
HEMBA1001291	76.537	40.444	50.226	18.776	38.423	55.355	46.692	35.972
HEMBA1001294	82.258	72.319	157.642	42.143	20.735	29.333	17.711	34.443
HEMBA1001296	53.487	17.150	31.045	10.275	15.918	21.120	15.842	13.595
HEMBA1001297	13.397	24.306	19.513	11.631	14.701	4.543	9.800	8.121
HEMBA1001299	122.378	135.140	326.747	90.817	73.749	56.152	49.803	80.999
HEMBA1001302	56.839	29.036	56.412	19.108	20.078	34.481	51.929	37.087
HEMBA1001303	14.975	18.442	43.778	16.797	10.985	11.442	9.787	19.264
HEMBA1001306	262.869	135.864	244.234	109.949	109.582	147.334	146.509	115.543
HEMBA1001308	174.017	96.705	220.049	56.953	61.486	74.225	56.171	58.657
HEMBA1001310	103.029	52.915	67.714	22.895	38.245	67.233	49.204	51.006
HEMBA1001312	98.664	47.333	61.080	18.118	33.555	47.007	41.795	38.627
HEMBA1001319	2.396	8.234	13.960	1.828	5.485	3.003	5.682	3.780
HEMBA1001322	139.794	39.912	105.709	27.700	41.977	70.428	70.602	46.470
HEMBA1001323	33.347	16.728	25.356	11.399	17.982	11.181	6.356	12.033
HEMBA1001326	86.190	37.984	69.933	24.331	30.078	49.223	46.365	16.347
HEMBA1001327	7.232	9.387	23.180	7.314	5.185	9.563	4.423	5.267
HEMBA1001330	115.768	106.951	275.315	73.389	24.661	70.535	40.088	77.680
HEMBA1001348	15.770	21.874	26.347	9.575	13.666	23.703	12.647	13.724
HEMBA1001350	75.857	38.749	51.454	16.428	34.291	56.400	34.055	24.753
HEMBA1001351	52.274	55.313	56.544	30.521	46.408	29.604	44.212	30.972
HEMBA1001352	68.321	46.617	54.427	17.559	29.887	39.484	52.789	29.131
HEMBA1001353	39.891	57.492	54.971	31.425	27.945	45.687	29.741	66.188
HEMBA1001358	45.659	52.406	59.774	46.865	40.225	47.618	32.581	59.101
HEMBA1001361	22.908	16.519	28.635	11.897	15.569	13.635	13.938	16.914
HEMBA1001364	18.896	17.205	23.355	7.224	9.469	13.379	76.125	15.026
HEMBA1001375	61.506	22.179	38.795	12.798	25.778	40.077	21.715	22.300
HEMBA1001377	140.430	131.029	307.084	83.191	100.026	74.475	63.988	96.351
HEMBA1001383	23.974	26.206	28.704	11.442	17.819	19.160	16.899	7.766
HEMBA1001387	58.343	34.130	63.677	19.556	30.371	42.397	40.247	49.239

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Table 18

HEMBA1001388	48.601	24.690	39.877	18.958	10.634	32.922	22.224	33.218
HEMBA1001390	132.003	94.390	254.352	56.412	64.490	47.169	44.169	57.372
HEMBA1001391	18.302	9.686	12.994	6.299	10.600	8.500	7.116	5.544
HEMBA1001398	91.232	50.992	142.408	36.081	29.548	29.490	28.704	29.984
HEMBA1001405	58.645	22.354	32.227	15.864	9.285	19.993	24.564	13.964
HEMBA1001406	36.434	22.693	105.808	18.094	19.994	13.316	18.019	16.592
HEMBA1001407	38.781	19.637	24.599	18.935	13.107	23.014	18.826	15.060
HEMBA1001411	28.412	7.180	21.950	8.303	9.708	14.302	8.598	6.663
HEMBA1001413	66.736	26.480	35.635	15.400	24.013	18.356	24.304	20.769
HEMBA1001414	20.720	7.567	18.414	12.522	9.722	12.903	18.283	18.581
HEMBA1001415	76.802	54.702	159.510	34.156	20.989	32.235	21.694	26.676
HEMBA1001416	41.784	23.474	29.453	12.230	24.881	24.993	25.847	28.651
HEMBA1001432	74.066	60.077	190.870	40.409	63.619	36.879	66.751	33.675
HEMBA1001433	132.672	110.163	246.542	77.852	61.676	50.447	37.821	64.403
HEMBA1001435	138.669	108.645	334.104	89.523	68.855	59.723	58.393	56.483
HEMBA1001442	13.093	8.604	11.177	7.985	15.704	7.291	6.742	6.336
HEMBA1001445	102.450	63.255	146.442	40.086	27.976	37.353	30.266	41.647
HEMBA1001450	72.339	35.494	55.103	30.799	31.322	42.457	42.764	41.349
HEMBA1001454	146.726	128.060	438.247	88.679	43.129	54.712	41.131	31.250
HEMBA1001455	5.879	8.197	8.325	5.561	4.437	5.252	4.300	7.359
HEMBA1001459	17.432	15.927	16.490	6.749	2.733	5.888	7.836	10.963
HEMBA1001461	61.531	52.734	57.136	38.874	24.764	19.473	23.241	32.318
HEMBA1001462	10.875	14.911	16.843	12.984	13.465	48.381	7.061	25.992
HEMBA1001463	137.907	83.753	340.496	93.114	51.866	61.784	37.705	68.960
HEMBA1001469	85.416	21.757	29.463	15.911	84.887	77.440	27.033	29.537
HEMBA1001473	20.582	31.855	36.498	8.307	3.680	16.703	21.371	19.890
HEMBA1001476	135.720	113.851	246.800	65.595	57.431	63.903	65.229	67.697
HEMBA1001477	5.228	2.001	4.505	2.645	1.540	3.243	1.426	2.876
HEMBA1001478	14.335	10.180	12.692	5.468	4.474	5.444	2.171	4.539
HEMBA1001480	88.891	28.381	49.689	21.660	14.126	36.334	38.272	30.563
HEMBA1001483	29.872	5.156	20.900	4.647	5.264	9.545	13.805	4.424
HEMBA1001490	6.867	6.967	14.148	7.289	1.585	5.016	5.792	5.999
HEMBA1001495	431.282	118.073	203.714	73.985	176.836	195.947	194.164	146.945
HEMBA1001497	93.817	60.807	227.867	55.576	41.006	34.182	23.206	45.223
HEMBA1001510	174.254	120.414	343.336	76.008	76.932	73.234	61.531	76.899
HEMBA1001515	45.158	26.337	67.169	15.756	15.962	10.664	9.567	12.346
HEMBA1001517	51.005	47.728	80.287	34.595	28.246	21.020	17.229	33.972
HEMBA1001522	7.431	8.980	7.032	7.566	5.011	6.466	6.447	4.824
HEMBA1001526	48.774	21.300	32.732	18.831	22.395	22.767	23.530	17.914
HEMBA1001533	129.423	85.570	262.800	70.163	46.649	44.926	26.457	37.421
HEMBA1001547	59.442	26.656	27.947	8.053	15.558	53.508	108.861	25.371
HEMBA1001552	41.663	33.242	115.535	26.222	30.447	18.258	21.358	25.853
HEMBA1001553	58.388	75.765	66.228	32.264	36.396	54.513	64.874	41.905
HEMBA1001557	182.516	80.827	161.852	69.344	80.644	123.765	111.732	70.946
HEMBA1001563	39.649	31.429	85.246	26.057	12.157	15.987	10.065	17.083
HEMBA1001566	37.835	49.964	108.284	35.793	23.255	25.180	21.368	39.375
HEMBA1001569	75.584	44.631	109.624	35.487	130.340	63.130	44.960	55.257
HEMBA1001570	198.300	125.319	444.153	119.332	74.267	79.979	64.732	90.896
HEMBA1001579	103.128	60.654	48.704	22.469	22.629	67.058	24.391	34.300
HEMBA1001581	153.698	126.225	312.570	131.687	142.104	91.884	67.267	94.418
HEMBA1001582	3.551	7.087	15.302	4.019	8.190	4.888	4.671	5.144
HEMBA1001585	27.271	18.375	25.179	14.108	5.648	14.993	7.628	12.297
HEMBA1001589	109.877	22.722	49.216	20.427	22.904	64.665	57.120	21.314
HEMBA1001595	71.600	62.349	46.938	34.447	29.362	34.516	45.233	35.562
HEMBA1001604	41.253	27.004	34.167	16.004	6.061	21.932	18.414	23.101
HEMBA1001608	35.073	29.270	41.525	21.276	22.867	22.699	14.094	15.366
HEMBA1001615	556.575	105.703	103.519	47.686	27.311	81.914	42.373	58.652
HEMBA1001620	134.940	29.972	79.824	31.924	62.056	54.423	64.359	36.203
HEMBA1001621	70.036	30.704	63.807	15.048	19.545	42.391	33.266	40.516
HEMBA1001635	39.932	29.397	35.653	16.214	18.765	19.655	22.405	14.095
HEMBA1001636	73.726	18.596	35.798	14.928	12.865	24.352	31.819	22.414
HEMBA1001640	48.402	45.105	79.588	28.452	22.449	25.101	30.009	43.819
HEMBA1001647	82.402	39.456	75.907	35.084	26.220	48.859	71.158	46.463
HEMBA1001651	390.307	66.648	181.929	51.802	112.530	208.201	178.161	96.640

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Table 19

HEMBA1001655	60.366	18.983	58.438	20.404	25.072	27.162	29.260	26.673
HEMBA1001658	6.754	15.270	17.542	13.420	5.060	4.800	4.973	4.979
HEMBA1001661	87.199	20.304	32.793	13.066	8.394	24.098	22.916	24.583
HEMBA1001665	160.583	20.830	54.460	12.363	48.457	86.024	73.847	21.248
HEMBA1001670	16.953	38.651	17.002	34.999	14.855	17.849	22.906	29.478
HEMBA1001672	32.013	18.885	29.000	10.798	7.763	13.782	17.314	12.393
HEMBA1001673	38.188	67.401	34.336	38.037	14.401	17.612	30.520	43.461
HEMBA1001675	25.652	15.594	33.810	5.390	15.796	13.173	20.020	12.830
HEMBA1001676	91.000	54.310	85.397	92.681	131.468	50.365	47.230	68.405
HEMBA1001678	218.382	128.995	336.408	93.889	115.305	80.843	48.879	83.933
HEMBA1001680	82.159	51.521	165.818	33.978	36.449	33.368	38.495	35.261
HEMBA1001681	1.654	0.785	0.840	2.142	2.581	2.772	2.146	2.424
HEMBA1001684	143.985	84.151	377.154	72.850	69.097	61.638	30.820	52.077
HEMBA1001695	16.068	10.112	14.571	6.860	4.930	4.572	6.164	7.330
HEMBA1001702	26.509	13.637	8.186	8.466	4.041	2.043	3.870	3.613
HEMBA1001709	67.279	26.552	35.845	13.982	21.742	28.610	24.540	19.603
HEMBA1001711	20.072	29.559	39.037	20.902	21.639	12.713	14.718	33.127
HEMBA1001712	80.448	25.222	51.628	19.393	12.482	38.014	39.474	14.831
HEMBA1001714	360.368	55.902	142.225	33.748	51.048	144.094	124.654	59.543
HEMBA1001717	78.599	137.380	18.549	12.298	5.575	38.689	10.120	6.047
HEMBA1001718	51.621	52.280	151.597	31.305	21.166	29.146	14.075	24.411
HEMBA1001723	17.072	13.658	8.525	5.653	8.811	9.350	11.097	7.268
HEMBA1001731	35.728	22.781	41.531	15.151	12.421	15.292	14.020	16.584
HEMBA1001734	52.546	40.599	99.556	25.099	24.031	28.537	17.389	32.936
HEMBA1001735	177.269	58.328	110.046	33.820	58.955	108.630	91.464	62.571
HEMBA1001741	41.432	12.649	29.883	14.886	16.207	10.446	11.420	7.286
HEMBA1001744	5.531	6.849	12.961	13.191	14.151	4.519	8.367	8.623
HEMBA1001745	41.752	17.786	36.239	12.476	21.118	23.635	15.410	16.514
HEMBA1001746	27.437	14.874	24.099	8.668	21.929	19.488	11.306	10.070
HEMBA1001761	93.148	46.911	179.597	28.212	33.421	34.026	19.164	25.901
HEMBA1001762	55.612	45.069	102.148	38.307	35.260	33.316	21.274	45.248
HEMBA1001781	13.298	21.385	26.693	6.898	17.098	52.601	11.768	23.068
HEMBA1001784	89.965	43.765	70.064	26.575	31.708	50.347	52.265	31.618
HEMBA1001791	182.379	81.719	171.066	44.628	49.350	82.856	58.215	48.207
HEMBA1001794	248.582	163.789	153.778	73.632	50.595	152.279	178.827	132.329
HEMBA1001800	23.432	21.165	27.668	11.281	20.728	24.910	36.900	22.729
HEMBA1001803	17.343	8.333	22.801	6.620	6.043	7.560	6.613	10.079
HEMBA1001804	109.775	44.797	59.456	29.337	34.849	44.372	36.696	35.851
HEMBA1001808	78.129	23.567	38.056	15.858	23.507	27.136	14.673	12.332
HEMBA1001809	66.887	31.733	54.127	33.314	26.179	35.618	41.552	46.141
HEMBA1001811	58.974	24.196	37.583	17.314	16.018	21.582	15.074	19.831
HEMBA1001815	71.286	63.775	155.707	37.153	29.944	35.297	25.257	24.172
HEMBA1001816	38.494	19.017	16.797	7.139	5.598	16.061	22.304	14.646
HEMBA1001819	18.590	21.371	38.109	20.938	21.358	15.313	14.917	25.144
HEMBA1001820	10.884	9.530	8.017	3.507	4.470	3.473	2.999	3.099
HEMBA1001822	74.239	95.719	91.314	62.121	28.285	42.988	38.222	47.532
HEMBA1001824	155.543	93.583	301.248	95.135	67.478	89.045	64.562	61.114
HEMBA1001835	23.616	7.706	25.753	5.777	19.660	19.809	12.020	10.462
HEMBA1001844	149.876	52.023	230.213	48.968	42.113	39.652	33.559	40.495
HEMBA1001847	52.045	19.220	40.636	20.235	5.196	35.109	20.186	35.814
HEMBA1001849	101.048	104.708	250.547	53.025	28.022	40.644	33.371	35.250
HEMBA1001850	105.331	27.032	39.813	15.808	31.525	42.751	44.306	18.213
HEMBA1001861	3.104	4.469	6.763	3.292	4.454	2.945	0.995	3.121
HEMBA1001862	50.279	145.708	102.412	25.750	34.563	40.833	22.588	71.713
HEMBA1001864	24.313	31.572	50.378	32.237	24.991	21.182	21.031	28.126
HEMBA1001865	57.711	54.190	146.615	31.714	19.527	26.041	22.874	21.249
HEMBA1001869	55.280	99.559	58.454	35.799	45.195	40.562	22.644	40.891
HEMBA1001871	75.011	44.336	77.195	41.540	39.300	54.584	34.598	42.631
HEMBA1001876	34.287	31.955	30.568	85.092	19.827	15.356	8.554	21.861
HEMBA1001878	17.361	17.619	17.545	15.644	5.481	11.657	14.965	18.117
HEMBA1001879	57.004	22.429	37.128	16.562	20.200	35.414	21.946	17.114
HEMBA1001884	68.009	84.640	41.930	38.470	27.460	36.604	25.345	26.320
HEMBA1001886	12.711	12.605	37.824	31.827	15.893	14.038	6.697	38.737
HEMBA1001888	63.251	46.960	165.623	41.706	21.154	29.117	21.131	33.090

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Table 20

HEMBA1001890	42.902	42.848	42.779	30.112	25.432	24.430	22.605	26.730
HEMBA1001896	66.448	24.720	44.103	21.972	17.708	30.703	19.628	23.571
HEMBA1001899	36.251	25.553	24.121	14.701	12.301	21.838	17.455	20.813
HEMBA1001904	54.904	256.020	233.857	243.646	55.587	234.548	188.571	526.744
HEMBA1001910	40.309	10.865	13.738	11.244	8.226	15.367	15.894	13.300
HEMBA1001911	35.962	23.128	26.357	25.151	11.860	24.224	22.870	18.238
HEMBA1001912	59.924	66.966	97.679	51.180	45.903	33.336	33.019	40.551
HEMBA1001913	175.368	39.664	67.432	33.132	26.376	63.459	70.607	52.824
HEMBA1001915	14.756	14.666	30.224	8.295	7.629	17.718	6.737	8.522
HEMBA1001918	5.018	8.961	27.591	7.538	11.032	8.265	4.852	4.772
HEMBA1001921	4.431	8.444	18.196	11.252	12.587	7.417	7.668	2.769
HEMBA1001931	3.948	0.000	4.664	1.422	3.480	2.935	1.127	2.898
HEMBA1001939	94.821	24.679	81.706	24.209	16.692	37.223	29.835	13.058
HEMBA1001940	54.512	33.931	145.138	26.273	27.653	18.649	13.136	19.614
HEMBA1001942	38.572	16.710	32.402	18.718	14.782	25.435	26.410	16.143
HEMBA1001944	210.898	71.197	96.883	48.156	38.533	82.132	92.097	74.740
HEMBA1001945	31.531	17.019	14.533	10.175	3.037	17.421	12.222	11.694
HEMBA1001950	7.103	7.424	9.611	3.281	4.091	7.632	5.310	4.044
HEMBA1001951	46.024	19.234	101.026	19.207	13.212	23.714	20.006	19.402
HEMBA1001958	44.554	12.806	35.277	17.321	13.181	22.652	28.735	20.948
HEMBA1001960	20.513	7.802	16.888	8.822	2.948	8.826	10.834	12.935
HEMBA1001962	4.367	5.104	4.205	2.811	3.031	4.870	2.364	2.994
HEMBA1001964	35.944	22.281	62.761	18.757	6.663	17.775	8.068	8.601
HEMBA1001967	47.345	29.504	42.717	13.526	22.051	33.555	23.601	37.521
HEMBA1001979	35.138	6.478	16.732	12.797	5.919	13.447	10.355	9.155
HEMBA1001987	60.083	52.275	190.331	45.735	24.898	26.381	17.514	28.891
HEMBA1001991	111.286	79.833	276.566	56.455	50.862	50.789	40.252	54.919
HEMBA1002003	66.389	23.989	53.710	17.039	17.174	30.547	28.422	24.474
HEMBA1002005	86.885	41.457	150.127	33.935	15.339	24.541	24.237	27.345
HEMBA1002008	32.101	25.375	86.511	18.349	8.912	7.593	18.519	14.967
HEMBA1002018	66.105	22.380	36.174	16.334	21.482	27.922	34.098	27.804
HEMBA1002022	13.986	8.018	13.490	0.000	2.985	5.730	6.036	1.433
HEMBA1002029	132.547	305.823	115.974	144.692	70.087	74.071	37.048	204.730
HEMBA1002030	17.077	10.337	14.524	5.906	8.466	5.897	6.258	6.824
HEMBA1002035	48.658	12.959	10.324	14.325	7.176	14.446	14.084	13.506
HEMBA1002037	16.343	34.097	27.567	14.451	12.568	15.087	13.819	12.140
HEMBA1002038	68.477	31.733	91.391	16.935	8.370	6.020	17.500	19.367
HEMBA1002039	15.944	22.707	17.807	13.914	7.910	3.306	4.716	11.003
HEMBA1002042	41.657	27.877	32.654	21.111	14.815	10.217	24.300	22.659
HEMBA1002043	149.364	92.912	208.642	70.906	53.861	84.089	81.242	61.829
HEMBA1002048	137.253	29.889	60.279	19.894	21.605	66.594	55.483	30.137
HEMBA1002049	98.417	84.099	271.170	63.157	87.434	48.247	39.557	53.676
HEMBA1002053	33.636	19.194	25.821	11.890	16.358	16.441	25.376	27.152
HEMBA1002055	67.115	34.916	39.511	37.518	17.449	25.297	28.606	39.067
HEMBA1002056	13.684	12.039	16.129	14.136	1.311	8.564	4.481	12.538
HEMBA1002061	11.815	14.960	29.478	10.168	10.973	11.179	9.701	8.124
HEMBA1002080	59.350	80.319	81.497	43.371	72.416	39.904	45.653	53.581
HEMBA1002084	11.331	7.502	15.981	7.301	10.773	13.652	6.835	5.555
HEMBA1002085	69.868	62.174	111.196	13.760	19.083	101.175	43.117	14.011
HEMBA1002092	127.409	33.016	60.924	24.219	32.654	72.141	50.433	27.770
HEMBA1002098	34.645	16.695	25.357	15.741	15.632	18.082	12.882	20.451
HEMBA1002100	118.301	90.733	129.453	60.276	41.079	89.713	44.294	67.352
HEMBA1002101	57.160	69.427	106.418	34.067	32.565	38.238	15.932	74.139
HEMBA1002102	104.746	76.058	178.766	45.801	50.114	53.399	40.628	54.459
HEMBA1002105	35.380	25.812	31.300	14.131	14.867	29.842	22.894	23.960
HEMBA1002107	62.621	45.738	65.486	28.199	31.808	52.057	163.850	77.437
HEMBA1002113	745.018	396.517	1335.986	321.385	369.500	391.825	236.013	348.025
HEMBA1002119	35.812	23.546	72.351	18.292	19.991	18.086	26.533	25.611
HEMBA1002125	42.106	14.033	45.440	15.858	20.474	47.217	28.894	33.563
HEMBA1002131	84.269	29.512	46.944	12.807	29.311	40.381	49.691	37.106
HEMBA1002133	37.736	19.103	27.034	45.990	11.161	21.694	20.410	24.305
HEMBA1002139	25.756	10.925	20.941	4.978	11.839	9.451	7.795	9.431
HEMBA1002141	20.036	14.349	19.713	9.608	3.638	14.521	10.225	10.190
HEMBA1002144	86.896	68.335	193.756	56.749	45.612	36.918	23.020	39.262

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Table 21

HEMBA1002147	135.045	48.848	87.208	42.412	46.318	67.257	83.313	45.988
HEMBA1002150	347.113	89.434	182.502	48.715	86.270	215.282	234.394	85.507
HEMBA1002151	60.410	19.140	11.868	10.122	7.938	26.996	19.485	14.196
HEMBA1002153	32.258	25.478	35.746	20.325	25.638	15.972	26.019	19.827
HEMBA1002156	118.226	31.167	44.382	21.446	21.743	47.426	40.620	16.858
HEMBA1002160	166.654	114.853	336.241	90.651	71.047	63.857	41.633	55.419
HEMBA1002161	72.851	68.019	132.156	42.302	37.035	29.438	49.436	41.818
HEMBA1002162	122.516	62.989	307.464	68.589	51.141	55.242	37.823	54.952
HEMBA1002163	49.889	43.602	64.932	20.426	7.151	0.000	30.979	32.578
HEMBA1002164	110.221	59.044	71.408	32.652	19.476	39.440	43.639	52.404
HEMBA1002166	312.686	256.137	768.834	194.638	171.071	159.271	134.442	213.993
HEMBA1002167	139.053	18.430	69.693	11.057	30.091	50.202	48.620	13.648
HEMBA1002173	137.562	47.918	197.006	36.833	26.164	29.478	20.169	23.078
HEMBA1002177	100.895	25.141	41.676	25.857	17.903	28.153	22.687	14.081
HEMBA1002178	102.831	19.500	46.717	13.290	32.323	37.856	44.115	27.390
HEMBA1002179	55.617	56.403	85.686	45.680	26.918	60.684	59.110	64.849
HEMBA1002185	85.236	71.958	212.844	43.915	27.049	32.172	22.480	32.386
HEMBA1002188	79.413	28.280	31.826	23.275	21.094	33.295	36.478	18.236
HEMBA1002189	56.349	70.609	148.011	47.092	32.460	30.101	34.751	30.532
HEMBA1002191	149.027	80.765	149.493	49.599	42.372	60.095	35.614	44.348
HEMBA1002192	15.125	24.996	24.821	15.373	16.495	12.778	5.075	13.566
HEMBA1002195	57.368	28.635	52.828	16.254	22.600	31.843	32.995	29.791
HEMBA1002196	14.884	12.040	36.633	16.632	15.443	16.808	12.691	17.451
HEMBA1002199	24.937	13.539	27.878	15.728	17.426	10.639	19.664	8.927
HEMBA1002204	9.525	5.141	14.869	6.784	4.619	10.508	27.818	9.410
HEMBA1002208	80.832	44.154	68.317	68.994	37.453	74.064	81.827	112.820
HEMBA1002212	8.709	6.241	10.946	9.855	2.602	5.864	5.366	4.214
HEMBA1002215	36.521	28.098	31.165	19.157	20.170	17.045	19.124	21.605
HEMBA1002217	50.834	62.759	64.668	59.460	28.990	37.379	29.963	64.813
HEMBA1002220	27.731	14.997	21.655	8.451	6.409	5.663	1.641	6.714
HEMBA1002226	91.222	113.507	269.906	85.183	68.283	59.461	56.996	78.924
HEMBA1002227	55.957	91.527	79.169	45.309	54.892	28.856	14.142	101.597
HEMBA1002229	170.518	117.589	418.739	112.916	121.703	85.889	63.450	90.668
HEMBA1002237	47.252	49.329	124.721	32.838	24.807	23.399	15.399	26.185
HEMBA1002239	103.363	107.010	190.830	54.740	72.381	50.451	45.873	70.581
HEMBA1002241	70.729	45.281	81.541	43.824	30.449	54.328	62.401	55.767
HEMBA1002253	25.559	27.877	35.744	16.605	13.851	18.938	18.391	14.286
HEMBA1002257	6.344	5.787	15.404	4.338	1.225	7.119	4.456	3.711
HEMBA1002259	48.436	19.578	38.228	12.875	21.884	23.928	18.619	17.988
HEMBA1002262	271.029	219.564	645.284	192.491	147.403	112.552	83.057	137.280
HEMBA1002265	56.947	30.786	32.747	24.827	15.078	28.043	29.609	27.237
HEMBA1002267	108.413	102.522	243.566	58.776	30.087	53.750	24.099	29.752
HEMBA1002270	51.540	26.396	27.766	20.313	15.579	28.348	19.144	16.695
HEMBA1002286	44.897	17.027	19.776	11.608	10.900	25.959	14.425	10.031
HEMBA1002290	46.449	29.289	34.095	19.879	8.778	26.461	22.368	13.907
HEMBA1002302	152.883	48.105	92.158	43.064	48.204	66.899	80.872	58.027
HEMBA1002304	6.050	6.814	19.492	7.905	4.038	7.098	5.307	1.737
HEMBA1002307	100.402	132.737	29.225	24.612	24.050	42.355	39.076	37.573
HEMBA1002316	504.772	93.620	191.534	46.814	134.386	238.599	265.167	88.087
HEMBA1002319	2.868	2.456	9.670	0.933	4.715	4.369	5.615	4.579
HEMBA1002320	10.783	7.936	12.646	4.775	10.008	4.330	5.128	3.630
HEMBA1002321	10.743	9.992	10.165	4.549	2.547	7.952	4.048	5.700
HEMBA1002328	89.382	28.578	41.753	17.175	20.280	46.772	34.722	18.301
HEMBA1002333	63.542	21.208	32.148	11.559	15.490	29.410	33.449	21.452
HEMBA1002337	93.059	61.863	189.067	60.545	43.745	40.085	13.954	34.456
HEMBA1002339	354.195	154.586	211.807	141.794	124.733	173.522	284.831	192.502
HEMBA1002341	116.488	29.538	63.800	15.812	36.228	50.321	45.600	28.278
HEMBA1002348	6.882	4.859	18.593	4.056	4.011	5.790	4.476	4.606
HEMBA1002349	6.318	7.600	13.603	5.490	2.590	6.088	1.306	3.748
HEMBA1002353	14.497	13.001	12.249	10.426	11.840	13.977	17.141	16.760
HEMBA1002356	104.283	29.278	40.945	24.892	20.681	42.242	45.108	28.190
HEMBA1002357	64.855	251.508	219.532	215.420	68.836	206.728	136.339	380.371
HEMBA1002360	87.281	64.882	77.475	30.773	56.108	61.060	59.371	56.291
HEMBA1002363	71.449	51.764	63.278	52.711	43.280	33.755	31.248	49.484

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Table 22

HEMBA1002365	13.435	10.346	9.534	5.175	9.470	4.446	10.802	9.325
HEMBA1002370	29.997	4.107	11.054	4.163	3.224	9.009	7.477	2.921
HEMBA1002374	91.498	18.475	11.325	15.862	10.204	18.275	29.203	18.856
HEMBA1002376	186.416	75.425	127.578	52.056	38.450	99.590	90.190	86.994
HEMBA1002377	81.350	41.908	63.893	37.221	23.657	110.374	162.166	50.770
HEMBA1002380	189.521	137.466	477.021	137.908	491.500	90.431	81.778	127.767
HEMBA1002381	195.037	101.891	447.953	125.938	88.330	90.756	70.293	106.965
HEMBA1002384	35.247	22.319	42.496	14.694	19.780	40.126	24.243	12.399
HEMBA1002389	44.796	8.467	36.790	11.793	9.362	18.736	15.497	20.728
HEMBA1002396	101.267	69.467	33.025	16.553	26.429	25.964	22.294	23.666
HEMBA1002402	75.818	24.148	28.457	8.848	9.913	21.219	16.569	22.818
HEMBA1002417	132.807	33.708	84.436	22.910	38.826	58.589	58.836	38.486
HEMBA1002419	75.547	31.202	41.690	13.558	16.457	27.281	19.705	13.013
HEMBA1002420	20.818	20.448	35.559	17.034	13.878	23.652	14.721	24.637
HEMBA1002421	23.903	25.285	59.023	7.957	14.189	24.230	61.011	21.849
HEMBA1002423	12.762	11.755	25.941	12.938	14.177	14.263	12.495	7.512
HEMBA1002424	111.995	32.293	46.657	24.424	25.667	42.797	41.513	31.249
HEMBA1002426	60.617	23.489	45.906	20.305	25.173	30.860	37.738	21.223
HEMBA1002430	24.143	3.128	4.900	1.517	4.594	3.316	8.552	3.069
HEMBA1002439	59.808	37.476	93.025	16.789	23.324	47.857	33.099	27.888
HEMBA1002441	77.869	99.262	110.341	38.723	34.562	65.309	85.421	66.581
HEMBA1002454	58.292	15.281	38.384	7.520	19.044	25.972	22.845	22.015
HEMBA1002458	57.329	46.103	101.242	30.906	82.184	61.800	26.094	59.039
HEMBA1002460	32.814	9.205	25.085	12.160	23.009	18.683	14.678	14.249
HEMBA1002462	98.420	38.135	55.208	10.919	24.257	49.697	43.851	32.387
HEMBA1002465	11.819	15.260	28.272	11.939	11.225	10.938	13.593	20.635
HEMBA1002469	129.538	61.348	120.187	39.999	39.213	76.320	69.012	86.309
HEMBA1002475	3.180	5.116	4.323	2.230	1.467	4.495	10.058	15.691
HEMBA1002477	93.696	64.730	238.114	55.207	43.349	42.487	29.532	52.786
HEMBA1002480	210.023	58.823	84.566	37.478	45.060	106.554	97.791	70.487
HEMBA1002481	104.499	76.474	222.903	71.502	68.097	67.421	42.334	82.875
HEMBA1002486	81.465	42.269	169.291	49.953	40.852	39.475	29.153	26.233
HEMBA1002490	66.695	11.331	31.314	14.602	25.852	35.945	35.954	15.278
HEMBA1002495	59.387	12.315	25.235	7.937	4.091	17.402	14.269	10.773
HEMBA1002498	56.425	23.969	67.108	11.632	15.655	24.420	8.272	12.219
HEMBA1002501	40.955	16.994	22.074	13.575	16.498	21.707	39.506	24.619
HEMBA1002503	81.763	65.044	154.595	39.638	33.778	31.214	32.219	26.800
HEMBA1002504	155.357	95.219	279.391	90.092	120.246	70.516	52.190	53.323
HEMBA1002508	99.443	88.234	259.961	107.085	79.039	59.181	59.924	61.423
HEMBA1002513	50.560	22.902	30.431	26.184	20.783	30.500	32.903	22.864
HEMBA1002515	60.938	23.064	25.098	16.172	5.716	20.264	20.643	13.727
HEMBA1002524	94.350	36.789	56.675	25.998	28.978	49.840	57.148	25.205
HEMBA1002538	116.609	19.632	26.764	12.798	20.203	16.422	17.588	15.759
HEMBA1002542	81.641	81.952	188.888	54.986	41.864	32.890	30.719	38.321
HEMBA1002544	52.394	49.175	98.415	47.569	28.375	28.766	20.948	21.614
HEMBA1002546	76.538	62.763	156.051	47.625	74.374	45.975	34.756	46.753
HEMBA1002547	11.448	4.516	10.647	4.733	12.220	11.801	9.959	7.127
HEMBA1002550	67.373	39.322	48.468	15.671	16.497	121.814	94.586	25.401
HEMBA1002551	94.391	14.109	27.085	11.976	8.787	41.811	16.656	18.665
HEMBA1002552	204.583	77.430	205.444	49.448	44.756	67.408	63.216	57.684
HEMBA1002555	25.583	16.987	6.743	7.020	5.608	14.795	10.111	7.416
HEMBA1002558	92.744	77.405	245.703	59.079	41.247	33.253	41.617	41.270
HEMBA1002561	53.810	51.725	155.895	34.956	27.689	17.264	10.138	27.124
HEMBA1002562	15.261	10.822	15.435	8.259	18.723	12.036	9.056	10.429
HEMBA1002568	24.946	17.442	35.354	17.552	10.576	15.262	16.158	22.328
HEMBA1002569	112.340	34.133	118.192	37.823	57.431	54.936	26.164	27.309
HEMBA1002570	43.528	50.809	52.195	34.901	23.728	28.874	9.812	50.494
HEMBA1002574	106.101	25.148	46.793	16.369	26.322	57.278	42.795	31.310
HEMBA1002583	36.042	17.582	15.178	12.456	13.418	20.158	16.837	16.418
HEMBA1002587	61.527	32.123	45.811	22.217	18.974	32.461	40.250	39.915
HEMBA1002590	151.583	106.074	287.276	84.766	32.321	58.221	38.642	53.855
HEMBA1002592	97.854	85.949	220.496	89.335	52.684	53.653	35.724	57.578
HEMBA1002595	146.016	25.688	60.427	24.156	31.909	86.770	79.174	26.760
HEMBA1002609	97.442	41.926	56.054	29.427	35.650	35.839	44.688	47.074

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Table 23

HEMBA1002617	26.792	86.617	59.446	73.277	12.909	21.055	16.612	49.136
HEMBA1002619	101.131	25.998	30.959	15.921	21.913	40.814	35.003	28.108
HEMBA1002621	14.592	25.845	18.082	8.927	7.391	8.869	5.823	12.283
HEMBA1002624	254.635	42.837	73.568	48.036	71.673	113.228	101.786	53.514
HEMBA1002628	13.044	21.509	23.649	9.956	16.559	10.257	7.527	11.624
HEMBA1002629	32.199	16.370	29.306	15.884	5.722	15.410	42.964	19.680
HEMBA1002632	55.206	48.044	90.986	36.904	27.840	28.811	37.912	40.048
HEMBA1002645	95.909	89.897	220.184	68.171	48.643	56.847	41.355	59.667
HEMBA1002651	39.882	27.730	33.313	16.958	11.617	23.904	29.214	16.599
HEMBA1002652	107.869	24.187	46.646	22.248	22.950	37.216	25.827	23.282
HEMBA1002659	133.320	62.916	259.854	57.860	53.172	46.511	45.193	47.291
HEMBA1002661	88.495	68.014	154.170	35.196	22.499	26.290	22.314	23.727
HEMBA1002666	34.174	20.511	39.391	17.036	15.852	20.842	19.202	13.470
HEMBA1002667	155.384	166.244	164.658	29.523	520.013	30.234	25.612	83.769
HEMBA1002673	71.650	40.718	73.822	33.403	39.914	40.129	38.619	22.532
HEMBA1002678	161.681	89.986	247.534	84.722	54.176	46.941	61.944	77.085
HEMBA1002679	56.416	61.838	66.537	37.679	18.172	29.420	38.238	44.113
HEMBA1002688	6.756	3.364	5.387	3.816	1.793	4.608	3.600	2.944
HEMBA1002696	49.639	17.555	29.241	14.788	12.463	31.752	34.100	14.772
HEMBA1002703	185.328	96.718	97.793	54.473	50.688	113.980	87.727	59.878
HEMBA1002706	49.533	30.340	35.679	18.469	19.118	26.777	29.277	29.224
HEMBA1002712	52.878	59.111	110.506	41.591	43.597	39.604	30.872	26.457
HEMBA1002715	149.045	59.858	87.643	47.473	41.264	95.279	127.808	65.580
HEMBA1002716	23.142	6.155	17.077	15.783	23.557	19.064	27.647	7.572
HEMBA1002718	26.328	19.063	41.749	26.345	16.735	28.367	26.822	21.779
HEMBA1002728	117.984	88.950	293.019	81.290	43.679	65.830	46.321	57.003
HEMBA1002730	131.726	26.862	67.877	28.628	36.686	49.987	50.380	43.208
HEMBA1002734	77.679	26.481	34.604	21.128	21.756	41.413	60.057	45.992
HEMBA1002742	10.730	11.276	12.768	7.910	1.394	8.502	8.297	10.909
HEMBA1002746	60.876	22.803	35.400	15.830	15.630	30.605	31.889	32.759
HEMBA1002748	76.748	26.130	38.669	17.760	32.833	43.493	53.440	49.691
HEMBA1002750	40.663	45.306	95.205	18.200	10.037	22.527	29.331	30.774
HEMBA1002755	94.758	62.505	220.964	63.414	37.572	44.593	28.497	39.737
HEMBA1002759	13.935	3.117	8.450	3.792	2.291	8.714	10.261	5.285
HEMBA1002763	430.941	88.931	172.920	71.623	88.921	195.471	197.995	118.224
HEMBA1002767	65.682	25.272	35.782	14.035	19.183	31.497	33.393	18.347
HEMBA1002768	100.803	57.554	59.457	35.570	28.006	43.770	40.930	38.215
HEMBA1002769	103.210	30.236	54.098	17.099	19.753	35.636	41.922	26.940
HEMBA1002770	20.350	16.268	28.054	21.736	10.754	12.030	14.991	11.776
HEMBA1002777	130.615	37.655	72.072	41.794	31.219	54.881	59.342	43.652
HEMBA1002779	97.457	29.259	75.705	22.719	22.643	33.689	38.357	27.804
HEMBA1002780	72.338	50.411	181.356	42.070	19.957	31.370	27.642	39.672
HEMBA1002790	87.371	61.291	152.514	38.033	29.616	28.032	20.352	34.761
HEMBA1002794	202.405	77.515	95.182	31.252	41.834	100.167	80.301	50.036
HEMBA1002798	9.194	21.334	22.468	20.281	12.823	11.156	11.647	15.735
HEMBA1002801	10.311	4.603	11.704	3.190	4.420	3.016	13.829	6.693
HEMBA1002810	42.583	45.313	55.088	35.416	29.480	60.935	44.046	51.794
HEMBA1002816	52.084	37.823	56.994	35.902	25.574	33.389	50.974	49.045
HEMBA1002818	321.516	100.826	187.799	84.893	81.695	152.339	171.186	117.409
HEMBA1002820	139.924	107.278	533.137	90.533	79.745	59.869	54.302	52.958
HEMBA1002826	40.776	6.495	16.825	5.349	3.319	11.765	7.355	8.363
HEMBA1002833	119.102	44.248	40.839	17.864	23.748	44.398	57.302	36.668
HEMBA1002850	5.941	8.407	13.251	6.179	2.932	4.352	4.844	3.735
HEMBA1002862	60.735	32.524	30.030	9.693	9.527	27.595	19.397	18.101
HEMBA1002863	77.126	30.401	44.872	22.577	28.639	50.264	55.374	45.005
HEMBA1002867	25.385	13.583	42.122	15.283	9.501	22.992	15.180	16.196
HEMBA1002876	101.249	55.603	38.073	36.480	23.017	53.318	51.363	56.689
HEMBA1002886	9.474	14.188	23.688	7.657	11.980	14.640	6.432	18.574
HEMBA1002896	78.580	27.420	49.774	16.754	20.366	36.684	35.283	42.662
HEMBA1002913	126.001	32.845	58.138	14.590	22.846	54.873	56.608	38.801
HEMBA1002921	63.378	25.443	37.615	15.333	19.054	28.881	37.595	34.298
HEMBA1002924	65.007	29.109	104.125	15.411	19.920	31.099	23.998	19.182
HEMBA1002934	432.841	308.291	644.522	180.470	145.293	273.733	166.153	242.809
HEMBA1002935	92.005	52.184	221.722	49.477	41.867	34.331	29.646	38.889

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Table 24

HEMBA1002937	38.698	30.844	33.817	12.784	18.251	14.107	24.131	18.662
HEMBA1002939	39.755	22.867	33.838	19.077	13.734	19.266	17.364	17.750
HEMBA1002944	53.762	33.349	51.861	21.860	18.241	23.920	21.112	16.286
HEMBA1002951	38.716	29.783	39.196	19.808	29.614	19.702	28.422	21.177
HEMBA1002954	24.907	8.542	20.941	9.265	13.758	15.056	7.297	13.424
HEMBA1002962	86.680	62.578	220.246	62.027	37.753	44.037	31.812	41.725
HEMBA1002968	105.871	78.850	221.414	65.545	40.380	43.093	38.816	50.281
HEMBA1002970	48.034	34.741	30.834	18.482	6.639	17.125	23.514	36.180
HEMBA1002971	39.492	44.145	35.618	25.614	12.932	25.193	14.823	23.202
HEMBA1002973	83.710	70.965	156.167	43.307	28.902	29.947	26.101	34.769
HEMBA1002978	35.833	19.362	27.056	13.075	20.398	11.324	16.059	13.956
HEMBA1002981	107.112	35.200	56.576	23.695	26.105	33.054	37.199	21.249
HEMBA1002985	79.217	44.154	116.532	27.950	26.158	37.462	28.927	20.335
HEMBA1002986	61.056	78.203	68.834	49.967	64.529	38.333	28.919	20.529
HEMBA1002988	37.307	36.609	71.802	20.621	8.965	16.229	15.956	22.796
HEMBA1002992	97.720	72.656	79.841	50.454	34.289	57.004	61.291	91.211
HEMBA1002995	51.473	63.779	55.081	36.903	25.007	38.630	19.510	48.529
HEMBA1002997	41.734	70.805	29.264	27.019	33.664	24.201	18.442	25.973
HEMBA1002999	35.341	16.456	18.357	11.146	7.034	12.086	13.966	9.970
HEMBA1003004	55.654	31.689	35.194	15.119	16.204	20.866	27.891	20.055
HEMBA1003006	40.582	24.886	20.750	20.903	26.595	25.445	20.310	20.924
HEMBA1003008	29.269	20.922	74.697	25.061	17.787	10.271	5.688	12.638
HEMBA1003021	130.889	123.646	311.225	101.957	95.443	64.844	60.969	90.296
HEMBA1003027	54.935	32.610	44.710	18.890	52.131	26.286	28.112	31.561
HEMBA1003029	33.333	42.436	60.787	20.829	34.111	29.704	49.230	45.833
HEMBA1003031	34.000	25.311	18.494	14.998	13.316	13.955	15.773	27.136
HEMBA1003032	171.114	46.990	71.365	23.640	50.526	81.278	84.036	46.352
HEMBA1003033	168.563	118.674	378.771	109.222	90.670	70.150	55.336	77.819
HEMBA1003034	173.162	127.221	484.135	108.238	85.630	61.733	36.799	63.312
HEMBA1003035	11.693	5.195	9.305	4.478	5.058	11.024	2.553	4.409
HEMBA1003037	261.159	89.481	145.321	58.521	65.732	104.677	89.571	71.674
HEMBA1003041	103.945	105.085	291.931	93.188	75.193	53.097	39.564	58.217
HEMBA1003046	40.264	39.965	46.856	26.192	11.615	35.659	25.378	32.416
HEMBA1003047	127.888	49.341	139.750	32.219	32.320	57.450	33.390	28.702
HEMBA1003048	87.433	35.962	42.305	12.040	20.442	39.108	29.597	21.461
HEMBA1003064	6.366	8.535	6.201	8.809	4.415	7.239	3.330	7.829
HEMBA1003067	55.833	34.508	77.097	26.154	20.523	28.755	24.783	17.488
HEMBA1003071	54.728	22.509	28.869	17.461	19.647	20.624	22.285	19.438
HEMBA1003072	62.421	30.769	31.225	26.146	22.906	21.483	17.616	19.134
HEMBA1003076	111.254	51.085	78.972	37.151	40.422	49.911	47.023	64.737
HEMBA1003077	36.471	15.407	24.522	8.009	8.453	18.661	13.797	5.837
HEMBA1003078	34.143	38.741	77.906	31.907	37.169	17.933	17.439	18.923
HEMBA1003079	28.559	39.563	41.646	26.110	25.889	25.576	18.026	24.526
HEMBA1003083	61.036	48.635	169.439	52.788	60.016	41.611	29.619	67.469
HEMBA1003086	49.032	40.488	154.409	29.869	12.063	16.544	16.039	19.219
HEMBA1003090	34.778	14.860	23.758	12.710	24.132	15.848	25.027	14.265
HEMBA1003094	184.999	43.363	72.116	30.096	53.636	78.251	84.551	34.775
HEMBA1003096	31.440	18.030	25.774	10.290	11.781	14.033	27.791	11.348
HEMBA1003098	36.774	64.970	88.562	34.074	24.271	25.656	18.003	31.059
HEMBA1003101	55.716	24.121	22.316	11.682	13.163	21.315	25.117	15.689
HEMBA1003109	48.411	21.093	39.285	21.315	21.724	27.826	31.034	21.809
HEMBA1003114	41.101	24.786	22.792	14.164	14.657	18.320	15.152	16.038
HEMBA1003117	22.939	13.535	20.191	6.812	10.538	14.917	18.015	12.566
HEMBA1003120	24.531	24.408	55.805	26.574	13.838	15.423	15.080	21.728
HEMBA1003129	40.276	46.792	104.463	37.995	37.989	21.990	26.267	38.207
HEMBA1003133	50.080	22.873	35.022	15.164	20.000	21.592	25.551	27.656
HEMBA1003136	146.630	23.706	65.990	18.301	31.049	69.754	51.669	25.346
HEMBA1003142	69.008	47.857	130.557	32.955	30.384	25.274	27.118	29.493
HEMBA1003148	59.282	20.084	32.740	18.292	18.973	32.206	22.003	24.674
HEMBA1003151	53.856	20.003	51.824	13.233	9.854	27.114	22.251	13.546
HEMBA1003152	20.577	9.803	19.388	10.017	5.761	31.586	23.227	6.853
HEMBA1003157	16.477	9.272	16.246	9.919	17.605	7.547	10.156	10.181
HEMBA1003166	293.814	257.380	671.361	260.521	221.325	137.459	148.208	199.758
HEMBA1003171	17.730	8.702	16.527	6.499	6.963	7.361	5.733	7.164

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Table 25

HEMBA1003175	38.620	40.445	100.302	29.594	17.624	21.152	13.386	15.936
HEMBA1003179	63.835	33.869	50.631	27.163	25.502	35.500	39.052	37.713
HEMBA1003186	100.461	75.611	231.787	75.781	58.278	54.222	55.862	61.615
HEMBA1003196	36.422	27.557	45.633	20.623	18.740	21.756	30.501	35.864
HEMBA1003197	8.462	9.564	5.534	5.965	4.051	3.138	7.054	7.066
HEMBA1003199	34.650	18.409	81.183	15.696	16.799	9.492	17.381	15.917
HEMBA1003202	79.337	59.764	236.822	43.286	41.820	31.105	32.936	45.183
HEMBA1003204	66.523	56.272	172.818	48.560	31.451	33.193	27.421	28.849
HEMBA1003210	23.713	52.768	35.498	5.529	38.451	16.353	59.417	17.563
HEMBA1003212	126.394	90.709	372.474	74.164	62.392	59.663	45.714	54.363
HEMBA1003218	19.415	13.105	13.670	6.371	4.792	13.681	10.789	6.536
HEMBA1003220	81.171	86.642	147.453	89.495	42.391	47.586	54.647	123.019
HEMBA1003222	25.803	22.891	28.577	7.994	11.404	10.413	9.856	14.985
HEMBA1003225	105.735	21.238	40.848	11.586	20.280	48.243	44.574	19.547
HEMBA1003229	30.394	26.363	41.333	22.998	17.475	14.707	20.154	19.749
HEMBA1003230	69.643	70.015	42.439	31.176	20.775	56.815	40.191	75.238
HEMBA1003235	44.989	43.337	105.267	33.038	19.405	20.834	22.018	29.856
HEMBA1003236	8.677	17.896	8.735	7.270	7.328	17.286	5.295	18.441
HEMBA1003250	7.260	12.598	12.993	4.750	4.815	7.242	5.982	4.378
HEMBA1003252	56.274	51.495	65.197	28.241	33.512	44.917	62.506	60.076
HEMBA1003257	71.751	16.083	40.414	13.391	19.441	38.988	28.614	19.028
HEMBA1003268	19.492	18.996	46.948	14.167	12.769	11.524	8.622	17.414
HEMBA1003273	48.113	38.933	125.242	29.404	21.135	22.989	17.240	24.704
HEMBA1003276	36.279	34.802	113.584	23.812	17.208	20.437	14.685	26.145
HEMBA1003277	31.363	12.827	21.514	10.462	11.287	13.206	16.182	14.465
HEMBA1003278	36.998	24.906	71.222	17.479	15.791	16.787	10.948	17.841
HEMBA1003280	50.716	16.000	38.057	16.933	20.792	37.901	30.931	31.493
HEMBA1003281	66.732	21.393	32.728	15.032	18.416	26.844	28.577	24.898
HEMBA1003284	9.746	8.482	12.941	5.779	5.747	5.813	3.545	3.499
HEMBA1003286	69.502	35.947	60.729	21.827	29.473	52.233	50.283	47.695
HEMBA1003291	13.248	9.951	10.909	3.504	18.100	6.561	6.341	7.647
HEMBA1003294	69.599	52.239	168.555	39.127	38.460	40.377	24.057	27.486
HEMBA1003296	61.933	31.456	37.947	21.206	23.199	23.249	34.580	37.768
HEMBA1003304	7.117	5.972	8.976	6.154	8.839	4.199	3.461	3.227
HEMBA1003306	17.590	15.590	22.443	8.410	11.282	8.448	6.333	9.387
HEMBA1003309	6.845	10.103	12.198	14.015	7.776	8.709	3.955	18.326
HEMBA1003314	637.052	210.608	238.618	105.098	198.106	299.884	273.738	171.516
HEMBA1003315	83.736	51.612	84.690	32.381	29.482	56.694	53.105	54.024
HEMBA1003322	108.401	88.539	256.570	51.502	51.083	44.130	42.804	45.519
HEMBA1003326	42.723	20.581	14.759	11.799	7.780	18.087	12.420	9.516
HEMBA1003327	61.811	36.702	87.698	28.181	19.784	18.596	17.453	18.377
HEMBA1003328	53.406	51.712	114.941	36.926	25.000	18.669	22.079	32.865
HEMBA1003330	108.955	82.099	207.708	73.413	52.244	50.838	55.920	55.390
HEMBA1003348	121.625	110.275	337.182	94.209	99.717	67.000	43.513	80.023
HEMBA1003369	5.861	23.644	14.930	4.979	1.726	9.064	3.020	5.373
HEMBA1003370	315.016	197.956	369.117	140.044	139.216	140.758	150.458	124.948
HEMBA1003373	50.135	31.291	53.330	17.430	5.513	19.164	8.117	19.638
HEMBA1003376	174.269	170.290	519.668	126.099	89.798	108.226	81.818	107.084
HEMBA1003380	43.015	24.657	74.071	29.281	24.407	19.711	13.485	20.047
HEMBA1003384	25.555	30.071	68.079	15.389	9.455	11.810	8.800	14.281
HEMBA1003387	6.515	2.588	2.697	1.577	1.109	1.803	1.986	3.464
HEMBA1003392	111.457	25.882	42.253	17.323	29.007	50.086	29.337	23.550
HEMBA1003395	16.068	18.666	35.483	15.254	9.873	10.355	6.207	12.514
HEMBA1003399	45.227	21.480	37.035	19.231	15.354	19.471	27.860	34.116
HEMBA1003400	116.210	36.907	58.706	24.811	49.133	53.819	60.041	53.109
HEMBA1003402	32.500	16.239	27.864	8.795	12.867	17.141	11.617	14.596
HEMBA1003403	60.260	43.377	46.720	20.221	26.579	36.738	44.891	45.870
HEMBA1003408	196.676	49.687	70.460	29.354	50.910	84.358	77.062	46.433
HEMBA1003412	104.813	43.934	55.699	47.250	43.763	61.953	59.463	47.139
HEMBA1003417	22.445	13.970	25.036	8.433	7.282	10.593	5.696	11.032
HEMBA1003418	57.411	57.397	76.232	97.795	45.336	43.450	22.206	90.604
HEMBA1003420	29.838	15.856	201.831	11.319	8.067	11.379	12.938	14.721
HEMBA1003425	17.466	15.895	21.662	4.733	6.723	8.483	10.838	9.083
HEMBA1003433	23.931	18.435	24.576	12.136	10.421	10.074	11.092	11.581

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Table 26

HEMBA1003440	91.727	41.727	39.257	19.755	26.941	45.998	31.620	35.845
HEMBA1003442	7.090	22.535	10.452	33.897	10.259	15.118	7.093	14.790
HEMBA1003447	82.161	36.670	48.248	26.789	18.587	41.591	42.314	35.065
HEMBA1003453	50.472	26.692	25.954	16.130	11.252	16.584	28.534	21.256
HEMBA1003461	55.687	25.328	42.686	17.261	18.856	27.281	22.795	17.854
HEMBA1003463	40.102	23.311	34.469	13.456	19.704	20.277	16.984	18.124
HEMBA1003465	92.245	40.963	61.816	28.410	36.051	39.389	40.220	36.851
HEMBA1003480	114.075	114.841	266.076	76.366	67.942	56.459	51.589	62.191
HEMBA1003485	44.403	28.836	33.659	14.371	8.636	26.284	16.036	14.582
HEMBA1003487	42.939	15.463	23.730	9.752	15.729	24.902	21.136	16.494
HEMBA1003492	31.026	21.538	56.674	14.934	12.014	12.082	9.567	14.655
HEMBA1003494	97.366	260.496	50.174	48.821	12.504	74.554	20.623	180.841
HEMBA1003497	39.000	17.943	24.659	11.432	13.881	21.376	18.562	8.072
HEMBA1003503	54.774	21.486	28.175	12.948	17.154	30.911	36.463	16.806
HEMBA1003511	18.672	14.740	43.023	11.794	13.330	8.925	16.405	11.615
HEMBA1003528	385.123	191.234	239.319	81.329	123.915	213.945	179.430	96.672
HEMBA1003530	43.820	12.384	23.693	10.695	21.216	20.067	28.030	16.204
HEMBA1003531	111.104	73.542	215.578	67.833	214.022	56.139	50.217	66.992
HEMBA1003532	145.137	62.379,	83.827	37.506	53.388	90.314	77.728	60.515
HEMBA1003538	61.123	20.746	32.949	11.160	19.286	34.305	28.231	13.837
HEMBA1003545	21.489	10.501	20.608	5.904	7.197	10.239	6.617	8.168
HEMBA1003546	31.371	32.365	28.613	13.365	226.243	16.427	16.554	24.821
HEMBA1003548	4.466	8.124	9.845	4.563	7.542	6.155	5.647	8.387
HEMBA1003553	79.837	51.515	50.379	23.327	28.564	49.154	63.525	48.955
HEMBA1003555	20.066	8.873	13.692	4.762	3.684	10.112	10.962	6.521
HEMBA1003556	57.280	36.399	128.391	29.283	16.426	19.257	18.121	24.622
HEMBA1003560	9.290	4.426	2.529	2.848	1.767	2.983	6.207	6.539
HEMBA1003565	42.648	29.588	20.996	8.344	13.984	21.927	21.847	22.043
HEMBA1003568	7.244	1.649	7.712	2.430	3.763	3.172	2.836	2.592
HEMBA1003569	25.048	20.536	23.764	33.957	13.740	16.235	19.512	16.518
HEMBA1003571	111.721	94.378	326.335	84.368	71.788	50.029	48.011	59.960
HEMBA1003579	3.335	7.399	15.353	6.553	8.948	2.872	9.198	6.421
HEMBA1003580	274.105	50.292	102.103	26.686	59.875	128.943	110.375	35.695
HEMBA1003581	112.013	31.295	94.083	21.641	36.215	54.336	50.711	21.238
HEMBA1003591	97.076	64.326	77.160	89.876	47.882	53.615	40.656	45.172
HEMBA1003595	32.697	22.842	84.629	19.075	11.339	6.305	5.581	18.085
HEMBA1003597	48.561	25.846	108.491	20.931	15.952	19.375	17.580	20.153
HEMBA1003598	49.728	20.134	22.468	12.142	11.688	18.934	21.743	15.025
HEMBA1003600	32.772	35.099	56.905	26.268	29.290	38.873	53.305	56.783
HEMBA1003602	18.248	10.116	16.162	6.182	10.970	8.064	14.736	17.188
HEMBA1003604	205.949	53.579	69.723	24.549	49.902	105.181	98.166	47.144
HEMBA1003610	140.996	29.255	95.048	15.492	103.150	72.233	54.670	30.688
HEMBA1003615	57.258	20.035	34.102	12.808	16.022	24.378	18.759	20.876
HEMBA1003617	48.414	20.375	29.789	12.148	22.291	18.199	18.770	18.242
HEMBA1003620	52.899	22.318	45.502	19.575	19.962	25.239	39.072	29.451
HEMBA1003621	102.827	102.094	226.373	80.194	64.742	58.874	67.142	60.680
HEMBA1003622	19.815	13.838	25.009	16.055	8.339	12.261	15.369	13.833
HEMBA1003630	20.008	16.381	30.244	13.871	5.573	9.992	10.303	11.422
HEMBA1003637	37.880	29.848	106.379	23.251	18.468	17.181	12.409	18.500
HEMBA1003640	39.068	31.672	100.901	22.572	22.223	21.513	17.417	20.420
HEMBA1003645	25.820	19.380	48.445	13.481	9.247	12.142	54.230	5.711
HEMBA1003646	38.243	16.329	22.003	9.624	13.311	24.606	19.177	19.938
HEMBA1003647	10.261	10.718	12.323	7.860	7.892	7.607	7.882	10.058
HEMBA1003656	40.171	31.269	66.874	28.981	19.429	18.898	23.172	30.178
HEMBA1003662	25.325	17.011	19.352	6.387	10.041	10.909	14.055	18.544
HEMBA1003666	23.086	11.187	17.407	5.803	8.262	9.774	15.332	13.851
HEMBA1003667	304.975	209.929	337.134	96.636	131.792	179.317	140.769	174.256
HEMBA1003670	12.944	8.894	15.235	3.344	2.565	7.057	6.425	7.073
HEMBA1003674	143.262	32.196	51.919	33.863	62.734	66.675	65.424	47.173
HEMBA1003677	80.516	45.946	220.695	45.985	43.474	38.916	30.594	46.808
HEMBA1003679	25.325	7.795	16.167	6.727	5.941	12.433	12.034	11.720
HEMBA1003680	42.317	25.723	33.794	24.664	23.985	25.419	38.990	39.343
HEMBA1003684	18.273	10.175	17.733	13.315	4.937	9.099	10.182	10.574
HEMBA1003660	115.021	65.531	75.876	46.324	43.039	71.797	85.431	56.592

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Table 27

HEMBA1003692	83.253	96.347	194.372	63.188	40.872	47.354	39.288	42.644
HEMBA1003702	88.125	35.028	48.251	23.719	29.023	42.879	46.956	36.550
HEMBA1003711	93.732	50.280	140.199	32.886	33.424	47.500	41.959	36.807
HEMBA1003714	75.923	20.696	37.340	14.414	28.237	32.029	29.145	16.214
HEMBA1003715	54.160	54.486	142.871	31.894	31.122	28.832	20.640	26.672
HEMBA1003717	70.553	38.574	120.922	45.101	29.491	29.344	27.200	38.418
HEMBA1003720	83.687	94.829	133.285	55.896	49.519	43.330	22.099	41.137
HEMBA1003725	46.157	55.932	71.704	30.085	21.305	22.378	18.643	31.573
HEMBA1003728	103.795	35.668	58.184	16.485	21.818	42.286	37.790	34.280
HEMBA1003729	49.957	21.508	47.663	20.231	15.376	18.567	21.294	17.427
HEMBA1003732	13.069	1.953	6.558	3.228	2.195	3.652	3.024	4.336
HEMBA1003733	52.409	32.781	76.684	22.919	83.426	18.921	13.867	14.220
HEMBA1003742	40.426	20.265	50.667	26.589	21.518	42.057	44.130	24.802
HEMBA1003743	26.918	22.118	23.392	18.886	18.530	12.506	17.162	18.069
HEMBA1003758	110.630	126.359	315.104	79.435	58.130	58.587	34.868	73.429
HEMBA1003760	78.949	0.000	26.318	15.194	14.440	32.057	34.468	19.471
HEMBA1003764	45.855	30.390	82.720	23.891	19.630	164.051	37.797	57.861
HEMBA1003769	87.589	47.227	62.942	27.144	32.047	46.499	39.296	38.944
HEMBA1003773	63.842	14.722	21.132	12.002	9.850	33.904	29.817	13.165
HEMBA1003783	17.751	16.975	23.942	16.465	13.884	6.842	9.757	20.650
HEMBA1003784	13.500	17.233	21.849	13.856	12.436	17.394	11.099	13.140
HEMBA1003794	386.642	303.008	322.299	109.371	145.316	286.778	287.377	239.938
HEMBA1003799	39.392	23.099	29.603	15.022	13.775	16.550	24.428	19.403
HEMBA1003803	63.548	21.899	44.323	20.132	18.580	28.795	24.744	35.938
HEMBA1003804	80.382	26.816	48.558	16.154	27.867	31.087	37.611	22.634
HEMBA1003805	103.669	42.485	42.930	19.994	36.377	43.797	32.147	28.376
HEMBA1003807	21.717	13.940	25.512	9.492	6.870	9.649	8.812	7.611
HEMBA1003810	20.102	11.572	7.558	20.338	17.855	7.640	4.451	6.585
HEMBA1003827	432.964	219.520	240.291	155.416	219.584	266.037	283.204	241.127
HEMBA1003836	177.311	135.831	482.334	146.466	136.063	93.790	92.728	122.237
HEMBA1003838	223.674	185.295	641.368	134.002	79.993	115.711	87.137	118.957
HEMBA1003843	13.867	10.178	27.409	17.850	21.104	13.382	11.701	13.634
HEMBA1003846	133.994	57.556	58.738	34.962	50.550	56.395	40.861	60.253
HEMBA1003856	27.378	13.868	16.982	14.248	8.662	11.259	9.145	9.934
HEMBA1003857	101.908	95.527	253.525	75.110	52.628	51.958	45.837	48.871
HEMBA1003864	52.130	18.071	24.567	9.568	13.009	16.810	29.271	16.795
HEMBA1003866	27.257	12.805	22.440	12.069	15.414	19.103	9.229	7.524
HEMBA1003868	95.701	54.991	58.923	31.090	41.733	69.461	48.174	43.486
HEMBA1003879	62.950	44.572	159.217	48.098	42.446	37.097	36.010	45.824
HEMBA1003880	134.462	70.074	103.271	50.699	47.956	67.668	44.498	30.581
HEMBA1003884	99.190	48.465	73.499	34.796	54.399	57.269	63.551	68.830
HEMBA1003885	77.675	69.096	172.968	55.129	49.424	41.309	24.247	31.596
HEMBA1003887	60.203	22.185	33.582	16.896	21.181	29.281	31.275	22.835
HEMBA1003890	12.753	8.056	15.506	7.762	16.057	139.271	387.408	5.124
HEMBA1003893	386.525	281.955	515.307	187.300	180.355	212.964	137.297	122.335
HEMBA1003896	411.418	232.899	382.182	144.104	165.806	233.857	186.700	143.577
HEMBA1003902	39.732	39.491	114.984	20.297	23.509	16.793	14.124	20.479
HEMBA1003904	32.775	21.109	45.629	10.006	13.109	14.294	24.342	17.444
HEMBA1003908	8.660	8.873	15.689	7.298	15.429	6.307	2.267	5.699
HEMBA1003926	132.636	253.614	316.882	183.017	124.195	147.955	105.962	360.995
HEMBA1003937	87.005	63.862	200.940	40.687	36.238	35.284	29.695	40.418
HEMBA1003939	28.064	25.844	35.675	20.306	20.378	19.070	16.457	15.626
HEMBA1003940	27.800	13.368	18.045	10.235	10.394	14.633	17.733	9.868
HEMBA1003941	57.997	16.835	24.582	17.381	15.884	23.428	19.757	13.795
HEMBA1003942	38.168	19.747	45.852	32.660	22.333	24.695	10.791	21.900
HEMBA1003945	59.457	32.900	46.079	23.037	21.163	36.632	32.279	26.903
HEMBA1003949	12.870	13.019	20.678	7.159	38.521	442.120	272.494	21.625
HEMBA1003950	8.366	8.726	5.814	3.195	4.756	3.396	8.814	5.401
HEMBA1003953	23.527	10.310	11.872	9.390	8.494	10.637	10.973	5.252
HEMBA1003958	131.082	90.718	253.084	74.499	85.036	62.450	34.852	86.629
HEMBA1003959	12.105	11.228	18.520	6.548	7.960	18.122	12.612	10.591
HEMBA1003960	53.133	29.785	31.879	18.932	16.178	21.708	32.094	35.333
HEMBA1003965	58.245	19.415	68.506	20.791	26.975	28.975	27.825	25.303
HEMBA1003967	1.859	3.908	9.364	6.033	4.054	4.384	4.208	4.986

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Table 28

HEMBA1003968	40.219	26.894	55.357	16.296	14.511	28.531	22.648	15.420
HEMBA1003974	147.167	439.547	139.030	117.010	33.973	54.122	29.356	338.820
HEMBA1003976	20.167	17.809	13.159	9.187	5.748	6.826	6.962	10.367
HEMBA1003977	32.761	12.350	24.212	6.558	6.776	12.413	17.016	9.367
HEMBA1003978	40.564	13.858	10.812	11.585	11.203	23.881	20.489	17.488
HEMBA1003981	65.803	34.462	71.399	26.801	31.348	48.051	31.355	42.728
HEMBA1003982	15.104	89.360	20.946	18.086	1.620	3.781	3.102	64.356
HEMBA1003985	15.199	10.866	21.715	9.199	1.517	8.041	5.977	7.569
HEMBA1003987	48.695	30.080	108.473	25.632	23.222	28.008	21.302	24.940
HEMBA1003989	47.841	51.466	128.889	32.288	24.298	24.627	15.392	23.174
HEMBA1004000	36.424	35.098	34.843	16.292	19.541	20.604	16.803	21.872
HEMBA1004006	8.411	42.393	12.931	2.863	3.395	0.000	4.943	9.742
HEMBA1004007	135.300	114.014	286.000	90.971	64.473	74.153	71.985	79.319
HEMBA1004010	58.331	152.845	38.786	18.676	18.819	35.229	31.514	80.599
HEMBA1004011	62.306	16.294	38.336	12.356	13.756	29.683	26.091	7.986
HEMBA1004012	47.010	38.053	139.110	42.415	22.159	34.340	27.215	32.550
HEMBA1004015	24.416	26.249	27.372	12.243	13.962	25.082	25.133	12.269
HEMBA1004024	149.457	114.788	479.037	80.679	77.896	75.066	57.366	93.859
HEMBA1004029	81.485	31.944	43.520	19.897	20.191	38.768	36.482	19.376
HEMBA1004038	26.629	15.823	19.708	12.109	7.832	14.400	12.855	17.771
HEMBA1004042	8.177	10.678	12.830	6.612	11.484	7.963	11.320	10.405
HEMBA1004045	24.675	30.855	37.128	20.069	23.538	15.509	17.299	17.447
HEMBA1004048	95.795	48.977	78.760	36.608	40.779	45.132	47.334	63.844
HEMBA1004049	55.947	543.954	47.428	49.034	19.297	56.209	23.320	68.865
HEMBA1004051	69.776	31.608	51.948	13.046	25.684	38.632	30.423	32.553
HEMBA1004053	29.222	70.670	84.481	24.394	15.007	23.414	13.218	23.973
HEMBA1004055	39.564	23.202	34.928	8.151	5.353	28.619	15.237	14.807
HEMBA1004056	136.121	122.072	413.353	75.363	81.883	66.439	41.004	85.794
HEMBA1004060	17.642	11.826	29.995	9.507	4.910	13.895	8.679	8.388
HEMBA1004061	17.144	13.460	20.009	16.913	8.228	14.145	12.424	5.810
HEMBA1004067	165.029	79.589	104.390	62.419	50.783	89.115	94.004	91.850
HEMBA1004071	28.405	34.722	37.707	19.775	14.692	17.342	23.864	27.554
HEMBA1004074	128.445	51.388	148.050	35.606	37.851	50.216	53.461	46.373
HEMBA1004078	26.126	14.714	20.940	9.721	16.211	17.398	17.388	14.057
HEMBA1004085	42.006	24.067	36.862	15.417	17.609	19.555	28.362	21.993
HEMBA1004088	27.330	49.843	21.238	43.213	24.232	16.260	12.409	22.262
HEMBA1004097	45.296	15.292	27.795	13.971	26.928	26.002	33.192	19.361
HEMBA1004100	40.930	37.210	48.942	23.245	10.184	25.744	21.452	28.594
HEMBA1004103	101.036	101.281	184.668	64.176	44.322	55.385	41.050	40.000
HEMBA1004110	89.903	65.107	57.751	43.841	27.836	21.315	27.631	34.280
HEMBA1004111	171.907	134.108	296.310	95.474	115.874	78.450	80.011	98.760
HEMBA1004124	177.408	71.838	103.065	37.865	46.198	68.531	109.364	77.083
HEMBA1004130	64.543	54.797	171.602	50.628	35.382	25.601	19.599	23.097
HEMBA1004131	41.654	24.184	33.975	26.913	23.365	28.790	20.022	24.999
HEMBA1004132	55.906	42.840	162.243	42.708	30.251	28.863	19.780	22.237
HEMBA1004133	64.624	30.838	38.522	29.390	20.897	28.027	28.747	33.333
HEMBA1004138	61.197	21.853	23.858	17.376	9.337	30.080	17.345	22.082
HEMBA1004143	15.715	9.656	21.209	10.565	10.539	14.067	11.441	9.994
HEMBA1004146	40.893	21.789	90.537	30.633	32.870	23.542	14.368	20.982
HEMBA1004148	59.990	18.796	22.167	11.049	17.531	18.309	29.374	22.628
HEMBA1004149	16.284	11.131	18.385	7.758	7.634	7.677	5.890	13.683
HEMBA1004150	5.223	4.403	4.468	3.044	2.553	2.158	2.062	2.260
HEMBA1004154	111.110	40.836	69.965	31.437	46.253	58.472	62.983	47.866
HEMBA1004164	139.670	107.565	315.189	77.326	47.327	57.372	46.726	67.257
HEMBA1004168	24.042	16.530	18.698	9.347	9.400	13.838	3.054	13.060
HEMBA1004199	22.894	9.047	10.461	8.631	7.704	7.849	6.889	7.253
HEMBA1004200	33.301	51.362	83.462	26.185	27.548	17.580	17.235	32.109
HEMBA1004201	54.766	23.783	32.370	17.449	21.835	22.123	25.993	20.006
HEMBA1004202	14.526	10.484	12.784	6.804	5.704	9.594	8.672	11.673
HEMBA1004203	47.655	20.140	34.882	13.604	14.171	19.946	16.079	18.151
HEMBA1004207	6.344	3.206	11.421	3.936	6.145	5.704	21.692	7.780
HEMBA1004210	33.071	43.543	33.120	16.340	41.396	21.814	19.639	15.015
HEMBA1004225	73.182	63.749	226.133	59.565	43.156	32.703	25.781	40.078
HEMBA1004227	83.820	31.222	42.541	16.931	17.786	28.177	25.468	30.978

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Table 29

HEMBA1004235	99.954	57.144	62.536	27.672	34.345	69.613	47.182	38.807
HEMBA1004237	27.504	21.542	17.029	18.289	11.697	19.212	12.031	16.922
HEMBA1004238	79.210	38.454	102.493	34.130	27.841	36.089	27.438	34.578
HEMBA1004241	5.663	2.654	7.035	2.556	1.072	2.912	4.422	1.294
HEMBA1004242	256.862	65.757	191.327	80.010	76.455	85.478	89.242	62.567
HEMBA1004243	72.699	55.276	60.764	28.287	47.148	36.800	28.491	47.743
HEMBA1004246	44.915	30.967	100.300	22.414	17.109	15.470	12.686	18.700
HEMBA1004247	66.750	16.238	24.674	18.889	22.763	31.897	38.415	17.377
HEMBA1004248	13.953	18.412	17.581	11.953	11.378	14.538	12.794	9.562
HEMBA1004250	24.439	10.494	10.631	6.401	5.142	14.218	12.652	11.966
HEMBA1004252	37.349	20.650	22.246	9.949	9.550	14.570	21.841	18.200
HEMBA1004260	10.994	19.320	16.415	15.707	20.374	13.845	11.265	19.838
HEMBA1004264	22.716	14.715	13.358	7.615	5.234	12.282	15.089	11.397
HEMBA1004267	235.310	195.750	654.331	171.071	174.292	115.073	102.973	144.125
HEMBA1004272	28.776	19.025	23.678	13.063	12.012	15.529	14.123	14.593
HEMBA1004274	62.157	50.491	53.598	30.356	36.472	42.005	58.020	51.617
HEMBA1004275	70.423	38.514	45.176	17.443	18.132	34.031	36.295	22.171
HEMBA1004276	33.630	4.481	14.011	9.548	9.099	14.035	10.406	8.615
HEMBA1004279	16.536	11.082	13.356	14.834	7.333	10.255	8.919	12.068
HEMBA1004284	29.688	30.297	64.483	13.658	17.646	17.327	17.630	13.770
HEMBA1004286	32.471	16.566	18.049	12.391	6.773	17.625	23.811	13.547
HEMBA1004289	81.573	62.930	165.571	49.704	34.785	37.379	28.939	41.740
HEMBA1004293	72.466	34.902	48.669	32.705	17.408	57.764	53.695	45.065
HEMBA1004295	37.595	12.116	29.975	11.634	5.514	25.018	23.797	20.926
HEMBA1004302	10.880	5.912	7.885	10.025	5.190	6.060	5.264	9.355
HEMBA1004306	426.811	177.321	335.168	107.646	123.947	256.397	251.772	134.005
HEMBA1004312	37.953	30.864	105.533	30.747	25.847	16.140	16.283	24.272
HEMBA1004314	29.396	23.332	95.584	22.179	18.544	11.015	8.804	20.974
HEMBA1004321	47.670	29.150	105.316	35.655	23.139	31.309	29.736	47.858
HEMBA1004323	87.295	65.931	221.440	44.690	41.425	36.609	34.117	39.135
HEMBA1004327	65.869	21.284	21.540	11.985	14.419	27.213	27.030	20.118
HEMBA1004329	67.920	44.687	132.755	32.977	21.556	32.356	17.478	26.773
HEMBA1004330	8.765	7.655	16.827	7.164	3.843	9.511	7.660	4.615
HEMBA1004334	16.438	21.355	31.680	15.109	26.670	13.368	10.581	13.568
HEMBA1004335	204.961	102.859	325.226	69.979	64.392	78.772	71.641	83.525
HEMBA1004341	186.677	30.208	61.439	15.995	41.404	87.221	89.558	40.224
HEMBA1004344	261.676	76.316	123.332	42.705	51.432	26.797	42.054	59.071
HEMBA1004347	65.249	32.610	97.858	37.038	21.953	33.115	33.526	36.846
HEMBA1004349	22.353	35.727	29.441	19.803	18.786	23.126	19.103	18.719
HEMBA1004352	75.508	65.544	237.050	49.039	34.141	32.597	28.166	46.343
HEMBA1004353	54.322	66.042	132.169	40.563	27.380	39.551	30.556	56.886
HEMBA1004354	43.687	29.352	79.264	22.784	20.533	21.755	16.860	22.429
HEMBA1004356	44.730	22.201	27.487	10.404	8.280	22.159	16.039	15.038
HEMBA1004360	91.412	28.429	71.634	26.232	36.259	59.602	38.361	50.410
HEMBA1004366	9.956	10.099	14.263	5.481	5.631	6.802	6.791	6.167
HEMBA1004372	3.613	4.593	5.338	0.000	1.638	1.507	3.555	1.568
HEMBA1004377	53.834	41.410	47.048	29.140	26.163	34.545	30.827	33.572
HEMBA1004389	20.540	22.800	24.474	14.497	13.968	16.620	14.951	17.114
HEMBA1004391	60.284	22.653	44.013	14.283	19.018	31.716	23.931	23.617
HEMBA1004393	177.786	197.548	108.554	32.455	75.399	76.587	39.777	44.665
HEMBA1004394	28.949	11.849	12.442	5.544	10.440	17.825	10.981	8.836
HEMBA1004396	37.907	26.956	102.760	18.571	16.519	15.025	13.681	21.980
HEMBA1004401	22.519	21.858	30.601	14.945	13.592	15.418	20.530	20.774
HEMBA1004405	42.933	38.835	117.844	34.528	23.557	19.155	18.506	29.842
HEMBA1004408	50.497	27.151	55.000	25.559	15.351	19.522	15.546	20.863
HEMBA1004414	45.769	51.722	64.316	19.655	19.324	39.735	26.527	36.385
HEMBA1004429	61.867	59.067	190.058	39.014	50.304	38.462	27.517	46.317
HEMBA1004433	49.568	39.828	146.938	37.521	28.383	24.241	24.651	42.005
HEMBA1004440	31.849	22.469	37.132	18.742	22.366	23.183	21.969	35.073
HEMBA1004444	59.488	46.586	163.763	30.695	29.990	24.833	22.908	37.635
HEMBA1004446	22.134	12.309	29.426	11.920	3.385	14.862	10.855	16.078
HEMBA1004451	31.688	21.261	28.136	18.194	15.678	19.695	21.159	27.156
HEMBA1004452	36.593	5.268	18.479	3.443	5.737	17.680	14.173	7.972
HEMBA1004454	50.056	27.897	32.786	24.382	20.631	24.494	22.897	29.042

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Table 30

HEMBA1004460	138.550	96.143	356.058	74.883	54.735	70.698	38.344	55.945
HEMBA1004461	64.074	19.163	24.808	12.846	16.373	23.508	22.827	10.137
HEMBA1004468	134.439	72.774	210.409	77.409	60.142	56.229	42.361	49.457
HEMBA1004479	82.994	32.899	92.282	35.519	44.435	43.183	31.836	37.116
HEMBA1004482	5.602	7.682	11.248	36.034	2.926	5.535	5.693	5.972
HEMBA1004491	16.736	6.285	17.615	14.018	11.729	19.804	10.683	11.280
HEMBA1004499	94.095	71.456	148.355	58.479	48.596	46.968	46.648	57.279
HEMBA1004502	21.523	9.344	18.265	7.282	9.979	2.762	3.174	13.389
HEMBA1004505	26.042	15.980	43.855	17.516	15.469	22.190	22.873	15.812
HEMBA1004508	12.004	29.395	42.664	21.849	21.426	14.469	9.224	9.845
HEMBA1004507	96.377	87.688	99.177	103.472	34.160	81.068	54.939	151.142
HEMBA1004509	52.657	14.880	19.120	16.228	17.009	24.783	24.565	13.476
HEMBA1004523	20.156	18.209	11.197	16.529	14.651	13.004	20.267	19.467
HEMBA1004528	42.620	27.819	48.069	14.426	25.267	43.038	40.239	37.718
HEMBA1004534	75.090	41.159	44.399	31.300	16.686	31.317	21.009	18.589
HEMBA1004535	31.531	13.343	23.664	14.085	4.408	13.133	12.981	15.201
HEMBA1004538	352.363	181.508	233.819	97.018	122.402	183.507	100.197	150.062
HEMBA1004542	47.360	17.733	29.238	17.280	12.324	17.317	22.764	15.212
HEMBA1004552	63.401	29.585,	26.857	43.567	39.674	38.686	23.830	33.542
HEMBA1004554	62.231	11.953	25.084	16.273	32.820	33.809	20.812	5.536
HEMBA1004558	30.217	12.133	31.036	15.840	30.638	65.183	19.155	30.921
HEMBA1004560	68.901	16.566	17.908	16.431	10.034	30.093	22.379	22.683
HEMBA1004564	48.119	14.911	35.565	31.983	32.464	30.028	20.965	32.479
HEMBA1004566	32.479	29.553	20.970	32.788	42.949	40.715	23.273	32.960
HEMBA1004573	17.728	13.843	7.118	9.972	19.952	9.755	9.278	8.100
HEMBA1004576	39.572	26.733	42.044	10.704	37.505	32.441	17.232	25.361
HEMBA1004577	46.233	11.570	97.881	39.434	13.437	41.089	34.426	35.314
HEMBA1004586	82.532	71.398	213.814	70.289	52.589	45.729	23.395	38.312
HEMBA1004596	72.534	32.493	45.820	27.585	27.854	34.997	33.847	38.473
HEMBA1004604	99.019	48.582	103.587	36.723	49.392	48.377	56.558	69.256
HEMBA1004607	53.557	37.013	100.999	27.559	26.143	28.796	21.692	42.044
HEMBA1004610	20.690	14.854	69.908	15.349	12.120	9.108	8.858	15.087
HEMBA1004617	22.592	20.386	42.426	22.819	15.568	10.691	6.697	10.317
HEMBA1004622	78.025	46.803	209.059	49.931	29.836	29.902	12.194	27.438
HEMBA1004626	38.170	36.312	110.684	22.791	14.118	17.193	15.579	20.821
HEMBA1004629	33.858	37.886	87.440	53.228	47.341	28.160	12.170	28.096
HEMBA1004631	35.946	10.475	4.434	7.390	17.128	22.775	9.569	32.852
HEMBA1004632	27.084	13.891	23.598	10.209	7.802	11.754	22.566	6.362
HEMBA1004633	78.391	33.135	114.054	17.197	49.008	60.659	48.857	40.810
HEMBA1004636	52.397	20.706	34.962	10.085	22.609	21.255	13.502	25.039
HEMBA1004637	4.228	4.304	6.747	5.278	9.756	4.086	2.597	5.024
HEMBA1004638	0.241	0.000	0.000	1.008	0.000	0.000	0.113	0.000
HEMBA1004645	57.971	29.263	111.067	32.645	17.998	27.214	20.560	24.845
HEMBA1004656	16.139	9.194	21.399	12.766	18.216	14.099	17.122	12.004
HEMBA1004657	20.820	23.742	69.842	9.422	138.932	42.697	9.048	13.383
HEMBA1004666	7.321	3.174	18.097	5.962	9.830	5.098	2.525	7.512
HEMBA1004669	94.910	36.291	111.210	30.591	20.021	28.018	25.500	25.624
HEMBA1004670	57.231	17.070	60.538	23.280	13.173	24.312	23.413	14.342
HEMBA1004672	63.471	50.154	146.619	39.883	31.559	25.617	20.328	28.099
HEMBA1004689	152.993	93.435	103.311	81.212	50.901	83.998	57.329	84.276
HEMBA1004690	28.240	10.247	13.401	8.159	4.952	13.963	13.991	11.785
HEMBA1004693	18.359	15.228	20.803	14.290	13.070	16.726	9.014	13.531
HEMBA1004697	81.532	48.847	148.587	58.849	34.416	51.983	42.641	50.271
HEMBA1004702	97.518	62.966	49.904	20.714	42.224	58.936	64.906	37.506
HEMBA1004704	99.561	48.717	236.687	38.866	33.457	38.377	24.626	31.783
HEMBA1004705	12.717	12.313	40.950	9.649	17.803	10.638	5.969	4.810
HEMBA1004706	33.616	9.825	16.175	10.779	10.830	17.906	13.036	12.703
HEMBA1004709	51.126	39.934	136.723	32.285	25.072	21.674	15.230	23.755
HEMBA1004711	46.766	9.203	57.020	12.805	14.304	16.154	12.982	9.790
HEMBA1004723	121.283	47.643	73.497	30.236	56.917	65.719	56.298	52.009
HEMBA1004725	56.905	32.051	70.171	12.721	48.208	34.021	35.739	12.501
HEMBA1004730	36.072	10.037	30.016	7.633	13.361	7.545	8.989	34.832
HEMBA1004733	30.769	29.884	23.348	6.988	2.998	8.055	8.031	2.822
HEMBA1004734	11.912	11.974	36.595	3.988	12.556	7.653	4.303	15.670

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Table 31

HEMBA1004736	55.309	25.331	132.333	45.653	38.696	23.516	19.970	34.509
HEMBA1004748	53.832	20.004	172.069	29.562	22.161	14.904	12.665	18.349
HEMBA1004749	127.285	45.137	73.698	27.788	33.184	60.214	44.636	42.250
HEMBA1004751	81.283	64.830	173.888	54.165	36.368	41.802	31.283	43.505
HEMBA1004752	59.058	32.785	109.428	32.254	29.090	34.259	30.970	33.029
HEMBA1004753	204.044	247.466	406.165	156.689	102.755	131.323	83.515	263.882
HEMBA1004755	57.638	59.677	83.850	22.148	29.800	30.642	13.064	23.261
HEMBA1004756	9.965	16.228	11.023	8.349	6.780	9.109	111.628	14.885
HEMBA1004758	36.487	26.558	116.970	22.341	14.553	14.773	11.840	14.406
HEMBA1004763	67.343	19.641	33.742	13.841	16.720	25.489	23.061	18.650
HEMBA1004768	29.177	24.043	38.303	6.673	10.298	3.197	10.352	13.391
HEMBA1004770	10.327	14.492	10.901	6.416	6.310	7.963	10.868	7.955
HEMBA1004771	46.910	34.314	76.491	31.609	22.830	23.102	30.433	32.358
HEMBA1004775	39.253	28.706	63.968	24.931	18.754	43.049	32.720	26.795
HEMBA1004776	22.604	11.017	10.103	5.466	9.000	16.400	10.105	8.046
HEMBA1004778	78.144	77.681	223.475	37.540	33.791	32.337	24.067	43.529
HEMBA1004784	9.826	18.370	102.812	8.313	15.151	11.373	9.479	6.329
HEMBA1004785	25.723	16.345	26.216	6.651	10.649	10.674	13.732	11.615
HEMBA1004789	18.173	14.508	16.096	7.804	8.691	10.011	7.713	11.389
HEMBA1004795	14.283	12.973	25.122	11.028	9.351	9.757	9.905	12.028
HEMBA1004797	65.927	33.745	73.888	34.142	28.246	40.067	32.715	25.583
HEMBA1004803	36.634	41.124	65.880	27.072	30.957	22.607	22.520	26.554
HEMBA1004806	11.997	8.183	21.467	8.868	9.653	9.000	7.894	8.399
HEMBA1004807	16.352	14.481	22.459	11.249	12.009	13.340	7.935	9.118
HEMBA1004816	29.782	24.075	95.884	18.110	29.259	8.180	12.578	10.934
HEMBA1004820	8.636	7.466	8.862	4.249	4.018	4.269	6.876	3.493
HEMBA1004833	159.947	50.729	81.248	38.650	64.754	83.155	56.657	65.121
HEMBA1004847	51.456	25.570	40.694	21.115	36.572	35.053	31.537	40.529
HEMBA1004850	77.254	24.014	38.620	21.854	26.080	54.413	50.197	24.185
HEMBA1004863	57.117	32.704	72.480	23.951	31.887	25.058	20.050	20.982
HEMBA1004864	46.043	27.344	59.824	26.750	13.898	16.719	20.308	17.843
HEMBA1004865	12.257	14.642	31.748	44.090	14.331	13.454	13.835	15.797
HEMBA1004880	56.788	50.021	126.837	35.420	26.589	24.064	20.647	23.264
HEMBA1004882	42.450	18.453	29.340	16.782	13.013	13.652	10.676	19.977
HEMBA1004885	8.545	4.947	5.350	4.891	2.933	3.711	3.652	6.615
HEMBA1004889	28.103	22.485	32.049	17.078	14.363	23.391	15.605	16.916
HEMBA1004900	19.922	15.709	33.254	10.423	9.045	6.539	5.245	9.440
HEMBA1004909	88.522	49.269	163.284	48.147	35.537	36.045	18.861	27.933
HEMBA1004918	64.384	43.134	105.868	34.899	22.323	24.073	15.857	25.370
HEMBA1004923	47.731	37.996	69.168	19.659	26.441	18.192	10.213	20.111
HEMBA1004929	11.048	14.003	10.808	12.050	7.539	9.882	8.967	11.809
HEMBA1004930	101.277	92.425	279.652	80.664	66.618	34.331	31.091	41.874
HEMBA1004933	9.145	5.566	12.895	7.786	12.296	10.327	96.467	5.417
HEMBA1004934	7.311	7.106	43.966	10.208	4.750	5.866	9.143	12.805
HEMBA1004937	43.331	27.219	38.802	15.368	17.734	15.280	15.784	46.365
HEMBA1004943	51.072	26.833	32.001	21.614	16.458	27.585	29.628	38.533
HEMBA1004944	84.363	46.788	126.294	41.803	28.989	38.514	31.589	23.074
HEMBA1004946	64.638	28.144	37.908	17.163	24.332	27.854	34.636	31.712
HEMBA1004952	90.835	18.893	40.862	12.824	20.090	33.568	20.062	19.020
HEMBA1004954	14.656	36.003	41.485	27.126	23.696	20.777	6.946	29.261
HEMBA1004956	5.975	9.923	6.635	7.743	0.953	4.578	1.565	5.188
HEMBA1004960	86.030	77.420	136.061	60.735	49.221	47.560	29.646	45.929
HEMBA1004971	31.046	5.439	7.559	12.468	17.946	16.068	19.705	18.480
HEMBA1004972	77.318	38.259	56.654	35.819	27.295	40.233	30.004	50.710
HEMBA1004973	35.524	13.502	16.731	9.641	11.726	14.716	19.197	22.580
HEMBA1004977	6.756	9.870	11.419	9.684	29.373	8.701	2.217	10.523
HEMBA1004978	8.689	11.088	13.909	9.999	5.158	5.699	2.642	10.106
HEMBA1004980	34.093	33.440	87.268	25.974	18.071	16.453	11.605	22.124
HEMBA1004982	14.750	8.271	17.944	9.205	8.250	11.553	6.083	5.456
HEMBA1004983	38.285	13.488	20.831	11.831	3.348	10.309	11.455	8.305
HEMBA1004995	27.256	28.515	26.297	18.434	25.474	22.491	24.452	33.683
HEMBA1005004	13.855	10.490	33.238	10.381	7.816	13.134	7.576	14.698
HEMBA1005008	64.714	26.633	22.502	18.478	23.532	28.617	18.581	16.940
HEMBA1005009	34.543	15.673	19.462	18.045	14.122	26.432	12.593	23.116

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Table 32

HEMBA1005019	49.260	24.872	25.349	20.834	30.144	32.629	20.777	27.016
HEMBA1005021	37.224	63.713	38.065	17.061	15.647	20.369	25.859	32.656
HEMBA1005029	30.265	17.783	35.352	16.531	19.588	26.517	15.798	16.604
HEMBA1005035	393.404	200.167	574.746	133.872	210.689	177.872	156.563	170.510
HEMBA1005036	115.345	41.961	73.015	39.541	44.451	66.623	55.833	51.349
HEMBA1005039	28.850	19.922	57.018	13.971	11.999	26.427	15.206	7.350
HEMBA1005047	93.995	31.868	54.335	18.576	28.338	31.562	31.930	23.751
HEMBA1005050	78.015	41.690	73.330	29.830	26.504	35.887	21.640	35.653
HEMBA1005062	23.050	15.803	29.553	15.707	7.836	15.618	19.435	13.336
HEMBA1005066	10.980	11.364	31.553	13.509	5.668	10.541	5.005	10.849
HEMBA1005067	39.308	34.578	39.795	44.519	24.643	21.272	19.379	20.121
HEMBA1005070	73.155	34.949	68.556	29.956	38.004	38.211	48.007	31.733
HEMBA1005075	88.089	37.798	148.675	40.537	33.271	33.074	28.661	30.201
HEMBA1005078	100.064	37.746	66.827	33.115	41.170	55.560	51.231	17.112
HEMBA1005079	137.757	86.238	294.118	73.304	76.035	75.084	47.255	76.170
HEMBA1005083	18.102	7.642	17.087	6.711	6.184	8.675	9.287	9.609
HEMBA1005084	82.712	38.248	47.063	26.664	27.435	37.552	38.419	28.349
HEMBA1005088	31.610	22.435	76.774	22.700	18.926	23.875	8.895	12.447
HEMBA1005089	68.944	55.156	178.226	34.742	32.350	38.645	22.869	28.148
HEMBA1005090	148.861	86.156	117.997	94.811	57.034	81.098	54.187	116.066
HEMBA1005096	83.125	30.911	63.940	33.378	33.962	48.589	35.467	36.021
HEMBA1005101	69.080	14.020	34.136	10.197	13.998	34.420	22.696	15.975
HEMBA1005107	82.659	25.203	36.223	11.215	21.514	32.720	25.972	21.337
HEMBA1005113	7.977	17.225	31.501	7.563	44.493	5.157	6.957	9.761
HEMBA1005123	173.637	77.260	555.672	126.908	94.628	90.446	70.735	90.016
HEMBA1005133	58.192	40.749	122.920	29.864	16.700	17.652	8.802	18.988
HEMBA1005135	8.259	9.125	14.962	2.213	16.732	6.892	3.383	6.189
HEMBA1005145	185.299	101.220	352.159	92.082	88.750	122.118	76.475	90.044
HEMBA1005149	220.122	109.352	274.492	120.663	125.192	96.704	92.083	128.030
HEMBA1005152	125.948	96.291	226.882	58.505	33.738	46.323	27.534	34.457
HEMBA1005159	15.760	11.274	9.399	6.198	6.191	6.861	12.001	4.556
HEMBA1005172	1653.208	89.658	73.666	54.667	33.118	55.680	32.520	70.907
HEMBA1005185	9.954	17.248	10.492	34.452	3.558	3.117	6.026	11.173
HEMBA1005186	23.745	10.048	27.091	13.067	7.719	15.412	15.086	15.591
HEMBA1005195	14.573	8.648	11.038	19.306	6.313	25.313	13.510	9.183
HEMBA1005201	52.322	13.197	47.505	13.091	12.078	8.531	23.532	9.848
HEMBA1005202	98.566	30.141	71.588	27.954	44.381	66.294	42.390	39.695
HEMBA1005204	184.429	287.156	382.039	168.753	203.458	222.970	143.609	358.646
HEMBA1005206	148.946	61.309	84.791	34.139	49.115	66.295	83.608	76.159
HEMBA1005219	21.685	17.755	9.606	8.236	8.038	13.031	7.751	11.441
HEMBA1005223	79.969	42.665	113.460	40.547	32.099	53.017	26.025	32.004
HEMBA1005229	26.819	9.926	21.841	3.135	5.090	6.656	4.681	7.079
HEMBA1005230	71.184	67.313	201.065	79.279	59.679	77.484	47.808	66.511
HEMBA1005232	7.374	6.386	17.522	8.552	3.285	12.098	4.975	3.965
HEMBA1005238	96.780	44.134	51.932	8.128	20.776	69.291	49.474	35.019
HEMBA1005241	142.598	104.185	428.635	78.773	78.033	74.434	42.333	63.097
HEMBA1005244	76.771	32.597	37.797	16.459	12.489	35.934	31.814	35.602
HEMBA1005246	241.316	60.348	73.077	25.067	41.351	117.666	88.193	54.014
HEMBA1005251	37.505	33.247	108.631	23.585	14.915	23.393	14.302	16.409
HEMBA1005252	53.401	25.532	37.199	15.002	20.744	31.279	24.207	27.562
HEMBA1005267	17.238	39.564	20.097	27.506	31.874	11.013	14.526	14.024
HEMBA1005274	16.538	8.744	18.308	9.021	10.103	11.943	8.914	11.978
HEMBA1005275	69.133	43.329	216.468	46.290	57.647	37.411	25.040	41.913
HEMBA1005288	65.401	50.495	150.714	33.833	34.633	28.241	24.910	40.164
HEMBA1005293	17.403	9.430	23.201	4.467	3.192	25.620	6.775	8.771
HEMBA1005296	223.097	811.623	894.835	738.361	220.523	698.319	418.435	1376.785
HEMBA1005301	36.708	16.970	29.798	11.929	12.544	22.221	35.726	32.270
HEMBA1005304	83.978	71.914	260.016	50.686	36.101	36.160	24.896	47.838
HEMBA1005305	44.218	33.773	74.215	27.494	27.352	34.920	21.424	38.882
HEMBA1005311	33.034	20.140	48.263	13.836	7.908	8.958	9.090	10.440
HEMBA1005313	11.165	36.175	17.550	7.047	11.502	14.209	63.072	9.124
HEMBA1005314	6.948	2.955	22.604	6.336	3.812	5.787	4.089	4.891
HEMBA1005315	72.349	54.139	156.842	34.545	43.132	26.415	28.942	28.442
HEMBA1005317	20.230	8.451	17.258	9.796	11.664	9.976	9.263	8.017

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Table 33

HEMBA1005318	14.755	5.931	13.883	5.228	5.376	9.013	5.511	4.846
HEMBA1005324	98.070	33.348	44.270	26.052	35.446	48.523	30.889	17.915
HEMBA1005331	24.826	335.211	15.947	26.496	14.744	21.427	16.942	29.580
HEMBA1005337	19.080	18.022	19.429	5.217	20.830	29.867	32.481	44.585
HEMBA1005338	61.533	38.788	63.113	23.657	30.437	48.455	40.921	36.285
HEMBA1005344	384.481	88.937	143.574	53.983	72.524	167.620	135.992	68.042
HEMBA1005353	111.629	68.949	220.401	62.090	53.484	67.048	30.456	42.612
HEMBA1005359	87.635	64.332	175.543	59.707	36.743	34.233	21.666	47.596
HEMBA1005362	25.674	25.093	18.642	30.797	21.917	19.092	20.883	12.720
HEMBA1005364	6.677	2.817	5.168	13.116	19.753	5.180	2.877	7.198
HEMBA1005367	51.911	28.536	74.559	28.446	30.138	27.987	16.766	22.415
HEMBA1005372	11.289	6.819	11.700	5.659	9.177	6.402	9.312	4.913
HEMBA1005374	64.639	57.505	120.218	32.738	30.987	24.792	23.695	30.728
HEMBA1005379	29.549	13.813	12.040	8.862	7.648	11.978	9.051	4.019
HEMBA1005382	140.116	94.743	104.609	70.213	26.226	53.452	88.235	85.480
HEMBA1005384	33.109	15.221	21.713	10.250	8.543	11.030	7.498	9.010
HEMBA1005386	111.062	30.547	52.790	29.541	31.691	44.619	35.179	29.136
HEMBA1005389	56.821	32.429	129.272	42.528	35.894	16.765	11.513	24.601
HEMBA1005394	35.794	18.327,	22.715	25.833	26.639	30.857	16.944	24.443
HEMBA1005403	40.404	14.030	54.041	14.621	15.504	27.461	15.586	32.390
HEMBA1005408	51.701	45.069	71.813	44.257	67.383	35.010	23.690	44.612
HEMBA1005410	4.534	4.269	11.774	12.035	10.197	6.188	3.955	8.910
HEMBA1005411	75.220	94.039	163.001	67.133	50.499	41.243	22.652	35.008
HEMBA1005423	35.745	26.430	69.138	35.773	15.442	19.286	14.057	23.010
HEMBA1005426	14.366	12.073	14.418	5.345	11.591	8.954	3.082	7.203
HEMBA1005427	66.444	99.596	61.088	47.865	59.821	53.861	25.223	46.397
HEMBA1005430	52.945	15.385	36.316	19.210	23.854	37.895	19.556	18.127
HEMBA1005438	51.806	28.359	33.314	17.787	19.295	21.754	13.422	29.941
HEMBA1005443	108.954	165.667	426.408	91.550	77.559	76.024	105.042	108.232
HEMBA1005447	51.383	39.578	65.244	29.171	28.000	21.457	18.763	23.755
HEMBA1005449	86.452	20.253	41.861	15.939	27.647	39.311	28.567	27.508
HEMBA1005452	110.567	52.128	74.119	42.532	39.847	53.326	67.529	72.233
HEMBA1005454	7.997	16.821	17.998	14.293	14.436	8.454	6.498	11.445
HEMBA1005458	185.066	78.008	126.372	56.026	56.490	78.922	61.083	57.511
HEMBA1005469	88.419	54.761	196.280	63.682	53.661	42.639	23.441	30.144
HEMBA1005472	37.878	41.710	88.807	34.196	28.126	21.983	24.350	30.575
HEMBA1005474	89.169	55.263	212.086	51.664	50.480	66.508	39.590	30.322
HEMBA1005475	212.273	98.359	182.707	110.945	105.968	98.316	56.095	68.647
HEMBA1005489	61.603	40.439	42.459	21.361	21.335	31.130	11.578	25.898
HEMBA1005497	10.325	12.396	5.705	8.252	5.611	9.949	2.213	16.039
HEMBA1005500	86.636	39.755	180.843	46.031	28.664	31.809	14.951	31.189
HEMBA1005506	24.029	3.468	17.794	7.400	5.464	9.419	6.593	3.517
HEMBA1005508	12.944	12.524	22.247	8.536	16.857	11.561	7.741	12.059
HEMBA1005511	116.338	59.193	267.636	59.921	58.995	43.190	30.786	51.049
HEMBA1005513	167.332	70.217	88.519	56.620	54.920	73.797	80.751	68.624
HEMBA1005517	37.667	10.443	23.901	8.903	17.777	21.966	23.844	18.611
HEMBA1005518	109.105	25.679	71.345	23.319	36.856	47.397	27.618	27.825
HEMBA1005520	200.267	104.176	459.373	133.255	106.207	95.070	67.199	94.086
HEMBA1005522	36.421	15.946	24.796	12.598	8.472	14.558	16.899	13.857
HEMBA1005526	116.274	72.899	292.397	82.002	73.603	66.198	34.319	47.682
HEMBA1005528	13.037	9.406	30.550	14.612	15.947	16.516	7.583	24.988
HEMBA1005530	56.516	26.583	63.811	13.686	21.441	29.159	24.254	21.717
HEMBA1005538	5.523	17.373	36.952	7.017	10.885	11.406	15.411	35.789
HEMBA1005539	76.498	30.847	69.424	17.584	24.989	35.829	28.772	25.913
HEMBA1005545	46.912	10.940	32.124	15.206	46.822	33.595	31.865	24.090
HEMBA1005548	57.779	14.326	15.050	10.139	18.638	22.115	22.271	39.291
HEMBA1005552	141.489	120.695	363.831	84.934	81.893	79.223	60.281	62.088
HEMBA1005558	52.488	20.021	24.397	9.638	22.919	24.422	21.466	8.178
HEMBA1005568	74.152	61.206	184.989	53.681	38.261	33.077	24.038	37.014
HEMBA1005570	54.151	68.747	74.768	17.273	26.562	31.212	27.080	30.221
HEMBA1005576	71.454	57.260	39.016	21.283	8.931	30.461	29.371	19.991
HEMBA1005577	40.771	13.448	21.181	13.021	6.610	18.266	12.838	10.181
HEMBA1005581	81.577	27.270	38.708	10.847	19.565	33.479	28.804	16.842
HEMBA1005582	24.681	30.135	30.933	14.220	7.764	10.454	12.847	13.157

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Table 34

HEMBA1005583	23.564	22.466	98.629	9.735	10.545	12.468	10.523	17.884
HEMBA1005588	96.041	96.264	266.022	69.126	54.588	44.105	34.310	52.441
HEMBA1005593	61.102	40.350	125.688	37.987	35.953	41.577	39.834	47.357
HEMBA1005595	52.429	18.652	31.240	8.095	8.750	14.586	12.433	7.264
HEMBA1005597	125.119	43.335	90.414	24.402	44.780	74.946	66.352	45.322
HEMBA1005606	141.646	66.667	95.041	30.084	57.974	107.329	84.655	46.145
HEMBA1005609	77.991	60.190	244.951	52.002	41.602	40.406	26.928	42.614
HEMBA1005616	47.760	62.865	190.870	42.670	41.809	32.256	23.683	43.139
HEMBA1005621	33.797	18.993	22.515	11.333	11.545	16.964	12.122	13.910
HEMBA1005627	128.661	66.487	148.021	45.359	42.161	42.054	30.884	43.319
HEMBA1005628	43.539	36.758	85.714	25.524	46.601	19.229	82.784	36.636
HEMBA1005631	21.340	8.467	38.068	22.476	18.318	17.813	12.599	28.199
HEMBA1005632	113.190	73.661	233.637	59.097	45.388	52.090	29.944	37.461
HEMBA1005634	123.668	195.912	390.579	101.523	107.528	72.729	54.939	130.473
HEMBA1005662	15.391	11.345	23.021	7.453	5.561	13.084	8.973	5.282
HEMBA1005666	33.844	30.419	34.983	13.220	31.573	24.609	13.796	28.043
HEMBA1005670	91.667	63.609	255.523	57.730	46.927	45.285	23.794	46.684
HEMBA1005671	63.448	55.388	34.948	26.297	20.567	2.367	5.666	13.509
HEMBA1005679	53.089	33.284	126.705	39.666	32.151	40.446	37.522	36.817
HEMBA1005680	115.289	72.018	220.408	76.653	55.707	68.735	32.613	36.282
HEMBA1005685	68.783	46.211	72.197	30.110	32.724	43.022	37.740	33.510
HEMBA1005698	37.890	35.679	44.793	29.794	25.150	48.613	15.651	20.648
HEMBA1005699	14.243	17.539	37.269	9.035	12.276	5.454	5.259	6.787
HEMBA1005703	19.524	15.116	20.249	7.662	15.489	11.648	8.488	10.229
HEMBA1005705	35.316	35.677	66.552	26.492	29.605	90.298	18.303	44.730
HEMBA1005712	20.312	29.695	30.267	17.829	17.668	17.695	14.517	23.820
HEMBA1005717	47.313	15.037	30.499	6.950	13.391	32.044	15.084	7.078
HEMBA1005718	88.576	81.734	176.773	75.414	46.080	58.797	49.803	76.705
HEMBA1005721	84.981	42.340	58.434	18.134	34.246	43.284	34.523	41.460
HEMBA1005722	174.952	92.346	194.868	55.652	48.768	63.471	92.755	56.031
HEMBA1005724	32.655	8.284	5.342	4.000	14.801	15.671	9.324	5.953
HEMBA1005732	89.624	24.907	32.546	5.638	21.753	30.046	28.487	20.595
HEMBA1005737	25.179	16.797	16.017	10.703	12.731	12.444	8.579	7.257
HEMBA1005742	11.547	23.162	24.345	20.921	29.934	18.597	13.749	22.702
HEMBA1005746	36.098	14.407	21.907	16.923	13.431	12.235	10.908	8.606
HEMBA1005747	80.718	30.396	44.843	21.861	30.274	80.588	47.082	26.037
HEMBA1005749	35.749	31.758	64.769	22.766	28.853	26.733	31.698	30.753
HEMBA1005755	34.680	39.133	30.663	37.837	21.308	24.392	15.905	25.470
HEMBA1005760	118.125	41.490	33.276	25.724	28.933	46.295	36.173	31.205
HEMBA1005765	94.451	70.516	200.826	48.023	37.340	35.414	31.098	40.041
HEMBA1005768	112.861	70.359	87.247	48.958	51.073	52.147	72.391	63.859
HEMBA1005780	55.961	34.713	89.816	28.466	46.254	28.283	25.156	29.122
HEMBA1005795	18.800	38.386	19.666	10.007	13.009	11.811	13.106	14.493
HEMBA1005809	67.301	66.510	87.390	53.061	43.975	35.574	35.334	57.818
HEMBA1005813	52.911	84.881	160.064	38.752	43.727	30.799	23.426	57.177
HEMBA1005815	30.398	30.434	43.366	19.911	16.123	39.746	26.743	28.548
HEMBA1005822	40.948	47.746	65.298	51.932	30.845	20.187	22.641	29.114
HEMBA1005829	114.982	70.536	272.004	48.816	36.558	40.259	23.443	35.824
HEMBA1005833	59.540	25.743	29.266	15.545	24.711	26.964	17.968	18.807
HEMBA1005834	151.440	82.917	322.413	102.348	74.711	59.590	35.082	70.415
HEMBA1005844	66.624	11.865	96.556	95.719	56.133	75.546	55.974	122.840
HEMBA1005852	71.743	77.830	72.218	53.009	85.623	78.593	90.291	87.310
HEMBA1005853	62.809	83.326	343.381	63.897	79.208	48.939	27.359	58.468
HEMBA1005878	139.991	109.928	447.600	93.748	65.325	53.917	35.383	63.446
HEMBA1005883	5.211	6.310	6.808	14.769	10.070	6.635	4.486	11.850
HEMBA1005884	9.136	10.768	29.442	9.504	7.302	9.142	4.561	12.287
HEMBA1005891	8.927	12.500	12.662	5.996	7.370	7.346	1.250	5.470
HEMBA1005894	70.006	59.347	177.879	49.407	29.584	23.227	14.651	36.934
HEMBA1005898	84.399	61.254	234.549	59.872	43.955	25.491	23.019	41.130
HEMBA1005902	38.306	16.873	52.804	16.742	33.189	39.317	26.778	43.681
HEMBA1005907	4.806	3.997	8.804	5.339	3.957	17.078	5.311	4.941
HEMBA1005909	4.140	3.733	23.479	2.443	4.661	6.683	0.750	10.643
HEMBA1005911	143.926	92.633	316.302	83.107	51.954	60.593	39.302	55.189
HEMBA1005912	18.801	17.269	13.568	32.298	21.976	14.454	12.917	26.318

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Table 35

HEMBA1005913	10.533	16.117	14.368	16.655	8.179	7.135	7.907	12.918
HEMBA1005921	83.262	45.648	252.573	51.044	41.764	22.286	23.762	46.202
HEMBA1005922	64.440	17.427	35.136	20.084	33.779	24.835	18.394	14.883
HEMBA1005929	173.002	139.696	378.444	96.543	83.075	72.298	55.205	94.716
HEMBA1005931	146.354	89.551	224.601	83.623	63.406	73.122	54.973	59.891
HEMBA1005934	141.558	91.791	227.012	89.834	99.341	96.876	62.967	55.492
HEMBA1005945	144.693	21.871	38.980	19.915	46.699	78.590	80.430	30.052
HEMBA1005962	67.209	34.719	63.745	21.004	17.931	29.331	21.199	20.008
HEMBA1005963	18.320	6.954	9.127	5.913	2.497	8.674	7.674	4.873
HEMBA1005990	581.646	117.336	139.967	53.671	242.262	424.182	418.873	85.511
HEMBA1005991	67.437	59.327	188.570	42.994	21.101	33.868	19.164	11.619
HEMBA1005999	193.878	135.695	450.789	126.399	129.150	103.289	53.193	115.911
HEMBA1006002	73.560	26.438	22.156	12.657	16.731	16.116	10.600	19.305
HEMBA1006005	59.620	7.083	16.863	8.213	29.019	53.513	52.130	23.838
HEMBA1006011	25.811	30.413	39.888	21.434	54.488	30.978	27.996	25.339
HEMBA1006013	51.604	13.251	19.743	11.817	15.364	28.363	21.493	18.674
HEMBA1006016	101.929	42.149	115.996	36.228	39.875	46.607	33.305	26.397
HEMBA1006019	31.772	18.482	22.979	15.207	22.984	24.244	26.246	14.100
HEMBA1006021	26.984	10.213	45.937	9.253	20.615	14.587	14.203	12.296
HEMBA1006022	100.930	40.046	62.368	42.744	23.660	46.057	25.008	19.323
HEMBA1006031	42.088	41.281	14.729	11.264	12.725	36.716	13.037	5.133
HEMBA1006035	10.089	10.059	27.290	8.123	6.309	6.629	2.039	5.229
HEMBA1006036	188.431	82.469	443.914	119.939	80.135	81.126	54.157	94.631
HEMBA1006042	69.906	33.773	134.462	30.108	23.244	29.765	29.479	29.607
HEMBA1006044	53.721	10.199	12.818	4.725	8.467	5.436	2.586	4.088
HEMBA1006045	48.078	43.730	61.128	28.336	25.311	26.461	23.478	44.272
HEMBA1006048	35.685	18.435	41.495	19.225	19.636	34.213	26.302	28.809
HEMBA1006053	0.000	356.500	78.844	24.270	47.030	114.986	63.574	385.970
HEMBA1006055	7.603	5.331	12.625	4.484	13.776	12.227	9.079	5.545
HEMBA1006058	51.872	19.394	14.828	7.834	11.877	25.640	15.830	21.486
HEMBA1006063	72.886	52.429	63.882	34.021	30.125	39.536	28.303	35.860
HEMBA1006067	6.005	14.253	7.505	3.169	2.242	3.352	4.358	0.888
HEMBA1006081	70.282	19.151	25.838	8.981	9.908	26.560	16.837	23.976
HEMBA1006089	54.392	23.145	42.709	18.278	17.433	17.768	18.372	23.981
HEMBA1006090	71.092	20.389	36.832	15.386	17.868	38.904	35.031	18.238
HEMBA1006091	69.022	28.947	126.425	16.353	30.302	56.034	53.660	66.468
HEMBA1006093	111.885	11.435	50.738	16.185	27.687	43.178	26.048	14.980
HEMBA1006099	40.381	27.136	39.149	18.199	31.100	31.158	28.536	26.484
HEMBA1006100	36.979	48.991	259.267	41.090	50.094	24.833	13.379	34.466
HEMBA1006108	40.170	19.301	21.811	11.126	8.795	12.441	8.780	16.453
HEMBA1006114	42.849	44.783	46.702	33.193	23.220	34.626	28.294	51.756
HEMBA1006121	160.208	21.943	26.728	10.160	21.331	17.129	26.838	25.137
HEMBA1006124	63.151	11.764	15.994	17.764	14.099	57.249	29.200	8.240
HEMBA1006125	72.730	70.406	57.020	50.057	45.287	40.856	45.665	68.939
HEMBA1006130	36.221	31.688	34.742	7.817	28.246	34.473	25.726	21.315
HEMBA1006138	160.258	170.815	435.120	106.719	139.660	100.947	67.854	89.604
HEMBA1006142	127.194	85.725	238.562	54.531	52.936	65.032	45.938	59.791
HEMBA1006150	66.777	58.231	76.666	59.941	19.605	46.114	33.261	75.731
HEMBA1006151	189.265	57.959	104.921	29.646	46.546	66.736	74.155	88.383
HEMBA1006155	141.288	19.560	50.142	11.752	32.711	79.435	60.621	32.838
HEMBA1006158	17.276	12.039	19.210	7.139	7.468	23.241	7.360	13.357
HEMBA1006164	140.272	70.843	382.965	97.488	87.832	69.460	42.210	85.135
HEMBA1006171	66.839	48.304	34.618	13.911	21.700	40.783	26.049	37.233
HEMBA1006173	83.939	35.393	52.598	22.894	32.403	35.413	40.872	67.870
HEMBA1006176	51.671	222.661	52.703	39.369	29.305	59.271	24.272	83.343
HEMBA1006182	72.842	38.362	132.455	29.730	26.735	30.382	19.907	34.405
HEMBA1006197	16.655	31.338	37.528	55.808	23.143	18.848	13.456	40.765
HEMBA1006198	30.466	15.178	21.337	16.185	25.764	15.643	14.389	18.561
HEMBA1006213	38.783	20.120	38.136	15.627	10.604	25.761	21.716	35.282
HEMBA1006217	32.003	18.510	33.960	4.079	17.107	31.018	36.526	19.419
HEMBA1006226	40.304	60.090	110.529	40.359	39.915	62.796	35.202	59.281
HEMBA1006235	40.954	9.021	21.361	7.280	14.241	13.056	4.951	7.077
HEMBA1006248	42.946	17.521	32.092	10.747	12.992	19.331	18.339	17.999
HEMBA1006251	84.944	24.303	30.554	15.291	24.212	30.870	18.154	10.996

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Table 36

HEMBA1006252	36.069	24.612	74.170	29.506	28.055	19.517	14.085	15.356
HEMBA1006253	75.854	7.002	20.773	16.455	11.705	12.936	6.506	11.398
HEMBA1006259	37.456	48.402	135.000	39.735	19.462	25.242	19.832	25.931
HEMBA1006261	23.677	23.578	6.874	13.012	7.127	69.427	7.141	17.143
HEMBA1006268	35.886	12.563	30.879	8.970	7.077	19.793	22.288	18.289
HEMBA1006271	122.980	98.618	185.469	77.610	45.268	47.910	36.533	47.867
HEMBA1006272	16.261	12.829	9.416	4.968	5.925	27.766	15.997	7.567
HEMBA1006273	47.890	12.641	71.219	20.880	30.446	30.473	18.419	22.459
HEMBA1006276	79.296	11.878	30.854	34.032	8.760	27.168	16.165	7.501
HEMBA1006278	40.093	7.717	26.091	4.506	18.669	11.680	11.224	9.893
HEMBA1006283	16.994	23.586	25.614	25.226	23.447	59.086	28.267	25.848
HEMBA1006284	29.982	22.166	27.891	20.874	8.594	18.386	15.293	13.396
HEMBA1006291	22.745	13.071	36.861	9.670	4.059	11.649	31.851	7.519
HEMBA1006292	17.718	8.916	20.081	10.169	4.378	7.903	9.259	7.898
HEMBA1006293	31.307	10.056	8.749	4.645	4.097	6.631	8.473	7.189
HEMBA1006299	21.091	5.917	6.157	1.371	4.543	2.465	1.701	2.648
HEMBA1006309	69.975	25.568	110.869	33.191	19.510	31.160	24.850	17.764
HEMBA1006310	40.983	23.265	36.585	20.570	11.748	29.056	27.263	17.748
HEMBA1006311	85.398	20.844	64.711	8.925	20.171	92.798	9.481	19.313
HEMBA1006313	27.762	12.975	47.707	17.417	7.455	13.117	9.891	6.082
HEMBA1006316	23.345	3.751	3.303	2.158	8.774	9.668	8.505	3.270
HEMBA1006328	79.937	83.744	185.981	41.111	28.820	37.527	35.377	85.968
HEMBA1006334	22.524	16.717	17.679	5.994	8.506	9.813	3.866	5.361
HEMBA1006335	72.666	41.477	35.235	27.435	6.110	5.851	24.375	8.434
HEMBA1006344	34.707	67.866	132.978	46.518	34.812	40.158	41.934	25.330
HEMBA1006347	34.301	16.445	32.190	19.603	16.749	20.762	20.884	15.376
HEMBA1006349	139.389	26.300	48.767	43.275	22.026	24.648	22.876	21.499
HEMBA1006352	21.127	17.873	15.526	9.410	8.472	14.845	7.491	9.414
HEMBA1006357	94.337	82.319	287.531	67.888	76.120	47.179	41.500	59.557
HEMBA1006358	48.925	31.345	132.494	32.473	25.019	28.197	13.250	24.899
HEMBA1006359	57.203	18.522	160.314	70.923	17.441	30.686	11.154	47.991
HEMBA1006360	29.518	10.133	15.515	17.275	6.141	13.876	6.804	8.361
HEMBA1006364	59.236	7.900	27.522	12.114	5.401	15.432	17.981	6.672
HEMBA1006377	67.120	31.113	57.269	33.567	23.849	45.246	31.609	20.280
HEMBA1006380	73.227	57.029	182.581	57.870	22.288	33.416	23.618	40.932
HEMBA1006381	359.346	122.755	376.090	126.304	112.826	146.346	91.469	93.252
HEMBA1006385	60.234	62.166	257.945	59.429	59.157	40.136	35.385	17.281
HEMBA1006390	71.393	38.752	46.828	25.848	16.455	41.253	16.013	27.609
HEMBA1006391	61.261	18.765	20.686	10.972	10.022	39.431	27.305	11.797
HEMBA1006398	42.089	3.225	18.036	5.299	25.386	6.480	0.000	3.308
HEMBA1006405	137.413	28.645	40.904	17.896	18.180	84.926	41.325	24.773
HEMBA1006410	149.580	32.840	61.022	20.027	39.718	54.551	23.826	33.928
HEMBA1006416	96.031	62.892	198.896	50.538	38.551	37.025	37.809	33.447
HEMBA1006418	23.236	18.335	23.851	11.378	10.280	28.208	46.245	36.223
HEMBA1006419	189.293	101.979	476.145	90.626	79.213	64.306	40.042	52.384
HEMBA1006421	39.702	26.487	127.221	23.773	16.184	14.460	12.270	13.523
HEMBA1006424	4.484	36.452	10.588	3.778	4.512	7.346	2.324	3.323
HEMBA1006426	88.597	67.224	230.530	60.836	32.273	40.489	17.284	36.244
HEMBA1006430	61.672	17.989	69.151	15.913	11.038	15.595	9.696	17.632
HEMBA1006438	45.084	34.475	111.512	27.012	15.035	34.111	12.678	11.056
HEMBA1006445	48.245	13.919	53.981	9.326	15.672	34.167	27.442	18.331
HEMBA1006446	22.911	3.160	3.324	1.568	4.341	2.585	1.331	0.000
HEMBA1006456	36.915	28.165	141.114	18.927	65.823	33.549	13.651	33.405
HEMBA1006461	60.747	42.392	161.108	40.447	22.274	32.823	18.018	27.165
HEMBA1006467	13.357	6.130	15.734	10.759	4.032	4.471	6.183	2.655
HEMBA1006470	73.960	30.706	103.625	27.235	29.870	33.756	33.818	24.286
HEMBA1006471	19.032	4.504	7.503	2.933	2.522	5.224	10.020	1.873
HEMBA1006474	25.718	12.420	21.381	11.498	9.614	19.875	17.655	13.491
HEMBA1006476	180.042	91.936	63.588	43.462	42.248	109.725	88.725	65.945
HEMBA1006482	129.627	169.312	167.982	151.338	57.839	95.521	75.480	239.325
HEMBA1006483	99.620	64.773	232.207	50.445	29.074	37.572	23.818	27.130
HEMBA1006485	41.690	4.055	17.445	11.682	4.522	9.351	6.411	10.066
HEMBA1006486	76.250	36.421	29.634	46.687	17.302	21.229	17.832	15.706
HEMBA1006489	5.771	32.673	2.141	5.240	2.356	4.324	4.739	7.328

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Table 37

HEMBA1006492	14.002	19.916	24.662	35.451	8.836	8.075	11.419	12.090
HEMBA1006494	7.279	0.000	19.790	3.750	8.718	8.343	5.851	5.887
HEMBA1006497	41.284	12.396	23.326	6.590	7.186	11.228	9.062	5.781
HEMBA1006501	160.565	16.895	26.893	13.446	17.608	65.467	41.560	6.197
HEMBA1006502	53.451	19.114	39.593	25.366	10.919	15.054	17.536	15.658
HEMBA1006507	19.274	8.180	10.287	4.521	7.939	5.288	15.480	10.062
HEMBA1006517	95.989	30.085	91.871	18.732	21.918	45.881	29.819	16.672
HEMBA1006521	31.224	27.873	37.864	18.318	9.774	14.205	14.646	13.907
HEMBA1006529	28.702	20.010	34.050	20.150	16.588	7.353	8.993	17.327
HEMBA1006530	18.445	16.411	29.175	14.433	12.214	16.734	15.731	8.081
HEMBA1006535	11.627	7.208	18.048	3.956	8.160	19.824	5.837	3.457
HEMBA1006536	68.087	40.009	142.475	43.263	34.343	42.050	42.157	23.975
HEMBA1006540	20.393	10.867	35.153	8.637	8.656	15.027	11.094	10.350
HEMBA1006544	30.281	4.662	59.940	7.791	7.169	15.883	8.745	8.693
HEMBA1006546	68.722	53.155	127.193	49.337	73.807	60.506	22.328	34.045
HEMBA1006549	13.885	13.666	21.800	11.666	8.491	14.211	8.987	6.080
HEMBA1006559	26.976	22.040	38.197	16.910	14.550	14.058	13.018	17.217
HEMBA1006562	55.924	24.663	75.789	20.363	17.181	26.651	18.158	19.510
HEMBA1006566	20.849	6.116	14.933	8.767	9.572	6.937	5.229	4.788
HEMBA1006569	67.508	20.299	44.291	27.048	12.798	15.243	24.739	31.861
HEMBA1006572	21.817	4.339	15.862	1.796	3.407	11.582	8.381	5.922
HEMBA1006579	5.427	18.336	4.219	3.440	2.139	5.460	3.967	5.110
HEMBA1006583	31.967	15.854	29.307	14.271	11.747	26.889	17.058	10.451
HEMBA1006595	59.014	41.577	148.359	30.860	16.681	19.571	13.265	24.768
HEMBA1006597	111.817	64.480	210.001	47.574	27.392	47.009	27.887	28.666
HEMBA1006606	79.184	47.311	131.822	40.177	33.228	35.403	25.240	31.687
HEMBA1006612	43.105	20.909	46.913	39.205	20.348	25.383	18.706	17.150
HEMBA1006617	79.139	62.924	235.236	60.258	30.407	40.264	28.184	38.643
HEMBA1006624	449.384	84.050	165.494	39.352	209.908	291.427	208.533	65.478
HEMBA1006631	168.309	108.316	381.778	89.696	71.812	80.634	39.325	50.996
HEMBA1006635	51.406	33.730	158.286	28.605	19.347	19.781	9.639	12.894
HEMBA1006639	67.363	30.354	51.867	15.409	33.210	43.083	25.295	12.985
HEMBA1006643	229.685	30.246	56.218	16.406	35.196	68.642	41.724	17.931
HEMBA1006648	80.985	32.464	39.607	14.926	36.718	12.135	32.217	48.853
HEMBA1006652	118.455	69.232	231.917	50.609	51.023	50.716	21.698	29.527
HEMBA1006653	46.971	16.614	46.472	16.579	12.358	15.364	13.867	9.224
HEMBA1006658	89.823	28.363	60.976	37.660	28.124	47.014	33.470	16.872
HEMBA1006659	79.863	33.625	48.217	49.132	29.124	33.070	25.182	33.784
HEMBA1006665	25.726	26.740	39.661	13.975	13.287	15.240	12.046	10.419
HEMBA1006666	8.276	4.281	10.565	6.319	4.257	10.392	2.791	2.171
HEMBA1006671	39.553	178.623	135.413	18.941	17.294	37.782	10.166	32.048
HEMBA1006674	100.472	44.108	176.724	46.922	36.367	44.809	43.576	43.269
HEMBA1006676	120.417	42.888	163.816	29.504	40.435	60.162	32.540	34.825
HEMBA1006682	27.104	2.556	23.174	4.035	8.982	19.092	3.958	0.000
HEMBA1006688	57.351	56.288	111.358	60.597	65.322	37.545	20.757	20.789
HEMBA1006695	132.496	140.334	315.655	97.296	56.206	54.392	37.622	57.596
HEMBA1006696	65.136	25.204	42.137	26.654	26.490	30.156	6.159	27.512
HEMBA1006702	4.275	4.328	8.881	7.114	3.362	1.846	7.796	1.965
HEMBA1006707	52.417	20.766	26.862	21.409	19.843	32.229	13.146	18.546
HEMBA1006708	126.875	38.520	66.803	31.253	33.294	55.347	32.071	18.229
HEMBA1006709	67.500	31.686	94.432	24.924	17.365	30.329	18.603	23.474
HEMBA1006717	110.641	21.536	29.255	12.654	16.091	54.326	26.752	11.544
HEMBA1006724	34.421	23.073	25.607	18.231	12.305	27.570	10.585	17.797
HEMBA1006731	36.072	18.255	41.441	15.382	16.479	17.272	10.826	15.482
HEMBA1006737	60.467	14.107	30.096	14.542	20.232	22.606	10.316	11.440
HEMBA1006742	80.258	45.190	134.964	35.452	21.316	21.889	15.223	23.529
HEMBA1006743	41.970	22.864	31.760	22.024	15.126	23.989	13.179	16.281
HEMBA1006744	181.068	97.273	433.004	103.006	69.785	59.354	46.770	61.806
HEMBA1006749	51.776	9.753	37.994	13.564	23.164	34.516	28.426	23.238
HEMBA1006752	124.800	60.318	88.111	59.765	47.490	69.461	37.541	47.074
HEMBA1006754	49.957	30.459	86.726	23.747	17.745	16.269	10.783	12.424
HEMBA1006758	75.460	21.737	26.190	19.832	18.249	38.492	30.654	15.933
HEMBA1006767	14.002	15.106	11.961	16.059	5.628	13.334	8.382	8.573
HEMBA1006770	120.485	21.505	62.144	29.559	32.512	49.739	45.952	28.318

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Table 38

HEMBA1006779	81.492	51.077	162.657	41.163	39.166	36.722	18.025	29.256
HEMBA1006780	78.359	78.052	345.442	73.371	68.858	55.888	41.524	39.494
HEMBA1006789	29.455	21.233	20.440	14.349	11.547	38.549	19.736	25.701
HEMBA1006795	143.727	88.701	218.732	55.068	49.500	46.284	21.141	40.750
HEMBA1006796	87.214	15.814	115.542	17.685	16.790	38.694	15.525	15.352
HEMBA1006805	68.116	31.212	153.041	33.162	30.301	34.197	24.275	30.733
HEMBA1006807	94.524	86.723	157.559	64.349	36.505	62.933	23.097	55.508
HEMBA1006813	40.696	4.415	4.750	4.264	10.978	7.562	6.201	3.198
HEMBA1006819	53.717	15.217	30.071	14.679	17.006	30.866	20.346	6.250
HEMBA1006821	39.052	30.425	111.325	35.769	34.975	22.216	18.924	20.698
HEMBA1006824	68.491	61.498	201.721	47.107	40.322	27.255	21.689	27.074
HEMBA1006832	84.462	89.500	102.038	77.046	40.147	75.996	66.799	71.706
HEMBA1006834	123.958	57.085	160.407	48.909	41.460	61.443	30.402	31.940
HEMBA1006835	33.705	19.529	38.470	23.193	18.979	22.344	22.426	16.742
HEMBA1006843	52.436	44.642	96.773	258.615	195.878	33.141	8.256	13.117
HEMBA1006849	88.931	34.224	158.388	39.483	30.349	34.943	15.743	28.240
HEMBA1006850	44.733	24.923	67.667	24.186	15.829	36.593	11.223	18.454
HEMBA1006861	215.207	94.180	158.997	67.349	259.512	135.856	371.932	44.063
HEMBA1006865	124.996	59.773	124.376	43.328	69.356	71.072	66.350	45.129
HEMBA1006867	16.632	11.094	39.646	14.084	12.902	11.855	5.865	18.338
HEMBA1006873	9.965	9.279	7.010	5.013	6.262	5.127	7.141	8.422
HEMBA1006877	44.043	18.321	20.546	8.172	14.670	13.165	16.493	9.073
HEMBA1006878	100.427	34.418	109.029	25.739	29.525	48.800	41.513	17.905
HEMBA1006879	108.299	42.811	121.051	60.872	47.507	40.075	14.429	51.924
HEMBA1006884	95.426	29.331	67.556	27.787	25.909	106.818	47.878	47.793
HEMBA1006885	107.720	54.342	127.920	62.272	55.739	51.739	36.790	50.612
HEMBA1006886	50.841	22.970	51.528	12.561	20.660	23.207	26.952	19.149
HEMBA1006889	81.809	20.952	21.474	12.691	24.681	41.822	48.768	15.196
HEMBA1006896	68.030	97.285	75.370	52.746	23.109	44.481	37.701	50.662
HEMBA1006900	61.515	36.410	61.016	23.329	21.390	38.404	27.583	22.774
HEMBA1006902	43.283	19.713	47.129	12.105	11.602	27.830	26.548	13.885
HEMBA1006912	183.904	90.995	338.160	78.230	79.588	63.729	39.994	64.953
HEMBA1006914	54.548	39.053	48.945	35.736	25.895	38.586	22.479	33.810
HEMBA1006916	62.872	0.000	65.115	29.982	32.625	61.537	62.750	30.818
HEMBA1006921	64.867	21.840	74.902	15.692	30.866	41.257	25.569	10.362
HEMBA1006926	51.195	10.616	76.671	24.435	20.300	84.402	29.503	20.967
HEMBA1006927	24.016	13.778	23.573	5.335	15.250	11.291	11.672	7.086
HEMBA1006929	7.146	8.487	5.431	5.526	1.676	5.970	5.688	3.134
HEMBA1006936	68.233	22.847	45.566	20.391	16.346	25.493	20.196	17.720
HEMBA1006938	14.202	8.409	31.234	7.743	5.002	6.780	6.773	5.945
HEMBA1006941	30.559	24.290	40.928	13.779	16.040	34.253	22.542	18.507
HEMBA1006942	147.487	57.842	121.883	69.207	55.456	76.853	61.942	66.640
HEMBA1006945	80.546	64.930	104.037	63.709	40.444	54.676	33.533	31.915
HEMBA1006949	10.292	41.467	23.921	1.860	15.813	7.071	10.866	5.231
HEMBA1006952	58.685	12.572	34.750	8.032	18.283	39.764	15.332	12.456
HEMBA1006960	91.939	38.895	93.164	24.834	34.400	36.160	36.715	34.791
HEMBA1006973	74.208	24.793	50.621	17.619	22.844	24.971	24.844	16.167
HEMBA1006974	48.691	39.013	59.414	48.064	16.799	38.579	21.301	46.006
HEMBA1006976	35.907	15.675	32.116	19.091	14.522	30.574	25.042	18.348
HEMBA1006989	6.422	2.207	2.374	3.336	2.670	3.696	2.557	3.536
HEMBA1006993	334.266	64.150	357.947	46.138	95.466	144.777	109.174	54.000
HEMBA1006998	9.183	9.870	15.032	9.483	5.722	9.518	8.368	9.637
HEMBA1007001	117.610	95.668	334.868	56.093	55.288	47.863	27.205	56.828
HEMBA1007002	93.134	41.846	72.311	21.453	16.249	59.722	46.434	40.628
HEMBA1007013	65.734	23.106	53.712	16.933	20.783	34.293	29.163	29.338
HEMBA1007016	36.649	14.972	27.491	6.385	9.597	17.982	16.658	15.035
HEMBA1007017	6.290	0.000	8.194	2.155	5.231	2.329	1.949	0.000
HEMBA1007018	19.457	15.664	19.767	14.280	10.586	15.084	9.105	14.124
HEMBA1007044	139.784	50.078	125.738	15.913	53.729	123.367	90.838	36.173
HEMBA1007045	49.576	7.913	39.757	9.069	10.104	19.099	12.683	7.276
HEMBA1007051	36.374	44.117	129.384	27.586	19.407	24.088	15.546	9.363
HEMBA1007052	69.582	19.611	40.507	19.050	9.213	19.409	18.969	10.939
HEMBA1007053	25.326	27.611	21.861	14.031	14.266	20.128	7.847	9.544
HEMBA1007057	45.897	13.545	33.857	18.616	25.861	36.241	14.769	13.902

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Table 39

HEMBA1007062	129.012	18.903	40.670	21.323	29.469	40.252	29.408	15.700
HEMBA1007063	81.681	45.884	187.380	52.391	36.943	28.608	35.303	41.236
HEMBA1007066	98.396	32.970	35.373	22.961	11.085	42.430	26.631	14.760
HEMBA1007069	23.449	21.519	78.409	16.835	27.425	17.217	9.095	16.163
HEMBA1007073	54.833	42.548	40.682	29.352	11.879	7.937	24.282	19.372
HEMBA1007076	83.020	48.746	248.260	61.189	50.193	68.045	43.836	35.650
HEMBA1007078	151.561	159.600	446.445	189.146	130.283	98.734	65.934	117.079
HEMBA1007080	43.963	44.765	174.545	66.950	45.879	43.194	43.909	50.100
HEMBA1007084	78.948	60.672	268.327	63.769	63.088	60.307	35.006	46.866
HEMBA1007085	263.538	108.018	162.599	48.155	77.545	161.321	63.614	80.640
HEMBA1007087	85.598	25.085	47.862	25.580	13.918	62.815	143.461	30.856
HEMBA1007089	21.131	32.023	21.145	14.738	7.213	19.681	9.036	10.026
HEMBA1007095	147.777	215.051	136.910	63.992	170.706	117.992	103.152	86.452
HEMBA1007101	78.959	53.790	147.891	35.676	28.082	27.200	19.131	25.922
HEMBA1007104	66.308	23.279	45.417	11.902	19.468	48.054	26.760	16.647
HEMBA1007106	28.449	17.761	41.268	28.670	17.681	14.174	10.999	7.534
HEMBA1007112	12.759	8.412	16.340	9.319	7.661	7.304	13.296	6.622
HEMBA1007113	126.702	0.000	229.408	64.551	40.242	39.032	13.319	26.174
HEMBA1007121	219.036	207.410	696.658	149.217	168.827	131.628	642.099	128.755
HEMBA1007129	50.726	42.510	63.847	31.663	26.417	24.371	18.928	20.103
HEMBA1007147	111.299	117.722	312.811	79.949	67.395	74.391	35.758	54.184
HEMBA1007149	83.453	6.442	19.831	7.332	11.043	9.349	9.831	8.756
HEMBA1007151	97.211	33.530	53.944	24.544	18.501	35.246	36.228	24.174
HEMBA1007172	52.683	25.324	438.704	42.182	28.599	38.126	26.167	25.770
HEMBA1007174	52.921	13.482	44.770	21.384	19.520	28.559	22.332	20.471
HEMBA1007176	89.919	24.768	53.414	32.841	44.643	73.679	87.040	30.762
HEMBA1007178	93.941	73.120	135.427	34.313	32.040	34.622	22.898	24.897
HEMBA1007185	62.558	18.807	36.824	15.490	20.528	37.568	22.260	12.783
HEMBA1007186	70.967	31.546	59.038	21.059	21.332	35.648	42.864	11.346
HEMBA1007194	53.376	38.911	126.660	33.992	23.875	21.109	12.122	23.307
HEMBA1007200	74.955	53.829	44.212	23.979	20.225	32.762	55.417	22.176
HEMBA1007203	87.803	26.807	41.357	14.648	9.791	23.392	30.167	17.274
HEMBA1007206	82.800	73.675	225.293	44.461	28.674	37.091	14.673	34.505
HEMBA1007224	25.614	40.402	50.116	21.484	14.920	22.548	13.197	20.053
HEMBA1007226	88.512	43.606	93.121	22.209	17.911	38.704	43.759	31.721
HEMBA1007240	131.657	62.804	86.650	9.510	21.890	53.116	42.250	16.655
HEMBA1007241	12.225	7.719	18.461	5.051	6.724	15.945	3.135	5.390
HEMBA1007242	21.409	14.030	13.648	11.068	6.265	17.370	8.487	5.236
HEMBA1007243	61.824	25.854	40.264	17.235	23.438	38.197	31.904	20.347
HEMBA1007251	37.660	16.946	37.149	16.699	12.180	19.482	30.321	10.262
HEMBA1007256	53.905	43.642	113.110	31.642	27.946	30.492	18.548	23.645
HEMBA1007267	80.741	40.085	207.160	61.174	38.220	29.008	32.292	29.672
HEMBA1007273	41.062	9.087	11.906	5.193	6.445	7.723	9.225	4.483
HEMBA1007279	54.376	20.734	133.494	27.987	21.355	19.941	17.364	19.503
HEMBA1007281	8.523	5.717	4.731	3.403	2.317	2.497	2.740	0.000
HEMBA1007283	25.940	14.444	24.974	23.487	19.771	23.418	19.378	26.409
HEMBA1007288	57.959	39.576	155.227	28.725	24.689	25.110	16.998	16.095
HEMBA1007291	37.974	19.069	59.253	20.445	13.404	17.376	13.060	13.147
HEMBA1007299	446.640	93.668	199.852	61.423	94.129	249.346	241.373	85.323
HEMBA1007300	103.752	25.694	24.914	18.217	40.413	26.018	31.407	16.669
HEMBA1007301	49.752	18.178	32.677	18.170	33.650	33.786	22.892	12.782
HEMBA1007319	13.312	10.598	23.453	16.511	4.278	9.382	2.996	8.570
HEMBA1007320	53.723	23.595	62.301	29.439	16.672	32.932	28.191	18.418
HEMBA1007322	45.986	125.362	77.545	43.693	17.955	45.689	39.556	80.836
HEMBA1007323	64.720	16.869	22.970	11.238	11.687	32.209	25.350	7.506
HEMBA1007326	313.094	189.188	862.276	214.045	178.109	171.587	70.819	115.174
HEMBA1007327	78.767	61.102	219.980	55.002	29.411	44.095	29.354	42.286
HEMBA1007332	71.516	9.318	34.879	5.559	7.452	24.826	12.763	20.050
HEMBA1007341	89.805	53.431	207.395	82.402	105.877	47.861	32.826	50.162
HEMBA1007342	22.063	17.289	28.253	18.196	17.751	26.378	13.820	9.173
HEMBA1007347	112.392	64.499	230.022	60.348	47.557	63.758	30.683	33.285
HEMBA1007353	1.685	3.520	0.575	1.860	1.976	0.107	2.061	0.788
HEMBB1000005	60.047	46.027	121.870	38.241	20.699	18.268	20.068	26.957
HEMBB1000008	97.929	53.604	274.179	68.681	38.935	39.328	26.881	34.873

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Table 40

HEMBB1000018	122.130	127.861	329.165	120.419	57.867	95.203	75.902	92.924
HEMBB1000024	181.606	97.019	373.954	102.401	70.406	70.591	40.304	66.798
HEMBB1000025	85.919	29.049	45.055	23.789	13.946	24.397	29.349	13.072
HEMBB1000030	108.167	68.316	303.677	83.010	68.378	81.687	34.886	37.617
HEMBB1000036	107.960	11.573	50.484	11.277	20.480	41.381	25.378	14.730
HEMBB1000037	77.688	29.380	69.658	56.679	27.020	54.062	30.086	15.311
HEMBB1000039	52.550	48.503	140.795	30.096	18.739	26.012	15.151	21.723
HEMBB1000044	134.136	75.469	218.667	61.596	32.667	29.659	43.360	42.831
HEMBB1000048	17.937	21.052	31.004	18.291	11.321	20.120	21.506	15.078
HEMBB1000050	74.210	33.681	207.484	35.691	22.905	25.584	18.572	17.494
HEMBB1000054	68.273	47.191	246.350	44.008	24.522	29.259	22.570	21.316
HEMBB1000055	72.875	112.284	61.172	110.297	21.358	70.636	93.824	132.288
HEMBB1000059	331.577	184.687	662.540	182.481	130.065	131.364	90.002	121.903
HEMBB1000072	240.733	98.890	326.893	75.919	67.742	118.222	108.108	91.458
HEMBB1000081	23.738	27.174	85.100	21.146	30.856	20.458	7.513	15.351
HEMBB1000083	120.759	58.163	188.224	40.609	37.789	59.334	33.712	39.101
HEMBB1000089	67.618	54.952	191.832	56.629	24.609	36.847	30.680	26.912
HEMBB1000094	355.534	116.828	161.958	31.504	29.300	49.613	36.239	35.197
HEMBB1000097	27.834	63.724	51.488	14.249	22.834	34.068	18.547	16.455
HEMBB1000099	157.641	91.912	456.470	71.078	50.739	64.471	32.108	43.354
HEMBB1000103	75.781	59.392	114.974	44.216	31.915	47.628	23.669	56.268
HEMBB1000106	62.814	44.996	77.918	35.044	19.825	40.409	26.156	46.001
HEMBB1000113	43.660	33.435	95.987	42.744	19.714	20.114	15.899	21.606
HEMBB1000119	57.350	21.211	42.528	17.770	19.517	28.754	23.570	30.104
HEMBB1000133	92.950	65.230	58.619	69.544	53.706	104.229	39.058	80.858
HEMBB1000134	44.120	20.654	76.693	40.611	24.712	37.185	42.327	21.963
HEMBB1000136	21.810	7.191	44.517	15.599	7.339	22.582	12.399	24.899
HEMBB1000141	163.867	99.946	331.822	95.807	55.858	64.560	36.737	52.602
HEMBB1000144	96.831	97.019	183.423	88.529	36.185	15.577	29.259	32.144
HEMBB1000147	59.253	9.088	62.426	7.391	11.451	7.175	11.502	10.693
HEMBB1000152	56.391	28.723	34.597	15.309	19.424	32.469	29.105	19.117
HEMBB1000154	85.308	47.878	101.061	33.881	19.477	27.298	20.174	15.366
HEMBB1000155	35.691	36.132	109.038	28.164	29.608	22.283	16.557	17.041
HEMBB1000173	170.611	173.001	494.253	143.666	83.705	123.932	65.317	76.388
HEMBB1000175	32.273	19.114	23.481	10.948	4.039	29.180	7.135	13.322
HEMBB1000178	56.984	51.334	90.749	69.004	40.144	52.980	25.845	19.359
HEMBB1000198	70.426	12.768	26.381	10.237	6.266	11.215	8.858	5.363
HEMBB1000208	42.474	8.966	34.929	10.418	12.883	9.285	12.335	7.978
HEMBB1000209	43.846	10.700	9.943	10.934	8.858	12.135	9.049	4.168
HEMBB1000212	27.532	12.579	76.077	15.361	33.518	17.471	13.132	16.552
HEMBB1000215	178.324	89.053	294.606	95.420	68.598	89.720	51.270	61.235
HEMBB1000217	148.073	45.416	96.614	47.569	37.572	89.989	48.073	33.510
HEMBB1000218	88.298	123.000	347.859	84.124	41.828	57.417	21.147	34.605
HEMBB1000226	70.693	14.949	41.586	31.786	30.261	28.577	14.779	27.177
HEMBB1000230	28.681	8.910	13.549	5.500	3.547	9.616	6.632	3.293
HEMBB1000240	44.662	12.588	13.211	10.455	4.589	41.554	8.171	7.082
HEMBB1000244	22.390	13.510	42.662	18.503	18.758	11.192	2.111	13.188
HEMBB1000250	20.878	6.254	20.741	9.109	1.841	13.561	9.540	2.708
HEMBB1000258	101.717	75.034	336.781	79.281	52.303	67.231	33.313	34.880
HEMBB1000264	99.327	57.280	269.540	83.791	39.799	96.654	62.346	79.783
HEMBB1000266	70.747	23.082	23.217	14.456	28.745	34.547	15.022	15.672
HEMBB1000272	14.990	14.502	10.270	6.954	12.730	6.133	4.205	16.611
HEMBB1000274	105.245	46.925	190.978	49.759	41.568	43.127	18.199	25.826
HEMBB1000276	6.479	2.218	2.501	4.783	1.754	2.070	2.079	1.252
HEMBB1000284	4.790	5.088	7.884	3.489	2.213	3.213	1.981	3.304
HEMBB1000307	52.330	30.191	128.450	28.961	22.039	15.869	9.113	21.677
HEMBB1000309	86.347	36.463	96.140	43.964	34.442	33.118	18.805	21.507
HEMBB1000312	41.862	30.986	40.349	24.933	7.383	79.360	24.114	16.788
HEMBB1000317	49.311	18.053	26.189	10.490	10.102	21.107	12.632	13.384
HEMBB1000318	87.180	33.847	208.954	43.556	23.043	27.764	9.191	17.641
HEMBB1000332	3.892	11.256	14.087	42.331	28.145	14.132	2.408	14.319
HEMBB1000335	27.939	30.864	21.167	28.071	12.651	30.027	12.746	21.753
HEMBB1000336	68.463	26.023	48.843	10.608	22.871	23.654	23.868	13.927
HEMBB1000337	289.853	59.290	93.527	52.168	54.197	125.769	126.562	60.614

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Table 41

HEMBB1000338	54.685	45.765	123.480	44.612	17.722	26.663	17.708	29.721
HEMBB1000339	144.258	108.124	265.125	105.421	89.798	89.055	56.944	50.241
HEMBB1000341	113.271	46.622	132.906	32.751	40.166	37.986	28.017	30.881
HEMBB1000343	130.737	71.935	259.845	80.183	46.681	45.761	43.928	46.721
HEMBB1000354	202.146	151.264	495.642	157.908	153.529	142.579	67.161	105.322
HEMBB1000358	92.244	22.827	29.160	24.670	22.387	48.989	59.506	28.803
HEMBB1000369	55.720	25.874	97.758	27.483	21.576	23.750	17.278	16.569
HEMBB1000373	52.572	59.105	70.779	61.379	38.792	44.185	31.504	45.653
HEMBB1000374	153.545	115.183	389.274	108.150	98.073	80.319	58.214	75.906
HEMBB1000376	95.394	132.554	369.986	146.818	60.328	63.876	73.647	43.202
HEMBB1000383	37.023	35.429	24.954	13.017	10.381	22.638	16.842	8.781
HEMBB1000391	127.327	30.055	106.971	24.962	30.891	57.827	37.484	11.921
HEMBB1000399	35.143	10.865	22.406	8.561	4.100	8.569	2.643	8.889
HEMBB1000402	82.616	20.485	44.946	25.430	13.012	19.024	7.725	18.695
HEMBB1000404	18.903	12.568	10.300	8.593	9.455	9.301	2.672	7.956
HEMBB1000407	19.286	8.572	18.593	3.281	2.599	13.454	2.473	3.407
HEMBB1000420	95.847	66.573	138.307	54.950	39.330	56.220	37.608	43.081
HEMBB1000430	274.820	161.981	153.601	40.874	406.081	489.107	693.805	115.638
HEMBB1000434	350.936	139.481	599.497	199.198	125.426	113.500	65.776	77.687
HEMBB1000438	67.342	10.187	25.472	7.736	8.148	27.875	7.217	6.701
HEMBB1000441	84.086	98.109	312.643	78.842	60.934	76.141	46.589	35.267
HEMBB1000447	76.519	88.156	54.883	26.628	31.157	24.328	25.777	38.008
HEMBB1000449	22.367	11.282	25.245	11.267	1.700	13.053	5.731	8.109
HEMBB1000453	26.781	29.875	49.056	22.139	35.305	22.456	14.006	15.902
HEMBB1000455	37.937	43.401	129.423	29.222	40.584	24.577	21.227	20.356
HEMBB1000472	146.390	61.195	235.753	80.306	44.122	82.882	52.783	87.457
HEMBB1000480	138.135	67.904	194.466	46.367	41.944	60.409	34.897	40.785
HEMBB1000486	78.511	63.045	211.876	47.786	39.049	36.558	20.396	17.632
HEMBB1000487	21.510	22.091	29.116	10.718	21.056	15.854	13.086	10.892
HEMBB1000490	232.419	148.116	562.064	159.218	134.370	107.861	60.296	110.306
HEMBB1000491	149.070	107.169	349.100	81.342	44.330	51.147	33.633	59.342
HEMBB1000492	18.194	21.930	19.080	9.690	6.821	10.632	9.805	5.454
HEMBB1000493	286.390	34.074	64.876	31.406	23.065	49.816	39.824	39.921
HEMBB1000510	133.225	95.239	380.177	165.002	101.728	72.504	64.646	83.048
HEMBB1000516	137.574	35.610	61.963	35.305	10.932	78.851	39.905	19.224
HEMBB1000518	8.388	3.267	26.133	5.489	1.531	1.500	1.611	1.901
HEMBB1000523	153.793	88.071	329.880	82.474	43.568	69.756	32.830	51.127
HEMBB1000530	46.151	13.390	40.950	8.319	32.799	6.126	10.689	8.426
HEMBB1000542	57.808	36.831	46.332	20.306	19.414	5.489	13.314	22.747
HEMBB1000550	39.123	26.036	79.169	22.945	10.597	23.147	37.266	20.568
HEMBB1000554	192.214	105.635	349.184	148.874	90.632	98.169	55.377	100.995
HEMBB1000556	100.759	22.180	68.289	37.737	35.176	41.190	47.163	40.726
HEMBB1000564	101.412	37.586	144.386	37.463	27.344	59.939	31.447	9.452
HEMBB1000567	361.516	76.515	125.177	66.960	83.698	221.216	145.840	54.204
HEMBB1000569	63.847	46.712	54.356	18.197	23.752	36.942	31.264	39.479
HEMBB1000573	99.088	89.487	373.557	76.986	76.236	63.534	39.587	58.548
HEMBB1000575	74.071	67.726	296.427	63.469	37.530	42.388	33.544	46.151
HEMBB1000579	27.868	12.805	18.934	6.889	3.743	24.452	24.367	23.262
HEMBB1000585	30.826	34.244	65.882	26.172	19.828	26.184	16.826	33.888
HEMBB1000586	85.397	75.643	187.543	99.762	48.456	35.430	28.693	50.228
HEMBB1000589	135.404	58.619	243.853	51.181	36.284	29.883	21.561	27.997
HEMBB1000591	99.680	60.946	242.306	54.695	36.589	52.616	32.332	33.066
HEMBB1000592	30.320	18.740	34.338	11.753	8.732	28.305	13.707	12.164
HEMBB1000593	148.639	68.816	255.892	61.084	46.829	61.565	49.545	66.588
HEMBB1000595	27.140	21.001	29.869	21.272	9.199	21.841	16.487	29.680
HEMBB1000598	39.074	31.891	85.011	22.815	13.772	21.958	13.576	26.747
HEMBB1000611	14.828	6.552	11.601	7.498	7.461	15.614	9.246	9.161
HEMBB1000617	193.986	137.945	458.678	127.725	87.855	84.583	46.273	77.986
HEMBB1000623	65.566	26.480	50.777	19.193	18.923	40.974	28.571	23.219
HEMBB1000630	62.606	23.074	40.815	18.796	14.186	31.973	21.492	13.779
HEMBB1000631	61.311	41.283	27.586	23.498	24.433	35.043	48.566	22.826
HEMBB1000632	58.747	55.433	156.750	30.460	29.661	33.497	21.899	21.857
HEMBB1000636	127.885	47.562	59.456	48.965	33.643	65.366	42.360	37.349
HEMBB1000637	817.391	628.017	1645.738	524.605	482.307	443.855	191.753	265.704

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Table 42

HEMBB1000638	55.058	47.453	95.751	42.262	25.684	15.056	22.121	28.829
HEMBB1000642	179.188	88.317	251.754	80.865	42.468	81.296	37.696	52.009
HEMBB1000643	43.411	25.689	113.037	18.985	11.038	14.245	8.276	18.743
HEMBB1000649	27.852	45.202	137.371	34.816	24.496	9.967	11.881	22.322
HEMBB1000652	84.942	61.856	126.562	78.131	42.090	36.343	22.852	31.597
HEMBB1000655	418.308	73.377	56.858	57.166	32.733	57.424	38.897	44.477
HEMBB1000665	16.253	13.954	10.766	20.817	6.796	13.110	7.987	4.458
HEMBB1000668	28.587	13.435	14.606	13.788	25.844	15.049	12.549	11.202
HEMBB1000671	239.020	122.952	561.221	119.970	96.244	75.058	66.812	88.267
HEMBB1000673	11.633	5.779	14.629	14.904	5.916	4.811	2.141	12.812
HEMBB1000679	16.899	7.357	23.438	7.697	1.049	30.246	7.774	7.063
HEMBB1000684	188.240	157.754	430.254	128.150	66.411	89.722	49.173	67.832
HEMBB1000692	4.978	9.265	11.569	5.085	1.158	3.240	3.421	1.785
HEMBB1000693	63.119	40.561	59.522	22.326	25.408	13.898	31.488	20.706
HEMBB1000705	15.560	31.798	122.757	36.451	19.928	11.568	2.839	10.179
HEMBB1000706	22.553	13.626	23.777	8.621	11.683	41.509	10.019	7.584
HEMBB1000709	74.737	77.864	245.726	50.833	51.093	50.427	37.955	51.357
HEMBB1000714	23.726	10.733	6.625	12.298	6.349	9.891	2.142	14.350
HEMBB1000725	24.239	9.575	11.437	13.761	12.596	17.372	8.105	16.144
HEMBB1000726	86.971	84.395	208.396	65.157	43.881	37.441	22.020	39.067
HEMBB1000729	51.556	25.288	140.931	23.005	27.775	18.629	12.838	14.902
HEMBB1000738	39.002	38.955	166.616	42.588	21.380	43.330	7.181	21.192
HEMBB1000749	115.917	94.942	454.741	136.454	54.340	39.253	32.933	49.141
HEMBB1000763	47.835	25.201	36.488	16.952	21.036	31.919	14.990	12.111
HEMBB1000770	30.598	45.410	167.003	32.786	26.482	25.698	18.186	24.127
HEMBB1000774	27.168	21.690	33.470	20.937	12.916	22.598	8.092	17.606
HEMBB1000777	246.286	57.131	58.743	31.851	40.345	119.113	81.364	53.990
HEMBB1000781	41.945	36.620	34.149	24.543	23.561	16.383	14.371	20.775
HEMBB1000788	10.756	10.608	5.481	6.429	2.950	5.995	4.522	4.589
HEMBB1000789	28.490	9.620	26.151	16.088	11.640	16.477	7.916	7.672
HEMBB1000790	74.318	56.925	185.959	63.749	33.523	24.232	24.414	28.423
HEMBB1000794	18.080	17.254	38.876	24.305	7.427	10.338	5.445	9.305
HEMBB1000807	50.070	31.869	22.751	19.865	20.934	27.002	18.350	27.280
HEMBB1000809	334.541	42.976	42.300	26.454	9.545	31.526	31.677	44.152
HEMBB1000810	189.365	50.676	163.325	33.349	38.994	74.400	45.398	19.262
HEMBB1000821	40.710	9.304	21.006	6.841	5.422	15.981	10.835	5.685
HEMBB1000822	8.726	3.570	3.541	1.411	7.255	5.519	1.285	1.525
HEMBB1000826	68.485	40.348	201.149	68.467	43.204	31.769	32.812	55.367
HEMBB1000827	50.671	34.326	108.391	32.945	15.076	25.813	18.713	25.457
HEMBB1000831	38.060	20.466	29.131	12.368	19.990	20.562	25.373	6.415
HEMBB1000835	59.181	56.345	127.358	58.150	44.350	35.831	25.687	35.108
HEMBB1000840	117.639	63.375	340.802	61.186	48.924	38.995	20.712	30.526
HEMBB1000848	98.938	53.024	210.423	42.569	28.984	47.603	29.642	29.431
HEMBB1000852	1.827	2.160	0.621	2.559	1.621	1.272	1.364	1.086
HEMBB1000857	16.897	16.768	19.951	14.921	12.912	17.270	10.179	14.915
HEMBB1000858	25.634	16.531	8.162	8.209	14.482	12.749	92.823	10.102
HEMBB1000867	106.946	56.331	264.748	50.278	36.949	41.202	26.795	29.760
HEMBB1000870	68.550	62.423	192.351	52.406	39.303	55.641	23.738	27.427
HEMBB1000875	21.813	12.044	24.968	11.314	7.689	10.690	11.143	26.241
HEMBB1000881	30.089	16.478	28.345	14.926	18.419	17.763	18.901	20.494
HEMBB1000883	11.669	10.263	26.185	6.975	2.780	8.223	2.906	3.540
HEMBB1000887	42.638	32.274	66.780	22.979	31.512	42.842	20.622	22.566
HEMBB1000888	20.318	8.193	11.483	5.178	4.073	8.708	6.801	4.342
HEMBB1000890	40.795	42.287	112.076	25.031	11.171	23.116	15.491	16.447
HEMBB1000893	38.227	10.603	88.306	24.535	14.440	12.863	9.734	17.727
HEMBB1000900	23.814	8.709	17.013	9.267	10.928	12.199	14.105	11.108
HEMBB1000905	63.589	43.501	37.125	41.367	26.379	29.649	38.699	31.891
HEMBB1000908	42.944	54.674	120.821	34.982	28.838	28.194	15.897	26.230
HEMBB1000910	72.960	51.795	161.850	41.050	36.594	37.378	13.612	23.263
HEMBB1000913	33.820	35.219	96.448	24.688	12.371	26.067	14.715	19.268
HEMBB1000915	1910.513	222.511	693.345	124.825	532.993	1548.228	1159.943	223.176
HEMBB1000917	99.638	64.212	310.142	53.316	39.091	34.989	22.324	40.667
HEMBB1000927	80.569	11.252	19.448	8.653	21.944	24.546	17.769	17.391
HEMBB1000932	33.128	33.556	95.029	29.041	17.945	21.758	22.973	31.034

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Table 43

HEMBB1000933	883.639	393.035	605.052	289.543	312.660	538.431	353.155	291.706
HEMBB1000936	23.212	17.243	46.380	14.205	25.527	13.908	8.530	11.716
HEMBB1000939	105.016	36.905	52.525	19.304	30.111	35.223	41.856	37.146
HEMBB1000941	6.540	27.555	15.872	4.660	6.130	17.648	83.246	9.541
HEMBB1000947	36.384	18.020	47.143	21.361	9.565	34.299	13.482	13.269
HEMBB1000954	16.970	17.878	19.810	11.407	6.851	17.302	10.023	8.877
HEMBB1000959	22.223	21.226	78.296	22.443	5.599	10.268	10.673	12.183
HEMBB1000973	11.584	10.364	21.189	8.579	7.102	23.845	5.510	9.891
HEMBB1000975	99.598	37.022	69.027	23.084	27.137	40.162	56.997	30.316
HEMBB1000981	10.199	12.524	23.602	20.141	5.813	6.152	13.771	4.102
HEMBB1000985	13.065	8.026	7.574	4.776	6.642	2.985	6.049	3.612
HEMBB1000991	67.124	17.092	28.053	8.864	8.560	28.394	25.072	10.907
HEMBB1000996	170.256	127.636	352.650	90.350	64.926	71.240	60.014	102.622
HEMBB1001000	48.257	19.380	16.573	15.226	10.611	14.541	7.698	9.642
HEMBB1001004	0.797	1.839	0.439	0.000	0.000	0.318	0.000	0.000
HEMBB1001008	17.533	13.975	16.434	11.194	6.400	12.238	6.478	9.235
HEMBB1001011	39.743	19.337	28.396	15.752	15.302	17.720	15.586	16.702
HEMBB1001014	121.726	46.352	244.715	50.619	33.004	55.708	30.100	34.469
HEMBB1001020	86.065	68.022	243.352	67.763	53.522	50.406	30.247	49.844
HEMBB1001024	66.546	59.010	205.347	41.480	31.865	35.052	21.045	39.489
HEMBB1001026	36.265	27.027	76.443	19.990	25.484	27.657	12.014	23.129
HEMBB1001037	64.392	37.810	120.090	20.652	22.459	27.294	18.918	28.917
HEMBB1001042	58.936	20.428	42.468	17.255	15.600	32.463	20.274	18.506
HEMBB1001046	76.790	22.021	40.791	13.932	17.825	47.853	26.672	30.056
HEMBB1001047	76.665	39.237	208.757	53.469	44.539	37.624	16.049	20.262
HEMBB1001048	133.028	58.176	140.515	48.390	34.614	42.111	29.526	34.858
HEMBB1001051	22.699	8.465	13.142	9.942	10.065	9.946	5.881	8.790
HEMBB1001056	40.040	16.494	45.000	22.674	18.685	21.131	18.431	12.498
HEMBB1001058	88.873	59.116	223.822	45.122	34.696	29.783	21.562	25.222
HEMBB1001060	35.486	18.631	33.852	60.851	26.807	13.499	12.993	19.391
HEMBB1001063	53.418	36.359	125.166	33.156	24.220	19.182	16.188	14.597
HEMBB1001068	79.181	46.879	78.756	35.034	26.835	79.006	63.198	43.296
HEMBB1001082	66.296	58.491	173.393	49.675	25.253	33.015	14.189	22.904
HEMBB1001095	64.435	31.409	20.825	17.116	14.939	41.581	21.497	13.792
HEMBB1001096	43.372	28.562	94.366	32.120	13.089	21.236	15.814	22.034
HEMBB1001101	79.652	21.131	40.775	18.757	35.350	46.263	18.855	13.874
HEMBB1001102	51.740	27.685	86.794	21.160	12.958	16.450	7.215	8.605
HEMBB1001104	61.846	33.489	28.997	14.789	10.623	20.859	15.993	10.658
HEMBB1001105	69.199	32.868	132.855	27.292	32.605	49.984	20.779	23.761
HEMBB1001112	161.356	78.361	73.588	64.617	86.150	93.363	87.696	95.854
HEMBB1001113	114.744	130.208	298.139	107.218	73.757	61.718	32.824	66.952
HEMBB1001114	105.358	95.960	365.719	66.457	62.314	35.251	34.480	51.970
HEMBB1001115	67.274	16.815	13.190	26.838	17.638	29.948	23.803	34.239
HEMBB1001117	2.434	10.619	14.951	4.152	4.937	2.694	2.729	18.952
HEMBB1001119	18.198	17.501	58.077	15.560	5.202	13.437	5.261	9.614
HEMBB1001126	306.301	111.345	266.365	81.302	76.905	130.782	58.863	61.487
HEMBB1001133	39.673	36.703	178.312	45.328	36.363	38.712	14.400	26.997
HEMBB1001137	53.424	19.209	46.849	14.453	13.705	30.395	18.865	15.761
HEMBB1001142	105.888	131.411	405.403	98.008	104.700	62.754	32.598	75.485
HEMBB1001145	114.864	106.329	348.161	78.364	57.587	54.983	24.738	51.568
HEMBB1001151	149.618	23.632	66.607	14.582	34.238	68.060	46.084	19.806
HEMBB1001153	92.263	53.444	153.351	44.131	37.191	34.991	21.708	32.599
HEMBB1001158	64.416	30.844	50.578	22.880	32.523	47.046	24.553	39.658
HEMBB1001169	96.424	70.158	253.814	76.490	44.058	37.113	24.102	38.757
HEMBB1001170	34.989	7.730	32.617	5.324	4.217	11.418	7.623	5.208
HEMBB1001175	46.512	27.401	45.252	21.001	15.416	20.636	17.361	36.021
HEMBB1001177	126.389	86.212	396.633	84.357	48.470	40.910	34.438	42.680
HEMBB1001182	70.825	30.508	45.077	19.262	28.316	32.507	25.771	26.488
HEMBB1001192	30.059	21.703	61.610	20.151	5.688	22.456	24.299	31.214
HEMBB1001199	1.469	0.000	0.000	4.430	0.797	2.148	1.260	1.223
HEMBB1001200	2.266	1.426	2.071	5.734	0.000	2.413	1.567	2.969
HEMBB1001208	111.969	37.738	122.154	28.426	28.653	55.253	32.443	21.624
HEMBB1001209	103.602	77.445	233.649	60.849	25.456	40.993	26.273	33.636
HEMBB1001210	14.499	40.527	32.902	6.231	10.125	16.413	17.251	28.930

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Table 44

HEMBB1001215	219.922	83.033	126.326	63.007	71.733	115.441	61.961	72.210
HEMBB1001217	63.633	22.116	41.047	17.479	20.160	53.164	31.645	18.739
HEMBB1001218	98.226	47.137	142.266	53.412	29.467	23.819	20.495	24.079
HEMBB1001221	0.524	1.310	12.795	0.988	0.992	0.867	0.000	1.767
HEMBB1001224	52.109	37.281	86.318	28.364	24.177	19.072	16.478	20.321
HEMBB1001230	38.785	17.158	30.714	15.256	12.698	31.469	27.596	17.436
HEMBB1001234	335.966	64.817	131.669	43.601	69.385	167.134	101.415	57.258
HEMBB1001235	152.870	67.952	84.726	40.262	26.665	52.686	38.623	49.693
HEMBB1001237	16.971	23.623	33.663	30.744	21.161	18.495	18.264	25.643
HEMBB1001242	26.787	15.776	22.922	4.200	5.187	11.277	10.621	7.589
HEMBB1001244	280.439	9.589	9.743	8.128	2.116	4.366	2.735	2.871
HEMBB1001249	51.892	27.766	106.010	25.983	19.890	21.254	16.839	21.542
HEMBB1001253	50.869	33.773	58.857	31.656	8.253	38.144	20.639	25.942
HEMBB1001254	28.109	8.716	61.080	12.779	6.376	18.461	22.558	8.559
HEMBB1001266	2.010	9.088	3.704	1.682	16.420	18.653	1.717	1.611
HEMBB1001267	131.334	93.697	391.730	88.886	45.610	62.418	33.457	63.350
HEMBB1001271	31.480	28.408	63.773	19.821	15.244	12.530	8.683	10.739
HEMBB1001282	41.166	11.440	25.546	10.847	7.531	21.762	15.737	10.592
HEMBB1001287	195.274	200.678,	131.870	63.454	15.491	70.758	43.360	52.931
HEMBB1001288	40.232	10.227	25.481	9.789	5.520	21.519	16.538	9.861
HEMBB1001289	84.233	74.730	246.417	61.615	31.689	36.447	24.521	38.077
HEMBB1001290	57.742	13.181	11.174	33.921	23.320	24.860	82.615	15.369
HEMBB1001294	80.761	23.745	72.937	16.689	20.147	45.268	37.686	22.951
HEMBB1001299	58.616	17.094	44.424	13.532	14.650	31.325	32.822	12.329
HEMBB1001302	87.107	24.979	56.357	23.389	20.784	37.921	28.849	21.981
HEMBB1001304	12.134	0.119	5.246	19.403	1.810	3.978	2.153	1.580
HEMBB1001314	6.410	5.111	25.042	5.961	3.244	7.037	2.954	2.258
HEMBB1001315	3.706	8.398	10.733	3.067	1.405	3.652	1.659	1.943
HEMBB1001317	39.137	34.918	87.084	32.290	25.473	21.551	14.009	18.118
HEMBB1001326	13.902	5.726	7.704	2.886	2.324	1.546	2.008	5.612
HEMBB1001331	34.871	17.866	37.859	11.626	6.188	23.138	24.975	17.786
HEMBB1001335	22.550	20.911	19.341	12.458	15.964	18.477	15.941	5.614
HEMBB1001337	61.645	43.894	187.675	45.250	52.185	20.178	25.750	29.233
HEMBB1001339	20.634	25.030	21.230	11.541	12.874	18.490	12.601	13.466
HEMBB1001344	31.209	8.322	15.710	5.412	6.749	16.517	16.482	9.869
HEMBB1001346	44.149	21.512	38.191	15.415	9.432	26.936	17.706	15.965
HEMBB1001348	66.624	40.319	173.356	39.887	26.835	31.783	20.641	26.670
HEMBB1001350	103.603	17.400	35.832	13.555	13.837	54.503	34.694	19.925
HEMBB1001356	12.440	11.385	25.095	8.592	6.787	7.806	8.759	8.923
HEMBB1001364	28.525	14.483	31.452	11.829	13.494	12.620	13.025	10.117
HEMBB1001366	57.883	53.690	210.263	52.112	27.208	41.191	29.156	32.064
HEMBB1001367	140.660	59.744	283.101	54.260	46.338	67.368	43.944	48.485
HEMBB1001369	17.341	20.708	71.044	14.855	7.629	12.537	7.158	14.407
HEMBB1001380	50.204	67.647	124.463	41.290	43.730	41.591	29.026	63.358
HEMBB1001381	19.588	19.545	34.218	14.113	18.710	9.428	10.202	13.801
HEMBB1001384	17.779	11.154	26.926	11.606	19.030	10.038	7.367	14.535
HEMBB1001387	20.705	16.837	19.148	9.955	8.901	15.994	7.831	13.345
HEMBB1001394	21.419	19.091	32.720	17.551	19.172	11.590	12.282	11.322
HEMBB1001407	39.158	17.718	75.721	24.299	17.481	17.410	20.342	15.525
HEMBB1001410	18.880	3.346	6.042	2.907	2.655	0.000	2.839	2.094
HEMBB1001413	32.291	25.769	80.279	17.033	21.102	11.132	12.610	24.207
HEMBB1001419	36.323	42.415	185.239	24.790	21.849	17.972	13.895	31.342
HEMBB1001421	29.464	57.495	109.370	12.065	15.685	64.181	165.647	23.322
HEMBB1001424	9.663	7.148	10.294	6.073	6.773	7.183	5.215	8.524
HEMBB1001426	36.471	25.897	86.872	20.138	17.823	19.534	15.347	23.782
HEMBB1001429	60.351	47.669	39.928	29.802	21.695	39.456	39.474	41.210
HEMBB1001436	168.445	86.814	350.902	88.825	54.546	86.724	48.813	58.527
HEMBB1001443	20.733	11.137	12.445	8.769	16.707	14.531	9.581	12.477
HEMBB1001449	70.239	34.064	146.511	28.311	23.391	19.979	16.080	22.377
HEMBB1001454	60.851	40.766	133.878	33.168	28.709	36.541	29.720	26.623
HEMBB1001458	77.938	28.808	33.472	15.970	29.260	40.965	25.268	28.079
HEMBB1001461	44.192	44.580	179.531	65.974	16.217	45.935	14.669	27.974
HEMBB1001463	57.949	102.937	230.980	60.751	41.957	48.857	25.233	38.517
HEMBB1001464	18.058	9.999	14.908	10.039	7.528	8.680	2.638	2.964

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Table 45

HEMBB1001466	31.340	22.324	20.480	15.496	3.611	15.533	10.020	13.761
HEMBB1001482	12.741	4.057	9.987	4.175	4.887	24.039	4.114	4.470
HEMBB1001500	26.823	21.417	65.107	17.492	9.196	12.958	6.167	14.603
HEMBB1001505	116.783	105.297	302.199	104.682	36.419	54.346	38.027	46.591
HEMBB1001521	55.379	38.602	133.188	25.792	20.204	23.504	18.628	22.786
HEMBB1001527	331.186	160.160	252.225	131.308	116.694	179.333	72.732	79.869
HEMBB1001530	24.722	25.693	57.090	19.457	7.662	20.875	31.031	23.503
HEMBB1001531	43.913	51.679	130.225	34.674	21.061	27.704	18.966	32.578
HEMBB1001532	6.957	3.901	34.322	7.593	1.875	8.172	300.808	7.501
HEMBB1001535	71.654	59.202	131.794	46.369	28.936	34.644	21.690	23.017
HEMBB1001536	73.109	48.204	106.813	35.175	16.411	22.356	19.126	20.785
HEMBB1001537	40.809	54.756	140.043	43.830	21.583	31.273	8.692	29.500
HEMBB1001542	79.436	33.152	94.294	34.360	26.100	44.300	19.679	22.657
HEMBB1001543	55.819	14.588	8.417	4.239	7.702	20.740	11.834	18.032
HEMBB1001547	10.746	8.433	12.415	9.202	10.101	15.047	10.631	8.198
HEMBB1001548	163.125	42.223	39.134	33.781	26.421	115.789	76.174	67.211
HEMBB1001551	32.248	10.176	8.937	9.728	20.037	69.247	7078.074	11.439
HEMBB1001555	62.998	58.959	166.842	57.865	40.731	30.981	17.189	40.721
HEMBB1001562	67.088	35.544	83.929	24.475	18.852	28.472	27.682	23.295
HEMBB1001564	139.467	320.422	580.390	304.052	124.857	300.720	202.502	439.361
HEMBB1001565	56.749	43.545	123.727	39.891	29.530	30.029	17.527	28.501
HEMBB1001569	34.482	26.904	100.487	28.883	16.462	19.020	8.403	16.605
HEMBB1001573	48.940	40.308	65.598	41.979	32.247	35.238	25.583	36.979
HEMBB1001585	153.364	57.831	211.685	61.076	40.832	38.446	18.915	42.636
HEMBB1001586	44.946	40.343	113.224	34.426	18.386	24.673	16.535	26.124
HEMBB1001588	157.947	130.811	402.650	111.293	69.831	80.240	46.050	75.499
HEMBB1001595	12.602	11.160	44.464	13.949	6.811	11.538	4.359	11.569
HEMBB1001596	53.986	20.798	39.629	25.473	20.578	32.621	23.309	36.564
HEMBB1001599	29.275	7.352	13.267	11.568	5.279	15.756	10.260	5.135
HEMBB1001603	3.581	2.642	7.782	4.279	3.051	0.341	1.424	3.160
HEMBB1001606	6.897	7.220	7.226	7.657	3.104	5.383	5.658	4.364
HEMBB1001612	101.576	58.128	240.469	58.770	36.287	42.917	27.221	40.063
HEMBB1001618	52.604	38.648	141.745	37.723	24.274	24.922	17.197	24.223
HEMBB1001619	59.431	78.268	138.545	63.285	52.275	37.035	22.185	38.081
HEMBB1001623	33.128	8.489	11.122	6.318	8.326	16.007	3.331	7.918
HEMBB1001625	10.068	16.076	8.496	7.577	2.293	8.389	1.716	4.647
HEMBB1001630	7.144	5.464	31.186	8.383	3.256	11.196	3.053	5.942
HEMBB1001635	18.151	8.186	33.138	13.501	9.143	9.688	44.037	8.859
HEMBB1001637	40.224	35.174	58.964	24.082	26.640	26.340	20.792	26.243
HEMBB1001641	21.655	10.768	33.553	9.122	5.845	7.210	5.796	8.300
HEMBB1001653	76.468	45.984	138.114	33.606	30.023	33.136	16.720	25.949
HEMBB1001665	3.000	0.352	5.654	0.275	0.718	0.106	0.899	0.407
HEMBB1001666	48.027	23.276	59.669	22.201	9.196	20.512	10.659	15.687
HEMBB1001667	2.570	7.909	3.107	5.847	8.690	2.748	1.999	8.738
HEMBB1001668	2.545	8.886	13.392	8.498	18.131	3.355	1.531	3.932
HEMBB1001669	5.751	5.364	10.395	3.219	4.970	5.110	4.341	2.139
HEMBB1001670	17.795	10.903	34.891	20.715	11.725	22.401	12.909	20.514
HEMBB1001673	69.924	44.194	58.806	53.036	21.640	40.433	25.038	49.339
HEMBB1001675	58.961	13.650	21.648	10.914	9.356	22.270	15.894	11.977
HEMBB1001679	51.245	9.166	29.461	6.718	11.101	24.642	13.266	4.383
HEMBB1001684	27.854	11.218	30.139	14.666	11.546	25.422	15.072	13.683
HEMBB1001685	9.626	8.721	34.446	7.134	4.659	1.316	3.180	6.172
HEMBB1001695	2.706	4.723	4.741	1.162	8.059	1.109	1.036	1.119
HEMBB1001703	116.774	37.756	115.693	36.901	34.790	69.383	44.901	43.576
HEMBB1001704	67.385	52.606	211.228	52.452	40.406	43.432	33.952	54.662
HEMBB1001706	122.282	70.476	227.746	77.627	63.608	53.010	38.740	56.789
HEMBB1001707	111.416	69.815	154.286	51.656	60.773	50.260	33.306	43.746
HEMBB1001717	14.112	16.260	60.454	10.609	5.688	9.921	4.816	8.073
HEMBB1001731	29.550	36.222	21.992	33.872	22.551	35.654	37.976	32.089
HEMBB1001734	75.818	39.477	107.419	26.507	15.856	20.715	17.010	17.320
HEMBB1001735	63.245	22.136	169.823	34.289	26.478	18.371	17.292	27.924
HEMBB1001736	20.722	18.061	27.944	17.598	12.534	9.551	10.504	13.178
HEMBB1001747	21.158	15.281	18.501	9.967	9.806	11.088	17.268	12.572
HEMBB1001749	89.421	90.342	429.206	126.585	53.728	56.733	28.560	64.467

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Table 46

HEMB81001753	85.135	63.020	101.881	44.766	60.100	46.138	48.988	44.990
HEMB81001756	86.556	37.048	83.531	33.276	42.763	54.273	32.005	30.821
HEMB81001757	1.981	3.522	5.232	3.590	1.394	7.486	3.256	3.014
HEMB81001760	13.573	14.554	27.053	7.204	5.280	8.129	5.242	4.088
HEMB81001762	26.210	15.945	24.826	8.467	6.461	26.934	6.893	9.656
HEMB81001780	18.738	33.363	27.562	17.311	13.893	4.277	14.584	19.429
HEMB81001785	3.266	2.954	7.974	3.522	3.900	7.429	3.964	4.008
HEMB81001788	77.710	51.716	232.298	72.096	40.555	41.418	29.586	33.423
HEMB81001793	221.348	29.215	45.528	20.500	22.918	33.927	36.095	25.245
HEMB81001797	4.049	9.015	10.442	4.015	2.532	8.773	2.904	6.333
HEMB81001802	430.563	24.213	34.832	14.183	17.392	26.448	23.001	29.744
HEMB81001812	91.804	71.389	218.174	56.457	56.645	54.459	15.772	55.255
HEMB81001815	506.853	426.652	275.995	120.005	129.468	289.852	148.011	122.368
HEMB81001816	90.696	55.478	178.334	52.637	25.170	45.331	35.194	47.899
HEMB81001831	22.874	14.551	46.474	16.825	9.329	19.975	9.745	18.634
HEMB81001834	456.615	299.793	406.927	241.146	284.283	499.103	267.485	306.611
HEMB81001836	138.292	91.469	348.309	101.544	73.058	67.103	40.539	76.261
HEMB81001839	9.720	6.600	7.318	0.000	2.606	4.296	2.217	2.738
HEMB81001841	345.524	134.230	67.049	25.938	60.560	21.530	21.177	18.486
HEMB81001844	61.041	25.820	34.819	14.237	14.648	34.333	20.655	31.102
HEMB81001847	126.241	111.341	239.722	147.873	65.849	86.164	47.980	108.378
HEMB81001848	40.802	39.856	24.837	12.646	9.727	18.893	18.093	17.754
HEMB81001850	171.151	101.141	118.680	33.622	64.050	118.364	50.599	75.857
HEMB81001859	133.676	77.853	231.163	65.024	41.660	123.173	103.961	48.695
HEMB81001863	115.353	92.421	255.141	83.601	85.833	53.693	30.832	49.888
HEMB81001867	15.427	15.822	8.336	10.061	4.673	8.415	6.299	9.816
HEMB81001868	24.470	17.457	24.238	7.996	8.810	8.133	10.520	11.923
HEMB81001869	82.894	76.711	234.322	61.007	44.801	45.547	29.853	39.008
HEMB81001872	15.921	7.288	5.998	10.151	2.561	5.674	9.542	5.964
HEMB81001874	36.336	11.065	22.113	15.221	9.515	14.138	6.058	5.891
HEMB81001875	7.615	19.234	13.755	26.314	11.646	3.662	5.863	7.228
HEMB81001880	107.638	82.806	115.014	59.163	39.712	47.440	27.454	37.214
HEMB81001899	15.785	11.630	15.181	7.571	2.259	12.203	4.190	3.366
HEMB81001903	59.215	24.149	27.564	15.205	8.601	28.805	15.592	15.765
HEMB81001905	29.932	24.402	20.256	15.117	8.559	17.138	12.021	12.009
HEMB81001906	15.456	13.077	51.260	10.147	16.547	10.906	7.943	9.129
HEMB81001908	35.095	32.316	100.465	26.514	24.742	20.649	8.759	14.223
HEMB81001910	67.419	35.922	139.126	58.266	43.100	26.178	19.330	29.710
HEMB81001911	50.456	46.682	196.311	58.337	31.782	35.278	19.934	32.009
HEMB81001915	40.796	27.017	19.351	20.885	15.345	12.662	9.798	36.052
HEMB81001921	95.398	115.190	314.157	85.049	59.940	59.397	36.034	60.585
HEMB81001922	54.587	37.299	107.814	29.796	15.712	23.741	15.662	16.568
HEMB81001925	35.478	39.156	106.631	23.241	15.055	16.405	13.936	15.471
HEMB81001930	9.272	7.467	11.545	7.045	3.402	5.636	2.969	5.808
HEMB81001944	122.259	83.163	268.572	86.582	66.995	51.236	27.262	45.542
HEMB81001945	55.555	20.668	28.702	7.169	21.076	24.208	18.042	10.472
HEMB81001947	47.254	12.987	21.887	16.223	6.133	25.673	16.697	13.440
HEMB81001950	99.345	31.711	42.202	32.724	17.168	68.211	28.763	30.429
HEMB81001952	67.117	40.169	164.691	39.168	16.287	31.103	11.276	24.511
HEMB81001953	56.049	47.572	147.635	34.659	22.662	21.660	13.445	22.280
HEMB81001957	43.669	20.350	106.261	26.369	16.837	16.589	5.199	12.837
HEMB81001959	26.731	45.573	72.402	48.003	21.477	24.564	17.194	36.361
HEMB81001962	59.585	38.413	125.747	48.471	52.786	46.598	20.834	29.320
HEMB81001967	156.252	96.306	460.639	121.361	89.090	70.066	46.606	68.839
HEMB81001973	62.418	55.111	203.353	61.777	40.564	39.531	24.193	43.482
HEMB81001978	205.611	67.998	184.804	55.506	42.195	56.711	62.043	55.171
HEMB81001983	115.219	97.908	189.950	79.417	69.496	62.957	41.995	65.291
HEMB81001987	23.094	30.009	63.743	16.838	10.970	10.414	5.543	10.645
HEMB81001988	26.549	17.876	71.399	12.651	11.631	11.873	6.563	10.248
HEMB81001990	61.049	28.808	125.791	31.477	30.752	26.525	9.894	24.366
HEMB81001996	40.435	12.303	17.096	14.159	3.837	18.573	11.696	13.433
HEMB81001997	91.453	62.313	247.838	64.724	40.131	29.522	27.492	42.942
HEMB81001999	28.583	9.839	33.748	34.520	11.455	23.048	14.798	25.158
HEMB81002002	19.354	10.115	14.415	9.527	16.781	12.044	7.088	14.724

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Table 47

HEMBB1002005	127.202	87.407	314.165	82.406	66.505	55.577	40.792	64.185
HEMBB1002009	0.000	1.364	22.770	0.807	4.369	1.295	0.000	0.000
HEMBB1002013	28.258	13.676	16.813	10.399	10.765	17.046	7.782	9.691
HEMBB1002015	105.576	48.524	66.937	36.377	38.220	74.637	28.221	34.621
HEMBB1002024	216.724	27.841	16.159	12.961	10.268	16.725	13.378	30.580
HEMBB1002035	46.139	20.267	93.090	25.830	19.155	14.290	9.089	10.861
HEMBB1002039	56.819	33.510	91.779	23.686	12.816	13.451	13.710	16.666
HEMBB1002041	64.639	34.426	51.061	22.611	27.241	31.364	25.209	28.240
HEMBB1002042	108.989	70.262	244.087	61.596	54.097	58.195	45.407	53.478
HEMBB1002043	45.022	36.752	179.777	48.242	21.779	25.603	30.919	28.446
HEMBB1002044	13.181	2.012	5.797	1.053	1.982	1.313	3.432	2.045
HEMBB1002045	289.530	197.322	441.790	143.182	150.349	206.083	108.290	118.515
HEMBB1002049	35.193	24.481	83.015	26.999	19.710	27.535	16.278	24.921
HEMBB1002050	37.095	16.954	49.110	12.868	13.580	16.690	9.422	14.540
HEMBB1002051	36.389	19.655	68.218	18.665	8.800	22.352	16.403	17.616
HEMBB1002068	75.935	30.174	53.312	27.588	23.758	28.553	40.522	36.664
HEMBB1002069	213.038	176.212	471.114	127.141	113.252	145.813	82.555	84.929
HEMBB1002075	42.631	31.316	161.071	28.782	21.239	25.996	13.087	18.589
HEMBB1002079	16.958	10.592	15.974	7.658	4.913	11.054	12.406	9.170
HEMBB1002080	43.775	32.579	72.576	24.001	9.827	28.608	17.214	17.433
HEMBB1002082	26.775	8.257	21.193	4.448	6.280	19.090	464.903	8.346
HEMBB1002084	17.127	6.840	43.925	4.043	9.757	26.316	9.627	6.512
HEMBB1002088	90.318	38.977	65.816	40.755	47.974	81.367	57.452	75.281
HEMBB1002092	192.949	59.522	268.965	49.978	47.797	60.595	48.524	38.080
HEMBB1002094	127.875	84.707	379.671	89.066	80.779	70.636	38.807	57.037
HEMBB1002103	29.830	9.307	18.867	12.419	117.011	11.825	10.555	6.133
HEMBB1002109	28.380	23.579	104.568	24.307	17.018	17.089	11.301	21.844
HEMBB1002115	71.073	86.440	117.523	95.976	28.307	85.908	60.445	114.378
HEMBB1002120	16.393	10.090	4.147	2.085	3.568	9.594	4.954	4.539
HEMBB1002121	12.050	2.757	6.522	1.146	2.007	0.000	1.999	1.549
HEMBB1002134	784.781	365.377	605.805	262.168	223.204	719.592	534.370	450.949
HEMBB1002136	109.220	32.405	75.010	27.402	26.278	36.231	38.283	23.593
HEMBB1002138	17.812	14.057	17.210	7.413	9.287	10.613	20.319	9.644
HEMBB1002139	51.267	37.549	168.617	27.467	17.855	27.091	16.428	23.177
HEMBB1002141	82.369	29.424	54.387	14.566	15.214	39.768	33.139	22.856
HEMBB1002142	70.553	42.309	156.252	36.636	14.797	26.769	15.277	22.894
HEMBB1002145	40.661	16.263	15.725	8.229	13.984	21.757	14.873	15.525
HEMBB1002152	46.728	36.893	105.608	65.422	40.064	25.225	29.211	42.935
HEMBB1002162	40.153	34.008	96.274	29.709	19.847	47.860	22.055	40.550
HEMBB1002173	53.191	41.151	147.055	26.912	34.538	16.431	19.449	25.327
HEMBB1002189	73.406	88.057	211.287	73.810	54.029	46.682	45.749	55.885
HEMBB1002190	33.242	51.561	233.972	49.809	19.665	27.376	13.129	61.389
HEMBB1002193	69.174	22.324	33.672	10.803	18.423	27.938	24.748	16.109
HEMBB1002217	50.175	37.602	98.092	38.769	24.723	33.043	18.735	39.436
HEMBB1002218	596.902	272.867	712.867	191.461	186.314	373.711	195.571	197.556
HEMBB1002228	88.583	45.763	205.932	47.852	46.693	41.923	37.485	53.876
HEMBB1002232	56.752	32.790	128.643	36.535	28.693	32.710	31.447	41.940
HEMBB1002245	31.084	9.332	17.943	11.049	11.834	11.864	17.012	14.199
HEMBB1002247	151.502	27.325	64.167	10.018	26.829	62.501	35.734	21.698
HEMBB1002249	153.327	94.814	380.989	101.573	65.579	80.049	62.653	85.673
HEMBB1002254	43.885	36.758	118.582	29.328	19.323	11.675	12.693	22.229
HEMBB1002255	8.633	2.293	14.174	8.771	1.813	2.385	3.358	3.589
HEMBB1002266	5.303	5.716	8.530	6.222	1.842	2.404	4.411	2.295
HEMBB1002271	160.682	46.654	157.828	58.291	63.843	72.913	62.659	73.702
HEMBB1002280	24.597	13.246	76.763	13.976	7.742	9.196	9.200	16.479
HEMBB1002296	67.004	21.270	52.536	34.388	49.938	53.045	123.030	41.218
HEMBB1002300	94.815	28.682	50.102	35.939	13.923	29.792	25.246	21.629
HEMBB1002302	51.059	31.157	28.441	17.568	17.905	26.026	22.516	30.501
HEMBB1002306	35.213	49.812	33.017	23.300	15.072	17.296	14.490	16.293
HEMBB1002316	19.773	8.638	19.354	3.667	9.274	9.974	8.613	6.883
HEMBB1002326	201.896	126.797	406.052	154.628	89.356	85.970	54.052	98.198
HEMBB1002327	85.792	48.221	184.126	47.724	32.764	29.959	17.415	34.542
HEMBB1002329	69.191	21.714	43.746	25.618	17.775	24.892	32.481	27.906
HEMBB1002340	18.233	28.462	7.730	3.702	3.055	4.522	2.914	5.745

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Table 48

HEMBB1002342	74.746	83.579	169.482	40.919	23.495	26.453	33.215	66.420
HEMBB1002358	149.857	132.962	286.214	85.160	50.855	67.646	36.624	78.432
HEMBB1002359	160.804	77.260	219.199	68.995	44.093	58.049	35.955	51.139
HEMBB1002364	102.885	74.409	188.270	50.973	55.276	45.770	40.780	59.739
HEMBB1002366	152.074	77.016	248.465	68.268	81.100	64.637	39.912	60.303
HEMBB1002371	44.433	12.342	26.565	13.307	36.600	10.553	9.238	5.351
HEMBB1002381	134.427	77.953	207.310	57.210	48.215	64.049	51.493	77.629
HEMBB1002383	164.205	52.312	94.064	31.346	31.368	30.947	43.038	47.640
HEMBB1002387	196.859	164.904	235.139	49.485	25.102	93.004	52.536	43.092
HEMBB1002409	82.986	49.978	112.097	29.207	15.402	37.667	36.064	38.132
HEMBB1002413	123.367	87.690	361.106	87.505	57.485	48.097	23.254	49.302
HEMBB1002415	87.091	31.703	92.595	31.804	23.352	27.293	21.815	24.444
HEMBB1002424	13.162	19.511	15.995	5.848	21.533	16.980	18.246	25.253
HEMBB1002425	84.086	69.689	238.147	82.198	36.928	41.171	26.823	47.957
HEMBB1002427	143.727	26.894	50.430	25.865	40.707	52.937	38.610	47.517
HEMBB1002442	163.853	121.153	501.168	129.909	73.231	81.033	47.108	287.238
HEMBB1002447	107.214	80.007	214.338	58.963	41.313	60.452	49.159	44.523
HEMBB1002453	163.250	93.442	384.443	93.027	68.808	58.555	46.254	58.810
HEMBB1002457	116.756	104.520	330.657	83.026	46.720	50.971	38.415	57.991
HEMBB1002458	18.721	11.278	23.232	9.587	7.205	6.051	4.659	4.343
HEMBB1002463	229.657	146.001	663.683	193.622	138.458	104.827	52.827	110.558
HEMBB1002465	44.210	23.316	33.631	20.895	17.932	26.471	19.122	19.703
HEMBB1002477	98.948	27.813	153.875	11.062	36.071	16.072	13.791	8.347
HEMBB1002479	23.249	59.003	73.224	14.014	10.084	13.246	1.980	8.949
HEMBB1002489	78.748	24.690	71.038	31.400	39.869	43.673	44.800	75.957
HEMBB1002492	9.080	6.989	26.130	3.092	1.453	5.606	1.415	2.381
HEMBB1002495	95.752	104.949	301.328	60.728	72.404	45.161	24.771	61.121
HEMBB1002502	17.132	17.866	14.643	16.170	15.224	14.056	4.504	23.313
HEMBB1002509	0.913	2.235	7.269	4.304	0.743	1.283	1.504	6.154
HEMBB1002510	0.732	0.000	0.000	1.858	0.926	0.000	0.000	0.000
HEMBB1002520	249.875	127.604	585.470	169.423	138.712	90.360	100.598	112.828
HEMBB1002522	24.741	27.480	12.342	14.142	17.462	5.861	8.292	8.541
HEMBB1002527	63.012	61.066	87.388	46.392	29.555	37.187	25.642	36.089
HEMBB1002530	72.655	45.682	83.329	21.750	21.479	53.227	440.333	38.710
HEMBB1002531	40.398	18.832	10.308	9.953	5.539	16.743	11.880	8.115
HEMBB1002534	78.552	49.139	154.741	68.211	30.154	46.591	28.712	37.112
HEMBB1002536	27.609	22.843	52.264	17.646	8.234	13.078	23.458	15.919
HEMBB1002544	24.012	6.185	27.814	13.117	39.363	15.921	9.427	14.017
HEMBB1002545	108.234	31.929	243.949	50.972	16.032	40.343	31.828	13.472
HEMBB1002550	31.850	11.452	10.668	11.228	11.049	10.100	14.262	14.910
HEMBB1002556	125.621	89.607	311.607	79.974	50.209	57.837	53.696	54.119
HEMBB1002571	33.047	21.526	54.457	14.847	25.892	21.961	5.482	18.608
HEMBB1002579	75.252	55.132	229.479	48.891	31.521	43.266	24.667	31.554
HEMBB1002582	100.572	56.574	258.453	63.093	45.740	39.580	26.474	45.912
HEMBB1002584	8.325	7.614	13.574	6.883	1.796	7.855	6.183	4.955
HEMBB1002587	57.430	44.383	60.900	47.981	30.048	30.562	19.161	20.854
HEMBB1002590	114.241	78.587	179.926	65.737	28.629	43.657	33.101	34.032
HEMBB1002596	278.617	90.944	275.018	69.006	68.247	114.505	88.149	59.750
HEMBB1002600	17.618	16.003	23.907	4.699	9.726	10.133	7.945	8.940
HEMBB1002601	67.910	48.188	183.948	45.346	38.021	37.423	21.860	31.698
HEMBB1002603	69.793	43.222	141.343	36.733	28.849	35.264	22.033	29.436
HEMBB1002607	64.941	36.284	134.598	39.424	22.220	31.501	15.575	31.024
HEMBB1002610	22.852	9.200	51.294	16.832	6.664	12.856	6.433	6.515
HEMBB1002613	85.026	60.872	161.891	47.532	36.559	44.841	24.569	31.062
HEMBB1002614	65.074	30.721	39.687	10.970	15.910	13.297	10.461	5.438
HEMBB1002615	230.370	55.581	35.517	11.758	7.258	46.064	22.857	86.789
HEMBB1002617	69.016	67.288	254.296	42.530	30.217	36.395	21.284	37.688
HEMBB1002623	92.506	78.124	204.116	60.739	20.110	48.078	32.253	43.355
HEMBB1002624	77.755	27.026	163.976	33.209	25.309	20.104	21.741	24.486
HEMBB1002631	10.297	18.892	12.879	14.916	7.219	5.864	6.990	11.537
HEMBB1002636	88.049	68.172	141.149	41.853	40.290	23.649	21.781	44.425
HEMBB1002644	98.956	65.380	26.659	19.268	9.200	38.890	35.668	29.597
HEMBB1002654	127.571	78.659	51.653	28.747	32.125	137.732	315.048	39.477
HEMBB1002661	106.501	46.651	47.116	19.470	20.684	30.561	24.281	118.028

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Table 49

HEMBB1002663	100.783	42.600	100.008	36.841	24.382	35.028	41.975	18.150
HEMBB1002664	179.828	131.008	395.057	51.235	74.731	89.130	40.814	55.262
HEMBB1002677	2.206	3.466	5.138	4.981	2.314	4.033	3.301	1.422
HEMBB1002683	118.247	69.327	247.117	55.886	44.381	26.944	27.017	42.278
HEMBB1002684	40.291	21.056	46.317	17.772	9.039	5.460	8.120	14.377
HEMBB1002686	30.893	12.882	26.031	19.059	3.146	12.807	18.055	9.131
HEMBB1002692	48.969	24.335	52.440	29.779	19.960	25.893	38.755	15.268
HEMBB1002693	129.760	76.886	322.740	70.620	62.314	67.760	73.429	39.005
HEMBB1002697	41.673	38.793	25.105	8.999	2.058	7.613	10.266	29.797
HEMBB1002699	223.756	165.884	369.080	116.529	77.378	109.419	79.393	99.532
HEMBB1002702	13.506	15.782	24.367	3.561	6.434	15.699	13.253	24.914
HEMBB1002705	29.934	20.276	16.478	21.230	7.599	11.487	18.202	30.589
HEMBB1002712	29.588	10.805	47.572	15.673	13.434	15.691	7.559	16.536
IMR3210000028	77.081	39.937	40.934	18.725	8.281	41.195	27.733	21.472
IMR3210000031	50.644	21.357	34.754	22.184	15.786	31.242	22.705	14.148
IMR3210000034	76.518	63.230	37.290	51.243	23.808	43.858	26.605	67.455
IMR3210000039	66.895	68.027	83.136	36.653	27.339	62.232	57.760	88.100
IMR3210000044	1.614	0.000	0.000	0.000	0.000	0.000	1.970	0.000
IMR3210000063	131.633	84.822	66.499	84.753	43.262	73.363	69.831	80.878
IMR3210000085	157.704	34.180	42.747	11.752	50.766	66.106	54.160	47.424
IMR3210000089	52.645	22.980	31.408	17.365	13.731	36.296	27.222	10.181
IMR3210000091	39.993	32.664	43.895	41.311	25.143	35.002	20.444	63.906
LIVER1000004	45.674	30.112	69.445	16.874	11.073	28.505	106.044	24.660
LIVER1000008	23.703	14.444	22.304	9.381	15.657	274.776	344.333	11.282
LIVER1000011	107.957	31.187	106.032	30.434	41.030	41.256	348.474	63.939
LIVER1000022	402.839	177.843	270.232	82.143	125.292	206.780	141.934	124.260
LIVER1000025	61.584	42.776	172.307	36.300	26.856	33.045	34.820	42.189
LIVER1000030	62.987	24.034	69.275	29.784	17.581	22.393	51.178	22.556
LIVER1000045	27.941	4.859	27.468	7.384	9.755	14.426	20.651	24.802
LIVER1000046	180.297	117.998	24.240	23.527	16.373	7.466	27.795	66.724
LIVER1000072	24.097	35.964	6.976	11.158	7.657	8.260	16.555	4.898
LIVER1000077	90.518	39.165	17.306	13.193	25.835	52.139	348.056	37.506
LIVER1000080	17.084	4.918	5.980	9.600	2.294	5.176	6.495	4.479
LIVER1000085	82.711	55.169	150.708	18.858	19.278	176.018	481.085	27.747
LIVER1000092	61.883	36.836	116.592	27.330	16.805	25.266	35.863	24.160
LIVER1000095	54.562	13.959	104.146	23.878	13.158	200.163	137.395	5.508
LIVER1000097	138.286	11.401	12.265	8.127	9.389	9.669	32.751	7.159
LIVER1000098	58.055	39.291	47.410	18.991	19.124	20.338	142.508	19.104
LIVER1000100	81.693	64.546	94.504	29.185	18.588	42.254	23.727	58.633
LIVER1000101	52.507	16.303	57.500	10.286	8.662	17.642	6.129	27.273
LIVER1000108	46.259	32.121	32.438	11.568	9.377	13.216	102.126	16.904
LIVER1000108	26.277	50.565	62.172	25.422	16.619	17.243	38.369	18.508
LIVER1000115	23.571	18.673	71.367	14.244	11.023	17.910	427.626	11.136
LIVER1000120	100.902	21.640	35.183	16.565	26.236	39.037	87.151	16.249
LIVER1000138	69.624	27.584	56.479	22.794	25.076	42.015	35.937	23.833
LIVER1000146	107.757	63.296	209.735	54.534	42.231	45.210	254.168	42.466
LIVER1000148	141.467	42.327	108.510	37.031	31.920	62.584	125.466	65.728
LIVER1000157	97.282	37.198	50.979	49.952	35.021	43.954	52.527	43.221
LIVER1000161	100.902	24.883	57.647	28.329	31.562	42.781	89.198	30.740
LIVER1000167	97.214	29.093	41.460	25.700	26.316	112.706	332.789	30.702
LIVER1000174	53.927	23.440	26.353	13.595	12.625	36.580	71.460	10.512
LIVER1000185	49.746	20.428	31.630	13.964	13.391	16.773	16.676	14.878
LIVER1000187	38.332	8.211	15.200	4.654	8.084	9.846	567.808	8.320
LIVER1000190	93.672	29.635	50.518	15.812	18.768	23.709	41.865	11.496
LIVER1000192	141.875	53.337	99.330	32.936	41.210	79.500	128.608	47.907
MAMMA1000009	99.036	77.266	234.005	72.924	40.612	44.930	25.218	35.909
MAMMA1000015	40.458	7.192	19.901	13.017	12.921	18.315	13.014	8.185
MAMMA1000019	62.999	29.927	150.049	52.037	36.450	42.958	38.148	30.172
MAMMA1000020	58.696	30.055	181.093	40.615	38.572	34.176	18.169	20.807
MAMMA1000024	15.610	5.088	15.411	7.263	3.468	11.662	37.960	9.224
MAMMA1000025	53.706	37.358	123.944	37.766	29.177	24.650	18.530	21.156
MAMMA1000043	170.220	108.774	290.077	126.472	100.059	82.087	70.843	76.243
MAMMA1000045	83.118	48.873	22.107	10.125	5.779	15.440	7.895	8.811
MAMMA1000046	117.084	44.858	285.890	66.458	43.862	36.388	23.428	22.376

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Table 50

MAMMA1000055	65.118	40.884	57.307	29.859	27.445	33.405	22.066	23.563
MAMMA1000057	170.331	108.479	421.160	100.366	84.331	77.475	42.047	55.847
MAMMA1000060	79.698	50.265	153.319	49.223	28.927	42.539	25.636	52.458
MAMMA1000069	118.921	35.010	182.272	48.764	43.720	61.342	45.357	33.115
MAMMA1000084	128.354	92.819	277.404	87.542	63.176	65.262	34.266	45.092
MAMMA1000085	40.199	20.019	40.608	21.956	13.181	18.822	36.347	26.209
MAMMA1000092	77.338	37.915	167.474	43.988	16.101	26.961	15.531	22.390
MAMMA1000096	55.344	38.495	38.888	25.605	11.893	44.990	24.784	25.160
MAMMA1000097	62.546	54.694	52.522	52.269	24.807	65.730	25.787	23.238
MAMMA1000102	67.585	32.797	91.551	31.689	19.430	26.892	22.353	16.842
MAMMA1000103	63.752	26.301	89.530	30.004	12.188	31.709	11.461	14.718
MAMMA1000106	37.916	23.228	90.795	22.075	14.445	24.686	16.649	17.569
MAMMA1000117	58.533	24.502	43.190	22.445	16.140	27.418	15.487	13.269
MAMMA1000118	104.168	58.433	63.822	8.833	24.039	42.731	38.062	43.242
MAMMA1000129	170.665	72.256	98.813	45.970	22.181	58.739	50.197	14.587
MAMMA1000133	62.435	25.090	33.061	20.713	14.310	34.686	18.642	14.101
MAMMA1000134	106.522	79.090	246.344	90.530	127.758	76.596	45.325	60.360
MAMMA1000139	78.566	47.362	99.179	34.535	22.772	37.601	28.841	28.280
MAMMA1000141	30.121	20.528	28.150	13.910	5.510	14.314	12.120	15.748
MAMMA1000143	16.647	8.669	41.797	8.690	9.949	10.059	4.040	8.280
MAMMA1000150	128.128	259.413	21.844	28.777	86.623	42.827	51.840	42.986
MAMMA1000155	205.031	88.642	291.247	110.884	80.817	97.755	63.045	78.585
MAMMA1000163	43.643	36.898	57.239	22.848	21.852	41.672	11.036	10.618
MAMMA1000171	141.225	46.928	265.746	98.189	60.007	66.037	34.872	50.109
MAMMA1000173	103.027	21.955	68.080	33.572	25.668	45.271	40.340	52.609
MAMMA1000175	19.316	8.683	7.960	4.550	3.535	7.894	5.974	4.015
MAMMA1000183	57.490	35.830	148.702	42.892	23.250	23.680	21.050	46.992
MAMMA1000191	88.722	31.449	40.834	26.064	22.392	26.766	36.253	27.729
MAMMA1000192	53.467	25.096	30.205	28.380	21.976	101.288	128.339	44.025
MAMMA1000193	83.936	36.823	36.836	29.409	18.905	35.131	35.059	36.667
MAMMA1000196	132.127	93.550	347.292	70.840	49.278	62.924	38.858	66.720
MAMMA1000204	64.455	59.079	71.789	26.771	29.275	55.156	62.132	49.295
MAMMA1000207	45.771	62.052	52.332	19.986	16.418	37.618	225.196	18.506
MAMMA1000214	100.292	62.311	289.223	62.541	32.825	57.748	32.755	39.770
MAMMA1000220	91.389	23.816	43.034	13.919	12.649	42.421	29.143	20.494
MAMMA1000221	39.338	35.655	11.931	39.315	9.426	18.802	27.741	17.121
MAMMA1000226	65.096	20.174	11.901	11.838	17.236	23.487	43.016	24.801
MAMMA1000227	94.333	64.156	183.365	82.763	58.478	66.811	43.961	53.250
MAMMA1000230	116.378	47.908	97.869	47.218	38.196	56.380	71.726	37.727
MAMMA1000241	53.737	85.177	107.748	60.815	31.230	51.839	36.525	22.770
MAMMA1000245	107.413	148.468	205.417	144.478	51.682	86.017	93.183	198.398
MAMMA1000248	205.478	88.411	342.827	76.468	51.702	110.723	70.650	60.978
MAMMA1000251	115.401	47.888	209.360	39.959	42.597	57.904	34.572	51.015
MAMMA1000254	43.161	20.910	114.081	20.548	9.699	9.885	5.348	32.024
MAMMA1000257	142.781	70.118	332.822	104.425	84.387	124.673	78.270	116.103
MAMMA1000262	18.952	34.301	19.786	32.516	14.840	15.513	23.805	35.519
MAMMA1000264	59.532	20.630	124.043	44.847	29.466	21.390	22.616	37.039
MAMMA1000266	55.476	28.959	122.654	35.663	27.018	24.021	20.212	38.284
MAMMA1000270	142.968	64.234	270.948	75.022	64.760	68.130	64.006	73.994
MAMMA1000271	53.605	9.611	35.682	12.139	16.139	24.236	26.722	26.433
MAMMA1000277	56.407	16.435	98.448	19.751	12.725	33.047	23.839	33.012
MAMMA1000278	40.286	13.365	19.395	9.730	12.609	20.423	25.204	22.237
MAMMA1000279	68.661	36.984	173.379	46.809	34.441	42.500	26.143	48.597
MAMMA1000283	55.199	27.095	46.168	22.395	15.870	21.308	16.298	18.504
MAMMA1000284	76.726	67.676	42.784	39.851	34.586	47.651	39.169	48.342
MAMMA1000287	73.583	58.726	142.953	39.301	31.007	27.370	29.006	35.599
MAMMA1000294	457.450	361.106	313.407	116.696	112.848	343.951	155.948	100.375
MAMMA1000298	31.731	25.511	41.413	16.220	16.320	14.676	22.043	20.205
MAMMA1000302	109.379	58.532	280.880	69.156	44.790	36.788	28.220	40.861
MAMMA1000303	67.505	14.147	18.804	11.073	33.859	26.599	30.177	30.810
MAMMA1000305	32.363	19.693	108.733	15.375	12.695	14.455	13.353	15.189
MAMMA1000307	279.600	75.098	397.421	75.020	45.244	68.757	131.117	116.800
MAMMA1000309	11.679	39.455	13.529	3.502	3.904	8.895	10.500	6.744
MAMMA1000312	22.645	50.288	9.368	4.180	3.450	4.882	7.079	7.576

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Table 51

MAMMA1000313	79.577	69.550	54.317	10.741	60.526	42.964	18.206	37.303
MAMMA1000331	80.910	48.868	139.047	33.811	22.564	15.207	18.580	21.385
MAMMA1000335	54.800	22.399	33.190	18.244	16.273	30.688	26.611	30.790
MAMMA1000339	69.222	40.948	83.679	13.158	20.941	22.134	20.026	10.739
MAMMA1000340	57.498	34.708	164.968	32.922	28.610	23.069	18.858	23.519
MAMMA1000348	78.099	102.955	374.737	55.033	32.546	66.256	22.303	23.575
MAMMA1000356	152.238	116.086	454.516	67.232	34.525	47.884	22.865	61.267
MAMMA1000358	34.367	56.332	15.362	15.091	16.743	17.405	19.645	7.358
MAMMA1000360	71.104	74.351	246.244	43.414	24.093	24.945	14.842	14.739
MAMMA1000361	101.653	93.468	230.215	73.577	45.022	37.236	37.987	42.992
MAMMA1000363	71.108	19.232	39.013	13.717	23.713	30.739	27.813	32.485
MAMMA1000370	171.867	108.830	110.466	80.949	52.076	79.266	57.877	247.810
MAMMA1000371	100.543	32.223	80.873	48.039	49.442	91.739	57.647	46.599
MAMMA1000372	206.850	114.326	609.068	130.138	79.980	80.890	54.857	97.509
MAMMA1000385	72.074	60.911	238.462	40.061	34.528	31.361	22.458	45.681
MAMMA1000388	118.855	69.094	105.789	42.626	50.059	55.389	37.396	37.825
MAMMA1000395	97.031	44.493	34.493	20.201	19.036	27.695	24.269	17.433
MAMMA1000402	126.085	107.637	256.584	68.415	45.669	61.486	30.340	30.943
MAMMA1000403	87.558	63.749	208.574	64.857	45.578	44.799	22.710	42.239
MAMMA1000410	43.073	43.539	94.207	39.613	19.880	22.573	16.272	21.003
MAMMA1000413	30.829	13.370	70.418	17.102	13.392	15.291	11.599	15.353
MAMMA1000414	125.550	111.622	81.672	15.722	51.528	14.549	28.214	13.858
MAMMA1000416	179.864	103.793	427.214	107.383	105.899	121.441	55.040	84.667
MAMMA1000421	131.712	73.475	307.780	70.841	55.037	49.498	34.519	46.482
MAMMA1000422	12.614	14.628	30.167	16.100	11.675	22.441	18.843	54.831
MAMMA1000423	34.100	22.150	69.677	18.461	13.815	15.645	8.500	8.869
MAMMA1000424	9.330	4.056	36.234	8.171	0.971	2.769	0.745	7.267
MAMMA1000429	575.321	219.603	317.414	158.529	150.779	290.300	196.161	149.619
MAMMA1000431	143.825	79.993	275.497	82.499	52.496	63.425	43.337	66.733
MAMMA1000432	65.212	17.117	24.472	28.083	17.360	33.881	27.547	29.615
MAMMA1000437	89.375	88.947	265.572	60.025	69.885	45.195	30.823	31.510
MAMMA1000444	120.017	124.234	477.772	115.966	65.200	66.888	31.943	88.274
MAMMA1000446	50.201	66.027	41.406	8.991	18.971	29.395	7.985	37.220
MAMMA1000449	81.386	41.427	180.761	40.414	25.983	35.232	23.109	27.942
MAMMA1000457	47.862	13.862	15.095	11.981	7.566	21.142	12.971	10.872
MAMMA1000458	34.485	13.749	22.864	12.116	11.199	18.881	15.924	10.046
MAMMA1000468	8.235	7.843	6.029	5.004	5.503	8.258	7.138	1.618
MAMMA1000472	250.243	67.964	110.774	68.614	73.186	111.758	88.016	79.409
MAMMA1000473	54.174	16.506	40.489	16.002	17.450	26.506	17.741	13.900
MAMMA1000477	77.316	50.237	238.943	56.460	38.807	32.776	36.438	35.332
MAMMA1000478	201.299	157.097	496.514	127.872	82.832	77.444	49.296	86.763
MAMMA1000483	107.340	74.564	252.463	60.824	31.055	44.198	44.167	87.449
MAMMA1000490	14.473	14.068	16.023	12.496	8.202	15.654	11.091	12.344
MAMMA1000496	32.756	10.554	20.693	10.676	19.830	19.282	13.204	13.410
MAMMA1000500	23.016	17.584	49.151	15.706	13.914	19.063	11.094	22.904
MAMMA1000501	196.637	102.490	468.793	104.118	67.761	83.834	76.446	86.912
MAMMA1000503	7.083	4.085	3.866	1.004	1.005	3.752	4.005	3.248
MAMMA1000506	201.452	116.279	151.434	56.847	78.502	149.780	99.352	64.069
MAMMA1000510	70.898	18.432	60.927	39.187	33.327	42.829	40.993	33.127
MAMMA1000515	43.923	30.031	85.637	35.744	18.805	21.837	19.339	17.922
MAMMA1000516	74.742	48.811	148.307	43.452	18.069	34.061	19.122	26.985
MAMMA1000522	53.273	23.845	132.197	22.861	14.594	24.776	12.095	27.578
MAMMA1000524	130.806	61.389	266.529	71.558	50.972	73.691	47.484	55.510
MAMMA1000528	38.579	27.136	46.940	35.839	15.860	29.316	19.300	24.797
MAMMA1000534	32.603	20.088	33.950	10.973	7.185	10.580	7.972	10.160
MAMMA1000541	165.518	58.806	85.648	63.188	27.705	52.036	46.200	39.018
MAMMA1000550	119.597	203.059	41.184	24.393	5.859	48.433	766.194	63.005
MAMMA1000556	31.963	15.056	15.588	8.634	11.294	15.698	21.467	16.597
MAMMA1000559	57.738	31.181	242.155	29.443	19.030	26.908	13.520	41.571
MAMMA1000565	118.770	30.318	289.829	37.509	33.728	38.720	18.344	26.847
MAMMA1000567	77.050	44.379	224.645	48.804	41.102	56.039	36.496	63.529
MAMMA1000576	271.038	180.600	661.566	221.987	157.443	132.385	93.679	129.843
MAMMA1000582	54.936	43.406	272.366	14.342	18.896	29.396	46.333	40.210
MAMMA1000583	90.692	51.670	147.946	34.905	17.175	23.177	19.077	40.824

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Table 52

MAMMA1000585	89.865	50.008	288.673	52.259	29.243	39.188	24.088	46.734
MAMMA1000587	47.955	14.789	58.279	12.415	6.584	14.410	15.734	6.826
MAMMA1000591	77.705	38.280	81.784	28.019	20.094	28.578	24.299	19.949
MAMMA1000594	194.593	94.384	488.898	91.064	59.244	55.681	43.577	75.029
MAMMA1000597	496.923	264.906	751.636	196.294	121.483	306.397	199.968	160.426
MAMMA1000605	324.584	183.667	990.246	209.555	135.844	158.096	97.598	149.183
MAMMA1000612	68.113	22.051	42.999	14.074	19.294	41.220	29.460	15.713
MAMMA1000614	580.099	136.874	402.890	69.022	127.808	309.892	249.344	194.110
MAMMA1000616	2.590	16.442	13.809	1.109	3.011	7.500	3.036	3.188
MAMMA1000621	19.258	12.723	14.307	13.200	5.971	12.028	11.561	11.081
MAMMA1000623	60.189	23.285	25.913	12.057	10.648	23.327	19.218	20.667
MAMMA1000625	651.334	249.117	346.876	155.944	192.671	373.924	300.473	274.263
MAMMA1000635	4.459	2.994	4.756	2.883	0.000	4.118	5.584	9.542
MAMMA1000643	24.259	51.698	115.511	47.881	17.554	52.330	16.308	38.448
MAMMA1000646	72.487	111.121	22.868	9.213	27.074	81.604	46.859	34.048
MAMMA1000652	152.920	94.568	319.943	76.610	67.817	87.605	41.747	77.720
MAMMA1000657	116.830	41.097	278.504	38.131	36.289	67.327	34.224	32.593
MAMMA1000664	48.908	37.993	133.863	26.712	16.308	21.135	14.102	35.215
MAMMA1000667	77.285	24.312	99.732	25.027	29.493	43.769	22.193	24.502
MAMMA1000668	42.561	28.100	54.970	17.454	18.336	50.398	38.233	26.553
MAMMA1000669	22.797	14.382	57.803	14.670	6.337	12.841	7.392	12.088
MAMMA1000670	66.748	22.566	46.836	26.498	25.826	33.332	38.768	39.130
MAMMA1000672	128.331	25.209	67.913	35.262	28.783	64.713	38.934	40.592
MAMMA1000681	66.397	40.677	32.249	14.404	13.181	26.710	30.054	37.369
MAMMA1000684	85.908	107.381	66.100	35.992	32.881	41.006	36.719	77.834
MAMMA1000696	165.293	107.442	551.458	130.714	88.510	70.985	43.857	55.551
MAMMA1000702	82.316	25.689	52.797	22.639	22.884	48.899	39.297	29.636
MAMMA1000706	81.416	25.442	34.529	20.432	15.562	39.909	33.303	25.371
MAMMA1000707	128.277	17.100	51.835	15.001	33.473	48.628	46.555	24.075
MAMMA1000713	75.263	59.677	109.995	37.970	23.975	33.874	30.149	39.491
MAMMA1000714	228.366	288.017	246.261	56.045	25.380	80.480	51.219	64.589
MAMMA1000718	98.208	92.149	245.750	79.940	49.064	50.180	40.223	49.032
MAMMA1000720	158.737	111.227	446.586	101.175	73.612	78.021	29.904	60.252
MAMMA1000723	64.930	49.053	148.286	40.276	28.806	19.434	18.845	24.784
MAMMA1000731	31.516	11.357	68.834	12.436	11.755	7.989	7.536	7.367
MAMMA1000732	121.291	56.513	230.064	68.746	51.582	53.763	35.440	49.335
MAMMA1000733	24.525	14.171	58.717	16.852	7.153	14.100	8.586	10.632
MAMMA1000734	113.011	127.466	142.152	102.345	44.860	84.456	43.098	98.011
MAMMA1000736	142.978	48.490	130.520	34.595	40.252	73.418	82.810	69.461
MAMMA1000738	110.304	61.504	28.831	38.642	18.942	31.735	48.926	35.128
MAMMA1000744	140.264	94.669	281.287	76.261	79.000	63.977	43.557	40.380
MAMMA1000746	26.385	50.110	37.264	16.895	10.790	35.280	3.177	11.010
MAMMA1000748	73.879	36.619	52.587	30.957	36.810	46.899	25.359	24.846
MAMMA1000751	42.505	27.882	58.087	44.924	28.537	43.075	32.581	61.052
MAMMA1000752	55.785	55.799	193.100	53.436	25.798	29.655	21.969	44.384
MAMMA1000757	314.709	210.647	536.246	187.416	161.327	151.926	112.625	152.076
MAMMA1000760	218.937	178.377	534.346	131.736	100.173	95.443	58.158	91.220
MAMMA1000761	147.993	73.793	349.399	85.319	65.436	75.180	43.310	63.428
MAMMA1000775	75.873	25.684	170.040	34.150	30.063	20.938	15.825	18.992
MAMMA1000776	101.206	81.986	253.211	57.436	51.043	51.597	28.394	33.452
MAMMA1000778	71.839	47.596	214.100	42.749	28.124	29.701	17.866	26.497
MAMMA1000781	67.961	30.437	97.580	26.658	23.265	29.056	17.488	26.972
MAMMA1000782	286.062	65.796	174.951	84.753	88.062	151.891	90.446	86.369
MAMMA1000784	135.655	91.366	264.154	67.248	65.127	26.625	29.991	78.501
MAMMA1000788	143.478	49.979	98.983	34.503	30.600	55.026	29.032	46.210
MAMMA1000798	62.822	41.315	139.860	37.055	26.873	27.100	11.942	32.539
MAMMA1000802	132.633	86.328	341.638	76.811	64.234	64.772	38.532	61.561
MAMMA1000810	150.779	88.200	372.241	99.538	80.592	81.887	42.150	57.891
MAMMA1000813	31.571	14.636	31.497	9.531	9.356	14.627	12.633	10.718
MAMMA1000814	197.602	134.253	279.885	107.679	82.142	99.046	64.626	62.091
MAMMA1000824	65.693	21.602	64.020	38.421	35.405	29.268	31.671	38.813
MAMMA1000827	146.098	70.894	157.448	47.656	39.428	44.524	33.051	44.519
MAMMA1000831	55.332	19.954	29.847	13.557	9.407	21.580	16.602	6.497
MAMMA1000838	39.583	28.962	39.815	28.681	49.251	39.669	14.663	19.273

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Table 53

MAMMA1000839	157.898	138.792	503.964	113.084	86.648	85.964	57.386	102.963
MAMMA1000841	44.843	37.288	50.074	28.351	19.319	37.537	13.012	20.655
MAMMA1000842	174.347	36.747	169.008	44.926	48.610	78.492	50.804	35.389
MAMMA1000843	8.643	4.650	14.084	4.758	2.185	6.547	5.283	1.757
MAMMA1000845	40.044	33.955	33.012	21.488	15.747	23.310	17.728	15.607
MAMMA1000851	197.033	79.321	307.054	96.446	73.025	75.853	98.526	72.039
MAMMA1000854	66.548	33.221	63.298	17.429	20.157	33.288	22.320	21.685
MAMMA1000855	10.264	4.185	17.702	3.794	3.995	2.454	9.158	3.568
MAMMA1000856	186.269	40.945	84.561	27.973	38.378	82.629	60.529	25.726
MAMMA1000859	64.234	121.939	60.662	34.958	42.945	39.557	20.320	33.032
MAMMA1000862	40.107	21.345	23.693	16.808	28.277	22.661	14.238	14.693
MAMMA1000863	98.576	70.285	234.996	67.796	55.216	72.466	36.802	70.885
MAMMA1000865	1.106	0.000	0.000	0.000	2.321	0.000	0.000	0.000
MAMMA1000867	46.228	24.216	64.376	21.736	17.699	18.758	10.742	6.964
MAMMA1000875	124.814	80.537	231.558	88.627	57.015	82.859	46.826	53.611
MAMMA1000876	87.475	36.523	94.191	19.763	21.466	42.434	27.201	24.439
MAMMA1000877	201.968	107.716	538.232	164.333	86.827	114.380	80.171	97.872
MAMMA1000878	99.671	67.833	257.022	71.323	29.066	47.487	36.714	37.365
MAMMA1000880	76.396	60.884	153.335	45.836	17.649	44.996	19.238	35.353
MAMMA1000881	63.646	33.072	177.731	43.034	30.410	31.086	12.184	38.045
MAMMA1000883	71.807	24.931	43.109	16.630	18.675	40.320	44.419	55.440
MAMMA1000897	88.466	0.000	7.404	0.000	0.000	0.000	0.000	0.721
MAMMA1000898	380.818	62.977	134.846	45.311	63.221	164.332	122.071	52.933
MAMMA1000905	97.555	63.528	161.117	57.777	42.205	50.312	28.216	42.710
MAMMA1000906	57.788	33.146	125.096	29.019	13.531	29.380	16.982	14.930
MAMMA1000908	30.597	19.222	40.351	11.584	5.445	10.392	13.469	11.612
MAMMA1000911	9.952	29.425	3.998	9.963	1.886	7.419	5.350	126.406
MAMMA1000914	82.184	23.137	69.228	20.659	18.111	35.329	22.616	18.859
MAMMA1000920	92.123	62.032	37.206	16.675	15.550	47.235	47.680	26.801
MAMMA1000921	107.169	69.026	207.821	102.347	60.403	64.787	35.902	77.424
MAMMA1000931	211.796	140.234	424.498	95.390	40.229	51.643	49.349	95.211
MAMMA1000940	145.411	82.982	268.876	70.972	55.532	61.420	51.119	60.328
MAMMA1000941	182.800	134.847	509.857	131.193	79.478	106.717	53.292	91.187
MAMMA1000942	195.078	123.131	446.428	117.435	68.234	90.801	63.506	75.814
MAMMA1000943	196.926	99.988	558.754	109.551	89.006	81.092	51.063	85.539
MAMMA1000952	161.019	97.081	355.265	78.330	98.779	104.172	79.021	96.980
MAMMA1000956	43.741	16.217	14.918	11.103	5.840	41.230	24.471	6.893
MAMMA1000957	95.532	53.066	225.645	64.794	42.610	47.323	34.337	45.567
MAMMA1000962	281.600	192.048	781.968	204.962	120.611	123.900	84.354	140.995
MAMMA1000966	151.087	157.558	417.591	111.282	64.746	81.685	51.694	78.953
MAMMA1000968	217.975	107.043	313.251	58.469	41.964	45.044	41.392	63.998
MAMMA1000972	18.150	48.148	119.482	22.427	18.041	15.672	12.870	33.135
MAMMA1000973	36.667	18.879	24.787	11.758	12.527	19.441	17.828	22.312
MAMMA1000975	44.972	19.058	38.995	20.137	30.793	22.864	65.817	45.398
MAMMA1000976	122.625	67.075	216.981	70.671	60.470	91.475	60.614	81.173
MAMMA1000979	81.812	102.452	145.415	68.435	53.443	56.902	38.749	89.759
MAMMA1000986	118.211	39.368	239.204	68.513	49.208	56.431	42.354	94.152
MAMMA1000987	81.466	50.679	249.660	43.686	35.580	49.753	23.004	41.997
MAMMA1000988	150.907	68.191	242.562	63.946	34.252	81.162	48.528	86.723
MAMMA1000994	101.984	21.000	41.248	21.154	26.136	49.152	44.373	50.523
MAMMA1000998	166.669	75.193	367.111	91.202	105.673	107.213	56.957	84.216
MAMMA1001003	73.580	37.252	146.092	47.279	34.315	35.674	26.101	59.032
MAMMA1001007	3.055	0.000	5.547	0.000	1.411	3.633	0.800	0.000
MAMMA1001008	40.892	31.048	65.220	38.501	74.831	38.859	47.979	31.121
MAMMA1001013	135.486	126.855	372.544	93.280	57.270	56.674	44.237	52.328
MAMMA1001014	85.681	25.361	77.414	32.516	25.227	20.809	35.346	16.624
MAMMA1001021	93.867	49.224	180.659	41.205	34.542	34.975	35.352	29.726
MAMMA1001024	141.736	49.918	229.735	52.670	41.069	54.541	41.726	36.711
MAMMA1001025	13.661	8.964	12.310	5.843	13.733	6.698	4.305	5.091
MAMMA1001028	36.353	24.719	14.061	10.363	34.518	16.233	15.746	11.316
MAMMA1001030	33.596	27.602	35.295	20.296	15.861	14.989	25.031	23.535
MAMMA1001035	235.880	125.555	517.898	181.208	139.149	129.655	96.375	134.509
MAMMA1001036	133.350	45.689	152.344	60.632	47.114	60.433	40.803	40.973
MAMMA1001037	180.875	100.457	403.651	52.277	55.761	72.026	38.313	51.826

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Table 54

MAMMA1001038	26.248	12.160	150.692	32.729	5.309	10.436	15.903	27.263
MAMMA1001041	113.237	27.602	43.846	32.708	45.924	47.820	46.929	16.614
MAMMA1001043	218.483	23.847	68.163	22.306	10.449	41.046	45.779	31.087
MAMMA1001050	157.361	80.096	220.216	71.548	69.197	49.684	13.493	49.872
MAMMA1001054	102.456	62.728	134.003	63.324	43.343	21.184	38.007	39.478
MAMMA1001059	136.357	48.942	59.998	52.931	26.061	111.283	69.714	40.010
MAMMA1001066	387.798	103.377	293.890	140.850	119.334	176.295	158.563	60.324
MAMMA1001067	82.327	39.420	127.017	37.076	29.891	30.670	19.782	14.257
MAMMA1001072	150.398	31.601	52.273	21.983	32.143	57.421	47.051	26.375
MAMMA1001073	101.957	23.218	17.217	11.405	43.228	24.053	24.142	5.176
MAMMA1001074	104.201	41.827	240.332	94.124	56.071	89.717	16.387	14.966
MAMMA1001075	32.081	34.601	23.705	29.782	21.196	23.184	14.757	17.497
MAMMA1001078	102.185	111.402	317.478	75.869	35.841	49.660	67.285	67.244
MAMMA1001080	367.248	210.764	130.259	89.003	81.982	186.406	141.739	266.507
MAMMA1001082	50.264	39.773	20.039	17.602	43.163	26.358	17.452	14.352
MAMMA1001091	3.576	11.403	27.522	0.000	18.321	4.593	0.000	0.000
MAMMA1001092	50.554	25.306	48.577	16.425	15.153	18.849	11.524	4.155
MAMMA1001094	353.180	72.506	112.379	42.145	78.386	130.358	113.824	62.964
MAMMA1001105	138.777	111.226	113.121	82.426	80.960	45.158	16.891	45.652
MAMMA1001110	15.141	8.661	7.407	3.823	5.537	6.280	3.216	4.392
MAMMA1001126	299.120	223.060	683.480	194.522	164.920	119.375	96.413	88.784
MAMMA1001133	243.826	187.024	529.603	144.907	119.301	111.573	67.515	94.605
MAMMA1001139	291.212	867.784	447.960	473.187	227.579	348.627	121.382	173.640
MAMMA1001141	36.320	18.295	40.066	9.930	5.202	26.277	16.337	13.996
MAMMA1001143	163.308	70.387	153.588	67.249	59.919	67.023	43.805	40.903
MAMMA1001145	110.718	43.148	141.067	30.890	31.851	11.000	10.119	13.322
MAMMA1001150	80.076	29.005	50.289	16.249	7.495	33.674	48.052	22.629
MAMMA1001154	203.206	129.777	429.878	121.700	90.014	77.333	45.155	71.154
MAMMA1001159	46.847	28.763	19.301	13.704	8.444	23.404	21.664	24.248
MAMMA1001161	185.601	233.229	485.605	141.151	109.607	107.154	96.161	79.043
MAMMA1001162	196.299	51.198	67.587	29.962	40.684	78.949	43.247	18.714
MAMMA1001181	116.505	35.688	88.127	33.728	40.701	41.280	16.749	26.312
MAMMA1001186	155.118	85.120	303.506	69.532	51.017	85.296	42.211	48.082
MAMMA1001189	60.587	31.052	16.618	30.386	22.337	29.809	50.065	54.044
MAMMA1001191	120.521	18.093	41.909	22.249	21.661	39.122	50.157	24.623
MAMMA1001198	229.338	561.556	755.924	695.028	205.811	536.623	412.766	746.035
MAMMA1001202	322.950	274.854	664.569	248.672	218.550	168.136	144.829	179.567
MAMMA1001203	170.551	101.121	330.599	85.243	72.915	53.390	44.564	52.183
MAMMA1001206	132.103	114.504	202.256	65.195	71.217	61.327	43.601	48.988
MAMMA1001208	55.417	28.101	30.608	21.282	25.686	27.394	20.016	15.433
MAMMA1001215	199.721	123.016	194.852	82.919	72.839	87.841	68.245	60.078
MAMMA1001220	223.133	154.557	404.346	110.968	91.387	74.073	58.534	62.841
MAMMA1001222	5.585	4.936	6.763	1.952	0.474	2.171	20.800	5.022
MAMMA1001223	94.809	29.294	42.345	15.601	20.861	20.316	32.446	15.726
MAMMA1001232	130.199	45.692	227.125	47.671	38.837	45.692	59.906	32.862
MAMMA1001234	129.344	27.935	227.692	95.815	64.344	61.799	49.210	34.673
MAMMA1001237	29.560	11.083	23.224	7.241	4.489	20.199	16.883	11.003
MAMMA1001243	20.832	11.598	47.127	7.253	32.689	20.073	7.954	6.544
MAMMA1001244	44.925	10.751	11.473	9.770	11.102	14.902	16.779	4.470
MAMMA1001249	43.758	23.671	15.616	19.023	10.556	26.846	10.975	13.758
MAMMA1001256	169.303	81.917	266.686	187.649	131.656	44.850	55.325	59.786
MAMMA1001259	70.213	24.036	18.445	18.447	25.202	45.289	34.303	19.546
MAMMA1001260	154.426	64.153	81.115	52.438	46.566	80.874	64.937	87.761
MAMMA1001262	153.326	53.618	54.054	40.354	54.252	66.416	134.449	25.835
MAMMA1001268	97.760	53.599	146.494	47.068	42.826	34.360	20.976	28.286
MAMMA1001271	305.116	66.364	106.518	32.761	65.392	128.314	130.796	39.913
MAMMA1001274	73.329	94.857	235.488	85.814	64.385	71.860	51.087	62.114
MAMMA1001280	66.399	17.595	13.218	9.853	3.831	37.015	12.303	6.374
MAMMA1001283	145.535	67.060	129.301	56.055	38.490	56.397	52.661	34.076
MAMMA1001284	253.434	60.199	204.903	48.739	63.272	100.485	93.658	76.590
MAMMA1001286	86.284	38.290	49.421	32.175	40.490	57.666	59.470	32.210
MAMMA1001289	169.737	90.053	62.200	32.142	102.670	66.398	64.913	47.082
MAMMA1001292	103.898	20.400	28.796	15.498	31.006	29.378	26.545	31.970
MAMMA1001296	225.022	173.717	324.251	133.662	60.125	88.173	70.926	89.316

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Table 55

MAMMA1001298	80.876	60.189	230.669	38.485	32.838	36.675	27.032	27.836
MAMMA1001305	153.258	67.563	147.529	35.286	31.766	65.281	41.627	30.730
MAMMA1001309	6.490	8.306	6.534	3.627	4.269	0.000	5.861	6.705
MAMMA1001310	148.253	53.093	165.786	46.753	41.171	63.488	82.639	54.927
MAMMA1001322	20.005	14.809	29.403	19.332	11.227	14.549	14.163	15.700
MAMMA1001324	82.605	28.652	85.996	52.506	31.339	47.688	30.365	20.779
MAMMA1001330	180.949	117.040	245.119	52.680	15.121	97.891	81.121	27.980
MAMMA1001333	101.707	75.972	213.812	59.950	49.965	59.640	32.340	37.307
MAMMA1001334	156.564	108.340	81.315	64.901	34.949	73.570	65.555	73.287
MAMMA1001337	105.507	35.111	33.563	17.119	20.426	44.148	21.930	33.068
MAMMA1001341	100.751	32.100	79.257	23.788	38.019	38.614	42.286	29.671
MAMMA1001343	128.875	95.425	301.822	74.316	77.337	85.437	18.963	98.899
MAMMA1001344	32.880	35.930	40.648	21.963	23.320	30.315	16.394	27.074
MAMMA1001346	49.749	17.537	51.635	21.147	20.480	22.107	26.805	24.306
MAMMA1001383	202.565	186.453	597.532	117.676	100.238	103.083	68.993	76.274
MAMMA1001388	149.105	66.100	213.624	45.488	52.686	66.868	85.346	57.974
MAMMA1001396	197.435	81.919	430.433	80.848	94.812	95.399	75.293	90.889
MAMMA1001397	116.167	86.809	175.125	67.323	58.676	56.833	61.558	52.233
MAMMA1001401	101.761	72.090	194.999	62.960	48.162	57.422	73.403	78.023
MAMMA1001408	62.875	17.757	62.603	9.779	13.557	44.301	11.008	20.408
MAMMA1001411	271.344	54.507	67.489	20.558	68.557	157.085	134.884	38.338
MAMMA1001414	74.836	21.511	88.459	27.219	20.603	32.791	16.798	25.126
MAMMA1001415	207.635	38.228	51.690	26.716	68.700	89.184	99.527	41.848
MAMMA1001418	103.090	36.102	91.976	39.234	28.949	27.016	31.339	23.195
MAMMA1001419	106.299	52.357	210.943	52.570	45.256	41.351	37.624	25.914
MAMMA1001420	133.835	25.587	149.981	15.816	19.703	28.670	26.323	15.896
MAMMA1001426	265.539	180.062	165.308	87.320	89.096	170.869	109.848	84.772
MAMMA1001428	310.313	180.134	229.960	136.337	147.398	262.499	135.345	83.047
MAMMA1001432	266.375	107.317	387.676	86.786	60.159	83.974	37.205	60.775
MAMMA1001435	99.596	48.079	193.151	53.623	27.154	41.869	30.388	39.835
MAMMA1001442	103.071	100.872	193.544	78.030	54.054	54.359	43.164	50.728
MAMMA1001446	180.367	105.551	197.748	98.484	72.694	46.485	39.641	61.589
MAMMA1001450	67.785	51.961	68.660	34.362	32.591	32.211	28.904	9.424
MAMMA1001452	180.732	124.244	432.438	115.549	111.829	104.153	92.517	96.081
MAMMA1001465	528.588	255.549	770.820	359.206	364.762	388.404	209.219	264.053
MAMMA1001476	33.639	19.551	25.289	5.909	17.988	24.584	26.252	17.981
MAMMA1001478	117.183	61.333	147.393	46.785	39.649	32.143	33.776	40.723
MAMMA1001479	156.131	59.931	31.646	28.808	44.671	62.901	69.911	26.759
MAMMA1001487	67.613	53.042	92.480	34.978	30.928	40.427	27.489	11.238
MAMMA1001498	96.522	111.213	222.159	50.813	14.811	23.385	56.209	28.054
MAMMA1001501	216.969	55.879	84.459	38.369	49.731	88.169	43.395	32.036
MAMMA1001502	124.674	57.815	131.281	46.452	43.478	54.854	34.762	36.860
MAMMA1001510	27.993	7.591	13.577	10.197	11.745	6.993	14.922	8.048
MAMMA1001522	56.601	24.819	109.236	27.569	21.472	26.994	29.481	17.416
MAMMA1001529	83.190	23.330	52.489	20.883	31.879	41.170	29.923	20.596
MAMMA1001532	47.058	33.575	98.780	33.881	17.641	23.522	25.583	30.896
MAMMA1001533	97.390	40.032	30.146	22.218	20.573	25.298	46.390	16.233
MAMMA1001534	0.341	0.000	0.000	0.000	0.608	6.274	0.000	0.000
MAMMA1001535	32.482	21.042	23.902	24.788	14.317	27.839	5.277	10.537
MAMMA1001547	122.717	75.842	186.325	45.519	46.073	43.338	36.590	24.660
MAMMA1001551	103.124	52.282	155.615	43.540	38.692	47.685	20.767	32.781
MAMMA1001569	47.916	19.726	56.549	24.376	18.319	34.666	36.128	11.381
MAMMA1001575	137.304	30.090	50.539	31.981	29.095	50.896	55.992	33.156
MAMMA1001576	355.571	57.322	87.851	39.259	62.142	115.580	85.589	39.636
MAMMA1001584	59.860	30.398	60.438	23.526	24.246	30.161	16.694	22.305
MAMMA1001585	6.157	32.887	0.000	2.133	1.210	6.758	2.949	4.371
MAMMA1001590	150.616	76.439	214.250	84.714	45.244	67.639	37.913	52.869
MAMMA1001599	40.717	29.889	37.283	14.016	19.295	24.401	27.880	19.119
MAMMA1001600	109.112	32.647	49.324	13.148	24.411	44.599	35.258	20.344
MAMMA1001604	153.185	34.765	63.275	52.861	9.643	15.339	24.456	16.253
MAMMA1001606	217.088	99.469	248.919	91.848	90.788	88.514	79.192	78.377
MAMMA1001609	64.637	23.619	74.281	18.302	10.063	9.100	19.011	13.860
MAMMA1001614	74.839	29.828	9.202	11.550	18.036	35.992	21.716	14.483
MAMMA1001615	71.970	10.164	10.048	11.622	4.999	35.674	12.056	11.852

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Table 56

MAMMA1001619	361.714	66.104	138.945	35.137	88.004	177.280	155.721	44.365
MAMMA1001620	113.233	68.799	320.014	88.182	65.387	62.891	47.797	49.428
MAMMA1001623	32.719	16.493	22.246	8.396	13.561	16.233	7.490	7.940
MAMMA1001626	75.279	8.514	13.728	10.774	12.665	56.613	57.493	6.962
MAMMA1001627	28.468	7.652	39.356	8.734	4.064	8.190	14.443	7.576
MAMMA1001630	36.419	36.649	115.287	20.971	7.371	8.511	10.371	16.570
MAMMA1001633	77.945	25.597	143.786	22.273	51.279	40.689	37.952	19.350
MAMMA1001634	132.937	95.570	297.140	83.974	56.835	62.263	58.952	66.333
MAMMA1001635	140.754	47.359	225.161	34.126	24.717	38.086	34.792	34.698
MAMMA1001649	30.569	12.321	20.513	11.727	13.713	19.299	12.550	9.106
MAMMA1001654	150.282	91.691	90.096	34.969	64.959	66.853	62.712	58.197
MAMMA1001660	133.470	97.805	42.199	61.020	54.089	65.813	66.019	54.874
MAMMA1001663	394.964	202.523	572.820	154.372	162.177	148.843	118.542	79.262
MAMMA1001670	109.171	38.230	119.077	31.362	18.030	43.797	53.194	28.426
MAMMA1001671	145.809	21.188	31.621	20.983	11.973	13.009	10.867	8.816
MAMMA1001679	74.490	17.313	20.426	10.837	8.375	23.180	9.271	18.786
MAMMA1001683	147.044	87.078	260.375	71.805	39.630	48.331	49.633	41.012
MAMMA1001686	12.824	14.464	46.223	12.860	21.575	12.528	5.274	9.906
MAMMA1001688	290.960	584.756	484.182	407.762	105.060	319.616	241.392	1824.687
MAMMA1001689	74.686	28.294	39.725	20.248	8.261	19.721	31.387	18.923
MAMMA1001692	90.375	64.474	198.053	56.976	35.470	19.914	16.899	28.825
MAMMA1001711	111.425	82.300	189.195	30.269	36.663	51.227	10.898	27.229
MAMMA1001715	67.545	40.330	71.553	28.616	19.372	25.019	24.223	13.907
MAMMA1001730	33.925	17.096	21.837	11.464	4.477	36.743	11.375	8.587
MAMMA1001735	79.384	42.172	38.240	23.675	25.390	20.932	27.963	11.313
MAMMA1001740	100.894	25.218	94.454	17.836	17.794	23.366	21.945	16.107
MAMMA1001743	199.112	118.364	141.535	72.049	46.384	86.104	96.828	100.038
MAMMA1001744	23.256	20.454	0.000	2.086	2.551	2.098	5.703	0.000
MAMMA1001745	121.679	94.047	301.292	106.455	100.677	125.697	46.388	55.894
MAMMA1001751	58.670	37.967	90.572	30.921	14.618	26.060	33.416	32.380
MAMMA1001752	284.221	89.024	175.680	74.746	86.008	159.864	103.908	99.685
MAMMA1001754	57.620	30.193	53.390	14.833	35.182	39.454	17.523	12.754
MAMMA1001757	14.456	8.290	7.632	7.247	6.076	15.580	5.382	5.641
MAMMA1001760	283.527	155.103	596.815	118.229	106.868	115.717	105.154	147.707
MAMMA1001764	33.825	15.661	33.885	14.429	5.043	11.697	22.420	16.539
MAMMA1001767	41.791	27.578	112.242	22.484	21.848	16.357	11.576	9.367
MAMMA1001768	50.861	34.645	129.707	25.692	23.037	24.674	27.811	11.075
MAMMA1001769	206.737	82.818	645.195	110.913	102.640	105.607	80.653	102.144
MAMMA1001771	123.973	30.551	49.772	16.877	55.099	52.348	41.113	48.806
MAMMA1001773	47.743	27.204	35.277	8.450	18.002	17.141	23.713	30.755
MAMMA1001778	104.585	49.619	92.589	42.249	35.085	50.584	39.215	26.862
MAMMA1001783	140.821	89.274	371.095	82.231	85.003	87.248	61.999	71.448
MAMMA1001785	119.072	65.819	256.400	60.491	37.351	65.802	45.875	54.652
MAMMA1001788	37.967	8.305	25.708	9.749	9.870	11.494	13.172	10.408
MAMMA1001790	202.092	181.258	279.482	57.700	22.737	29.284	28.819	46.106
MAMMA1001800	24.282	11.444	30.466	12.517	1.763	8.501	13.065	25.671
MAMMA1001804	150.744	16.771	51.213	14.975	33.630	67.533	64.799	20.701
MAMMA1001806	62.312	54.896	146.142	37.371	11.402	36.501	43.675	52.846
MAMMA1001812	17.002	11.569	32.023	10.166	5.995	9.576	10.245	11.255
MAMMA1001815	50.743	27.272	61.778	19.704	15.636	25.863	15.187	22.130
MAMMA1001817	10.653	7.578	15.446	7.044	7.758	3.611	7.974	11.601
MAMMA1001818	48.733	19.657	87.193	21.647	18.566	18.770	19.255	18.678
MAMMA1001819	165.340	99.233	343.318	111.523	112.261	57.848	73.268	87.725
MAMMA1001820	48.662	22.951	34.879	16.243	11.743	9.468	15.897	11.396
MAMMA1001824	125.683	53.824	187.383	58.214	53.691	47.999	45.347	37.548
MAMMA1001832	56.633	30.370	42.082	21.957	23.518	23.996	20.046	8.482
MAMMA1001836	128.477	58.280	179.541	45.913	43.465	44.952	56.814	24.346
MAMMA1001837	118.428	66.031	172.658	60.299	38.153	37.090	17.947	50.301
MAMMA1001848	42.562	27.622	82.759	24.693	20.435	22.941	15.102	19.124
MAMMA1001850	402.506	243.182	312.586	171.182	143.034	232.615	91.466	106.637
MAMMA1001851	123.305	30.035	69.870	64.763	41.560	39.454	33.329	45.924
MAMMA1001852	198.774	161.311	321.896	118.228	133.655	112.820	91.724	115.602
MAMMA1001854	158.894	117.462	234.984	44.823	77.240	42.929	39.634	45.321
MAMMA1001858	148.310	133.834	240.344	51.820	24.063	35.871	73.151	58.279

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Table 57

MAMMA1001864	169.742	52.389	185.785	37.880	50.896	67.999	55.272	23.142
MAMMA1001868	82.643	56.439	59.491	62.418	34.438	47.003	29.588	35.585
MAMMA1001874	9.192	9.651	51.178	7.405	11.275	9.054	7.189	10.453
MAMMA1001878	190.515	70.315	227.600	164.835	101.886	72.219	79.645	146.982
MAMMA1001880	159.918	94.489	292.528	95.467	48.528	98.588	39.271	81.114
MAMMA1001885	117.729	44.975	110.656	53.460	26.142	52.223	41.423	29.156
MAMMA1001890	127.969	47.712	247.654	60.558	29.367	36.838	39.109	41.483
MAMMA1001893	90.120	22.271	50.435	19.070	23.222	27.783	36.643	18.711
MAMMA1001901	78.854	67.274	188.894	57.356	38.856	45.633	22.050	26.367
MAMMA1001907	159.767	70.062	305.846	76.004	91.563	25.690	68.288	28.595
MAMMA1001908	44.964	27.928	41.967	55.852	40.219	53.008	32.123	40.375
MAMMA1001919	0.000	82.865	12.109	0.000	2.270	0.000	0.000	5.175
MAMMA1001931	59.705	9.869	29.213	49.582	13.981	18.165	29.466	11.467
MAMMA1001937	47.045	26.453	33.302	16.535	17.844	31.265	29.899	19.650
MAMMA1001951	114.033	76.574	311.618	70.531	55.661	40.552	39.990	40.224
MAMMA1001956	171.199	78.116	295.630	76.171	65.654	47.426	67.568	57.411
MAMMA1001957	114.304	40.789	155.366	46.819	41.429	43.671	26.153	26.982
MAMMA1001960	99.822	63.449	192.955	55.422	57.938	23.395	42.027	44.844
MAMMA1001963	6.938	3.651,	9.748	3.671	3.337	0.000	0.000	5.275
MAMMA1001969	237.109	164.919	517.768	178.594	149.500	109.284	97.612	137.120
MAMMA1001970	199.358	123.085	297.080	101.158	41.691	71.806	71.685	61.125
MAMMA1001978	1.206	0.000	0.000	0.000	1.081	1.561	0.000	0.000
MAMMA1001992	189.502	91.630	283.440	78.807	70.640	63.218	71.282	32.898
MAMMA1001994	85.231	21.385	143.259	40.178	38.484	54.686	24.893	33.837
MAMMA1002008	66.834	77.793	37.647	14.813	20.016	33.334	39.365	10.388
MAMMA1002009	144.462	65.030	407.911	107.350	55.438	47.107	40.434	57.138
MAMMA1002011	32.832	13.901	27.624	10.188	19.701	17.344	22.354	14.449
MAMMA1002022	107.727	67.057	159.576	65.640	59.239	37.381	36.122	50.747
MAMMA1002024	176.885	70.125	207.390	72.614	55.279	78.953	108.945	46.948
MAMMA1002032	270.523	130.983	362.313	98.620	95.826	104.970	73.966	83.780
MAMMA1002033	132.652	119.984	303.660	81.264	93.758	74.391	34.919	49.831
MAMMA1002041	19.611	15.313	18.901	14.070	10.859	15.705	11.098	10.476
MAMMA1002042	78.700	42.958	161.397	37.566	30.208	55.486	24.562	23.890
MAMMA1002045	7.131	8.948	24.018	14.459	14.811	11.172	1.533	10.371
MAMMA1002047	82.875	57.343	192.240	55.806	45.781	34.315	27.824	37.210
MAMMA1002056	212.189	152.323	474.785	146.238	94.617	84.218	104.806	75.923
MAMMA1002058	149.112	126.148	334.116	98.541	74.809	81.670	44.227	65.825
MAMMA1002060	13.278	7.931	14.514	12.643	5.782	6.917	16.902	5.536
MAMMA1002065	128.185	46.405	127.810	82.855	59.107	72.737	63.052	39.667
MAMMA1002068	110.652	64.982	163.753	51.583	45.893	40.656	37.400	24.128
MAMMA1002070	61.186	24.791	29.988	16.102	15.306	31.362	22.002	21.338
MAMMA1002078	170.197	38.633	93.014	30.633	33.682	90.533	42.110	14.299
MAMMA1002080	21.195	14.596	12.646	10.208	14.094	14.792	10.377	10.263
MAMMA1002082	111.870	77.716	117.819	55.009	54.940	28.457	25.946	21.254
MAMMA1002084	74.297	40.086	152.790	30.118	30.052	28.788	24.428	24.140
MAMMA1002087	17.991	17.619	30.479	8.932	13.026	13.365	9.996	6.344
MAMMA1002091	78.604	26.611	41.258	17.086	26.812	39.757	46.803	27.660
MAMMA1002093	17.498	0.000	5.942	5.592	5.630	8.103	11.278	4.689
MAMMA1002095	78.790	13.430	22.728	13.058	20.650	32.157	32.621	8.152
MAMMA1002108	91.919	6.035	31.027	13.639	7.939	32.486	27.923	11.735
MAMMA1002112	24.376	27.337	10.667	11.574	5.250	15.678	14.329	37.463
MAMMA1002118	12.060	5.100	8.756	5.943	6.502	7.856	7.396	3.149
MAMMA1002119	122.271	36.908	59.513	20.581	36.895	38.172	39.046	32.476
MAMMA1002125	159.277	83.844	373.786	60.523	54.991	63.367	35.366	35.797
MAMMA1002126	231.380	139.298	431.047	153.496	117.027	84.728	70.558	62.381
MAMMA1002128	102.647	35.864	48.863	19.098	20.911	44.235	39.193	25.406
MAMMA1002132	226.752	118.230	198.712	79.589	88.860	84.266	50.630	48.550
MAMMA1002140	54.642	53.227	115.593	42.121	33.524	31.026	24.905	32.121
MAMMA1002142	121.646	33.612	49.214	19.085	27.295	103.698	68.348	39.850
MAMMA1002143	150.595	15.368	78.681	36.118	5.895	13.974	10.806	45.937
MAMMA1002145	237.202	72.397	165.166	45.537	53.986	87.872	73.605	22.437
MAMMA1002147	73.366	34.088	45.076	27.984	33.648	53.571	33.082	8.766
MAMMA1002153	133.485	74.073	143.431	55.132	46.673	85.911	25.126	19.099
MAMMA1002155	320.181	146.275	552.191	86.240	120.874	124.338	93.185	96.378

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Table 58

MAMMA1002156	3.612	2.088	14.013	0.880	0.000	0.000	0.000	0.554
MAMMA1002158	70.916	40.655	88.575	24.125	14.786	21.144	21.721	31.526
MAMMA1002164	109.211	29.584	54.163	32.089	28.633	66.844	29.378	23.138
MAMMA1002165	166.029	111.787	135.468	73.710	66.970	77.137	88.540	53.125
MAMMA1002170	0.000	0.000	0.000	1.159	0.000	0.000	0.000	0.000
MAMMA1002174	139.902	178.299	326.262	182.252	147.225	141.399	87.695	71.650
MAMMA1002175	49.635	20.661	21.290	16.108	13.918	22.449	12.876	18.564
MAMMA1002180	117.470	55.089	69.154	18.969	36.764	45.946	59.721	45.237
MAMMA1002198	123.227	67.539	235.488	54.699	51.835	48.796	31.324	62.413
MAMMA1002205	114.861	63.437	420.688	47.331	61.775	61.499	42.296	74.029
MAMMA1002206	86.539	30.565	50.318	17.788	32.139	63.320	64.272	56.392
MAMMA1002209	124.961	73.557	143.211	32.601	43.486	64.448	43.661	36.987
MAMMA1002215	446.836	148.590	401.477	150.983	162.248	310.059	210.563	225.764
MAMMA1002219	103.054	68.338	110.047	29.595	35.094	50.008	34.183	47.670
MAMMA1002224	155.329	135.036	325.596	92.243	139.113	54.888	50.692	104.338
MAMMA1002229	54.055	19.297	24.594	8.408	18.280	19.024	14.880	18.482
MAMMA1002230	131.172	96.706	345.936	76.632	50.164	62.315	35.205	65.871
MAMMA1002233	40.299	20.503	27.780	14.645	13.380	24.157	18.866	16.294
MAMMA1002234	16.951	13.815,	19.460	7.251	4.128	10.631	13.812	19.438
MAMMA1002236	50.642	23.553	50.683	14.162	51.817	24.897	29.324	44.837
MAMMA1002243	88.955	30.943	38.127	26.451	21.889	37.268	32.369	10.849
MAMMA1002250	101.569	23.851	171.031	56.513	74.300	48.863	11.431	66.114
MAMMA1002253	515.185	161.871	322.750	80.630	175.660	370.878	217.429	157.156
MAMMA1002267	129.167	239.800	180.046	95.357	56.654	98.387	72.076	331.998
MAMMA1002268	36.456	16.771	39.216	17.501	24.043	16.873	20.704	13.929
MAMMA1002269	27.848	6.625	13.419	16.093	10.154	9.666	6.915	4.635
MAMMA1002282	53.648	58.269	178.298	38.160	60.059	34.106	22.977	37.892
MAMMA1002292	62.491	17.873	48.526	22.803	16.647	14.012	30.027	30.270
MAMMA1002293	236.280	162.513	481.000	154.526	85.449	104.060	60.152	54.729
MAMMA1002294	110.705	24.664	124.002	36.492	33.138	43.853	25.143	19.816
MAMMA1002297	66.424	40.774	88.229	32.940	16.126	21.061	14.524	17.505
MAMMA1002298	104.368	30.772	64.493	24.071	29.853	40.308	35.653	29.912
MAMMA1002299	102.764	41.185	67.139	29.656	30.944	33.813	19.722	23.248
MAMMA1002308	69.299	30.798	86.503	30.668	29.756	27.771	17.935	16.223
MAMMA1002310	494.257	272.509	645.571	186.568	219.463	344.867	183.571	203.149
MAMMA1002311	151.653	60.941	315.707	69.190	66.700	63.609	50.563	40.723
MAMMA1002312	79.548	36.483	113.839	34.110	19.878	36.852	19.114	16.993
MAMMA1002317	96.094	32.026	188.632	45.170	46.365	46.409	41.391	20.920
MAMMA1002318	141.320	69.599	218.472	74.218	50.463	59.927	44.261	42.418
MAMMA1002322	144.393	65.401	253.730	67.857	46.931	25.375	51.002	44.826
MAMMA1002329	49.002	17.163	28.349	17.067	21.239	27.218	20.223	13.611
MAMMA1002332	55.840	30.915	137.766	47.492	35.312	32.956	23.130	16.413
MAMMA1002333	75.478	17.882	32.309	19.280	28.576	31.145	41.629	17.637
MAMMA1002335	171.866	50.373	149.587	54.778	40.367	18.695	38.972	26.410
MAMMA1002339	91.741	62.618	152.049	63.915	53.097	48.035	33.591	31.797
MAMMA1002347	98.915	55.800	120.784	40.650	55.929	33.327	45.235	27.501
MAMMA1002351	70.045	22.016	35.600	18.333	20.122	33.583	21.722	19.631
MAMMA1002352	52.143	17.786	22.690	23.069	12.412	24.411	13.818	11.949
MAMMA1002353	128.336	52.785	144.030	46.481	46.561	36.806	12.132	34.575
MAMMA1002355	46.995	34.505	123.684	29.737	22.025	29.352	6.766	22.664
MAMMA1002356	40.901	21.732	86.932	22.189	25.451	22.826	13.215	18.951
MAMMA1002359	276.825	92.529	330.418	168.428	142.084	59.794	89.656	51.182
MAMMA1002360	42.725	25.740	47.382	16.661	18.409	9.982	9.481	12.121
MAMMA1002361	152.118	88.131	201.317	50.907	41.767	51.778	26.886	27.245
MAMMA1002362	39.281	22.692	119.094	21.154	14.517	23.579	14.318	19.590
MAMMA1002367	142.262	75.887	50.909	48.285	31.085	65.479	60.201	210.780
MAMMA1002371	119.755	66.644	278.090	138.658	42.317	49.599	32.494	49.257
MAMMA1002380	90.587	47.691	161.106	38.559	31.139	36.350	34.696	25.229
MAMMA1002384	90.935	85.538	249.278	71.113	46.508	40.126	29.975	44.417
MAMMA1002385	13.712	7.306	6.051	7.420	3.720	9.699	8.116	7.609
MAMMA1002390	119.086	26.468	66.535	12.989	40.464	53.956	37.080	19.518
MAMMA1002392	90.573	32.273	97.224	19.547	21.438	26.503	20.868	14.255
MAMMA1002396	167.171	132.603	370.476	113.135	82.112	77.745	28.921	53.900
MAMMA1002399	73.011	45.586	115.522	33.773	19.180	17.808	26.587	22.269

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Table 59

MAMMA1002400	10.797	7.113	11.587	4.041	5.847	4.732	4.516	4.194
MAMMA1002409	93.810	75.886	50.232	41.725	30.159	43.673	520.771	70.327
MAMMA1002411	81.111	34.713	76.973	23.185	26.301	31.997	16.726	11.902
MAMMA1002413	199.066	68.034	377.354	55.454	56.059	50.318	26.763	38.961
MAMMA1002417	30.976	26.195	58.136	15.593	17.649	14.266	7.765	11.383
MAMMA1002427	87.721	47.715	208.629	48.123	38.391	40.117	26.156	31.585
MAMMA1002428	108.360	83.671	293.146	88.263	84.156	51.786	57.518	57.126
MAMMA1002433	90.843	23.726	38.263	19.586	19.565	44.397	36.529	25.042
MAMMA1002434	117.152	72.024	272.113	68.694	66.706	54.616	45.191	46.511
MAMMA1002446	102.855	36.748	90.796	22.955	36.351	49.598	42.676	12.897
MAMMA1002447	77.962	49.457	171.445	42.653	21.446	36.510	25.929	27.967
MAMMA1002454	314.500	201.950	539.572	188.845	118.797	99.696	72.794	103.951
MAMMA1002461	204.681	47.899	153.652	28.137	56.943	63.968	55.245	48.401
MAMMA1002463	130.489	40.148	72.561	25.745	31.969	67.395	41.920	28.713
MAMMA1002464	94.697	34.520	44.484	18.573	24.045	50.857	37.103	17.415
MAMMA1002466	27.080	25.120	36.208	16.549	16.920	44.337	37.029	13.891
MAMMA1002470	66.277	10.542	19.623	14.778	9.384	20.022	21.241	15.324
MAMMA1002475	35.982	26.009	77.707	23.670	24.685	10.963	12.591	26.386
MAMMA1002480	85.342	48.419	144.499	40.755	50.788	48.101	35.187	30.058
MAMMA1002485	256.024	56.235	75.461	32.978	72.095	120.038	77.311	49.943
MAMMA1002494	66.749	23.381	164.418	25.376	48.947	43.136	11.733	14.401
MAMMA1002498	58.032	20.346	24.265	12.932	13.125	26.950	19.794	5.551
MAMMA1002524	73.628	20.842	11.923	21.047	20.268	27.749	12.366	14.645
MAMMA1002530	82.789	19.903	43.603	13.551	9.151	28.535	27.989	12.505
MAMMA1002538	101.182	27.725	28.460	21.181	31.900	45.529	26.380	25.658
MAMMA1002545	131.415	100.020	322.993	72.173	54.265	23.145	30.820	51.328
MAMMA1002554	51.033	30.923	62.549	16.548	18.644	38.344	32.052	17.411
MAMMA1002556	201.613	62.773	211.073	70.139	99.337	37.921	45.357	46.536
MAMMA1002561	199.748	128.004	586.968	135.854	118.280	54.740	81.217	51.656
MAMMA1002565	57.918	43.508	20.564	13.434	36.930	27.532	51.392	13.777
MAMMA1002566	29.155	16.405	7.906	3.460	1.967	13.518	5.709	5.318
MAMMA1002571	73.034	22.187	37.154	25.594	6.079	28.030	19.946	20.955
MAMMA1002573	218.479	62.669	183.544	61.350	46.029	113.781	65.617	60.521
MAMMA1002576	109.621	18.498	33.802	10.617	22.615	43.283	55.199	26.452
MAMMA1002584	244.467	197.626	384.879	79.185	103.251	112.917	113.914	151.642
MAMMA1002585	133.865	28.963	56.983	17.186	16.306	13.727	51.687	25.753
MAMMA1002588	67.168	39.043	34.776	15.656	19.252	29.596	35.555	19.945
MAMMA1002589	98.120	25.567	26.638	16.923	18.956	18.249	16.364	12.591
MAMMA1002590	268.176	57.804	202.329	36.276	77.487	180.923	123.883	42.552
MAMMA1002593	131.425	64.951	130.257	54.131	23.515	55.983	37.410	36.272
MAMMA1002597	76.091	50.352	131.097	33.606	42.551	25.425	36.396	34.764
MAMMA1002598	69.190	45.133	59.324	58.225	35.339	68.531	47.164	70.246
MAMMA1002603	122.932	40.124	155.801	51.386	48.672	98.075	64.732	66.103
MAMMA1002612	330.999	152.583	441.574	105.603	112.764	175.106	98.853	99.475
MAMMA1002617	363.139	211.631	557.754	145.485	146.260	203.052	110.009	118.254
MAMMA1002618	90.423	66.208	129.807	53.454	46.096	53.758	43.899	55.854
MAMMA1002619	34.076	14.223	23.292	10.350	14.540	15.236	12.465	13.642
MAMMA1002622	112.756	60.308	263.518	46.461	43.508	41.984	32.044	52.630
MAMMA1002623	89.689	68.083	149.811	64.401	102.216	102.611	54.682	73.325
MAMMA1002625	83.660	44.949	94.038	26.154	32.540	34.576	38.497	28.162
MAMMA1002627	9.090	2.616	7.631	2.675	0.000	3.940	7.852	8.826
MAMMA1002629	111.050	96.279	397.433	77.573	45.933	89.752	53.737	108.399
MAMMA1002631	50.470	10.960	11.524	6.679	3.741	10.219	10.741	11.301
MAMMA1002633	32.234	20.386	37.729	16.053	9.358	12.456	8.681	32.169
MAMMA1002636	59.898	50.529	142.123	25.014	15.348	18.150	38.018	22.608
MAMMA1002637	58.583	21.541	11.323	5.892	14.789	18.069	26.406	22.104
MAMMA1002646	55.442	29.770	36.308	23.176	15.750	18.816	26.997	38.809
MAMMA1002648	49.661	48.800	69.217	43.621	64.730	39.438	38.742	48.014
MAMMA1002650	15.384	6.907	9.595	4.820	3.958	6.140	8.225	6.042
MAMMA1002652	61.935	69.556	44.994	60.882	59.089	42.135	62.414	54.651
MAMMA1002655	49.617	25.105	13.568	11.569	8.462	23.347	10.991	22.157
MAMMA1002662	122.410	44.430	94.935	34.850	32.770	58.417	41.476	39.910
MAMMA1002665	236.733	190.056	600.904	183.784	112.684	133.133	101.570	153.389
MAMMA1002671	89.496	41.623	60.274	25.563	20.577	26.452	50.459	40.518

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Table 60

MAMMA1002673	94.294	135.347	302.435	85.978	116.544	122.876	58.765	72.402
MAMMA1002684	169.486	32.550	60.424	32.013	39.987	86.564	80.699	45.058
MAMMA1002685	25.020	18.401	21.785	11.312	11.628	3.402	5.660	25.002
MAMMA1002692	7.274	9.361	3.697	10.386	2.003	4.100	3.302	9.849
MAMMA1002693	66.711	52.339	15.641	32.934	10.671	20.167	32.429	30.795
MAMMA1002698	39.272	32.200	43.657	33.153	4.354	11.796	12.328	34.409
MAMMA1002699	18.348	10.645	5.272	3.333	2.314	3.625	12.679	6.883
MAMMA1002701	66.193	107.821	326.150	82.189	33.993	57.919	29.820	56.144
MAMMA1002708	232.250	119.730	163.846	75.850	65.245	76.116	103.624	109.697
MAMMA1002711	128.862	101.834	359.100	105.535	79.020	76.543	26.135	61.975
MAMMA1002712	55.151	50.304	36.811	8.507	18.857	25.978	44.085	47.001
MAMMA1002716	32.821	37.741	37.674	23.554	13.366	39.383	49.740	33.088
MAMMA1002721	128.620	78.060	360.516	86.920	49.826	57.925	48.421	76.576
MAMMA1002723	67.425	45.775	59.116	53.954	27.853	31.646	28.039	37.993
MAMMA1002727	4.194	5.317	4.081	4.586	3.879	1.679	6.885	6.203
MAMMA1002728	45.508	63.239	134.784	49.369	17.238	32.733	26.228	67.828
MAMMA1002742	486.871	191.088	183.567	79.031	108.740	257.374	156.771	126.280
MAMMA1002743	17.914	25.779	65.317	19.354	14.843	12.214	24.184	22.277
MAMMA1002744	70.172	65.184,	190.550	59.599	40.023	33.273	23.675	53.991
MAMMA1002746	14.967	8.271	6.293	9.116	3.957	9.800	1.039	7.011
MAMMA1002748	53.355	180.966	171.425	25.271	3.510	13.742	11.775	23.747
MAMMA1002754	64.093	69.489	189.499	44.022	29.371	15.039	15.857	30.299
MAMMA1002758	25.835	7.240	9.756	5.507	5.640	9.500	11.968	9.173
MAMMA1002762	65.824	58.122	104.988	33.940	18.698	86.679	92.471	84.012
MAMMA1002764	104.828	95.058	295.803	59.485	52.006	47.508	45.629	48.337
MAMMA1002765	81.926	54.425	185.685	56.838	25.634	30.254	22.519	36.212
MAMMA1002769	20.078	9.062	33.997	9.878	15.366	12.293	19.431	15.797
MAMMA1002771	92.652	248.038	91.136	106.297	36.324	95.235	52.022	929.910
MAMMA1002775	51.236	37.084	125.540	30.088	37.975	21.242	25.695	24.387
MAMMA1002780	23.190	24.572	73.778	29.564	12.337	13.199	6.027	19.175
MAMMA1002782	76.728	28.066	76.753	28.366	26.053	26.045	13.885	33.944
MAMMA1002795	17.412	3.178	14.907	9.264	2.359	6.615	10.186	19.921
MAMMA1002796	28.596	28.390	48.340	13.930	16.360	14.274	13.494	19.709
MAMMA1002805	25.198	16.430	30.126	13.856	9.933	47.769	23.312	13.432
MAMMA1002806	84.431	28.564	34.957	32.528	49.335	29.125	31.705	30.489
MAMMA1002807	64.374	42.471	124.060	39.454	51.288	34.538	23.265	46.125
MAMMA1002814	28.078	31.573	133.666	36.466	14.707	19.459	22.590	33.539
MAMMA1002817	8.719	10.443	6.527	4.036	1.155	2.240	8.038	11.128
MAMMA1002820	15.173	5.049	24.747	14.605	7.416	9.432	16.038	5.111
MAMMA1002830	91.438	212.662	185.761	75.492	49.491	111.835	311.632	133.132
MAMMA1002833	90.875	71.138	237.238	50.346	44.689	47.222	25.094	46.080
MAMMA1002835	28.488	23.244	28.102	14.935	9.604	12.597	16.302	12.709
MAMMA1002838	84.752	56.692	166.200	49.694	30.237	32.930	11.828	26.416
MAMMA1002842	98.706	53.519	151.875	23.902	32.033	41.236	27.950	47.227
MAMMA1002843	76.343	31.051	107.479	18.190	24.282	30.456	19.401	13.727
MAMMA1002844	311.853	139.150	228.560	66.881	72.282	201.758	152.946	94.166
MAMMA1002845	4.464	5.631	16.258	13.028	3.642	8.306	5.338	22.843
MAMMA1002857	77.604	209.913	235.780	167.148	50.200	178.228	129.737	278.807
MAMMA1002858	113.809	319.730	662.654	523.500	84.144	532.413	382.518	1000.090
MAMMA1002863	108.297	33.190	66.980	38.305	26.112	45.735	86.883	51.987
MAMMA1002868	65.375	102.643	253.035	92.062	91.774	46.567	38.439	58.468
MAMMA1002869	85.453	22.923	80.058	19.164	22.933	26.217	42.600	30.859
MAMMA1002871	28.097	6.998	5.660	1.623	3.087	7.477	5.467	3.406
MAMMA1002875	20.954	16.542	18.160	22.628	23.110	21.099	24.952	32.949
MAMMA1002879	33.352	14.773	9.446	6.359	8.506	13.275	30.077	23.108
MAMMA1002880	46.288	35.830	71.009	12.119	12.813	15.447	20.107	22.354
MAMMA1002881	57.225	55.154	238.977	25.333	27.378	18.964	34.053	52.410
MAMMA1002885	87.039	28.425	35.323	14.016	29.952	34.101	61.975	26.271
MAMMA1002886	398.174	39.003	88.206	52.831	26.325	197.562	39.216	20.561
MAMMA1002887	45.505	7.809	7.548	7.024	9.968	8.271	13.675	5.111
MAMMA1002890	65.426	81.707	153.034	36.444	19.739	40.974	38.649	41.029
MAMMA1002892	58.445	53.672	210.646	36.086	31.508	36.186	13.729	35.746
MAMMA1002893	76.469	18.593	25.600	5.864	9.192	24.826	20.585	11.290
MAMMA1002895	33.029	30.313	81.623	21.896	10.209	8.431	11.614	21.933

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Table 61

MAMMA1002898	88.538	24.524	42.725	9.653	16.551	32.137	42.359	30.615
MAMMA1002905	191.445	39.095	72.714	28.234	32.209	91.200	60.899	51.358
MAMMA1002906	92.692	27.862	53.273	26.259	34.130	57.141	67.635	26.917
MAMMA1002908	77.656	66.964	209.054	54.014	54.429	43.639	58.626	50.901
MAMMA1002909	157.128	123.626	554.652	152.777	89.304	83.884	61.550	89.879
MAMMA1002918	55.362	26.201	35.298	14.931	10.960	19.166	27.775	29.119
MAMMA1002925	50.571	70.116	54.395	18.071	27.814	43.511	11.984	57.467
MAMMA1002926	105.041	221.644	119.112	66.217	73.866	245.600	1218.974	550.265
MAMMA1002930	68.089	38.713	147.112	32.243	19.181	31.875	24.698	46.379
MAMMA1002937	207.866	61.711	89.764	38.377	38.050	97.677	156.876	119.279
MAMMA1002938	34.139	13.727	21.350	7.309	10.152	15.165	14.230	14.534
MAMMA1002941	18.884	30.845	50.805	19.591	7.699	16.322	11.528	24.529
MAMMA1002947	63.095	31.441	46.623	20.590	18.624	28.594	29.987	39.586
MAMMA1002964	43.981	37.785	133.836	22.173	11.661	25.346	15.389	28.296
MAMMA1002967	37.974	16.689	23.126	13.527	10.863	35.085	22.091	25.886
MAMMA1002970	178.268	124.368	533.590	120.984	97.317	92.795	66.069	109.854
MAMMA1002971	99.466	79.461	50.710	19.662	15.091	40.745	37.592	51.546
MAMMA1002972	83.922	33.377	50.911	16.436	12.354	42.113	50.137	45.819
MAMMA1002973	117.540	70.913	318.513	45.601	38.568	34.070	22.903	68.699
MAMMA1002979	80.771	204.398	227.280	56.459	375.745	119.386	122.750	226.538
MAMMA1002982	19.895	9.493	14.202	6.265	0.000	0.000	0.000	5.076
MAMMA1002987	65.397	50.918	156.507	28.534	30.958	22.630	16.594	36.952
MAMMA1003003	104.891	69.630	125.933	48.800	36.915	48.025	45.716	47.346
MAMMA1003004	41.353	106.059	274.622	111.746	92.691	59.597	33.719	77.654
MAMMA1003007	20.423	21.289	75.498	16.044	8.909	15.878	6.947	15.193
MAMMA1003011	45.615	37.641	29.754	23.843	21.157	33.395	48.907	39.054
MAMMA1003013	55.088	58.284	49.438	27.289	18.877	31.768	67.950	59.419
MAMMA1003015	36.817	29.585	89.251	19.826	4.679	16.602	6.959	10.432
MAMMA1003019	10.026	30.107	5.244	7.467	2.375	6.403	3.225	6.184
MAMMA1003020	48.046	31.761	50.515	13.842	17.142	19.341	28.497	20.218
MAMMA1003026	28.646	14.274	3.514	8.603	6.618	9.838	11.161	6.781
MAMMA1003031	248.219	140.526	311.997	98.494	105.194	112.752	66.462	132.570
MAMMA1003033	47.072	27.208	130.132	44.811	42.096	33.806	17.555	36.757
MAMMA1003035	102.528	49.560	45.025	30.912	25.924	64.046	42.175	56.246
MAMMA1003039	37.382	19.822	98.219	37.555	17.115	27.935	9.656	25.906
MAMMA1003040	76.014	95.416	243.138	114.795	84.250	59.989	42.107	100.448
MAMMA1003044	79.444	46.915	90.545	40.709	21.121	25.258	13.745	23.444
MAMMA1003047	376.340	121.483	150.100	91.015	100.397	168.621	175.219	122.400
MAMMA1003049	26.899	9.631	9.169	2.907	5.679	12.149	5.016	10.003
MAMMA1003055	38.639	24.977	76.695	21.811	15.758	11.937	6.277	20.034
MAMMA1003056	31.238	13.811	32.121	15.345	7.891	17.689	3.176	18.147
MAMMA1003057	68.258	35.596	34.053	23.862	19.335	28.373	32.521	36.634
MAMMA1003066	43.837	46.015	117.875	31.178	11.361	17.068	9.179	35.831
MAMMA1003075	16.366	6.334	32.629	10.374	3.215	6.507	2.433	11.804
MAMMA1003089	49.867	51.500	220.715	36.189	24.057	14.625	14.530	41.852
MAMMA1003092	22.129	73.102	15.615	27.304	11.693	9.575	15.986	84.963
MAMMA1003095	8.240	37.313	24.078	8.354	10.123	9.662	24.609	12.392
MAMMA1003099	44.094	27.545	96.117	16.060	12.184	15.519	4.930	23.720
MAMMA1003102	44.491	18.730	31.447	14.500	22.389	16.929	20.089	20.899
MAMMA1003104	35.977	19.146	34.647	14.588	10.720	11.459	11.385	18.999
MAMMA1003113	41.697	21.092	30.337	15.635	14.764	14.690	17.723	23.810
MAMMA1003126	20.042	39.595	102.916	21.241	15.167	17.921	20.876	26.563
MAMMA1003127	57.961	27.221	102.332	12.486	8.002	12.295	13.773	22.285
MAMMA1003131	267.516	37.924	129.263	66.563	86.667	135.209	95.293	83.256
MAMMA1003135	22.855	14.308	5.624	7.938	2.690	14.984	7.633	17.269
MAMMA1003140	6.575	9.140	33.040	4.487	0.895	1.900	5.064	5.312
MAMMA1003146	14.105	18.018	18.562	11.213	11.461	16.500	8.591	9.815
MAMMA1003150	311.806	87.992	58.938	77.271	104.739	165.139	115.042	46.945
MAMMA1003154	93.002	39.912	37.471	22.819	19.655	31.742	26.299	27.565
MAMMA1003155	41.709	26.308	36.508	14.326	18.674	30.842	23.489	18.046
MAMMA1003157	34.876	32.317	147.845	12.108	24.093	12.999	8.766	19.930
MAMMA1003163	37.900	25.338	29.052	18.551	20.826	32.639	35.893	33.749
MAMMA1003164	26.961	14.747	18.545	13.932	5.852	14.778	13.694	20.137
MAMMA1003166	12.213	5.478	7.671	8.749	1.781	3.094	8.412	7.640

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Table 62

NB9N31000010	31.105	17.113	26.284	14.271	7.540	17.180	16.220	11.568
NB9N31000016	63.431	16.195	24.879	17.001	16.740	25.216	14.845	17.364
NB9N31000043	87.438	35.161	58.144	20.813	36.473	36.956	51.575	34.673
NB9N31000045	83.399	109.448	62.101	95.653	93.734	94.218	166.554	74.328
NB9N31000054	41.821	12.636	37.831	15.025	15.265	18.963	10.894	13.189
NB9N31000076	22.822	22.709	57.320	14.223	12.517	9.029	11.713	24.494
NB9N31000086	31.281	74.504	22.661	29.164	11.744	29.951	13.909	30.012
NT2RM1000001	11.595	9.900	11.540	4.467	4.016	8.823	6.775	5.184
NT2RM1000018	333.185	68.022	171.103	77.680	48.418	138.131	122.906	79.595
NT2RM1000032	37.506	9.768	23.088	9.453	13.222	16.128	22.911	12.495
NT2RM1000035	185.573	46.513	81.354	56.890	39.846	82.885	74.450	52.553
NT2RM1000037	185.843	60.878	116.479	50.830	36.658	98.591	49.882	54.356
NT2RM1000039	228.804	172.849	444.715	104.606	82.108	214.282	139.766	101.078
NT2RM1000042	55.479	102.774	112.292	145.900	52.898	89.445	80.537	184.618
NT2RM1000055	1.083	0.593	0.000	0.000	0.252	0.000	5.227	0.000
NT2RM1000059	212.057	100.267	173.989	78.130	50.792	143.445	83.189	102.504
NT2RM1000062	11.755	9.438	11.334	1.925	2.705	2.434	25.015	10.555
NT2RM1000065	153.505	42.956	56.248	29.740	66.820	67.974	42.112	65.531
NT2RM1000066	26.794	6.539	7.914	2.716	6.609	8.275	11.533	13.605
NT2RM1000071	42.919	126.091	61.623	97.378	24.665	45.008	74.491	266.252
NT2RM1000080	12.803	1.714	1.023	4.022	2.135	8.919	13.254	4.329
NT2RM1000086	393.857	146.368	283.360	100.835	117.874	205.973	155.085	102.325
NT2RM1000092	12.949	18.015	4.187	6.602	2.600	0.000	5.579	17.636
NT2RM1000118	0.000	0.276	0.000	0.180	0.000	0.000	0.000	0.655
NT2RM1000119	18.719	5.828	9.051	5.794	3.873	6.048	19.700	10.812
NT2RM1000121	2.231	0.000	7.566	3.177	3.735	3.309	1.697	3.614
NT2RM1000122	309.647	84.904	138.129	58.379	75.966	213.166	141.553	57.569
NT2RM1000127	14.133	3.707	2.380	2.322	3.743	4.212	8.594	5.786
NT2RM1000131	1.661	1.269	0.348	0.000	0.768	0.000	2.271	2.221
NT2RM1000132	10.432	7.649	9.599	3.479	7.287	11.592	13.046	10.752
NT2RM1000153	39.773	9.302	10.314	3.465	4.419	11.775	17.131	12.503
NT2RM1000184	85.966	171.937	58.982	34.486	22.674	51.668	129.969	177.417
NT2RM1000186	2.149	4.607	0.000	0.000	1.586	1.226	3.974	7.121
NT2RM1000187	29.354	12.303	16.019	17.222	15.020	17.176	15.232	18.703
NT2RM1000199	16.274	0.000	17.316	6.834	4.725	5.212	8.917	6.720
NT2RM1000213	17.361	14.639	43.481	9.904	8.998	12.127	6.422	10.141
NT2RM1000215	8.787	10.858	90.070	4.505	89.435	12.158	6.380	7.453
NT2RM1000218	0.000	10.196	7.239	2.227	1.452	4.273	8.324	4.445
NT2RM1000224	35.730	65.418	0.000	47.537	20.172	44.102	26.563	63.368
NT2RM1000236	52.706	47.803	20.481	19.138	42.513	21.813	58.118	100.492
NT2RM1000242	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
NT2RM1000244	13.988	12.654	6.957	9.937	6.047	8.026	8.938	3.968
NT2RM1000252	283.006	144.306	358.324	169.383	149.200	192.609	174.288	239.093
NT2RM1000258	284.496	113.021	203.771	67.954	94.270	152.181	132.435	150.452
NT2RM1000257	8.203	8.081	9.713	9.716	0.000	5.002	7.893	7.694
NT2RM1000260	548.461	312.072	494.663	164.454	249.491	313.672	232.568	270.549
NT2RM1000269	9.472	7.461	6.606	10.004	8.876	5.844	16.818	6.933
NT2RM1000271	8.917	1.259	3.857	2.440	2.317	4.289	4.982	5.727
NT2RM1000272	83.425	97.598	29.246	80.462	22.650	25.350	34.266	157.515
NT2RM1000273	27.031	19.960	21.872	11.127	5.201	25.896	29.976	17.270
NT2RM1000274	42.234	91.340	28.306	26.224	11.534	34.723	32.623	85.440
NT2RM1000280	14.289	12.359	21.912	7.205	7.361	10.397	4.200	10.119
NT2RM1000295	8.249	4.916	17.445	4.671	9.099	9.454	2.185	1.092
NT2RM1000300	41.252	31.172	62.474	15.266	6.023	14.825	6.206	14.221
NT2RM1000304	130.855	217.805	133.583	142.504	77.271	155.874	78.198	321.054
NT2RM1000314	255.347	113.392	165.204	56.831	114.936	189.937	108.461	113.313
NT2RM1000318	4.002	22.985	8.505	14.343	0.836	6.124	14.391	25.194
NT2RM1000335	10.157	10.048	6.881	7.482	5.897	3.558	14.151	14.353
NT2RM1000341	41.219	3.681	1.562	0.000	0.000	10.884	5.578	6.704
NT2RM1000350	302.316	74.071	106.873	34.040	61.895	149.078	112.517	85.201
NT2RM1000354	6.027	0.000	0.000	1.807	0.000	0.921	2.303	1.256
NT2RM1000355	74.362	158.811	209.578	39.101	103.936	249.368	14.695	225.724
NT2RM1000361	16.299	10.575	9.446	7.432	8.424	7.383	4.356	5.053
NT2RM1000365	0.000	0.000	0.000	0.000	1.447	0.000	0.000	0.000

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Table 63

NT2RM1000372	93.583	9.616	49.097	28.761	33.904	61.678	39.147	31.524
NT2RM1000377	42.186	17.871	22.783	12.668	13.142	15.587	18.377	23.602
NT2RM1000388	8.811	19.351	1.155	5.242	0.780	5.795	6.201	11.464
NT2RM1000394	0.899	1.862	0.813	1.925	0.438	0.000	0.000	0.000
NT2RM1000399	1.641	5.386	0.000	2.270	0.570	0.319	2.023	1.257
NT2RM1000407	69.180	19.536	39.379	6.299	21.106	27.229	14.102	13.378
NT2RM1000421	0.890	0.000	0.000	0.000	0.456	0.150	0.000	0.000
NT2RM1000422	102.028	152.115	200.732	297.482	65.137	134.344	50.452	241.878
NT2RM1000430	16.769	3.286	12.402	4.398	4.506	12.149	11.238	7.508
NT2RM1000462	167.815	117.695	165.008	62.828	65.795	81.561	72.026	118.786
NT2RM1000499	16.037	22.127	75.152	12.507	7.415	7.335	41.299	22.217
NT2RM1000512	126.610	24.122	12.786	25.082	11.161	46.878	21.802	31.090
NT2RM1000519	7.852	28.718	9.178	14.716	6.756	27.934	11.081	10.474
NT2RM1000527	29.692	15.338	24.471	17.418	45.221	59.291	31.450	14.020
NT2RM1000539	14.790	19.300	31.135	14.824	2.560	6.669	3.751	10.774
NT2RM1000542	118.560	38.555	21.020	20.675	29.849	30.176	22.378	32.507
NT2RM1000553	37.329	18.841	47.329	24.533	23.901	33.590	34.084	33.966
NT2RM1000555	77.352	46.168	43.953	21.772	15.838	16.936	12.057	35.840
NT2RM1000558	55.132	15.424	20.508	7.987	7.249	8.886	23.984	21.919
NT2RM1000563	39.161	14.058	17.872	12.234	8.871	14.324	12.341	13.462
NT2RM1000566	3.172	7.323	0.000	2.755	1.243	3.584	2.944	4.754
NT2RM1000570	65.428	72.508	44.124	24.498	15.164	26.341	21.720	56.340
NT2RM1000571	20.300	15.881	9.841	14.197	7.525	7.964	16.668	9.893
NT2RM1000574	45.305	32.953	5.746	5.977	1.945	5.060	1.526	3.809
NT2RM1000580	10.540	9.295	12.139	8.734	2.114	6.532	5.687	7.120
NT2RM1000620	11.778	12.782	21.632	15.504	5.894	4.488	3.359	17.303
NT2RM1000623	3.914	2.515	0.416	3.125	0.251	0.715	0.355	2.159
NT2RM1000630	17.633	6.091	6.532	3.910	2.095	8.257	7.963	6.411
NT2RM1000633	5.563	70.230	93.799	22.316	42.967	24.174	6.091	43.328
NT2RM1000634	3.427	3.869	2.248	1.997	0.487	0.000	1.258	3.039
NT2RM1000642	87.902	31.353	26.846	11.421	21.495	75.074	66.152	42.393
NT2RM1000647	46.410	65.742	56.619	55.351	49.439	30.233	26.128	50.923
NT2RM1000648	25.285	9.969	8.914	5.538	3.383	6.086	5.045	5.201
NT2RM1000650	22.370	16.864	19.881	11.036	29.031	8.360	13.816	11.166
NT2RM1000661	23.325	6.294	12.692	7.551	6.360	11.076	18.036	9.158
NT2RM1000666	13.966	1.244	3.221	1.629	1.543	4.997	1.079	2.418
NT2RM1000669	7.339	9.184	2.145	1.453	1.159	1.973	0.824	6.789
NT2RM1000672	58.162	25.532	15.778	9.171	22.446	58.987	16.791	14.945
NT2RM1000681	21.724	106.663	3.979	14.842	2.185	20.284	16.034	21.688
NT2RM1000691	4.381	9.202	2.832	3.483	1.268	0.878	2.181	3.652
NT2RM1000698	31.943	17.379	9.609	16.495	5.185	8.614	8.628	12.092
NT2RM1000699	10.439	2.722	5.406	4.115	3.535	6.367	10.784	8.214
NT2RM1000702	32.110	7.097	17.438	3.946	5.019	19.783	18.192	9.778
NT2RM1000703	32.168	17.962	20.468	14.964	19.912	19.806	20.940	16.286
NT2RM1000704	25.926	35.690	22.230	11.998	15.536	38.075	52.384	26.689
NT2RM1000725	12.567	91.681	3.742	10.735	0.262	10.694	14.773	17.602
NT2RM1000726	7.525	9.354	5.608	7.297	2.528	3.884	3.237	8.489
NT2RM1000731	144.609	19.850	46.338	14.141	85.767	40.231	32.791	30.972
NT2RM1000741	14.291	4.715	6.122	2.576	3.554	8.230	5.265	7.328
NT2RM1000742	30.801	9.241	6.240	6.116	3.655	11.131	7.680	11.315
NT2RM1000744	69.419	21.887	27.283	15.799	11.433	38.093	24.162	24.347
NT2RM1000746	12.863	7.631	12.042	6.326	6.665	9.321	8.974	11.118
NT2RM1000747	24.565	39.958	11.215	5.537	1.866	7.009	10.940	21.461
NT2RM1000752	13.148	7.585	3.359	5.748	4.905	1.290	6.516	8.686
NT2RM1000767	146.795	35.621	33.719	11.495	31.430	63.425	41.576	22.788
NT2RM1000770	24.395	7.712	21.569	11.954	11.449	9.412	14.053	17.537
NT2RM1000772	2.148	5.100	1.271	2.181	0.000	1.505	6.132	3.034
NT2RM1000779	284.561	185.275	301.250	139.318	150.250	196.541	146.279	96.926
NT2RM1000780	9.227	9.621	4.260	6.864	3.591	4.298	8.898	2.912
NT2RM1000781	0.000	0.000	4.468	0.666	2.562	3.064	2.407	2.127
NT2RM1000789	79.877	28.387	74.545	23.140	28.956	35.852	51.230	46.548
NT2RM1000800	4.947	10.706	34.906	3.617	6.856	4.436	8.934	3.531
NT2RM1000802	209.372	41.025	60.767	12.693	69.721	155.310	133.291	27.049
NT2RM1000811	0.000	0.807	0.000	3.615	0.593	0.000	1.896	1.921

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Table 64

NT2RM1000826	55.971	29.000	28.733	20.800	12.255	7.195	28.144	23.708
NT2RM1000829	39.377	19.978	34.233	28.539	40.659	14.500	22.956	26.065
NT2RM1000831	92.244	176.233	212.504	115.234	47.485	121.255	114.428	264.692
NT2RM1000833	20.877	17.302	8.876	4.821	8.474	6.471	16.424	13.119
NT2RM1000834	7.920	13.142	7.973	9.896	4.809	8.919	6.281	8.562
NT2RM1000841	31.899	32.922	28.948	39.736	19.743	24.819	26.306	46.020
NT2RM1000848	10.486	17.213	11.047	9.143	7.207	4.310	8.632	18.858
NT2RM1000850	4.705	2.700	0.000	1.784	0.000	1.597	2.104	7.243
NT2RM1000852	27.699	10.440	14.655	3.679	11.796	13.435	15.920	11.316
NT2RM1000853	0.000	4.915	0.000	1.897	0.000	0.000	19.505	3.017
NT2RM1000855	295.899	111.992	196.426	53.443	65.232	138.673	132.776	97.678
NT2RM1000857	419.515	279.225	710.235	153.528	198.222	264.575	140.191	196.436
NT2RM1000858	450.537	223.032	628.109	128.574	92.997	272.161	183.324	165.845
NT2RM1000867	36.148	35.491	71.518	26.137	22.828	37.610	46.674	48.259
NT2RM1000874	94.766	25.329	40.690	15.917	33.235	69.767	75.898	34.795
NT2RM1000882	32.751	18.077	43.528	12.957	13.381	12.209	10.357	22.709
NT2RM1000883	312.282	118.317	233.345	90.226	109.110	311.111	130.746	182.823
NT2RM1000885	252.089	146.253	191.597	129.087	63.370	152.039	156.686	193.445
NT2RM1000893	28.474	12.532	13.539	21.087	13.367	23.959	22.465	14.066
NT2RM1000894	246.338	100.240	188.863	51.822	48.537	189.474	182.264	80.716
NT2RM1000898	8.028	11.716	12.431	3.461	8.055	10.349	3.262	8.889
NT2RM1000899	20.978	2.796	3.034	4.018	6.936	7.286	6.525	8.715
NT2RM1000905	90.972	37.943	146.214	36.300	72.541	61.959	55.239	46.935
NT2RM1000910	21.235	22.607	15.176	6.355	3.770	20.204	15.343	18.656
NT2RM1000914	199.944	90.792	169.446	46.693	65.449	122.556	87.145	72.117
NT2RM1000919	36.141	16.161	19.116	13.229	8.891	18.002	10.279	10.389
NT2RM1000921	0.242	1.831	11.629	2.787	0.000	1.344	1.305	2.292
NT2RM1000922	13.119	18.060	5.555	12.140	3.037	3.684	6.526	16.464
NT2RM1000924	29.895	12.894	4.946	4.788	7.984	10.841	16.108	5.749
NT2RM1000927	48.046	34.032	49.155	23.882	14.687	14.867	17.603	20.582
NT2RM1000951	13.349	11.379	12.531	13.272	6.919	7.215	10.192	8.882
NT2RM1000956	5.337	16.522	6.739	2.246	6.192	6.379	6.215	8.675
NT2RM1000960	24.574	14.841	49.930	16.747	44.584	52.121	23.270	34.312
NT2RM1000961	20.594	16.610	28.449	33.770	11.295	30.987	65.017	30.389
NT2RM1000962	1.479	8.158	49.309	6.863	4.421	9.226	13.337	10.246
NT2RM1000973	89.241	51.561	16.390	19.560	15.357	27.890	33.675	45.410
NT2RM1000978	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.368
NT2RM1000982	7.275	2.308	2.120	2.059	1.138	1.293	1.746	4.769
NT2RM1000991	13.759	6.798	22.345	7.467	6.192	11.494	1.942	9.039
NT2RM1000994	12.087	15.119	14.969	10.866	9.132	2.303	4.549	14.654
NT2RM1001002	46.263	5.707	19.271	15.499	18.065	33.283	21.225	33.831
NT2RM1001003	14.107	33.647	23.710	23.835	3.391	10.638	8.307	14.681
NT2RM1001008	4.937	4.696	0.740	4.466	2.544	3.192	3.215	10.971
NT2RM1001011	67.834	16.031	21.431	8.274	20.203	46.979	40.030	18.121
NT2RM1001013	25.323	6.694	3.303	6.673	8.650	15.882	23.168	23.126
NT2RM1001017	8.644	4.934	1.214	2.455	1.873	2.894	4.062	7.068
NT2RM1001018	224.654	234.771	124.092	68.774	75.070	85.777	124.713	184.612
NT2RM1001026	23.853	12.510	10.387	14.301	5.568	12.341	14.618	17.008
NT2RM1001028	11.717	13.271	17.437	18.862	5.641	12.231	8.930	11.443
NT2RM1001043	21.614	13.830	4.261	8.481	4.770	7.687	17.274	10.663
NT2RM1001044	21.983	20.272	44.315	8.181	4.171	5.809	4.623	9.566
NT2RM1001059	3.169	2.991	1.316	0.000	0.352	2.727	2.878	3.632
NT2RM1001063	0.879	5.544	0.768	1.254	0.973	4.181	1.761	5.391
NT2RM1001066	3.011	3.061	0.000	3.241	0.000	1.348	1.228	3.011
NT2RM1001072	13.706	7.601	5.972	2.306	0.165	3.139	5.672	5.851
NT2RM1001074	32.455	14.324	28.723	10.090	6.573	10.841	7.837	10.538
NT2RM1001076	7.339	4.891	0.792	2.511	0.000	5.644	6.602	2.026
NT2RM1001082	63.705	50.432	105.417	34.113	20.331	17.230	16.378	21.799
NT2RM1001085	13.921	7.236	4.420	3.206	4.563	0.966	5.984	4.704
NT2RM1001092	16.133	28.559	80.293	36.442	13.840	23.671	15.948	30.844
NT2RM1001102	2.299	0.000	0.000	0.000	0.000	2.006	1.301	2.772
NT2RM1001103	4.293	14.550	11.888	3.980	17.852	6.345	2.505	12.387
NT2RM1001105	0.000	0.418	0.000	0.686	0.000	0.000	0.000	1.156
NT2RM1001112	6.983	5.403	12.985	7.889	7.226	5.412	8.469	12.089

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Table 65

NT2RM1001115	100.486	24.788	67.251	18.301	19.421	53.304	29.318	21.097
NT2RM1001122	18.980	19.515	19.938	11.109	10.211	34.308	33.955	13.422
NT2RM1001136	4.811	3.751	2.520	1.126	0.765	2.194	2.817	5.117
NT2RM1001139	78.791	18.931	27.710	8.382	21.060	31.349	14.028	14.521
NT2RM2000003	27.773	13.438	12.296	3.254	10.288	4.103	14.697	22.880
NT2RM2000006	64.154	36.637	117.073	30.277	27.783	25.842	17.647	24.349
NT2RM2000010	57.806	33.217	60.148	20.749	86.788	23.487	19.722	22.651
NT2RM2000013	24.877	27.244	40.874	15.590	40.045	30.831	48.932	36.344
NT2RM2000030	68.595	26.308	27.271	17.595	26.608	41.165	43.837	27.939
NT2RM2000032	22.984	13.418	59.847	11.737	13.094	11.681	12.137	11.426
NT2RM2000039	35.892	5.887	28.101	23.568	9.740	51.053	23.006	23.405
NT2RM2000042	7.936	9.200	20.886	10.060	5.098	11.101	20.459	10.744
NT2RM2000092	12.085	11.085	15.415	5.779	5.195	6.720	11.106	5.712
NT2RM2000093	51.998	31.271	57.365	24.041	26.832	24.640	12.930	20.135
NT2RM2000101	34.341	46.687	64.294	27.692	29.563	48.487	33.388	54.246
NT2RM2000104	73.163	48.315	58.786	33.739	39.845	53.753	69.151	73.279
NT2RM2000124	35.818	16.923	31.954	10.723	11.012	23.770	21.401	22.254
NT2RM2000155	31.139	23.019	27.033	12.467	9.797	13.085	10.315	17.050
NT2RM2000191	151.075	54.651	87.171	59.579	62.006	74.514	126.950	91.326
NT2RM2000192	0.760	2.690	0.971	4.582	1.137	2.242	1.413	0.000
NT2RM2000239	92.578	36.060	71.933	31.157	21.570	60.155	49.672	39.127
NT2RM2000240	104.218	69.966	77.545	23.453	53.412	78.029	64.223	83.906
NT2RM2000241	70.281	31.167	42.733	18.007	14.544	13.466	26.176	42.298
NT2RM2000250	72.366	22.586	52.512	23.631	19.076	29.100	50.616	50.848
NT2RM2000259	90.122	33.799	39.931	17.198	9.865	44.083	74.558	29.086
NT2RM2000260	340.036	40.469	141.962	35.653	77.794	188.072	216.739	59.426
NT2RM2000265	24.506	4.177	38.440	1.951	3.495	14.217	14.995	14.683
NT2RM2000287	131.692	88.080	127.535	51.611	38.294	53.574	55.104	70.583
NT2RM2000306	45.342	24.950	44.593	13.884	40.471	40.133	22.666	33.254
NT2RM2000312	13.383	57.043	78.915	13.258	60.055	90.975	183.675	38.391
NT2RM2000322	33.318	18.077	22.354	11.030	6.002	8.829	16.962	15.344
NT2RM2000343	70.618	78.514	302.242	43.179	64.338	35.838	84.150	77.161
NT2RM2000359	79.203	25.437	34.945	19.556	16.348	47.922	31.041	20.663
NT2RM2000362	138.367	75.052	100.195	73.363	49.276	128.683	126.847	106.528
NT2RM2000363	41.249	17.128	40.363	12.316	18.047	6.982	11.907	9.239
NT2RM2000368	225.366	121.451	100.718	49.727	89.663	128.354	136.054	93.203
NT2RM2000371	88.897	208.325	97.848	212.525	33.081	80.287	140.890	131.756
NT2RM2000374	54.398	55.656	153.004	34.316	25.750	36.072	34.151	51.955
NT2RM2000387	31.537	35.012	44.269	24.245	23.611	19.094	24.288	26.745
NT2RM2000393	43.873	18.662	32.917	12.496	14.167	17.560	23.452	33.102
NT2RM2000395	11.936	2.901	3.145	1.722	4.564	6.102	4.725	9.257
NT2RM2000402	26.540	28.616	42.681	18.209	10.970	24.876	20.077	26.993
NT2RM2000405	29.390	26.302	56.236	18.191	18.624	17.673	19.408	19.435
NT2RM2000407	213.973	77.583	145.459	42.798	73.678	124.360	103.989	122.635
NT2RM2000410	46.375	23.782	29.096	10.711	13.331	26.855	27.992	20.820
NT2RM2000420	41.781	29.100	39.676	24.872	16.605	26.730	29.136	43.708
NT2RM2000422	400.274	145.824	265.042	61.828	73.571	186.812	131.563	125.088
NT2RM2000423	119.707	56.563	272.757	58.213	50.981	60.353	42.529	86.903
NT2RM2000452	44.543	24.735	36.727	13.780	10.160	32.134	23.468	26.716
NT2RM2000469	28.062	19.762	14.685	5.603	7.485	22.242	10.716	6.249
NT2RM2000490	57.984	29.556	42.743	16.403	19.316	36.503	21.106	31.221
NT2RM2000497	44.862	39.966	107.651	23.488	15.277	19.316	13.374	16.412
NT2RM2000502	49.184	33.683	39.515	14.256	18.792	23.598	23.921	27.778
NT2RM2000504	53.653	30.376	46.453	19.836	22.267	39.106	28.508	19.188
NT2RM2000514	40.702	23.938	23.980	9.704	12.601	20.319	19.147	27.441
NT2RM2000522	6.782	0.000	4.730	3.680	1.616	2.008	4.021	14.506
NT2RM2000540	28.543	24.938	24.326	8.984	9.799	16.595	10.471	17.045
NT2RM2000556	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
NT2RM2000565	52.454	32.231	48.697	17.373	14.758	42.730	24.240	28.218
NT2RM2000566	31.997	22.486	34.598	11.793	7.665	32.508	18.105	35.032
NT2RM2000567	57.110	29.153	45.058	10.738	15.606	44.727	22.394	28.766
NT2RM2000569	113.652	91.632	187.867	40.645	36.420	58.576	40.151	50.117
NT2RM2000577	61.308	16.114	35.195	12.694	14.986	83.608	36.221	60.695
NT2RM2000581	152.797	45.271	66.363	20.096	32.397	79.582	62.192	40.676

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Table 66

NT2RM2000582	96.163	83.789	104.868	37.893	45.777	67.766	50.428	50.631
NT2RM2000588	109.847	89.480	119.521	70.534	32.168	143.491	88.984	95.908
NT2RM2000589	91.130	45.398	66.143	21.774	22.548	80.656	43.864	35.379
NT2RM2000594	31.068	22.138	28.684	10.809	13.325	34.179	10.310	16.391
NT2RM2000599	275.423	132.063	221.911	86.738	66.363	237.294	209.381	119.304
NT2RM2000609	26.687	13.378	20.025	9.729	14.321	19.395	17.956	8.545
NT2RM2000612	40.704	19.012	36.338	9.471	15.531	27.049	24.872	30.269
NT2RM2000622	45.492	46.307	46.012	27.097	17.426	48.495	30.090	42.927
NT2RM2000623	279.041	219.374	245.200	90.410	123.723	286.194	221.925	144.950
NT2RM2000624	52.551	88.174	87.665	60.273	35.044	29.084	27.783	54.409
NT2RM2000632	15.461	13.673	11.853	13.378	8.044	7.114	6.910	5.808
NT2RM2000635	24.726	21.442	42.243	17.900	14.353	23.119	10.306	20.675
NT2RM2000636	45.247	47.662	62.828	24.460	33.311	28.868	35.751	35.343
NT2RM2000639	34.707	19.290	26.594	15.919	12.875	28.297	20.526	11.317
NT2RM2000649	39.662	37.102	62.088	31.152	32.252	42.335	27.796	50.424
NT2RM2000658	53.598	26.723	55.360	19.176	26.348	46.815	23.949	20.812
NT2RM2000660	84.441	62.193	66.364	13.329	36.417	48.267	23.694	40.215
NT2RM2000669	17.352	23.877	38.180	11.181	16.885	17.594	13.008	20.479
NT2RM2000689	118.126	102.565	102.237	102.435	37.057	156.147	96.539	140.413
NT2RM2000691	29.467	12.787	29.631	9.783	15.294	28.392	15.401	17.161
NT2RM2000714	238.396	61.067	122.264	38.290	60.785	222.914	188.827	77.434
NT2RM2000718	9.515	10.199	19.686	5.036	7.922	8.962	7.572	22.010
NT2RM2000732	44.022	24.869	42.915	12.209	29.863	38.537	30.201	17.415
NT2RM2000735	112.208	47.966	111.282	57.228	38.980	78.590	45.888	59.237
NT2RM2000740	23.990	62.438	143.286	24.030	26.159	35.449	22.001	29.845
NT2RM2000743	15.424	14.901	23.591	12.391	9.779	16.339	8.950	8.560
NT2RM2000772	79.885	34.020	54.908	31.068	31.256	64.893	44.735	55.557
NT2RM2000773	56.846	36.465	77.155	26.645	32.523	60.130	42.946	53.958
NT2RM2000776	56.550	40.820	69.793	43.736	22.285	89.348	33.285	45.221
NT2RM2000784	54.586	33.888	45.181	19.559	21.292	43.103	25.540	42.124
NT2RM2000795	169.462	132.660	456.283	117.450	94.702	91.566	59.832	91.914
NT2RM2000796	12.942	12.033	20.129	5.817	6.070	11.596	8.538	11.009
NT2RM2000798	67.292	147.984	71.980	42.802	43.127	85.427	63.126	132.706
NT2RM2000801	145.709	152.451	160.966	85.365	73.827	214.221	157.384	174.371
NT2RM2000821	29.716	25.994	36.976	14.293	9.638	63.476	12.133	3.427
NT2RM2000829	77.695	36.834	148.015	32.077	69.569	70.012	26.103	73.222
NT2RM2000837	85.748	27.100	51.022	19.432	22.405	48.733	36.614	45.277
NT2RM2000924	41.170	22.739	31.818	6.582	16.935	130.595	55.870	42.226
NT2RM2000930	45.514	31.120	39.165	20.017	17.433	49.111	28.135	30.171
NT2RM2000937	85.092	19.912	28.613	13.728	34.425	55.176	53.959	15.755
NT2RM2000939	63.956	41.986	59.137	18.909	23.056	57.088	26.370	29.465
NT2RM2000942	141.275	345.015	119.378	242.434	78.282	274.472	112.054	436.171
NT2RM2000951	32.383	20.717	32.763	17.041	10.179	32.704	19.494	30.498
NT2RM2000952	33.160	18.882	34.052	16.194	27.783	44.540	16.881	31.012
NT2RM2000966	54.007	44.546	57.551	30.397	27.965	78.353	44.947	77.916
NT2RM2000973	96.188	97.082	100.373	31.654	38.259	115.479	60.146	151.200
NT2RM2000983	66.024	27.357	40.970	16.277	25.768	44.322	40.901	34.882
NT2RM2000984	38.635	39.635	42.628	14.734	10.729	39.002	24.661	39.000
NT2RM2000994	38.406	43.907	36.416	29.496	24.408	22.384	18.679	31.517
NT2RM2001004	74.509	45.438	146.622	36.919	35.918	125.242	81.529	92.360
NT2RM2001022	195.677	346.056	350.501	243.410	179.341	419.711	214.981	540.668
NT2RM2001035	23.201	26.826	34.867	15.930	11.692	19.371	11.576	23.987
NT2RM2001038	18.846	16.860	28.577	14.251	9.432	21.182	12.726	12.544
NT2RM2001043	31.149	17.293	22.001	11.462	11.232	18.219	25.898	31.106
NT2RM2001050	101.638	45.617	56.097	28.126	32.674	61.600	49.621	79.938
NT2RM2001055	83.075	29.856	49.927	15.739	32.251	60.461	35.926	29.242
NT2RM2001065	21.466	21.970	40.162	20.006	27.398	26.370	15.034	14.433
NT2RM2001075	366.658	258.334	337.690	128.945	166.931	370.161	257.064	228.430
NT2RM2001083	230.683	79.913	107.950	30.576	63.142	203.365	79.590	24.253
NT2RM2001100	182.772	114.627	137.289	65.878	54.062	141.899	155.507	119.434
NT2RM2001105	101.949	70.116	95.624	50.863	39.812	104.272	87.573	85.122
NT2RM2001109	48.591	27.328	30.825	11.569	12.495	53.494	34.958	45.222
NT2RM2001110	99.871	68.967	152.982	31.616	42.715	78.028	71.894	63.509
NT2RM2001126	57.602	33.922	47.638	18.667	20.095	52.257	42.378	28.204

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Table 67

NT2RM2001131	59.454	21.547	32.934	24.063	22.706	37.676	28.873	17.418
NT2RM2001141	116.250	82.599	275.090	51.756	53.614	85.069	47.274	63.199
NT2RM2001152	20.261	21.814	23.297	10.506	9.194	20.068	10.068	22.007
NT2RM2001177	44.847	43.449	52.307	26.604	19.552	41.709	26.283	55.231
NT2RM2001194	164.727	54.905	97.293	28.358	44.057	146.597	99.019	118.606
NT2RM2001195	36.939	36.245	34.818	15.750	15.727	32.602	21.861	34.274
NT2RM2001196	125.134	23.362	52.729	15.781	26.090	77.518	62.058	31.794
NT2RM2001201	56.981	42.504	62.447	20.139	31.351	68.607	32.835	44.422
NT2RM2001221	65.764	32.746	40.357	19.556	25.529	40.240	33.849	36.497
NT2RM2001238	34.807	25.200	33.023	13.254	14.872	43.011	20.155	18.493
NT2RM2001243	50.316	49.076	42.361	34.148	33.121	68.021	35.734	60.810
NT2RM2001244	39.082	47.756	54.069	35.242	30.728	59.908	22.778	50.393
NT2RM2001247	138.825	184.906	146.564	65.082	57.954	94.133	78.544	136.745
NT2RM2001256	28.147	18.773	29.336	14.133	9.881	8.739	16.106	25.473
NT2RM2001269	21.655	19.444	36.676	14.235	17.978	11.919	14.441	17.847
NT2RM2001278	105.133	67.683	225.135	41.243	42.803	61.361	51.930	64.103
NT2RM2001291	21.264	19.798	31.162	8.619	11.535	15.945	16.243	12.482
NT2RM2001294	60.754	44.696	66.102	25.820	20.715	42.950	28.321	33.134
NT2RM2001295	43.856	35.189	40.675	10.220	16.301	35.694	20.908	35.879
NT2RM2001302	30.816	16.802	26.058	10.228	12.245	25.513	14.404	12.416
NT2RM2001306	11.584	52.176	16.722	6.379	6.616	13.560	8.347	10.145
NT2RM2001312	33.361	18.866	54.572	11.148	10.119	13.848	8.526	26.714
NT2RM2001319	13.127	22.841	23.586	17.119	10.492	18.998	4.495	38.587
NT2RM2001324	103.673	83.091	165.198	32.861	22.836	56.112	31.793	39.459
NT2RM2001345	49.634	25.168	35.284	14.837	16.900	100.618	25.540	19.919
NT2RM2001360	74.152	33.097	38.122	17.360	16.021	50.562	31.265	21.915
NT2RM2001370	28.821	12.859	21.986	6.327	5.734	26.406	10.631	2.394
NT2RM2001391	16.127	5.412	27.834	4.575	4.553	14.188	3.910	9.994
NT2RM2001393	57.930	25.241	58.135	14.781	20.544	47.187	32.903	28.104
NT2RM2001420	17.272	10.676	16.079	6.774	6.751	2.717	3.157	8.464
NT2RM2001423	17.345	9.837	15.261	12.233	6.527	15.432	10.007	10.935
NT2RM2001424	196.973	74.966	136.019	35.222	48.814	142.268	95.111	56.187
NT2RM2001482	265.035	123.493	274.926	59.811	62.022	227.572	99.155	72.372
NT2RM2001499	65.942	48.790	62.383	28.605	19.730	68.321	23.722	26.475
NT2RM2001504	39.282	24.742	30.958	9.395	16.991	46.880	13.034	16.709
NT2RM2001524	24.755	14.244	24.384	9.699	10.204	16.924	9.647	14.539
NT2RM2001530	5.573	8.914	10.768	5.856	3.286	9.623	4.337	7.511
NT2RM2001533	69.137	57.026	127.055	29.970	34.159	33.371	27.483	25.268
NT2RM2001540	65.400	54.541	73.017	63.277	35.636	49.097	31.308	76.346
NT2RM2001544	18.067	19.624	25.228	12.549	7.049	19.380	11.033	9.485
NT2RM2001547	22.357	25.608	19.122	11.755	13.130	14.503	12.339	10.697
NT2RM2001558	59.623	25.861	31.696	14.111	16.568	53.758	34.506	18.325
NT2RM2001575	53.128	46.425	111.368	27.392	24.257	43.005	25.405	24.423
NT2RM2001582	59.050	42.778	132.294	24.555	24.449	28.347	22.303	22.397
NT2RM2001588	35.342	21.815	27.343	8.806	14.132	21.498	16.451	22.464
NT2RM2001592	19.456	18.542	28.436	10.182	12.538	15.234	15.478	15.460
NT2RM2001603	42.456	15.253	41.037	12.377	16.738	23.117	21.517	12.277
NT2RM2001605	60.434	36.233	43.204	13.580	20.116	41.260	20.117	15.459
NT2RM2001611	54.771	39.056	128.984	17.180	24.100	40.047	19.191	16.136
NT2RM2001613	39.500	22.894	27.579	12.321	11.577	26.696	21.149	24.773
NT2RM2001626	202.358	40.774	93.458	19.731	45.138	168.993	96.729	42.842
NT2RM2001632	30.160	45.268	47.586	25.780	18.848	32.974	21.939	45.513
NT2RM2001633	6.521	9.885	12.546	7.571	6.017	11.226	7.294	20.798
NT2RM2001635	188.515	41.783	101.462	30.227	41.863	115.049	88.246	58.313
NT2RM2001636	26.880	23.087	31.788	15.679	14.225	22.589	16.870	26.264
NT2RM2001637	13.020	5.524	6.631	4.897	11.170	10.700	20.526	5.331
NT2RM2001639	71.531	28.740	32.389	12.149	15.813	54.897	28.931	13.443
NT2RM2001641	39.297	32.462	49.334	14.630	22.002	30.556	21.763	16.776
NT2RM2001643	25.535	12.621	15.764	6.658	12.027	21.274	22.136	12.847
NT2RM2001648	26.584	18.351	24.507	8.310	6.636	18.218	14.277	13.561
NT2RM2001652	18.655	15.854	22.304	6.782	9.644	25.729	7.851	20.144
NT2RM2001659	16.891	10.861	16.538	3.750	4.964	9.228	6.172	11.278
NT2RM2001660	17.414	13.987	20.619	12.709	10.544	12.482	10.671	11.244
NT2RM2001664	32.470	29.186	27.804	16.171	15.728	29.928	13.136	17.877

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Table 68

NT2RM2001668	89.325	61.356	52.221	32.055	34.144	88.196	46.704	35.968
NT2RM2001670	58.448	20.552	40.552	17.717	15.452	67.725	25.514	50.962
NT2RM2001671	31.368	15.752	21.018	19.630	8.980	62.746	15.913	35.807
NT2RM2001675	7.281	7.210	6.726	2.026	5.059	4.678	4.675	6.219
NT2RM2001681	6.784	7.472	11.234	3.584	7.454	5.095	5.298	21.547
NT2RM2001685	28.752	21.105	22.146	9.525	9.058	19.334	21.485	26.746
NT2RM2001688	35.233	25.279	43.734	11.154	11.656	30.491	20.238	33.991
NT2RM2001695	82.068	103.403	239.543	46.305	60.347	69.201	35.903	61.706
NT2RM2001696	101.355	65.027	68.822	31.652	35.701	110.799	51.358	52.359
NT2RM2001698	146.791	45.033	83.099	28.886	31.134	111.891	66.042	79.232
NT2RM2001699	24.737	20.994	25.919	13.654	8.984	19.132	14.447	42.307
NT2RM2001700	14.734	8.383	12.975	3.702	1.312	7.813	9.485	4.374
NT2RM2001704	50.393	27.867	50.059	14.943	24.129	36.190	27.006	62.522
NT2RM2001706	75.476	62.308	144.702	48.167	41.996	55.679	28.916	57.741
NT2RM2001714	14.876	12.916	25.654	7.345	10.946	13.341	5.670	10.957
NT2RM2001716	294.058	99.615	122.970	48.569	68.313	188.154	109.177	48.112
NT2RM2001718	109.052	48.161	57.895	15.717	34.379	105.548	62.864	26.050
NT2RM2001723	20.352	14.923	16.575	7.233	8.937	39.809	8.807	9.491
NT2RM2001727	57.044	41.046	46.272	22.665	16.545	51.332	33.590	46.539
NT2RM2001730	27.206	22.859	24.865	8.552	9.397	19.553	13.897	12.427
NT2RM2001738	25.036	6.229	18.054	7.967	10.452	22.532	14.238	26.610
NT2RM2001743	31.219	15.575	27.495	8.999	13.856	19.966	21.123	40.203
NT2RM2001753	41.699	57.379	66.833	29.155	36.474	48.608	37.342	50.583
NT2RM2001755	102.308	95.543	95.880	48.800	50.926	85.016	46.946	58.535
NT2RM2001760	36.852	29.592	43.280	11.529	16.235	41.973	21.095	36.897
NT2RM2001765	17.310	22.525	20.809	5.472	6.161	36.420	11.083	21.129
NT2RM2001767	507.383	198.624	244.752	82.225	86.662	313.630	261.579	156.449
NT2RM2001768	14.334	16.852	22.405	14.516	7.327	13.653	4.371	27.736
NT2RM2001771	33.884	31.815	59.888	20.959	19.261	40.662	26.114	70.587
NT2RM2001778	14.653	9.177	12.741	0.999	6.577	9.552	8.651	6.525
NT2RM2001782	49.540	17.667	39.944	11.809	19.235	60.433	38.302	42.078
NT2RM2001784	31.529	23.807	34.905	9.620	16.512	26.774	14.749	17.008
NT2RM2001785	73.444	32.799	54.722	14.868	28.332	74.431	52.678	40.155
NT2RM2001792	82.550	48.689	54.661	13.880	26.470	67.309	56.934	51.170
NT2RM2001795	130.534	65.803	79.887	22.935	40.781	108.971	66.672	68.900
NT2RM2001797	17.770	23.911	46.302	31.918	15.965	38.330	15.267	61.440
NT2RM2001800	32.076	15.750	32.039	9.323	10.196	25.569	24.848	32.579
NT2RM2001803	18.883	19.806	27.862	15.915	15.790	17.317	12.178	25.827
NT2RM2001805	10.973	6.105	12.362	3.395	7.748	17.242	7.464	10.576
NT2RM2001806	41.604	28.683	30.345	12.360	14.554	35.269	18.192	22.416
NT2RM2001813	11.155	10.752	12.187	5.926	6.671	17.463	7.004	10.764
NT2RM2001814	16.422	18.276	19.059	5.168	10.179	14.993	12.571	9.506
NT2RM2001818	37.340	15.047	25.378	7.050	13.614	28.082	23.903	16.747
NT2RM2001823	13.814	13.268	12.712	4.562	7.791	10.847	8.727	7.819
NT2RM2001825	27.524	37.936	22.505	15.145	17.486	21.050	17.161	33.945
NT2RM2001832	68.657	29.677	30.202	9.749	22.522	37.241	30.727	18.205
NT2RM2001839	53.715	31.908	39.273	13.944	12.144	27.291	25.952	18.816
NT2RM2001840	108.411	98.429	259.021	48.048	32.857	58.314	28.523	37.338
NT2RM2001851	52.202	39.752	63.088	24.308	18.778	32.821	26.626	85.666
NT2RM2001855	33.026	24.176	29.953	16.912	19.394	23.562	31.355	25.910
NT2RM2001867	30.838	22.957	35.457	14.948	16.183	32.799	17.562	46.800
NT2RM2001869	129.599	162.083	180.222	173.694	64.737	231.277	145.176	147.129
NT2RM2001879	14.477	14.016	20.104	6.241	7.997	18.463	6.634	17.934
NT2RM2001883	42.649	14.914	59.041	11.657	28.809	14.670	17.172	5.396
NT2RM2001886	31.621	19.917	31.650	19.861	14.683	19.396	24.619	18.912
NT2RM2001887	19.995	18.787	31.384	9.308	6.192	7.945	11.032	6.537
NT2RM2001896	5201.332	1475.462	2605.875	738.729	3013.651	5911.225	5347.627	1306.593
NT2RM2001902	9.512	5.176	9.030	3.230	3.539	7.418	7.583	3.383
NT2RM2001903	63.243	40.127	55.162	28.793	22.732	77.356	28.595	48.438
NT2RM2001910	108.255	64.649	109.195	31.339	39.123	80.005	62.289	59.426
NT2RM2001935	36.519	23.148	18.415	4.134	11.165	15.562	19.141	10.042
NT2RM2001936	78.536	47.939	51.879	18.980	21.013	48.576	35.554	52.419
NT2RM2001939	23.961	5.651	21.192	6.301	5.377	17.197	7.025	5.482
NT2RM2001941	71.450	49.630	78.923	19.738	22.274	54.128	31.260	34.949

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Table 69

NT2RM2001950	46.415	29.816	36.996	18.559	8.239	39.347	13.956	23.224
NT2RM2001952	2.871	2.886	10.623	6.195	0.000	2.538	1.846	8.237
NT2RM2001976	42.702	29.344	52.698	20.599	18.125	57.645	24.197	33.972
NT2RM2001982	20.947	25.776	25.162	18.275	10.576	18.050	9.191	14.830
NT2RM2001983	23.643	16.045	27.661	9.316	13.749	23.964	18.258	17.035
NT2RM2001984	147.043	51.662	81.658	22.066	35.725	120.259	90.102	44.130
NT2RM2001989	76.106	50.939	80.150	44.331	24.785	39.074	34.205	61.176
NT2RM2001996	37.798	41.931	43.246	23.083	19.109	45.858	26.665	31.923
NT2RM2001997	63.158	41.928	28.543	20.691	22.046	58.320	33.747	34.764
NT2RM2001998	47.869	29.374	50.969	17.042	23.450	45.674	22.546	20.062
NT2RM2001999	23.045	23.925	34.107	16.137	19.923	26.601	19.613	27.167
NT2RM2002003	60.554	45.534	133.518	30.271	23.148	57.270	34.688	36.304
NT2RM2002004	16.782	14.896	24.193	8.483	9.918	13.788	12.592	4.939
NT2RM2002009	22.784	26.292	37.573	16.205	17.990	24.047	10.371	17.159
NT2RM2002014	12.027	11.499	20.605	9.676	8.686	10.127	8.085	17.091
NT2RM2002019	45.009	49.617	61.370	29.641	24.044	45.990	20.852	29.924
NT2RM2002029	100.329	58.955	73.738	25.096	36.513	90.878	44.848	41.854
NT2RM2002030	53.030	36.122	48.637	23.542	18.217	49.856	26.265	32.557
NT2RM2002034	55.319	58.655	69.310	15.775	34.969	119.355	37.851	31.637
NT2RM2002049	30.306	26.333	67.224	12.461	13.486	32.196	19.763	26.143
NT2RM2002055	4.746	9.322	10.601	1.587	3.475	2.738	4.711	1.253
NT2RM2002072	274.106	142.825	221.668	99.170	111.051	240.179	193.919	147.089
NT2RM2002088	66.101	43.548	67.009	20.108	29.769	38.434	34.203	37.710
NT2RM2002091	157.752	95.255	103.301	42.530	51.107	91.971	64.745	58.827
NT2RM2002100	36.481	42.661	83.563	34.382	22.604	42.960	30.266	45.203
NT2RM2002109	65.961	25.178	54.629	11.426	17.601	56.066	33.542	37.167
NT2RM2002126	271.768	145.370	244.199	79.521	110.685	272.182	195.547	168.748
NT2RM2002128	30.978	20.989	35.773	13.699	15.221	20.446	37.022	29.430
NT2RM2002129	53.911	38.709	50.544	14.507	24.022	54.089	40.427	15.416
NT2RM2002142	157.794	95.271	127.900	44.871	54.994	121.896	116.748	122.762
NT2RM2002144	39.141	23.769	42.061	18.362	18.425	90.424	32.619	22.086
NT2RM2002145	69.465	33.538	54.629	19.065	28.804	64.861	31.013	26.312
NT2RM2002153	57.982	34.658	45.808	37.204	22.363	85.615	33.858	45.468
NT2RM2002163	46.164	22.611	32.853	10.533	12.313	28.767	18.529	24.578
NT2RM2002170	20.367	15.918	26.954	17.854	7.659	21.614	6.584	31.812
NT2RM2002178	72.826	29.934	35.113	17.819	17.814	57.676	53.788	36.064
NT2RM2002179	20.487	16.890	26.778	4.596	7.536	27.483	11.691	22.514
NT2RM2002270	75.965	30.835	59.481	19.162	23.264	67.579	38.824	31.179
NT2RM2002326	25.054	17.109	25.901	10.631	13.295	20.170	15.155	11.219
NT2RM2002337	49.608	30.430	44.382	14.424	20.214	49.783	38.536	36.266
NT2RM2002339	126.783	46.855	62.446	22.680	35.280	129.046	67.853	46.026
NT2RM2002345	34.662	27.251	30.489	17.636	9.930	27.503	20.940	24.302
NT2RM2002368	53.018	67.271	118.627	55.152	36.416	61.876	35.957	79.909
NT2RM2002381	29.049	17.380	20.968	5.965	9.584	35.715	13.371	27.731
NT2RM2002424	23.738	30.901	58.344	39.163	17.434	49.766	25.216	77.325
NT2RM2002450	40.370	29.535	54.082	14.242	16.219	34.988	19.676	33.464
NT2RM2002482	44.705	26.737	46.955	14.769	18.437	42.664	46.045	30.188
NT2RM2002492	113.197	127.579	109.738	72.932	49.321	103.335	74.905	97.173
NT2RM2002575	112.457	88.605	247.074	59.323	48.212	80.685	45.794	62.455
NT2RM2002580	64.838	62.853	111.962	57.513	26.109	65.998	30.240	69.813
NT2RM2002592	110.441	70.152	96.103	45.340	44.856	104.438	69.434	96.173
NT2RM2002608	20.462	46.581	29.949	14.231	13.430	29.384	17.823	61.212
NT2RM2002615	33.564	24.375	25.868	12.468	16.085	46.176	71.069	33.280
NT2RM2002622	95.365	53.669	62.071	44.205	38.612	108.504	47.073	91.258
NT2RM2002630	118.784	86.444	276.792	68.615	58.079	85.848	51.946	80.285
NT2RM2002634	36.887	30.749	31.925	22.948	20.353	42.111	32.736	22.117
NT2RM2002645	51.215	209.069	58.292	23.942	32.501	97.660	24.132	61.537
NT2RM2002648	69.318	57.452	61.629	25.645	19.295	50.329	23.768	24.267
NT2RM2002647	31.140	27.535	50.514	14.850	14.557	35.612	29.190	42.269
NT2RM2002652	42.576	30.866	34.782	11.897	12.829	46.172	14.955	30.578
NT2RM2002692	53.871	40.724	63.208	39.963	38.748	37.914	30.444	71.284
NT2RM2002721	81.740	78.721	123.105	75.203	80.050	98.931	44.593	72.005
NT2RM2002748	91.982	206.064	112.357	241.969	54.156	135.810	67.060	228.776
NT2RM2002764	46.071	41.769	48.814	22.081	22.119	34.365	32.761	36.777

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Table 70

NT2RM2002772	80.296	40.944	68.101	23.056	28.389	72.818	41.505	60.302
NT2RM2002811	63.439	38.909	43.044	17.983	20.375	56.523	23.815	28.434
NT2RM2002818	50.605	52.430	151.915	32.193	19.702	26.680	17.380	40.512
NT2RM2002879	24.562	28.586	34.172	8.860	5.095	18.514	12.159	30.354
NT2RM2002979	84.387	41.192	53.776	21.436	31.083	74.067	53.736	47.429
NT2RM2002981	59.340	25.706	33.191	11.478	15.597	54.899	35.830	32.861
NT2RM2002995	42.179	21.303	31.267	13.206	10.830	32.109	30.448	42.538
NT2RM2003031	44.114	29.430	46.063	16.774	17.437	43.222	40.155	25.053
NT2RM2003042	106.509	160.917	155.488	83.058	73.174	152.473	69.308	122.583
NT2RM2003044	33.909	33.603	47.142	12.698	45.517	25.310	25.508	29.529
NT2RM2003090	47.953	25.520	41.051	9.604	15.180	34.197	23.552	25.659
NT2RM2003095	43.943	31.580	32.103	11.759	18.398	29.592	34.666	28.874
NT2RM2003116	20.590	18.126	22.701	10.734	10.194	11.727	12.203	14.479
NT2RM2003222	21.198	10.313	27.148	5.349	13.395	13.068	20.550	25.145
NT2RM2003224	110.266	37.406	48.819	30.835	29.947	80.454	57.677	53.588
NT2RM2003250	30.062	26.498	38.776	15.773	16.547	23.997	24.660	26.915
NT2RM2003258	12.707	12.077	15.752	5.247	7.979	8.239	5.752	8.852
NT2RM2003262	37.575	42.567	50.603	27.374	33.378	31.965	36.375	43.803
NT2RM4000023	49.690	44.882	57.421	17.352	24.868	53.007	25.083	35.943
NT2RM4000024	33.710	23.142	26.564	7.803	10.308	34.975	25.466	17.156
NT2RM4000027	6.576	5.402	9.541	2.488	3.969	5.783	1.681	9.230
NT2RM4000030	107.340	43.649	64.579	25.595	27.984	81.398	45.801	45.851
NT2RM4000033	54.521	41.188	116.087	19.883	18.324	28.028	14.764	29.244
NT2RM4000034	8.646	20.135	21.495	9.212	9.086	13.100	7.920	12.176
NT2RM4000046	42.055	17.446	23.148	8.687	9.540	32.532	23.736	18.823
NT2RM4000052	23.740	17.236	25.146	8.065	5.341	17.707	13.080	13.561
NT2RM4000054	440.502	221.475	352.643	107.153	132.322	410.274	281.112	209.475
NT2RM4000061	30.264	15.792	27.807	6.396	10.845	21.557	14.902	4.276
NT2RM4000074	8.073	35.126	41.073	20.510	9.480	34.431	24.493	47.368
NT2RM4000085	22.897	19.315	23.277	16.541	12.977	24.111	12.451	24.618
NT2RM4000086	50.715	22.670	78.725	20.299	18.217	28.085	16.663	27.361
NT2RM4000100	17.872	21.935	15.019	10.707	10.091	15.556	12.260	12.129
NT2RM4000101	42.770	15.330	25.674	6.552	7.785	24.576	15.561	5.064
NT2RM4000102	407.848	190.329	321.537	152.733	208.613	334.316	212.009	231.229
NT2RM4000104	23.885	13.626	17.310	3.131	7.950	21.156	10.845	7.969
NT2RM4000115	32.088	10.072	16.134	5.693	9.226	13.512	10.582	7.588
NT2RM4000129	36.681	21.490	22.965	12.521	11.849	23.308	16.146	10.761
NT2RM4000139	25.930	23.620	31.564	24.607	22.610	18.556	14.008	44.620
NT2RM4000149	33.404	17.925	29.734	13.712	15.989	18.474	26.736	42.075
NT2RM4000155	21.566	44.820	46.750	15.598	16.524	14.928	9.733	8.224
NT2RM4000156	16.586	6.239	5.822	3.387	3.958	28.594	7.207	15.119
NT2RM4000167	20.171	16.879	15.859	11.667	2.739	8.443	3.474	21.050
NT2RM4000169	30.428	28.089	36.443	24.244	11.338	20.566	13.227	60.152
NT2RM4000191	52.656	25.321	40.946	12.980	18.787	41.092	35.047	38.394
NT2RM4000197	15.240	11.946	16.612	2.282	13.434	15.387	8.823	5.757
NT2RM4000198	88.525	63.904	196.728	39.099	37.803	49.371	53.195	32.774
NT2RM4000199	52.380	24.904	46.280	17.110	18.960	33.287	27.322	30.945
NT2RM4000200	33.395	16.462	28.537	10.600	16.103	20.714	14.030	6.949
NT2RM4000202	30.208	20.922	42.468	9.182	9.970	16.908	10.274	12.811
NT2RM4000210	66.407	27.815	30.474	15.335	16.812	41.212	27.389	47.172
NT2RM4000215	25.869	24.845	36.251	22.848	13.152	31.488	12.403	27.548
NT2RM4000220	47.201	39.573	38.877	20.267	19.583	51.592	35.424	51.912
NT2RM4000229	38.395	26.396	42.302	13.878	14.171	29.316	28.242	16.590
NT2RM4000231	54.697	33.959	43.440	18.016	23.895	29.537	28.746	34.406
NT2RM4000233	209.479	90.187	137.270	36.159	66.994	160.853	100.732	62.965
NT2RM4000244	16.916	9.010	13.401	4.357	9.911	12.907	8.771	8.963
NT2RM4000251	43.833	19.474	33.500	11.060	16.673	31.966	32.833	8.105
NT2RM4000255	35.799	17.398	36.446	10.625	12.098	29.741	23.847	15.929
NT2RM4000265	102.046	79.778	222.138	64.769	51.026	72.136	39.083	49.420
NT2RM4000283	285.571	172.391	189.067	109.857	94.953	255.306	162.352	166.824
NT2RM4000284	23.615	36.279	30.562	12.441	17.835	25.501	27.248	34.927
NT2RM4000290	74.673	36.513	57.081	15.623	22.008	73.912	45.709	43.178
NT2RM4000295	24.000	18.871	22.693	8.987	11.022	47.890	18.701	14.976
NT2RM4000306	140.029	42.148	61.817	18.306	78.561	140.760	92.030	34.220

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Table 71

NT2RM4000307	20.678	19.168	22.141	9.050	9.145	23.385	14.343	13.754
NT2RM4000309	41.662	20.618	26.408	8.581	10.787	30.894	18.116	11.868
NT2RM4000313	36.434	20.403	33.260	17.080	12.239	39.520	34.145	43.040
NT2RM4000318	52.262	31.467	139.471	20.774	17.880	23.820	17.441	19.608
NT2RM4000324	51.333	27.748	39.958	9.932	17.995	63.248	27.625	42.800
NT2RM4000326	32.179	16.471	20.536	8.435	10.621	23.791	17.926	20.620
NT2RM4000327	60.230	58.958	198.666	39.302	28.376	44.008	20.961	43.734
NT2RM4000344	63.708	65.489	173.360	38.949	27.536	34.270	15.519	42.106
NT2RM4000349	30.022	14.663	14.070	7.442	10.197	22.535	12.455	16.210
NT2RM4000354	46.698	15.085	27.013	11.329	7.922	27.895	13.694	15.005
NT2RM4000356	32.497	24.336	32.372	13.972	11.464	43.673	31.608	29.630
NT2RM4000366	528.262	330.865	423.109	167.985	170.232	378.411	215.606	442.307
NT2RM4000368	51.220	51.300	153.236	33.445	22.538	43.253	17.539	64.383
NT2RM4000373	25.297	22.861	32.020	19.516	16.128	25.045	13.784	37.614
NT2RM4000386	22.576	9.738	24.078	8.987	9.704	21.730	24.414	23.758
NT2RM4000395	61.364	79.696	124.563	37.133	40.433	107.248	46.227	46.047
NT2RM4000414	159.474	59.130	69.911	18.566	40.333	119.002	79.051	21.561
NT2RM4000417	15.712	20.634	23.502	7.213	7.502	15.030	7.412	1.867
NT2RM4000421	15.106	14.708	19.062	8.549	6.469	15.114	8.074	20.588
NT2RM4000425	101.441	83.854	259.486	55.511	39.319	53.250	31.739	69.026
NT2RM4000433	51.457	24.650	39.654	12.379	16.608	41.763	37.139	36.708
NT2RM4000436	51.207	21.755	29.307	13.444	12.333	34.290	27.223	37.320
NT2RM4000444	40.864	26.268	67.826	11.797	17.600	39.060	23.113	28.672
NT2RM4000457	63.983	39.080	61.124	23.292	28.748	50.040	26.813	31.965
NT2RM4000471	41.652	29.088	37.803	8.939	15.093	35.469	20.877	14.796
NT2RM4000472	68.502	62.226	206.357	48.752	23.646	77.597	28.412	104.099
NT2RM4000486	30.140	26.427	28.452	18.097	7.542	22.184	12.697	24.533
NT2RM4000490	51.124	23.641	42.235	9.300	14.683	56.785	25.625	17.105
NT2RM4000496	110.770	31.642	65.060	13.739	27.500	68.720	52.247	37.631
NT2RM4000505	134.100	84.063	126.035	43.665	56.053	130.720	81.120	71.520
NT2RM4000511	73.441	160.671	81.146	172.018	35.906	98.128	55.037	164.299
NT2RM4000514	24.804	23.670	34.085	13.945	16.589	32.103	21.758	11.170
NT2RM4000515	56.528	99.798	88.516	40.030	41.279	67.061	40.210	72.202
NT2RM4000517	94.295	97.384	143.107	76.451	43.905	144.940	69.520	145.604
NT2RM4000520	13.459	13.780	16.902	5.273	5.564	7.899	7.054	14.968
NT2RM4000531	29.188	24.283	26.738	11.063	12.826	18.929	23.443	20.712
NT2RM4000532	14.395	12.711	19.277	9.437	8.520	12.914	15.215	13.835
NT2RM4000533	18.380	13.704	18.165	8.534	7.454	15.515	10.288	7.686
NT2RM4000534	17.803	11.768	18.975	7.585	10.236	14.119	11.420	19.497
NT2RM4000563	53.983	34.056	51.401	17.700	36.352	45.609	32.373	33.367
NT2RM4000566	36.586	22.989	35.859	9.957	21.078	25.668	24.949	21.224
NT2RM4000568	59.423	29.845	36.652	12.139	25.850	70.617	54.001	29.192
NT2RM4000585	48.810	27.673	38.443	12.701	20.510	33.948	23.868	27.346
NT2RM4000587	29.705	26.644	25.876	12.729	11.927	16.240	17.926	19.718
NT2RM4000590	32.164	21.289	29.186	8.941	11.617	18.856	16.495	13.544
NT2RM4000593	61.080	32.766	38.970	15.411	20.360	33.032	30.484	25.715
NT2RM4000595	41.141	22.473	35.313	9.766	11.448	11.237	20.012	12.069
NT2RM4000603	78.976	52.410	58.176	24.839	24.042	50.072	40.363	31.910
NT2RM4000611	15.953	10.734	13.469	9.013	8.977	10.161	7.157	22.979
NT2RM4000616	45.814	37.309	35.175	17.505	23.768	40.117	27.918	39.007
NT2RM4000621	57.493	77.709	73.014	76.819	24.081	71.204	46.769	83.169
NT2RM4000648	28.637	18.518	26.908	8.210	13.083	15.965	12.644	11.022
NT2RM4000649	85.058	41.743	59.668	13.629	29.612	55.983	39.586	36.405
NT2RM4000658	135.688	61.028	120.722	28.197	43.765	79.777	46.011	96.630
NT2RM4000661	71.864	99.345	52.294	18.409	29.132	62.897	45.030	41.904
NT2RM4000673	135.680	61.584	75.017	24.321	20.618	70.048	46.608	45.107
NT2RM4000674	75.722	36.633	51.480	16.765	16.961	34.561	42.749	30.664
NT2RM4000689	41.790	28.540	39.966	15.401	8.448	22.615	15.641	20.045
NT2RM4000698	61.169	46.347	64.951	24.102	41.257	63.885	38.390	29.637
NT2RM4000700	27.239	106.106	27.114	9.273	11.699	12.813	14.815	12.082
NT2RM4000701	227.264	115.040	182.483	47.970	70.324	76.813	128.958	65.330
NT2RM4000712	43.183	27.951	46.394	10.240	14.168	19.562	26.208	16.644
NT2RM4000717	34.386	22.333	19.262	10.038	12.975	19.299	13.148	20.540
NT2RM4000733	75.958	43.996	58.928	24.743	28.885	88.871	65.331	37.193

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Table 72

NT2RM4000734	24.197	38.270	53.725	16.970	13.155	39.087	23.333	39.227
NT2RM4000741	43.844	13.589	30.427	10.346	8.744	26.119	12.592	26.083
NT2RM4000744	50.833	14.548	25.024	23.480	10.805	62.136	17.742	83.553
NT2RM4000749	80.902	71.083	91.633	27.354	60.031	198.030	52.328	100.669
NT2RM4000751	22.688	29.768	53.788	53.315	27.282	19.811	22.272	42.714
NT2RM4000752	52.247	32.866	40.812	14.427	15.224	9.355	23.407	43.927
NT2RM4000760	33.235	16.169	27.997	11.989	19.412	13.254	10.563	10.820
NT2RM4000761	2403.264	848.134	3887.956	172.265	1449.525	4450.958	2359.029	400.128
NT2RM4000764	301.709	144.132	163.494	49.659	143.743	257.369	245.639	103.045
NT2RM4000768	11.747	9.247	11.542	9.135	9.038	10.345	6.336	11.267
NT2RM4000778	6.893	5.725	9.950	5.466	4.458	5.886	5.079	5.685
NT2RM4000779	238.073	96.516	182.851	51.850	99.170	184.671	138.565	75.926
NT2RM4000787	69.121	57.977	157.708	28.426	29.213	21.609	22.633	11.420
NT2RM4000790	60.309	46.026	83.182	23.988	30.494	22.815	35.485	31.417
NT2RM4000795	453.425	108.548	204.710	17.809	92.365	272.802	147.653	47.088
NT2RM4000796	144.288	57.098	70.720	23.213	47.104	97.550	50.426	30.942
NT2RM4000798	59.938	28.301	25.839	10.244	18.327	23.444	20.572	11.548
NT2RM4000800	150.768	122.487	195.880	137.376	57.284	146.130	97.369	185.386
NT2RM4000813	37.084	20.876	36.294	12.655	14.527	25.975	22.848	11.921
NT2RM4000820	86.855	60.381	192.196	39.751	37.738	50.427	35.797	26.747
NT2RM4000827	41.788	28.006	51.622	20.945	21.631	21.541	30.438	31.570
NT2RM4000830	68.078	30.965	59.647	20.203	26.347	37.484	30.029	44.496
NT2RM4000833	111.407	74.480	77.732	17.832	39.802	56.697	25.292	36.404
NT2RM4000841	49.942	45.599	72.313	16.308	20.094	29.644	26.188	28.854
NT2RM4000846	104.561	76.278	275.932	57.490	49.037	63.058	36.772	14.948
NT2RM4000848	125.196	36.830	101.007	17.584	32.806	82.740	51.262	19.922
NT2RM4000852	113.009	77.800	126.639	43.464	43.880	57.479	52.365	44.156
NT2RM4000855	64.608	50.229	146.326	22.844	23.661	28.928	25.813	51.332
NT2RM4000859	24.418	19.759	24.141	10.385	14.916	34.345	18.598	11.625
NT2RM4000868	16.564	14.752	14.556	11.565	9.114	12.226	17.324	12.029
NT2RM4000870	55.531	47.020	57.796	18.791	30.154	39.778	25.127	26.057
NT2RM4000879	103.887	41.773	56.495	12.837	31.154	67.942	43.586	22.044
NT2RM4000882	81.982	42.561	80.304	22.840	38.713	36.853	45.646	48.992
NT2RM4000887	151.731	36.758	112.092	22.645	40.960	98.527	85.229	22.008
NT2RM4000895	84.679	41.293	172.935	28.755	27.724	44.297	19.644	26.291
NT2RM4000897	45.994	42.630	58.329	17.578	25.299	44.317	41.019	30.575
NT2RM4000901	13.138	13.528	18.046	7.930	5.669	7.738	9.304	5.798
NT2RM4000950	13.710	21.028	17.402	10.585	11.390	13.090	8.272	13.397
NT2RM4000965	54.459	36.282	50.127	15.952	25.327	23.064	21.414	26.049
NT2RM4000971	41.258	27.847	39.604	12.433	17.061	72.230	20.025	17.430
NT2RM4000979	33.580	21.677	32.692	7.475	11.647	22.259	16.549	12.389
NT2RM4000987	51.537	23.981	27.883	11.309	12.974	42.714	19.808	18.064
NT2RM4000989	43.246	16.680	33.780	10.504	10.430	22.581	33.282	15.269
NT2RM4000991	6.595	8.954	14.910	4.216	4.093	24.191	3.472	15.581
NT2RM4000992	61.901	44.659	179.747	37.376	29.327	33.667	22.750	38.582
NT2RM4000996	12.902	17.829	47.104	22.304	9.589	16.133	12.379	41.017
NT2RM4000997	139.754	107.958	216.478	45.750	59.135	79.871	47.855	52.159
NT2RM4001001	222.229	90.117	123.641	25.902	74.114	102.439	120.879	88.667
NT2RM4001002	22.453	23.223	34.127	15.841	13.942	17.616	10.393	26.669
NT2RM4001016	39.433	22.372	27.844	7.677	15.230	29.791	22.346	14.840
NT2RM4001025	123.159	184.713	262.665	136.422	89.809	167.042	104.628	258.452
NT2RM4001027	1.003	0.083	0.000	0.188	1.139	0.903	0.000	13.341
NT2RM4001032	15.446	8.560	20.283	7.827	10.702	9.129	9.798	10.321
NT2RM4001047	18.565	7.922	16.869	2.924	7.503	4.130	9.323	18.916
NT2RM4001049	87.157	64.640	99.050	20.618	35.192	44.265	24.923	27.816
NT2RM4001061	45.597	65.440	63.291	17.761	11.312	31.198	20.661	24.356
NT2RM4001052	83.704	54.084	58.884	12.670	16.509	36.706	54.060	39.934
NT2RM4001053	55.548	69.868	192.178	27.160	24.862	42.613	24.525	28.003
NT2RM4001054	29.223	12.533	27.929	5.313	10.023	15.125	15.911	14.263
NT2RM4001059	181.587	40.368	91.633	17.857	33.606	105.399	88.210	64.703
NT2RM4001071	29.020	21.136	81.470	8.928	13.093	5.999	16.142	11.555
NT2RM4001084	42.690	28.922	39.816	12.808	14.924	24.390	23.123	13.779
NT2RM4001092	102.531	57.027	86.268	31.684	25.916	49.946	45.616	58.081
NT2RM4001100	43.266	33.448	49.943	8.293	19.072	24.126	16.221	46.701

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Table 73

NT2RM4001116	27.726	26.051	28.521	6.793	9.001	18.038	14.406	8.177
NT2RM4001119	56.668	21.890	35.980	9.796	15.859	38.916	35.588	15.608
NT2RM4001140	136.817	79.720	322.522	72.609	64.281	53.073	51.451	56.047
NT2RM4001148	238.824	52.972	84.009	16.224	62.535	137.805	147.073	38.797
NT2RM4001151	49.119	18.810	31.963	9.013	16.522	24.362	37.118	17.496
NT2RM4001155	51.322	26.524	38.663	9.832	19.192	16.401	24.191	12.958
NT2RM4001157	29.926	19.538	29.560	8.442	11.794	23.764	9.393	5.071
NT2RM4001160	72.399	50.574	60.230	13.285	29.392	49.862	35.181	33.807
NT2RM4001163	150.688	70.942	95.070	47.204	58.092	77.447	65.645	40.117
NT2RM4001187	46.613	33.666	37.323	10.669	19.756	22.493	19.909	13.410
NT2RM4001191	62.821	78.568	138.398	23.085	37.250	19.851	28.068	31.505
NT2RM4001200	48.487	41.856	115.958	43.120	35.674	29.433	29.755	46.933
NT2RM4001203	29.740	33.257	26.183	10.711	18.414	17.515	13.820	29.510
NT2RM4001204	85.368	2.729	5.406	1.939	1.539	2.503	5.782	1.987
NT2RM4001217	22.326	14.483	20.894	6.910	10.252	17.142	14.178	16.377
NT2RM4001245	102.964	61.341	59.224	17.873	32.330	47.902	39.713	28.855
NT2RM4001247	60.472	48.248	105.685	27.869	20.131	20.633	22.912	17.998
NT2RM4001256	38.132	20.867	27.791	11.662	11.297	22.362	18.443	14.221
NT2RM4001258	13.173	14.508	15.622	2.115	6.064	10.903	11.147	31.184
NT2RM4001267	18.994	10.887	19.555	6.271	8.494	3.421	7.779	13.809
NT2RM4001273	57.388	34.293	59.413	25.522	17.714	21.978	30.691	39.740
NT2RM4001281	52.686	24.825	33.241	13.708	11.390	31.923	19.522	23.080
NT2RM4001286	481.183	1240.431	782.259	477.895	296.841	681.688	413.930	936.577
NT2RM4001290	25.298	23.154	13.373	6.552	0.000	12.469	8.723	14.611
NT2RM4001309	48.445	24.031	36.511	15.060	18.354	33.040	18.409	21.487
NT2RM4001313	61.618	55.950	171.030	27.704	18.541	31.137	15.527	37.397
NT2RM4001316	49.175	40.348	93.903	19.571	16.907	28.903	20.127	14.212
NT2RM4001320	73.145	43.895	149.769	28.755	24.031	24.203	22.793	27.654
NT2RM4001321	49.367	26.564	28.912	10.370	15.275	21.145	21.285	20.579
NT2RM4001325	38.855	43.433	53.158	15.234	25.333	31.624	26.184	15.840
NT2RM4001333	48.466	17.343	99.002	20.144	115.167	148.955	12.312	8.170
NT2RM4001340	30.804	28.992	40.576	27.062	32.009	10.155	18.551	26.573
NT2RM4001344	30.624	35.092	33.290	12.667	12.525	9.910	11.004	11.417
NT2RM4001347	14.549	14.691	20.853	11.657	13.229	14.366	8.959	54.748
NT2RM4001357	58.256	26.925	40.009	14.812	13.213	104.908	348.697	7.592
NT2RM4001360	86.062	33.099	53.959	12.261	27.140	48.858	36.604	20.008
NT2RM4001371	57.075	37.841	49.730	24.239	25.868	54.098	8.910	31.242
NT2RM4001377	101.216	75.138	68.626	19.407	36.169	52.589	30.583	31.839
NT2RM4001382	56.509	78.201	56.186	36.607	24.700	70.227	41.803	66.511
NT2RM4001384	13.506	11.432	7.793	6.199	7.970	12.881	6.788	7.108
NT2RM4001400	21.837	16.958	21.913	10.795	7.913	16.255	9.524	12.188
NT2RM4001409	28.309	17.011	26.656	9.796	12.960	23.632	14.054	20.949
NT2RM4001410	29.072	19.001	30.576	8.925	14.550	18.489	21.014	17.448
NT2RM4001411	8.505	7.030	30.358	2.388	3.324	0.962	1.969	1.931
NT2RM4001412	59.413	25.935	59.821	15.231	22.577	30.927	24.563	11.190
NT2RM4001414	64.093	33.321	33.046	9.873	26.265	24.538	20.805	20.958
NT2RM4001435	33.680	29.671	20.088	7.331	12.620	14.939	11.468	14.185
NT2RM4001437	70.569	41.529	158.116	28.707	19.302	25.565	23.649	23.787
NT2RM4001444	63.099	33.815	51.190	21.250	36.920	56.421	41.830	35.180
NT2RM4001454	15.293	16.251	33.213	14.589	11.226	13.235	7.237	9.931
NT2RM4001455	8.636	7.947	12.910	5.235	6.864	7.007	13.432	28.743
NT2RM4001483	74.168	64.931	192.825	43.272	33.854	44.722	22.451	46.563
NT2RM4001489	27.884	28.159	36.108	13.377	14.505	15.628	23.221	19.361
NT2RM4001495	260.493	117.396	133.602	31.705	64.659	91.833	54.255	51.382
NT2RM4001499	68.936	37.210	73.295	19.285	26.638	41.151	25.080	25.754
NT2RM4001515	11.646	7.906	18.332	5.318	7.167	15.640	6.612	8.512
NT2RM4001519	12.556	9.937	20.664	5.346	32.689	10.138	7.966	8.328
NT2RM4001522	71.440	69.438	164.718	40.425	35.841	32.755	19.774	38.742
NT2RM4001523	24.710	16.532	29.750	8.848	11.883	12.279	19.569	31.077
NT2RM4001550	24.908	22.060	34.537	19.909	20.432	20.143	15.284	28.090
NT2RM4001553	73.882	40.371	52.795	27.094	23.686	46.848	27.034	27.166
NT2RM4001554	53.585	30.046	33.134	23.878	15.283	26.877	16.771	20.649
NT2RM4001557	19.423	19.434	24.184	11.971	12.237	21.486	7.653	15.404
NT2RM4001565	65.552	37.852	90.440	18.538	17.294	23.128	23.413	18.529

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Table 74

NT2RM4001566	100.946	48.659	87.457	28.565	28.860	79.976	52.286	9.785
NT2RM4001569	7.010	5.598	41.076	3.288	8.597	0.981	6.611	1.304
NT2RM4001579	41.258	24.859	37.584	7.247	15.119	35.411	21.050	31.905
NT2RM4001582	36.827	23.162	29.372	10.109	10.956	22.015	19.971	25.442
NT2RM4001589	57.574	32.795	61.841	23.877	20.226	47.320	41.167	35.619
NT2RM4001592	32.950	21.429	32.007	7.221	14.392	17.425	7.965	10.850
NT2RM4001594	55.970	26.805	46.827	13.556	21.275	46.488	34.751	25.706
NT2RM4001597	113.189	66.565	189.284	36.307	35.658	51.457	41.254	42.293
NT2RM4001605	16.347	11.965	18.084	2.805	4.141	11.032	9.672	10.297
NT2RM4001609	173.865	587.184	265.155	76.761	120.584	182.319	73.643	191.832
NT2RM4001610	89.090	32.924	55.024	13.942	38.114	56.107	36.218	28.535
NT2RM4001611	30.709	14.204	28.060	6.394	11.242	12.351	22.333	13.486
NT2RM4001618	77.313	59.231	178.569	26.795	28.633	44.101	23.934	50.141
NT2RM4001622	42.484	50.813	37.378	16.153	35.073	39.451	29.062	30.213
NT2RM4001624	55.088	36.243	39.342	10.093	11.389	25.162	26.300	19.356
NT2RM4001625	165.457	44.283	55.076	16.243	29.704	87.349	62.707	32.707
NT2RM4001629	23.424	34.729	31.319	10.721	9.407	17.262	17.006	17.599
NT2RM4001632	49.318	105.740	108.162	80.539	33.853	62.834	39.339	102.299
NT2RM4001642	26.758	24.864	25.229	7.187	11.536	12.746	15.743	16.315
NT2RM4001647	140.643	83.479	257.397	53.466	49.798	64.749	33.054	65.546
NT2RM4001650	20.039	17.016	26.536	7.633	8.417	10.663	14.969	25.969
NT2RM4001662	93.433	61.261	62.868	18.713	28.801	43.545	39.576	18.233
NT2RM4001666	99.250	58.594	135.514	19.947	25.792	43.075	21.822	28.747
NT2RM4001670	108.596	50.059	60.195	8.757	26.897	80.647	55.639	44.557
NT2RM4001682	23.010	37.857	52.107	34.229	26.474	24.078	19.040	48.902
NT2RM4001710	71.974	22.009	43.652	12.553	17.193	33.805	36.338	25.346
NT2RM4001712	30.145	17.963	29.768	6.775	12.959	13.705	17.401	11.444
NT2RM4001714	39.284	71.253	45.168	23.590	23.852	34.014	32.992	44.464
NT2RM4001715	39.876	47.568	68.485	29.814	28.676	29.317	23.694	38.125
NT2RM4001727	18.826	16.671	24.630	8.765	12.634	14.525	9.624	7.446
NT2RM4001731	163.786	60.747	103.744	21.266	23.073	109.348	70.159	88.870
NT2RM4001735	25.147	42.977	27.836	33.257	23.484	16.531	22.623	48.984
NT2RM4001739	29.621	22.031	33.503	11.627	16.721	10.593	7.382	14.863
NT2RM4001741	117.616	80.979	99.834	34.861	34.797	49.703	68.739	91.553
NT2RM4001746	61.847	44.910	113.561	21.148	31.787	37.464	33.824	23.274
NT2RM4001754	72.161	34.709	70.656	13.473	25.420	34.023	22.194	15.154
NT2RM4001757	38.117	23.659	28.972	12.593	10.724	21.161	24.761	19.803
NT2RM4001758	24.391	23.518	27.924	5.579	12.781	14.153	7.027	6.943
NT2RM4001768	51.099	53.221	60.158	17.044	37.261	58.428	34.390	27.280
NT2RM4001775	15.024	11.154	13.303	2.644	9.532	9.892	8.237	4.050
NT2RM4001776	24.497	20.843	16.325	5.116	12.075	8.815	13.233	6.515
NT2RM4001783	44.218	34.754	35.521	11.654	27.683	28.899	24.397	19.284
NT2RM4001793	75.698	74.949	146.739	24.426	38.218	21.996	28.324	24.241
NT2RM4001810	25.287	22.294	22.627	8.986	12.014	13.754	22.602	19.691
NT2RM4001813	108.290	15.721	11.311	3.071	4.660	7.061	9.406	9.278
NT2RM4001818	55.110	32.332	35.827	10.603	18.181	30.893	25.538	20.147
NT2RM4001819	221.187	103.477	118.661	33.955	61.689	117.958	105.557	45.891
NT2RM4001823	31.566	19.207	30.580	9.100	12.589	18.948	23.046	12.498
NT2RM4001828	33.606	37.243	60.904	39.892	17.528	52.576	22.264	20.662
NT2RM4001835	31.946	48.485	36.681	12.402	10.874	32.404	26.073	33.367
NT2RM4001836	68.101	53.948	86.019	25.292	41.216	44.492	46.063	49.677
NT2RM4001841	77.551	75.005	64.963	39.736	29.180	60.179	38.346	53.737
NT2RM4001842	41.837	31.217	153.538	19.696	13.432	18.888	13.674	12.515
NT2RM4001843	47.451	47.021	41.491	12.355	14.857	30.666	19.358	23.477
NT2RM4001858	35.284	17.427	22.905	18.860	0.000	35.066	18.473	17.632
NT2RM4001858	34.556	13.809	35.731	11.606	5.891	13.370	14.536	27.815
NT2RM4001861	102.500	55.955	86.639	33.805	25.003	43.868	45.531	30.143
NT2RM4001863	41.449	33.911	68.502	24.321	16.482	31.445	31.424	32.578
NT2RM4001865	40.706	38.767	51.589	19.138	24.325	53.955	38.078	30.584
NT2RM4001869	87.261	35.753	43.743	13.720	22.315	49.946	39.651	110.541
NT2RM4001873	31.012	19.677	42.836	19.140	23.082	17.690	23.735	26.533
NT2RM4001876	263.450	78.666	162.933	35.889	80.574	217.874	135.056	71.907
NT2RM4001880	52.575	35.308	47.881	20.693	7.377	39.267	19.933	16.114
NT2RM4001885	62.625	53.956	164.215	33.733	28.285	40.932	20.399	40.632

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Table 75

NT2RM4001889	44.826	54.188	57.058	17.324	30.679	30.391	31.401	27.309
NT2RM4001894	33.180	21.032	38.644	10.368	15.617	23.290	26.653	24.028
NT2RM4001897	55.973	37.135	42.706	11.443	18.977	24.084	62.995	21.376
NT2RM4001899	79.426	37.833	50.793	22.892	10.010	19.933	39.828	71.231
NT2RM4001905	71.913	42.987	131.041	19.900	22.521	28.037	22.888	34.298
NT2RM4001922	68.361	66.765	167.103	32.535	29.282	32.842	21.101	29.820
NT2RM4001930	9.761	18.972	11.870	12.179	5.722	7.704	2.893	19.882
NT2RM4001938	13.300	9.323	20.059	5.226	22.340	8.605	6.836	2.737
NT2RM4001940	44.499	28.342	53.112	22.045	19.769	35.835	24.329	24.211
NT2RM4001942	71.378	109.603	137.250	99.314	68.782	123.550	44.362	143.236
NT2RM4001953	73.750	67.064	218.754	37.265	39.359	37.249	28.374	31.774
NT2RM4001965	27.774	33.648	57.473	21.916	18.921	11.704	7.776	32.933
NT2RM4001966	49.431	24.684	41.501	12.421	18.343	29.179	21.379	18.604
NT2RM4001969	28.734	22.964	33.007	12.456	14.747	23.958	15.690	13.553
NT2RM4001974	82.202	23.827	35.591	10.813	20.091	38.983	35.402	27.290
NT2RM4001979	50.759	32.744	64.327	26.669	29.268	32.957	29.294	45.426
NT2RM4001980	64.506	28.217	65.730	29.832	30.129	51.434	39.037	38.269
NT2RM4001984	8.940	10.121	18.976	9.204	7.020	7.587	10.490	17.931
NT2RM4001987	76.782	27.219	64.310	10.713	13.598	56.046	41.155	21.341
NT2RM4002013	19.064	9.935	20.167	9.513	9.423	13.449	15.551	64.982
NT2RM4002018	23.330	15.361	28.649	4.482	9.866	15.203	14.895	11.409
NT2RM4002033	103.629	76.058	255.894	33.739	36.068	40.994	22.684	32.604
NT2RM4002034	97.025	74.014	204.281	25.591	40.356	66.335	30.838	29.885
NT2RM4002044	128.284	97.260	283.326	56.682	49.448	68.685	42.993	58.693
NT2RM4002047	42.016	31.010	47.604	17.496	19.793	15.043	24.593	16.651
NT2RM4002054	75.334	24.437	33.919	5.362	20.426	36.508	26.858	12.455
NT2RM4002055	28.223	41.574	41.231	17.667	21.073	24.192	30.052	56.881
NT2RM4002059	24.790	47.792	30.688	32.255	11.889	26.659	17.375	42.684
NT2RM4002061	15.353	22.159	24.342	33.358	8.569	13.680	9.654	12.890
NT2RM4002062	35.603	17.782	25.712	9.437	13.693	23.679	11.468	12.877
NT2RM4002063	106.902	59.539	161.049	27.157	37.323	44.770	45.190	17.589
NT2RM4002066	69.187	29.278	44.089	14.142	12.777	47.854	23.625	20.028
NT2RM4002067	72.915	65.950	164.446	33.322	23.243	29.901	19.168	38.472
NT2RM4002073	26.509	19.553	24.129	7.501	12.225	19.453	13.427	15.358
NT2RM4002074	23.768	16.727	27.356	9.430	10.288	9.267	19.036	9.923
NT2RM4002075	14.729	8.566	14.082	6.113	8.179	19.921	8.913	5.764
NT2RM4002076	33.772	34.570	24.768	12.754	12.370	22.729	21.957	5.088
NT2RM4002078	65.837	45.074	59.931	29.244	28.319	38.890	38.136	27.441
NT2RM4002081	72.328	49.374	162.917	29.519	33.925	46.864	32.277	29.982
NT2RM4002082	31.523	20.963	24.293	4.626	7.828	18.917	11.824	4.512
NT2RM4002093	13.703	12.906	28.190	14.073	16.132	8.993	10.746	15.942
NT2RM4002109	48.477	33.601	44.587	16.373	19.020	42.752	31.367	24.718
NT2RM4002115	52.087	16.294	25.726	5.046	11.691	15.294	19.312	5.666
NT2RM4002118	6.461	10.205	16.364	2.841	6.221	5.928	9.423	8.612
NT2RM4002128	24.014	12.586	38.670	8.609	8.704	17.808	16.887	18.787
NT2RM4002137	50.650	30.735	54.930	9.746	20.827	30.629	27.756	30.682
NT2RM4002139	59.820	72.323	217.660	35.299	32.433	22.926	18.198	31.925
NT2RM4002140	61.939	27.988	54.095	19.817	18.951	36.147	28.930	19.620
NT2RM4002145	55.935	18.752	37.184	6.758	24.220	25.455	54.028	17.830
NT2RM4002146	10.714	7.232	14.881	2.330	4.463	6.475	3.969	22.927
NT2RM4002161	21.929	10.374	17.604	4.124	7.983	12.456	8.266	7.504
NT2RM4002174	36.217	21.020	78.760	11.488	14.155	12.056	10.913	19.766
NT2RM4002178	51.201	34.975	146.685	25.841	26.852	32.083	18.490	38.988
NT2RM4002180	88.245	86.565	200.162	36.530	47.240	50.257	25.291	41.037
NT2RM4002185	60.374	34.725	47.531	10.870	17.954	36.151	35.104	14.336
NT2RM4002189	443.685	125.746	233.812	62.020	80.189	317.532	213.671	55.692
NT2RM4002194	110.410	60.176	66.781	14.262	24.395	63.199	46.341	16.491
NT2RM4002198	19.112	25.320	30.650	6.006	16.046	10.695	12.653	18.533
NT2RM4002205	86.368	52.183	210.523	37.437	37.350	41.233	35.023	46.891
NT2RM4002213	87.023	29.632	69.582	22.287	36.169	49.771	58.648	47.205
NT2RM4002216	28.034	36.860	39.984	61.988	14.040	23.466	28.018	31.505
NT2RM4002226	59.214	25.842	44.190	19.726	22.840	30.160	21.306	34.363
NT2RM4002237	84.115	47.301	42.516	13.185	17.445	121.874	282.813	42.699
NT2RM4002240	21.140	20.818	18.200	11.226	4.270	17.260	9.804	24.400

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Table 76

NT2RM4002251	39.895	25.621	38.004	9.808	12.483	27.050	27.880	15.570
NT2RM4002256	62.880	50.437	132.459	16.059	20.051	22.911	18.973	36.148
NT2RM4002262	40.381	19.221	18.726	4.067	10.643	11.552	18.506	11.180
NT2RM4002266	33.927	16.247	29.395	7.271	10.706	15.907	16.746	45.558
NT2RM4002276	31.555	29.432	34.470	12.227	15.207	18.832	24.174	41.738
NT2RM4002278	24.493	44.932	54.554	19.947	24.631	19.085	14.211	28.361
NT2RM4002281	73.045	68.535	120.767	28.971	77.810	35.833	33.197	34.350
NT2RM4002287	95.529	67.191	148.977	16.383	32.822	42.647	36.149	22.550
NT2RM4002294	37.325	40.622	32.626	7.879	22.188	17.681	21.208	18.691
NT2RM4002298	15.253	25.056	14.186	6.186	12.213	8.996	13.334	20.467
NT2RM4002301	25.506	22.524	24.351	8.779	13.463	11.537	16.605	21.093
NT2RM4002306	64.514	27.130	40.307	8.697	16.098	30.071	33.558	17.520
NT2RM4002323	46.276	37.334	108.848	13.787	18.840	15.998	23.739	23.002
NT2RM4002334	84.665	44.953	240.849	13.009	61.866	67.867	63.381	16.555
NT2RM4002339	40.226	15.664	17.738	4.286	11.781	13.743	14.276	7.602
NT2RM4002344	15.209	14.735	15.127	5.186	14.835	5.571	6.021	15.852
NT2RM4002345	29.537	16.084	44.040	7.161	49.725	20.214	15.169	93.476
NT2RM4002352	25.146	26.320	39.068	10.070	10.828	17.765	20.622	16.556
NT2RM4002382	22.727	18.967	35.121	7.780	16.102	13.358	9.862	21.089
NT2RM4002373	49.413	25.049	39.501	16.293	10.820	16.723	21.117	10.960
NT2RM4002374	45.312	17.702	80.866	14.495	13.876	25.509	12.233	16.564
NT2RM4002376	44.035	32.785	33.965	15.793	15.635	33.518	17.499	20.037
NT2RM4002383	143.921	114.177	338.801	56.564	36.130	62.968	25.071	60.431
NT2RM4002390	19.946	15.647	23.593	13.554	0.000	15.764	10.120	21.189
NT2RM4002398	33.574	85.078	55.577	19.871	29.143	36.917	34.014	15.071
NT2RM4002409	62.430	25.690	44.155	15.629	15.274	43.916	36.612	24.609
NT2RM4002414	122.797	27.569	49.085	13.732	29.300	20.609	24.789	22.958
NT2RM4002438	60.880	24.210	57.361	13.303	21.819	19.128	27.861	33.288
NT2RM4002440	50.958	29.949	58.790	16.516	17.087	22.853	27.261	86.320
NT2RM4002445	85.102	43.893	64.557	15.166	30.454	59.828	43.072	34.360
NT2RM4002450	29.806	50.782	20.662	10.226	5.031	56.095	6.391	48.088
NT2RM4002452	38.119	24.046	27.781	13.792	11.741	21.974	28.908	14.192
NT2RM4002457	58.998	45.958	72.065	21.106	21.980	25.587	22.709	26.372
NT2RM4002458	17.499	9.159	12.416	3.859	12.704	4.423	1.634	7.476
NT2RM4002460	37.183	7.502	15.263	2.616	9.265	20.827	12.805	1.464
NT2RM4002464	12.680	10.529	5.512	5.737	10.707	1.669	5.391	12.187
NT2RM4002479	85.068	45.694	66.175	35.340	44.661	52.236	42.316	33.845
NT2RM4002482	714.577	349.138	482.476	135.984	180.855	462.386	321.086	260.860
NT2RM4002489	41.987	36.475	28.303	18.347	20.193	45.527	22.970	15.427
NT2RM4002493	101.547	19.009	34.214	7.129	20.617	58.926	20.613	6.136
NT2RM4002499	104.508	114.364	295.841	132.961	45.496	125.546	54.809	138.353
NT2RM4002504	130.575	85.186	319.621	58.095	51.615	65.385	43.397	39.625
NT2RM4002506	17.534	7.716	22.097	8.307	8.641	11.973	11.217	19.715
NT2RM4002510	20.570	20.274	28.261	7.195	10.108	9.354	16.982	8.405
NT2RM4002527	29.097	14.199	26.008	7.215	11.820	15.320	15.507	11.537
NT2RM4002532	119.266	103.485	252.069	38.479	49.581	51.534	30.506	48.759
NT2RM4002534	46.720	29.222	28.381	12.470	17.005	30.785	27.381	25.218
NT2RM4002535	150.736	124.425	370.470	71.472	69.884	70.122	44.328	39.348
NT2RM4002554	46.680	4.678	15.042	2.434	7.853	8.287	11.868	8.546
NT2RM4002558	64.523	30.756	60.861	17.849	28.435	32.697	50.330	26.839
NT2RM4002565	26.150	21.759	29.418	10.020	13.855	14.504	15.952	20.143
NT2RM4002567	13.750	9.555	16.128	7.961	6.533	14.816	11.242	24.778
NT2RM4002571	64.981	32.370	51.874	13.381	25.113	37.880	40.593	30.327
NT2RM4002572	21.932	17.415	44.482	6.169	9.094	15.081	8.955	11.463
NT2RM4002577	13.390	34.537	17.827	8.379	17.150	9.208	20.440	135.375
NT2RM4002583	43.872	21.818	41.335	7.938	12.820	25.087	16.879	8.165
NT2RM4002584	48.978	41.874	47.589	19.263	15.387	18.002	26.572	29.591
NT2RM4002593	43.140	21.408	34.068	14.481	17.846	27.459	22.581	18.025
NT2RM4002594	53.494	32.355	54.474	10.039	23.934	38.188	30.209	28.918
NT2RM4002604	49.799	31.218	31.584	14.197	10.658	52.255	31.422	27.262
NT2RM4002614	18.848	9.948	15.663	7.767	10.103	19.152	15.480	10.800
NT2RM4002616	52.378	28.130	31.691	6.189	16.589	25.551	20.412	22.945
NT2RM4002623	31.915	15.505	22.179	7.046	11.143	28.155	15.957	8.295
NT2RM4002634	27.202	13.607	23.468	4.566	6.856	27.565	17.040	9.308

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Table 77

NT2RM4002636	2.342	5.234	9.517	3.874	1.465	2.585	2.436	4.543
NT2RP1000002	114.491	47.508	61.586	25.000	29.448	84.026	73.878	59.624
NT2RP1000006	71.057	28.511	44.224	10.202	17.523	40.868	37.373	15.237
NT2RP1000015	7.192	9.953	16.089	4.506	3.649	7.738	3.651	8.661
NT2RP1000018	5.882	0.000	0.000	0.000	0.000	2.690	4.737	0.000
NT2RP1000034	273.802	61.801	59.676	50.413	101.761	283.598	21.883	51.696
NT2RP1000035	14.407	14.328	5.278	5.331	3.905	19.347	5.560	9.946
NT2RP1000040	2.229	2.143	2.569	1.482	0.842	0.251	1.226	0.963
NT2RP1000042	2.962	1.516	2.106	0.450	3.003	1.458	1.788	0.000
NT2RP1000048	3.312	5.643	4.404	1.520	1.452	2.742	0.779	17.389
NT2RP1000050	37.260	7.381	21.735	7.969	7.544	14.598	18.930	19.749
NT2RP1000056	2.575	8.244	12.209	2.506	2.248	50.055	1.919	18.856
NT2RP1000058	7.701	2.152	6.853	1.889	5.740	5.703	5.884	4.654
NT2RP1000063	17.863	6.661	8.488	2.745	0.000	7.494	5.484	2.401
NT2RP1000068	4.612	5.197	4.140	0.833	1.697	1.068	0.863	1.468
NT2RP1000072	143.838	99.413	72.321	37.376	27.104	99.463	69.787	134.954
NT2RP1000073	1.552	1.742	0.000	0.919	0.996	0.623	4.055	9.765
NT2RP1000078	2.896	0.000	0.000	0.230	0.741	0.763	0.567	3.421
NT2RP1000079	49.027	29.652	15.514	6.677	6.650	9.256	18.182	28.375
NT2RP1000080	16.385	13.693	8.875	4.934	5.832	9.673	15.737	12.194
NT2RP1000086	7.169	3.761	10.248	2.946	7.423	5.286	3.826	0.000
NT2RP1000087	0.000	5.038	0.000	1.221	3.506	2.887	0.000	2.053
NT2RP1000089	4.302	9.012	8.097	5.674	2.992	4.624	0.418	13.867
NT2RP1000090	52.428	58.867	69.998	38.821	17.374	29.637	36.043	79.235
NT2RP1000100	3.207	3.774	1.540	2.138	1.112	1.149	0.000	1.791
NT2RP1000101	92.707	46.496	68.186	33.782	33.861	36.104	55.994	56.718
NT2RP1000111	4.451	9.940	6.651	2.623	8.151	2.766	11.052	2.965
NT2RP1000112	3.985	3.478	0.000	2.480	0.000	1.727	2.041	2.374
NT2RP1000124	24.505	9.928	6.917	5.644	2.553	12.703	2.802	42.644
NT2RP1000125	24.817	79.995	139.555	49.819	97.770	62.060	44.484	52.427
NT2RP1000129	28.170	30.324	26.037	10.799	3.638	16.350	16.315	13.950
NT2RP1000130	5.381	7.279	14.556	2.578	10.778	12.987	0.000	20.710
NT2RP1000154	17.054	18.625	18.032	7.765	17.883	13.855	12.502	19.133
NT2RP1000163	18.531	7.739	9.822	4.142	3.589	2.512	6.952	17.030
NT2RP1000170	14.775	6.603	3.911	1.557	5.549	3.844	7.224	15.609
NT2RP1000174	10.066	4.006	4.875	1.601	3.951	1.497	5.060	0.857
NT2RP1000181	108.209	58.429	137.843	40.129	31.719	74.897	73.935	56.201
NT2RP1000191	9.285	6.645	5.460	3.099	6.842	12.624	5.864	2.766
NT2RP1000202	4.547	3.462	7.203	6.298	6.151	3.022	2.481	4.122
NT2RP1000239	0.000	0.000	4.313	1.852	1.396	1.558	2.101	1.136
NT2RP1000243	10.228	5.330	3.864	1.538	6.834	4.100	5.184	5.579
NT2RP1000255	6.844	3.187	2.512	1.848	1.326	2.012	5.711	5.678
NT2RP1000259	10.073	6.510	10.276	1.573	3.601	8.515	4.509	4.367
NT2RP1000261	0.000	0.000	0.000	0.000	1.606	0.000	1.763	0.000
NT2RP1000269	233.453	119.331	130.392	48.933	78.334	111.105	129.953	95.341
NT2RP1000271	504.212	314.887	684.003	191.587	126.841	351.080	221.963	268.189
NT2RP1000272	130.317	52.877	78.345	38.313	30.575	71.136	50.465	37.296
NT2RP1000279	103.540	36.699	55.522	23.329	29.320	68.415	50.629	9.388
NT2RP1000290	383.695	214.173	295.250	136.106	105.408	267.258	215.344	195.667
NT2RP1000293	139.263	71.666	91.679	43.735	54.577	85.003	75.589	61.144
NT2RP1000300	219.317	94.497	120.961	62.228	73.747	166.238	105.443	25.701
NT2RP1000324	205.212	96.463	109.241	73.482	49.779	120.952	75.697	54.085
NT2RP1000325	567.975	208.141	235.225	74.690	106.786	296.190	175.163	181.979
NT2RP1000326	114.548	37.978	60.587	21.766	22.713	70.707	48.865	22.186
NT2RP1000331	14.215	11.082	12.198	9.945	5.554	9.595	5.409	16.164
NT2RP1000333	175.329	62.474	124.398	35.732	30.723	116.009	80.360	48.737
NT2RP1000336	5.071	3.476	0.000	2.085	1.485	4.216	5.855	5.234
NT2RP1000347	8.732	4.239	0.000	3.444	2.753	3.942	4.829	4.180
NT2RP1000348	9.118	3.224	2.495	2.895	3.816	3.756	4.511	1.450
NT2RP1000349	6.925	4.441	0.000	1.180	2.776	3.407	3.025	2.512
NT2RP1000353	26.257	80.510	62.172	39.139	13.657	50.445	33.300	118.905
NT2RP1000356	25.146	46.385	82.299	43.972	13.987	49.489	26.724	110.239
NT2RP1000357	213.820	128.901	421.667	86.179	76.445	136.345	94.747	87.310
NT2RP1000358	186.987	64.055	108.939	32.778	41.723	110.904	74.510	67.426

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Table 78

NT2RP1000360	297.314	134.601	191.999	71.819	85.890	202.062	147.810	89.594
NT2RP1000363	364.040	212.933	280.442	136.437	123.748	247.266	256.906	128.344
NT2RP1000376	127.768	49.154	84.631	29.920	40.910	71.095	82.258	43.951
NT2RP1000386	39.353	145.725	56.520	52.245	252.336	185.039	121.336	65.534
NT2RP1000407	2.663	0.197	0.000	2.423	0.000	3.032	2.424	3.461
NT2RP1000409	0.000	5.878	0.000	0.850	0.000	0.424	0.000	0.000
NT2RP1000413	7.153	2.048	2.681	0.000	8.303	4.015	0.344	0.307
NT2RP1000416	0.000	0.000	0.034	0.000	0.000	0.000	0.000	0.000
NT2RP1000418	9.174	4.984	8.733	3.988	5.668	7.649	7.116	4.283
NT2RP1000420	2.125	0.924	0.000	0.000	0.000	0.000	0.147	0.000
NT2RP1000434	0.000	19.791	0.000	0.750	0.000	0.189	1.654	0.000
NT2RP1000439	134.853	56.272	115.668	51.887	49.782	73.229	64.079	15.355
NT2RP1000443	58.432	1.440	0.000	3.540	5.276	7.299	4.900	2.656
NT2RP1000447	3.820	2.955	0.800	3.240	1.187	3.303	1.052	3.063
NT2RP1000448	3.888	0.697	0.000	0.778	1.043	0.314	0.856	0.000
NT2RP1000451	5.766	4.110	3.245	4.480	1.272	3.036	1.022	3.138
NT2RP1000458	277.437	139.151	249.632	114.073	87.709	243.919	188.141	160.796
NT2RP1000460	216.381	129.722	192.470	86.161	96.273	135.913	170.172	91.267
NT2RP1000465	290.518	221.955	402.881	192.151	210.010	230.322	182.401	205.887
NT2RP1000468	29.203	30.933	61.862	19.161	13.854	16.791	11.220	11.713
NT2RP1000470	247.991	94.630	118.548	33.073	62.185	113.536	101.037	71.927
NT2RP1000477	3.039	1.894	0.000	0.887	1.636	2.721	1.261	1.757
NT2RP1000478	2.842	0.655	0.000	0.363	1.122	0.412	1.375	0.000
NT2RP1000481	5.676	0.693	1.376	2.294	1.991	0.993	2.480	1.941
NT2RP1000493	5.004	0.820	0.000	1.070	0.687	1.252	0.401	0.344
NT2RP1000513	183.214	62.178	133.983	29.869	42.569	122.982	62.701	55.329
NT2RP1000522	183.947	57.483	120.005	32.529	32.275	110.978	93.419	62.294
NT2RP1000533	21.686	8.198	15.700	5.816	6.071	12.902	9.030	5.528
NT2RP1000544	3.732	10.988	1.704	2.465	2.581	6.543	9.371	6.069
NT2RP1000547	0.300	0.310	0.170	0.000	0.000	0.000	0.000	0.000
NT2RP1000551	3.716	1.322	3.371	0.657	1.870	1.149	3.287	1.199
NT2RP1000567	18.148	4.535	7.630	1.128	0.978	9.115	8.337	2.192
NT2RP1000574	2.807	2.740	4.159	0.000	1.266	2.846	0.662	0.000
NT2RP1000577	5.767	6.059	6.234	2.033	4.066	4.517	1.545	3.168
NT2RP1000579	13.591	6.812	7.808	2.066	3.452	4.699	7.020	6.279
NT2RP1000581	23.446	8.664	15.950	5.531	6.046	15.075	12.761	9.085
NT2RP1000593	6.058	14.376	5.780	2.580	5.057	9.162	5.483	15.975
NT2RP1000604	3.081	4.126	5.413	5.134	3.748	4.785	3.835	2.255
NT2RP1000609	27.487	3.174	10.612	2.228	3.988	13.382	13.762	3.825
NT2RP1000613	4.356	2.265	1.529	1.001	0.000	1.184	2.710	0.767
NT2RP1000622	15.005	7.496	8.013	1.958	1.752	7.985	7.518	6.485
NT2RP1000627	17.344	14.772	22.410	6.441	12.047	16.356	20.729	10.336
NT2RP1000629	15.718	4.144	12.352	4.104	4.312	7.820	11.024	7.693
NT2RP1000630	65.249	32.499	52.699	15.138	14.415	30.508	33.741	18.936
NT2RP1000639	43.900	18.204	18.020	10.187	10.606	19.791	14.683	16.200
NT2RP1000640	86.217	156.971	37.078	60.057	32.726	29.102	17.026	76.883
NT2RP1000646	7.394	16.894	13.629	5.542	5.660	7.382	1.582	2.851
NT2RP1000659	25.494	13.979	53.935	11.276	9.119	12.945	10.602	15.936
NT2RP1000674	10.820	5.502	9.633	4.224	4.542	3.907	5.942	5.755
NT2RP1000677	187.310	76.173	99.589	25.959	49.679	90.146	95.230	63.227
NT2RP1000679	9.839	5.907	7.263	2.229	1.965	2.520	3.853	6.223
NT2RP1000688	30.741	21.137	41.993	9.852	14.205	17.736	20.738	18.729
NT2RP1000689	8.594	2.814	13.021	1.222	4.171	7.394	4.473	3.167
NT2RP1000695	1.813	3.104	2.068	0.810	0.000	0.000	0.786	0.000
NT2RP1000701	1.280	1.032	0.000	0.000	0.000	0.855	0.000	0.607
NT2RP1000702	4.112	3.346	8.473	1.156	1.698	1.616	4.749	0.000
NT2RP1000713	0.233	0.022	0.927	0.000	0.000	0.000	0.300	0.000
NT2RP1000721	199.937	95.449	152.563	45.581	64.142	102.872	121.431	76.919
NT2RP1000730	24.414	16.302	64.370	4.470	6.129	18.698	8.948	6.185
NT2RP1000733	9.992	13.894	13.138	3.593	3.087	6.945	6.918	10.277
NT2RP1000738	357.551	171.924	254.026	65.731	120.196	211.940	169.539	140.421
NT2RP1000739	261.372	106.684	146.597	37.731	77.574	193.277	164.547	67.465
NT2RP1000740	60.717	34.514	37.472	15.130	15.350	35.255	35.792	28.239
NT2RP1000745	13.275	9.551	20.132	3.376	1.635	3.601	3.265	3.969

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Table 79

NT2RP1000750	134.663	52.958	80.346	28.605	36.158	71.713	92.250	39.685
NT2RP1000751	17.717	44.325	31.941	32.295	15.461	19.059	18.084	64.708
NT2RP1000767	12.860	6.572	9.057	2.510	3.872	3.120	5.111	4.085
NT2RP1000769	27.412	21.636	18.089	7.324	7.758	13.441	12.436	7.317
NT2RP1000780	7.664	2.995	3.269	2.715	2.030	0.000	0.000	0.000
NT2RP1000782	11.618	23.259	28.607	5.886	16.596	14.946	5.301	7.061
NT2RP1000796	118.585	56.532	75.809	15.096	41.498	78.341	73.407	26.885
NT2RP1000797	215.680	107.927	100.844	28.806	53.841	131.952	306.946	77.792
NT2RP1000800	5.249	3.787	2.211	1.617	7.056	3.306	3.512	2.851
NT2RP1000825	49.312	22.623	29.009	4.529	15.271	16.815	24.570	12.101
NT2RP1000833	67.848	23.702	41.132	9.260	13.328	25.255	29.305	27.307
NT2RP1000834	21.157	17.555	15.686	11.112	11.392	19.117	14.348	17.998
NT2RP1000836	12.434	11.272	7.839	3.196	2.621	7.219	5.827	5.382
NT2RP1000837	98.743	40.415	104.822	21.833	23.029	41.395	35.068	27.483
NT2RP1000846	14.775	11.209	35.656	4.957	5.131	7.919	3.229	5.512
NT2RP1000847	27.431	18.237	16.588	10.757	10.320	14.784	19.182	10.029
NT2RP1000851	214.374	87.847	128.937	45.113	51.955	144.598	108.723	51.968
NT2RP1000856	26.023	29.514	67.757	23.663	28.185	38.015	15.874	11.458
NT2RP1000860	163.711	61.100	101.078	35.949	41.953	87.889	80.204	48.859
NT2RP1000902	24.271	31.899	49.716	12.862	11.237	22.189	17.326	17.501
NT2RP1000903	68.716	24.490	31.806	9.135	15.239	68.242	28.337	14.115
NT2RP1000905	25.662	13.385	22.530	7.568	3.894	6.452	12.011	13.929
NT2RP1000915	22.768	32.699	39.412	17.920	10.752	16.493	10.059	19.431
NT2RP1000916	36.356	17.076	24.787	8.241	2.752	29.963	18.336	4.134
NT2RP1000921	20.200	10.536	22.363	8.324	5.717	15.898	15.473	4.407
NT2RP1000943	9.440	4.278	14.836	10.665	2.682	3.445	1.686	1.791
NT2RP1000944	65.067	27.816	40.730	12.441	18.584	43.858	29.682	34.740
NT2RP1000947	18.414	12.386	22.697	15.197	10.849	17.723	9.687	20.200
NT2RP1000954	28.307	24.912	28.425	5.358	10.337	20.625	13.192	15.554
NT2RP1000958	21.987	38.788	40.914	23.030	11.285	20.525	21.953	28.920
NT2RP1000959	84.562	81.956	164.902	59.895	32.501	60.329	47.308	77.704
NT2RP1000966	104.461	73.705	101.907	58.853	28.479	65.560	39.891	37.125
NT2RP1000974	213.892	124.166	171.079	71.813	73.877	160.514	104.131	41.698
NT2RP1000980	16.802	11.080	6.958	4.146	7.799	7.626	6.311	2.017
NT2RP1000981	50.385	24.506	35.067	13.841	17.653	24.416	15.302	5.946
NT2RP1000988	19.623	11.058	22.064	9.003	7.658	18.310	15.545	11.394
NT2RP1001002	56.891	33.510	22.993	6.717	20.078	27.348	21.988	16.177
NT2RP1001004	23.268	13.134	13.405	6.295	5.883	11.999	12.399	18.783
NT2RP1001007	29.127	10.102	12.426	8.003	3.193	18.313	13.582	9.737
NT2RP1001011	36.507	27.547	42.002	16.657	13.048	28.628	24.654	12.589
NT2RP1001013	9.942	14.082	54.179	41.030	16.518	29.607	9.620	52.526
NT2RP1001014	19.677	17.977	30.913	10.101	11.200	9.468	17.655	12.776
NT2RP1001020	39.078	9.107	36.274	3.816	13.500	15.563	15.121	4.580
NT2RP1001023	5309.613	985.566	1698.618	284.967	1874.160	4332.654	3092.785	808.260
NT2RP1001027	73.098	53.184	34.629	18.681	24.296	93.325	67.199	51.245
NT2RP1001031	6.727	3.944	1.413	2.625	2.583	4.462	2.652	2.043
NT2RP1001033	34.383	18.547	52.827	11.061	12.794	15.798	10.825	16.802
NT2RP1001042	16.664	10.042	32.855	18.106	26.513	10.262	8.945	11.915
NT2RP1001045	189.863	33.846	51.766	24.186	48.474	72.682	35.437	30.767
NT2RP1001073	12.246	10.612	7.850	6.640	5.048	9.855	6.935	5.520
NT2RP1001079	91.852	71.311	176.776	25.199	28.090	49.291	51.519	16.408
NT2RP1001080	36.634	23.422	19.061	11.316	14.731	18.812	18.139	11.376
NT2RP1001113	14.930	5.617	8.219	2.444	3.358	9.872	5.861	3.904
NT2RP1001159	327.758	59.111	125.441	72.993	66.677	187.780	55.003	98.072
NT2RP1001173	16.780	13.137	27.175	6.169	17.090	13.269	9.476	11.252
NT2RP1001176	12.987	10.035	21.336	6.618	14.457	10.468	9.085	4.024
NT2RP1001177	47.481	25.797	35.864	7.900	13.900	29.446	22.230	7.579
NT2RP1001185	90.471	76.839	221.325	28.708	27.738	39.654	27.055	27.089
NT2RP1001199	15.790	17.518	27.913	11.849	14.093	14.390	10.829	11.780
NT2RP1001205	22.415	19.355	38.756	18.438	19.648	28.439	20.497	36.255
NT2RP1001215	26.469	21.856	25.048	13.068	11.039	25.483	15.692	15.808
NT2RP1001225	54.629	20.260	37.472	13.542	10.291	26.429	33.484	22.194
NT2RP1001245	11.787	8.531	12.195	4.229	4.219	12.906	5.042	9.166
NT2RP1001247	6.228	6.100	7.648	1.747	1.022	2.368	3.698	2.028

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Table 80

NT2RP1001248	49.226	25.943	116.648	10.461	11.820	12.652	13.256	17.837
NT2RP1001253	16.172	14.468	19.494	5.712	7.057	20.880	11.966	15.830
NT2RP1001288	31.909	17.523	37.293	9.003	10.973	24.180	18.180	18.610
NT2RP1001294	25.024	26.137	24.014	7.577	12.732	16.248	11.737	14.676
NT2RP1001302	20.570	17.865	14.990	7.914	7.089	11.711	10.424	6.370
NT2RP1001310	73.659	50.596	61.003	20.191	35.975	42.746	31.795	30.891
NT2RP1001311	107.757	35.881	46.474	17.712	21.645	48.944	43.729	26.945
NT2RP1001313	55.324	32.674	63.966	13.492	14.367	18.129	17.116	14.648
NT2RP1001324	35.171	18.577	22.653	7.819	11.963	16.113	15.675	21.371
NT2RP1001349	44.453	17.959	25.475	6.766	11.881	22.818	27.028	20.116
NT2RP1001361	55.753	27.902	58.131	21.682	28.045	60.728	52.605	27.148
NT2RP1001379	126.769	137.614	71.862	24.018	47.600	154.003	231.914	35.839
NT2RP1001385	74.494	89.642	123.622	19.403	22.929	45.989	34.307	19.045
NT2RP1001395	45.302	31.340	24.575	7.512	17.756	24.165	18.832	16.437
NT2RP1001410	23.514	23.629	40.104	12.632	9.318	21.843	13.537	8.295
NT2RP1001424	10.618	33.112	10.799	2.636	4.204	7.482	8.833	25.347
NT2RP1001432	12.466	40.995	9.503	1.789	6.323	5.098	8.187	7.252
NT2RP1001449	55.536	20.728	66.767	10.440	26.188	27.184	29.004	30.274
NT2RP1001457	30.322	32.721	37.777	8.330	12.956	20.340	25.841	17.849
NT2RP1001459	88.712	62.417	75.498	27.541	35.602	62.144	51.183	51.852
NT2RP1001466	16.844	23.355	27.785	10.621	12.274	14.384	8.050	13.792
NT2RP1001475	89.839	111.813	276.258	35.857	23.078	34.083	16.906	15.713
NT2RP1001482	9.804	7.238	3.123	7.419	2.367	3.451	2.538	1.692
NT2RP1001494	18.452	17.405	15.730	1.433	3.642	8.911	7.609	6.956
NT2RP1001500	2.143	2.316	3.634	2.456	0.000	0.086	0.162	0.765
NT2RP1001517	14.740	13.801	16.801	3.704	5.628	8.123	9.615	6.297
NT2RP1001540	50.226	35.070	52.423	11.150	17.869	36.090	28.195	7.025
NT2RP1001543	87.779	27.665	55.068	12.390	25.264	48.623	28.462	18.547
NT2RP1001546	51.476	99.385	143.880	25.320	72.799	104.259	38.212	42.007
NT2RP1001550	67.741	63.428	53.684	15.107	31.309	40.950	26.433	16.133
NT2RP1001553	34.956	17.566	22.966	10.039	10.915	17.367	20.710	19.945
NT2RP1001555	33.240	52.576	54.908	25.406	21.523	42.121	29.401	24.807
NT2RP1001563	30.536	23.522	26.745	10.623	16.136	20.228	17.699	11.340
NT2RP1001569	90.271	31.802	37.662	7.791	18.755	32.159	31.572	22.545
NT2RP1001584	125.503	64.642	101.860	20.979	38.153	69.983	85.177	68.021
NT2RP1001599	25.536	22.635	29.822	7.141	9.376	19.848	14.150	13.608
NT2RP1001616	38.077	18.321	20.981	7.268	5.256	12.873	14.067	12.210
NT2RP1001654	77.215	24.275	26.850	14.308	14.684	36.754	26.803	17.786
NT2RP1001665	20.132	15.451	16.433	5.156	9.958	5.979	8.761	8.109
NT2RP1001679	261.384	264.730	245.821	192.156	85.798	197.731	172.668	434.739
NT2RP1001681	21.960	21.892	16.974	17.231	5.379	21.608	10.982	20.811
NT2RP1001694	27.832	32.368	36.517	12.438	29.150	109.147	231.086	69.267
NT2RP2000001	79.348	34.825	26.858	8.546	17.604	24.165	27.629	18.039
NT2RP2000006	32.218	26.701	47.407	11.066	8.723	14.994	13.215	12.652
NT2RP2000007	54.262	32.503	34.116	12.829	11.972	20.410	21.705	11.281
NT2RP2000008	34.810	31.036	59.562	20.809	17.226	20.509	17.286	54.391
NT2RP2000010	12.320	9.820	24.557	3.019	5.341	8.149	10.076	5.865
NT2RP2000011	121.718	115.419	216.553	41.153	44.035	64.567	50.108	46.745
NT2RP2000027	74.085	69.757	136.369	23.981	28.217	40.308	24.108	20.710
NT2RP2000028	23.699	28.386	27.077	10.607	11.433	22.532	14.265	11.554
NT2RP2000032	10.199	6.568	16.529	6.282	6.462	9.523	8.119	8.527
NT2RP2000040	383.423	222.501	199.099	79.455	81.787	229.220	181.239	162.128
NT2RP2000042	97.011	62.254	67.677	29.525	13.003	45.921	45.196	41.158
NT2RP2000045	73.700	49.722	66.899	21.221	17.180	32.492	32.785	35.403
NT2RP2000051	37.323	46.342	93.958	33.924	13.292	43.534	29.174	17.962
NT2RP2000054	99.806	54.072	69.945	21.897	22.707	40.001	40.807	38.782
NT2RP2000056	57.518	40.207	41.868	18.309	24.303	26.794	25.564	25.156
NT2RP2000057	156.050	177.739	178.741	136.241	76.886	130.744	163.333	207.593
NT2RP2000067	59.366	13.414	39.371	6.372	16.511	22.699	22.699	5.023
NT2RP2000070	107.618	50.674	57.709	17.458	29.909	83.478	48.688	26.235
NT2RP2000076	48.409	27.260	29.570	12.733	8.235	32.852	11.701	13.485
NT2RP2000077	94.993	53.327	77.668	25.110	14.024	49.100	33.647	31.168
NT2RP2000079	62.685	66.203	139.230	32.930	26.739	30.432	16.329	18.678
NT2RP2000088	71.154	29.601	52.899	11.567	20.381	42.871	35.756	8.836

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Table 81

NT2RP2000091	39.115	38.293	35.366	17.159	14.253	18.714	15.927	10.202
NT2RP2000092	75.001	89.256	171.691	60.810	53.472	55.591	34.478	54.330
NT2RP2000097	31.201	13.401	27.451	11.261	15.139	18.293	17.851	11.653
NT2RP2000098	26.707	11.006	13.971	6.330	7.991	11.945	7.052	5.446
NT2RP2000108	169.612	134.647	385.078	90.234	79.343	81.573	54.191	92.458
NT2RP2000114	32.814	21.256	23.561	8.385	6.127	16.427	11.227	18.744
NT2RP2000116	24.247	26.308	35.305	21.085	8.128	21.812	11.292	29.326
NT2RP2000119	87.773	75.708	213.188	30.879	26.975	32.244	18.663	23.323
NT2RP2000120	28.158	40.341	40.702	11.423	17.144	20.974	18.758	14.232
NT2RP2000126	68.253	51.174	75.714	25.719	32.146	30.674	19.806	13.086
NT2RP2000133	40.974	21.406	31.855	9.468	16.094	19.158	19.716	9.703
NT2RP2000147	121.104	61.190	75.784	23.438	33.839	75.147	46.430	37.718
NT2RP2000153	96.598	63.476	66.144	23.377	31.821	72.069	43.415	32.773
NT2RP2000156	115.309	87.737	200.582	37.008	35.422	38.443	28.450	20.252
NT2RP2000157	24.318	18.096	28.697	14.121	12.284	22.086	12.179	10.763
NT2RP2000161	9.493	12.679	24.575	5.678	7.191	9.079	8.105	9.807
NT2RP2000168	11.413	14.646	19.908	3.979	5.383	6.466	8.554	3.206
NT2RP2000173	228.420	98.033	150.036	37.188	58.850	114.315	90.491	66.465
NT2RP2000175	78.839	44.514	71.096	15.404	30.614	50.131	40.431	40.206
NT2RP2000178	60.513	42.174	41.614	14.454	19.558	28.068	22.439	16.249
NT2RP2000183	120.139	90.798	139.074	34.168	44.541	64.271	60.391	53.828
NT2RP2000195	91.304	70.037	204.874	30.805	27.133	45.934	28.749	18.697
NT2RP2000204	91.419	106.652	263.856	91.981	356.822	154.895	68.553	248.768
NT2RP2000205	30.577	27.665	61.321	18.312	9.596	17.099	7.227	6.812
NT2RP2000208	53.204	48.346	85.459	22.464	20.371	37.407	31.136	31.123
NT2RP2000224	69.062	62.644	64.951	28.002	14.265	42.146	33.510	51.634
NT2RP2000230	56.320	38.161	51.891	19.712	16.865	28.186	30.382	25.164
NT2RP2000231	237.426	116.377	160.416	68.560	85.769	155.055	119.086	87.184
NT2RP2000232	49.708	32.849	24.700	10.366	11.881	31.935	21.623	13.775
NT2RP2000233	74.158	43.941	52.603	20.024	20.149	47.211	52.894	52.273
NT2RP2000239	32.380	15.399	30.197	8.574	4.025	17.013	20.268	23.735
NT2RP2000240	49.173	38.363	78.202	15.737	15.654	21.302	17.214	20.486
NT2RP2000248	17.308	13.339	13.368	4.823	12.687	8.493	12.992	9.218
NT2RP2000256	37.650	25.977	25.477	12.706	9.212	23.055	14.601	18.126
NT2RP2000257	69.335	66.181	244.979	45.881	37.192	46.969	31.322	46.624
NT2RP2000258	39.114	41.740	49.525	15.968	19.509	29.341	17.580	17.049
NT2RP2000261	46.051	30.214	48.737	10.438	13.441	22.674	19.894	19.556
NT2RP2000270	73.075	55.962	155.102	33.557	26.014	49.469	26.505	41.022
NT2RP2000274	15.514	7.310	20.284	4.327	6.428	13.479	7.807	4.833
NT2RP2000277	12.320	12.198	8.692	2.395	5.097	7.436	9.834	3.452
NT2RP2000279	12.294	6.735	9.825	2.486	5.467	4.265	7.545	6.898
NT2RP2000283	63.324	49.998	59.636	18.166	19.261	33.586	39.787	48.270
NT2RP2000288	38.289	22.877	35.809	11.594	14.150	24.632	25.978	24.657
NT2RP2000289	51.997	39.352	53.601	14.746	19.914	36.153	31.476	28.603
NT2RP2000297	76.236	71.227	206.854	45.839	34.290	40.991	22.703	77.905
NT2RP2000298	28.739	29.954	34.444	15.641	10.562	21.620	14.607	21.804
NT2RP2000310	29.075	14.696	16.125	5.503	10.245	16.627	19.121	11.456
NT2RP2000327	45.414	16.201	24.879	17.704	13.651	24.922	17.858	30.618
NT2RP2000328	36.600	35.521	50.933	15.515	23.798	33.981	22.925	32.863
NT2RP2000329	45.820	29.353	14.112	22.985	11.584	34.848	35.626	29.436
NT2RP2000333	33.894	26.367	89.382	12.302	13.127	27.377	10.155	15.517
NT2RP2000337	14.768	17.723	21.972	6.203	6.291	12.498	8.041	5.971
NT2RP2000346	53.051	82.391	46.420	15.624	13.030	26.358	27.011	31.395
NT2RP2000357	30.149	22.042	28.730	11.084	7.733	16.593	11.687	6.892
NT2RP2000358	16.228	10.853	14.700	2.291	4.114	11.789	8.150	7.184
NT2RP2000366	82.288	25.117	44.596	10.329	16.344	44.774	37.686	6.290
NT2RP2000369	21.429	15.884	19.746	6.532	11.361	9.148	7.691	12.275
NT2RP2000376	205.303	111.496	120.655	34.558	45.976	138.158	139.412	79.987
NT2RP2000394	31.766	23.882	31.577	11.745	14.448	23.860	24.285	20.279
NT2RP2000396	231.332	142.481	190.587	52.114	101.706	157.153	153.536	79.610
NT2RP2000412	67.028	66.250	119.740	21.685	25.253	30.952	32.657	39.766
NT2RP2000414	97.169	86.021	59.155	47.116	24.169	74.619	64.790	62.555
NT2RP2000420	34.977	33.139	27.658	7.585	9.872	17.817	19.531	15.065
NT2RP2000422	17.225	26.571	24.546	8.167	6.449	11.697	14.485	17.945

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Table 82

NT2RP2000426	114.626	117.810	111.501	29.759	51.358	87.480	90.640	100.150
NT2RP2000428	56.117	63.709	38.237	12.835	20.360	38.761	41.161	42.507
NT2RP2000438	54.621	34.534	49.392	15.765	13.700	27.527	31.816	22.667
NT2RP2000447	41.157	17.807	23.084	6.863	12.794	25.289	17.738	11.474
NT2RP2000448	26.410	27.807	28.584	7.787	12.459	20.751	18.164	12.208
NT2RP2000459	44.499	36.093	89.605	12.882	14.284	17.485	15.131	9.860
NT2RP2000479	21.922	30.183	53.808	9.553	8.835	9.648	8.854	6.739
NT2RP2000498	97.221	94.691	207.697	30.335	41.292	29.900	25.090	43.440
NT2RP2000503	15.067	15.551	20.810	5.166	10.196	9.766	10.763	12.056
NT2RP2000510	8.340	5.361	8.647	4.438	7.160	4.784	7.812	3.890
NT2RP2000514	10.423	8.148	14.693	2.596	1.773	12.792	6.695	2.902
NT2RP2000516	24.587	13.672	21.344	7.854	6.333	13.895	7.396	10.960
NT2RP2000523	10.281	2.981	4.878	1.371	8.071	0.000	6.857	1.961
NT2RP2000533	26.452	20.054	30.481	4.391	7.628	16.125	48.840	17.396
NT2RP2000540	52.523	22.512	28.503	13.567	14.612	28.427	22.545	11.372
NT2RP2000547	22.542	17.741	11.176	7.337	25.779	12.216	8.288	6.918
NT2RP2000557	91.024	63.951	163.497	30.438	30.047	43.813	31.490	9.367
NT2RP2000558	53.959	47.359	125.971	27.348	16.844	24.191	17.114	21.905
NT2RP2000564	30.446	23.046	22.258	13.084	14.165	16.265	14.861	11.150
NT2RP2000565	12.593	5.857	10.293	5.077	0.000	4.189	5.009	9.707
NT2RP2000583	92.921	56.070	68.992	29.211	14.291	50.282	32.844	34.467
NT2RP2000591	14.655	9.331	11.087	3.504	0.000	10.526	4.362	2.073
NT2RP2000599	8.002	4.780	7.951	1.807	1.614	6.232	2.299	8.293
NT2RP2000601	63.609	21.655	47.106	9.673	13.430	48.855	32.575	8.428
NT2RP2000603	101.578	37.142	48.248	16.412	25.194	51.543	39.363	20.157
NT2RP2000610	78.342	66.011	110.636	42.146	27.855	28.332	30.624	31.736
NT2RP2000614	139.380	106.590	188.604	171.750	58.678	83.079	86.298	185.276
NT2RP2000616	124.143	34.073	58.053	15.031	27.800	81.174	49.504	27.143
NT2RP2000617	50.724	37.802	37.086	17.602	12.086	34.751	20.157	16.389
NT2RP2000623	39.247	19.740	34.797	9.070	10.223	19.775	10.261	13.251
NT2RP2000634	29.431	24.224	35.865	13.077	19.480	16.373	23.806	11.338
NT2RP2000636	39.598	28.832	34.563	11.868	13.914	14.342	6.334	10.485
NT2RP2000638	43.027	34.379	58.259	14.094	15.200	22.724	21.525	6.843
NT2RP2000644	87.622	66.336	227.352	37.298	35.466	29.256	23.666	11.793
NT2RP2000649	28.849	24.035	32.562	15.166	18.629	25.012	15.485	15.528
NT2RP2000652	39.595	25.065	30.965	10.579	14.587	24.849	13.667	10.824
NT2RP2000656	12.851	14.986	7.925	2.952	4.388	9.997	3.990	6.959
NT2RP2000658	8.192	5.499	7.563	1.162	3.535	5.669	3.050	2.703
NT2RP2000663	38.633	21.653	37.840	5.964	12.174	20.777	13.553	39.917
NT2RP2000664	102.627	41.981	90.611	25.300	30.038	73.440	66.686	30.392
NT2RP2000668	41.209	35.434	46.568	16.251	14.705	25.339	29.016	11.020
NT2RP2000678	6.908	2.096	21.949	0.402	5.899	0.262	1.098	1.488
NT2RP2000694	47.376	19.986	45.832	2.636	16.192	24.523	19.843	12.311
NT2RP2000704	159.158	114.202	205.746	44.471	48.627	68.161	47.919	40.349
NT2RP2000710	33.138	26.994	21.890	10.683	6.833	17.938	13.596	8.070
NT2RP2000712	15.016	11.689	29.736	12.471	8.668	17.629	19.970	23.796
NT2RP2000715	61.771	35.912	115.757	20.470	17.051	26.042	17.159	21.325
NT2RP2000720	38.951	26.992	43.620	14.647	11.930	21.500	23.895	26.128
NT2RP2000731	8.039	11.373	11.261	2.986	4.755	2.127	4.657	5.827
NT2RP2000739	83.662	28.893	61.699	15.623	21.878	30.716	28.485	17.190
NT2RP2000748	21.953	22.377	38.996	16.815	15.564	15.846	20.219	20.054
NT2RP2000749	46.622	49.334	65.231	13.317	57.514	52.159	26.941	23.868
NT2RP2000758	79.204	43.258	49.681	18.768	17.058	49.245	31.463	9.472
NT2RP2000764	55.396	28.914	41.243	10.203	16.308	36.761	32.438	13.134
NT2RP2000766	40.275	50.060	83.340	10.610	48.180	26.508	18.850	15.663
NT2RP2000777	92.029	39.471	41.396	32.309	33.513	94.887	43.480	40.212
NT2RP2000786	91.676	61.265	70.189	16.798	30.669	51.517	41.968	37.840
NT2RP2000793	245.992	91.135	151.153	57.903	62.361	191.087	132.793	68.352
NT2RP2000796	24.053	16.664	26.693	12.773	8.297	14.258	11.004	10.440
NT2RP2000809	118.982	88.958	221.024	42.198	50.535	65.921	39.243	46.532
NT2RP2000812	23.931	28.037	26.224	15.476	9.968	23.492	19.671	6.489
NT2RP2000814	9.108	7.645	7.698	5.179	4.196	5.655	3.821	2.231
NT2RP2000816	49.615	22.174	23.358	8.758	4.975	23.109	16.789	17.124
NT2RP2000818	8.156	2.591	1.260	0.492	0.840	1.656	0.942	0.250

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Table 83

NT2RP2000819	18.931	14.180	22.186	4.470	4.973	11.664	8.535	5.164
NT2RP2000841	28.455	24.097	27.497	8.335	10.021	20.722	20.951	21.582
NT2RP2000842	34.381	17.071	34.845	8.688	13.092	22.498	16.807	14.291
NT2RP2000845	168.513	153.241	289.355	60.191	54.194	71.809	58.470	61.375
NT2RP2000863	43.408	19.456	21.479	5.334	8.450	25.326	17.757	8.334
NT2RP2000880	57.370	45.920	51.291	29.897	15.173	32.007	24.723	27.411
NT2RP2000892	10.063	13.581	18.264	3.215	4.302	10.360	11.152	10.295
NT2RP2000894	64.414	18.305	26.241	9.579	7.189	24.935	24.193	12.407
NT2RP2000903	38.945	14.595	23.755	3.839	8.850	15.625	14.467	11.189
NT2RP2000906	43.895	24.347	34.459	12.388	12.400	29.304	18.688	23.184
NT2RP2000910	76.036	47.430	175.193	28.258	21.020	30.976	28.638	37.229
NT2RP2000931	68.351	104.907	108.794	52.697	65.250	51.718	29.344	55.383
NT2RP2000932	30.706	39.023	31.030	6.448	13.290	15.553	11.313	11.145
NT2RP2000938	55.079	37.641	47.798	12.045	19.899	32.600	18.046	21.528
NT2RP2000943	64.610	32.689	54.181	11.802	18.241	33.817	55.424	23.572
NT2RP2000957	20.426	12.332	17.780	3.161	5.343	6.479	8.015	4.052
NT2RP2000958	74.825	23.934	37.910	10.227	22.164	41.633	29.369	21.256
NT2RP2000959	15.840	25.063	17.980	5.521	4.208	9.176	3.539	6.349
NT2RP2000965	57.687	40.458	51.330	27.882	16.372	29.535	32.993	35.643
NT2RP2000970	84.866	72.715	196.279	29.249	36.529	42.914	24.489	33.313
NT2RP2000973	42.690	30.786	42.102	8.964	13.498	23.369	20.702	18.360
NT2RP2000985	33.281	22.399	26.930	8.628	4.869	20.022	22.445	14.030
NT2RP2000987	47.736	66.487	94.477	25.911	19.844	27.890	23.633	33.551
NT2RP2000997	42.801	43.070	56.966	15.270	16.292	49.613	53.625	99.622
NT2RP2001024	47.605	28.976	34.658	13.810	14.526	32.054	39.269	22.962
NT2RP2001028	32.502	24.770	88.599	12.437	11.259	13.181	13.919	9.824
NT2RP2001036	206.163	234.625	568.339	116.746	85.893	125.996	88.623	100.568
NT2RP2001039	26.909	37.527	31.356	6.335	15.429	17.827	107.341	12.412
NT2RP2001044	51.134	33.868	42.988	9.015	23.633	31.422	25.682	20.463
NT2RP2001056	84.875	95.778	164.256	33.325	35.039	45.764	30.831	44.980
NT2RP2001065	57.092	61.052	49.599	18.558	20.229	29.013	30.628	32.966
NT2RP2001067	17.223	18.596	14.258	5.284	6.021	4.582	10.045	8.782
NT2RP2001070	92.615	68.975	230.584	37.646	41.225	36.295	43.293	26.959
NT2RP2001081	134.654	80.124	269.700	35.425	37.697	42.849	35.852	45.105
NT2RP2001087	54.476	40.059	74.079	12.377	21.043	25.654	22.663	15.956
NT2RP2001094	11.558	8.400	11.506	4.416	3.583	4.503	4.258	5.446
NT2RP2001119	66.924	57.741	177.347	36.523	37.388	40.013	41.672	39.968
NT2RP2001127	52.585	39.380	36.247	9.959	18.625	16.757	28.865	13.483
NT2RP2001133	94.638	97.465	155.477	25.417	36.346	28.836	28.731	38.218
NT2RP2001137	61.770	53.486	51.726	12.991	40.072	20.107	24.686	30.341
NT2RP2001142	54.131	38.507	34.342	8.552	14.688	17.434	23.807	20.602
NT2RP2001149	96.617	49.914	71.348	17.462	14.077	23.064	30.676	22.427
NT2RP2001168	313.055	217.008	205.763	65.294	77.914	146.883	169.121	159.484
NT2RP2001173	25.149	27.272	22.710	16.143	12.538	13.238	14.902	9.473
NT2RP2001174	21.134	17.440	22.879	11.089	14.190	18.125	50.600	22.839
NT2RP2001184	99.803	60.549	84.254	29.471	35.438	70.558	65.859	57.928
NT2RP2001196	19.492	14.580	26.749	5.551	9.060	20.695	9.289	15.340
NT2RP2001200	39.331	44.223	52.647	14.745	26.231	26.146	33.102	31.874
NT2RP2001218	32.396	16.531	28.960	21.387	13.855	8.618	18.872	11.236
NT2RP2001223	86.393	27.183	46.400	14.290	23.545	53.375	28.096	26.084
NT2RP2001226	223.868	143.880	155.700	46.575	60.808	148.876	100.150	92.898
NT2RP2001227	100.969	51.807	65.094	19.398	24.302	57.877	36.375	36.204
NT2RP2001232	49.733	30.526	64.154	11.691	29.542	27.238	22.294	35.950
NT2RP2001233	42.734	36.288	152.784	58.935	18.921	38.027	28.582	69.539
NT2RP2001245	28.251	16.266	32.594	18.419	8.746	38.272	8.565	38.035
NT2RP2001246	24.708	44.426	35.600	19.345	16.443	35.994	31.550	37.123
NT2RP2001268	44.328	34.570	58.263	12.894	20.636	54.014	31.715	54.645
NT2RP2001270	37.478	15.214	29.740	12.749	67.060	24.740	26.469	21.423
NT2RP2001276	15.931	7.905	12.674	9.235	4.389	12.549	17.273	10.235
NT2RP2001277	22.937	21.147	33.688	12.970	7.618	12.672	2.878	16.107
NT2RP2001290	66.867	20.688	27.890	13.340	37.970	38.444	27.073	34.029
NT2RP2001295	22.777	21.635	31.845	7.387	12.979	24.206	7.863	10.592
NT2RP2001297	105.753	198.744	183.982	210.648	32.481	152.615	178.985	399.018
NT2RP2001301	47.099	37.782	53.504	25.117	15.392	49.389	38.668	29.281

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Table 84

NT2RP2001312	493.097	175.989	324.513	96.070	132.150	315.768	282.270	146.542
NT2RP2001327	188.839	50.032	95.732	33.162	58.029	112.666	87.335	71.442
NT2RP2001328	177.255	162.267	495.438	96.591	104.203	93.675	57.120	68.709
NT2RP2001341	196.358	92.246	40.237	32.288	34.069	91.368	77.221	45.741
NT2RP2001347	148.143	157.594	486.643	72.828	67.867	81.012	36.464	72.260
NT2RP2001366	160.323	170.553	496.412	116.205	96.521	146.562	77.918	108.669
NT2RP2001378	217.791	51.524	110.978	31.128	51.690	147.191	118.132	56.442
NT2RP2001381	16.578	13.963	19.068	15.119	9.576	8.483	2.703	10.418
NT2RP2001388	84.013	52.476	228.213	47.276	49.007	52.881	33.168	44.592
NT2RP2001391	806.136	1438.949	1005.471	960.225	243.432	1160.112	1119.907	1127.811
NT2RP2001392	56.943	65.258	70.204	19.962	26.883	46.456	23.261	14.231
NT2RP2001394	104.258	120.852	350.764	78.963	59.635	75.686	42.505	53.751
NT2RP2001397	37.759	22.378	38.780	40.524	15.364	21.089	16.393	16.560
NT2RP2001400	24.214	10.586	19.685	10.414	12.173	24.380	11.796	22.055
NT2RP2001408	34.405	28.262	69.823	33.071	21.313	29.278	20.555	45.713
NT2RP2001420	74.700	70.462	212.932	44.495	49.469	33.427	30.009	41.019
NT2RP2001423	20.045	17.202	38.815	16.204	11.082	21.739	12.751	10.452
NT2RP2001427	88.620	91.272	206.946	51.057	36.829	49.854	34.587	57.012
NT2RP2001428	47.617	45.465	55.112	19.580	15.421	24.651	10.915	29.985
NT2RP2001436	19.654	25.606	50.345	11.202	18.548	32.033	22.720	5.351
NT2RP2001440	11.871	12.123	19.145	7.724	5.414	7.413	19.955	16.145
NT2RP2001445	11.934	7.217	22.053	5.885	6.872	7.794	3.377	20.818
NT2RP2001449	20.271	20.423	53.385	13.242	8.026	8.439	6.342	9.186
NT2RP2001450	47.497	32.496	58.237	18.660	21.208	28.880	23.620	30.207
NT2RP2001467	40.279	40.050	115.089	25.502	21.744	18.716	21.445	37.772
NT2RP2001469	66.890	35.784	93.465	23.588	33.470	54.095	54.103	33.386
NT2RP2001480	69.698	53.669	54.777	16.208	26.373	44.943	30.622	26.208
NT2RP2001495	14.156	12.199	18.018	8.178	14.762	10.694	8.800	14.613
NT2RP2001499	40.983	50.266	57.334	23.302	22.298	37.271	26.788	35.187
NT2RP2001506	83.528	66.377	104.162	41.795	65.692	61.567	55.661	35.667
NT2RP2001508	25.746	36.879	44.112	33.620	14.149	23.999	19.783	36.174
NT2RP2001511	231.898	147.751	199.611	46.927	77.381	122.787	130.829	108.021
NT2RP2001514	121.671	47.391	103.398	24.149	31.957	72.965	63.365	38.173
NT2RP2001520	38.773	20.470	34.140	14.159	13.366	19.602	22.077	7.741
NT2RP2001526	102.469	98.418	139.331	62.159	83.922	85.309	60.450	66.763
NT2RP2001529	189.308	69.082	103.704	31.713	54.543	173.158	96.700	74.482
NT2RP2001536	22.047	14.186	19.269	9.553	7.196	16.531	13.646	17.343
NT2RP2001538	123.315	222.563	281.173	191.775	90.257	199.255	133.592	422.435
NT2RP2001547	45.201	33.999	42.028	12.917	14.746	31.438	29.406	24.085
NT2RP2001560	146.079	68.501	131.623	35.625	46.061	88.704	90.584	78.703
NT2RP2001562	53.975	35.141	47.262	23.297	18.361	43.041	30.635	47.577
NT2RP2001566	55.453	48.563	91.463	37.157	27.507	54.780	37.595	42.663
NT2RP2001569	131.940	142.523	361.640	62.136	60.136	90.021	46.500	62.567
NT2RP2001576	103.537	76.306	58.434	23.607	34.648	91.306	67.270	45.219
NT2RP2001581	149.528	208.681	239.575	139.522	72.883	196.577	126.583	231.505
NT2RP2001597	52.409	27.790	43.630	13.807	18.650	35.875	23.646	43.012
NT2RP2001601	33.796	37.430	70.562	17.535	15.251	22.525	13.760	29.828
NT2RP2001613	10.438	5.350	6.715	3.155	6.423	9.119	9.830	14.501
NT2RP2001628	87.399	43.401	48.713	17.774	25.577	50.117	31.175	117.652
NT2RP2001634	38.792	56.546	47.793	23.992	16.006	30.530	21.235	42.849
NT2RP2001635	63.818	69.842	156.279	31.411	36.011	40.036	38.853	22.210
NT2RP2001660	31.664	25.538	25.905	6.081	11.137	20.048	20.365	48.159
NT2RP2001662	122.557	88.914	242.932	52.514	43.761	63.759	56.518	43.557
NT2RP2001663	33.056	34.206	58.783	11.163	16.477	39.485	20.869	25.608
NT2RP2001672	51.656	46.965	140.882	31.231	26.225	33.037	25.666	35.948
NT2RP2001675	8.589	6.791	12.510	1.982	5.806	3.149	4.861	6.461
NT2RP2001677	61.810	49.851	68.423	17.674	27.233	40.323	46.466	47.741
NT2RP2001678	70.100	86.779	193.110	58.566	46.915	85.668	62.835	64.186
NT2RP2001683	16.088	14.728	26.445	9.496	10.015	9.959	25.390	9.277
NT2RP2001699	116.996	54.743	185.463	33.235	33.217	64.457	41.391	50.672
NT2RP2001707	94.748	66.728	100.874	19.387	34.234	58.720	45.599	68.302
NT2RP2001720	81.079	33.745	39.415	16.859	16.907	38.973	31.931	30.227
NT2RP2001721	73.164	35.354	62.124	25.944	28.378	69.464	66.522	35.468
NT2RP2001740	23.081	30.430	27.131	12.949	12.248	21.055	20.053	28.546

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Table 85

NT2RP2001748	164.370	51.538	151.756	22.608	36.134	86.312	52.323	35.004
NT2RP2001755	10.363	5.707	7.354	3.303	2.490	20.122	2.133	9.371
NT2RP2001762	10.743	10.704	7.130	4.777	5.648	16.360	7.429	3.763
NT2RP2001768	122.047	71.860	129.000	29.098	38.722	67.999	58.129	48.111
NT2RP2001769	29.307	28.706	32.455	11.608	15.175	19.399	20.505	29.469
NT2RP2001784	18.824	19.322	24.434	8.167	13.814	14.835	14.266	10.332
NT2RP2001805	111.510	63.886	82.038	33.170	41.704	47.921	62.218	54.508
NT2RP2001813	15.000	10.225	13.797	4.221	9.786	3.548	11.805	8.246
NT2RP2001817	14.005	12.403	19.383	6.848	8.320	6.884	10.608	15.163
NT2RP2001818	30.494	21.374	23.441	6.808	14.438	12.858	13.055	9.397
NT2RP2001837	153.478	143.980	348.522	65.249	56.344	69.434	48.042	62.813
NT2RP2001839	68.237	44.006	65.237	21.186	23.824	37.874	35.524	54.235
NT2RP2001861	45.604	33.558	72.763	21.180	25.185	40.479	31.542	29.326
NT2RP2001869	79.101	52.967	123.399	29.766	25.811	40.870	38.251	38.150
NT2RP2001876	20.847	28.536	35.991	18.044	13.257	29.195	20.056	35.651
NT2RP2001878	105.429	34.989	86.887	21.675	33.547	76.806	64.301	35.521
NT2RP2001881	25.562	5.186	16.935	8.594	6.002	8.017	5.474	16.018
NT2RP2001883	162.487	96.494	76.800	26.663	40.257	93.069	57.806	50.662
NT2RP2001884	40.027	29.435	18.175	19.127	0.000	34.665	13.313	27.989
NT2RP2001885	41.527	29.494	60.284	13.719	9.345	26.427	24.717	30.448
NT2RP2001898	152.071	65.585	135.420	33.617	41.173	112.042	64.105	57.703
NT2RP2001900	20.075	16.336	54.207	10.431	9.790	20.098	19.168	30.123
NT2RP2001903	389.922	207.168	314.475	131.627	170.618	361.733	261.185	289.339
NT2RP2001907	118.240	77.557	213.664	50.816	46.691	58.895	52.711	56.061
NT2RP2001915	29.335	9.240	29.213	5.804	10.101	8.718	14.671	15.535
NT2RP2001921	70.657	42.199	23.786	27.411	23.817	52.083	27.655	30.244
NT2RP2001926	86.771	11.953	10.434	11.123	10.945	27.144	37.077	26.703
NT2RP2001933	210.457	80.003	159.875	38.312	53.192	114.539	90.251	48.849
NT2RP2001936	9.271	13.789	9.841	9.560	6.311	8.706	3.968	4.244
NT2RP2001943	329.800	151.136	357.167	96.135	99.997	227.342	186.800	161.131
NT2RP2001946	36.700	27.839	38.317	18.830	11.786	20.082	32.636	29.552
NT2RP2001947	49.825	40.322	58.260	17.399	25.524	30.411	31.309	15.258
NT2RP2001948	6.858	5.149	39.338	5.855	16.449	8.590	3.943	39.227
NT2RP2001956	204.499	97.036	150.184	34.215	55.776	144.746	109.645	45.142
NT2RP2001969	63.044	42.091	64.895	18.446	22.555	64.128	29.876	27.818
NT2RP2001976	8.014	10.925	13.322	14.259	2.776	2.729	6.432	21.452
NT2RP2001978	60.910	40.459	87.051	23.282	28.689	25.497	33.528	35.507
NT2RP2001985	73.126	35.661	72.052	21.029	30.385	52.486	46.885	41.899
NT2RP2001991	32.897	34.028	33.239	10.548	15.586	20.531	18.489	33.157
NT2RP2001997	38.265	33.006	69.711	20.057	29.835	29.074	30.213	39.156
NT2RP2002015	341.660	572.382	464.288	330.114	80.297	366.270	346.254	476.966
NT2RP2002017	33.468	25.736	55.897	13.982	18.424	23.720	12.540	17.897
NT2RP2002025	201.899	111.493	125.922	38.775	57.018	118.130	92.718	55.437
NT2RP2002030	147.806	150.643	447.960	95.773	104.163	95.260	65.007	88.254
NT2RP2002032	170.695	55.335	101.868	30.495	58.859	127.664	86.380	56.817
NT2RP2002033	147.111	92.379	481.152	84.872	61.493	72.667	37.144	74.278
NT2RP2002041	15.097	12.379	17.284	5.762	7.552	5.398	10.885	30.538
NT2RP2002046	15.094	19.275	25.228	11.030	8.158	11.642	14.255	15.385
NT2RP2002047	19.261	15.499	12.076	6.530	14.384	9.918	10.225	22.164
NT2RP2002050	71.226	75.633	97.017	33.238	36.421	49.003	42.580	45.656
NT2RP2002052	75.004	67.588	69.616	25.123	25.691	49.820	32.819	35.546
NT2RP2002058	9.803	11.955	11.648	6.527	5.940	8.570	15.678	16.434
NT2RP2002060	147.927	40.191	79.254	17.661	30.022	83.968	55.933	35.933
NT2RP2002063	8.334	10.615	17.124	3.910	9.032	6.499	6.095	43.967
NT2RP2002066	85.296	31.968	71.727	16.697	28.928	52.589	40.814	37.383
NT2RP2002070	24.791	21.309	66.961	13.511	11.537	11.893	11.300	28.065
NT2RP2002076	28.441	16.541	17.729	6.137	10.519	13.321	11.910	9.273
NT2RP2002078	75.992	38.941	77.227	23.502	30.063	65.434	39.358	28.599
NT2RP2002079	15.378	6.595	12.418	5.815	11.345	7.129	16.510	27.362
NT2RP2002099	78.520	17.490	39.514	8.705	17.165	51.830	37.473	36.146
NT2RP2002105	45.619	26.109	41.837	15.263	18.979	33.970	43.561	26.203
NT2RP2002115	4.270	4.361	2.711	1.795	2.838	1.055	1.725	0.659
NT2RP2002124	9.528	14.188	19.276	6.091	6.494	4.046	5.259	20.125
NT2RP2002137	42.205	16.739	58.339	7.326	12.132	22.097	14.684	13.003

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Table 86

NT2RP2002139	134.906	45.566	87.430	23.245	34.053	84.389	66.692	39.692
NT2RP2002154	73.877	40.956	58.084	17.359	21.276	53.977	32.847	25.981
NT2RP2002155	312.813	448.404	208.112	246.578	165.102	220.200	117.089	396.951
NT2RP2002172	30.233	30.674	55.659	15.991	11.479	50.028	14.567	76.933
NT2RP2002185	35.127	22.047	31.771	9.436	13.476	23.455	23.637	18.868
NT2RP2002188	281.595	70.032	141.729	44.333	58.463	164.587	118.094	78.046
NT2RP2002192	28.830	19.474	84.849	18.536	13.421	8.267	10.908	25.727
NT2RP2002193	51.545	23.270	33.672	10.534	17.989	33.897	31.972	33.050
NT2RP2002208	28.592	23.922	46.625	15.986	13.078	25.948	18.689	40.263
NT2RP2002219	13.529	18.299	23.304	8.697	7.005	20.832	6.994	4.421
NT2RP2002231	3.623	9.145	18.238	6.451	5.394	5.290	2.444	1.640
NT2RP2002232	41.922	30.600	40.665	10.290	12.646	31.637	16.070	23.193
NT2RP2002235	25.174	12.829	11.461	1.747	8.624	10.246	12.594	16.053
NT2RP2002239	123.863	99.627	183.537	54.220	35.311	68.845	72.486	114.538
NT2RP2002252	173.209	45.051	80.502	16.296	31.546	82.843	82.445	52.048
NT2RP2002256	6.776	3.892	12.301	3.488	7.236	6.566	9.391	9.526
NT2RP2002257	14.914	18.059	11.330	3.304	7.442	11.747	12.965	136.057
NT2RP2002259	25.623	20.902	41.590	9.164	7.968	18.892	22.893	29.020
NT2RP2002264	35.467	21.380	27.456	3.962	7.884	26.448	8.234	20.246
NT2RP2002267	99.224	90.968	353.970	55.091	43.373	63.895	30.469	55.401
NT2RP2002270	12.038	20.146	13.141	7.551	3.523	7.777	6.701	19.108
NT2RP2002281	49.615	38.410	43.936	21.926	17.935	51.455	14.825	35.239
NT2RP2002288	18.840	15.310	15.237	4.623	6.951	4.505	6.438	4.321
NT2RP2002292	70.138	79.487	98.062	32.152	32.815	48.306	41.287	55.682
NT2RP2002299	28.411	21.790	28.450	15.762	10.016	23.812	12.394	31.923
NT2RP2002304	17.776	27.505	25.401	9.478	10.570	14.112	10.173	10.213
NT2RP2002312	32.053	26.004	19.733	5.118	10.392	41.845	21.011	16.815
NT2RP2002316	15.618	29.406	20.363	11.321	29.588	16.866	17.862	43.519
NT2RP2002325	32.321	23.882	28.697	6.692	9.875	26.435	21.261	36.989
NT2RP2002333	117.384	75.765	92.724	37.475	55.245	56.768	79.089	134.509
NT2RP2002371	35.025	49.789	54.117	20.073	31.179	10.486	24.281	48.279
NT2RP2002373	73.024	55.638	58.797	24.729	33.686	48.754	58.440	58.483
NT2RP2002381	4.610	6.610	5.950	2.906	4.109	10.398	7.035	3.142
NT2RP2002385	73.600	28.798	39.973	10.268	23.738	57.377	29.062	18.367
NT2RP2002394	4.749	3.341	5.573	1.941	3.227	11.225	3.017	2.611
NT2RP2002408	30.199	16.610	24.803	8.840	17.966	22.778	22.751	14.463
NT2RP2002409	466.226	415.995	746.844	183.086	221.410	247.550	216.812	235.852
NT2RP2002424	73.955	40.022	38.781	11.417	27.269	38.757	36.192	25.977
NT2RP2002426	42.246	46.209	138.641	18.951	43.167	21.993	14.146	29.925
NT2RP2002429	38.796	37.515	37.290	13.976	31.959	40.592	16.576	28.408
NT2RP2002437	41.182	44.109	103.486	16.002	6.706	22.789	11.006	18.502
NT2RP2002439	300.787	110.081	147.018	33.619	60.331	171.025	155.332	90.923
NT2RP2002442	51.674	59.162	57.683	24.271	21.412	43.427	38.136	78.512
NT2RP2002457	87.804	91.782	200.265	53.883	50.903	42.083	43.069	58.125
NT2RP2002464	97.665	38.612	69.981	20.743	31.183	66.794	48.779	34.847
NT2RP2002475	87.229	49.226	48.473	16.952	38.579	51.432	45.816	27.604
NT2RP2002479	43.495	20.334	24.184	10.295	13.868	35.366	19.292	22.684
NT2RP2002487	95.041	44.922	72.897	21.815	31.046	43.590	37.943	47.177
NT2RP2002498	32.022	15.599	33.143	12.736	8.092	15.582	24.301	15.152
NT2RP2002503	143.137	80.337	119.421	48.392	35.509	96.570	63.743	69.363
NT2RP2002504	28.779	12.130	143.283	15.019	25.676	16.936	24.798	15.731
NT2RP2002510	389.826	185.539	464.842	123.573	125.657	192.079	171.751	115.972
NT2RP2002520	28.465	20.629	47.388	22.909	14.948	38.504	25.659	37.802
NT2RP2002527	82.404	66.911	163.583	35.753	34.220	51.754	33.562	45.539
NT2RP2002533	453.205	209.788	357.064	113.267	150.283	251.157	262.839	188.717
NT2RP2002537	39.475	40.266	89.504	25.635	20.657	31.517	13.708	23.210
NT2RP2002542	68.000	79.669	80.611	82.297	29.448	38.068	33.806	62.834
NT2RP2002546	27.656	17.241	60.211	11.584	0.000	26.089	6.935	5.274
NT2RP2002549	41.394	22.287	57.825	30.309	7.713	40.681	12.786	23.580
NT2RP2002564	135.808	83.403	115.471	41.607	30.969	95.939	62.575	50.150
NT2RP2002591	34.917	38.064	103.943	37.411	25.346	30.888	24.127	41.780
NT2RP2002595	29.155	28.991	47.139	17.440	18.604	24.511	28.272	25.178
NT2RP2002602	62.164	42.498	49.596	18.894	40.679	48.767	25.334	7.981
NT2RP2002606	23.368	18.641	18.058	7.405	14.392	5.066	8.402	33.190

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Table 87

NT2RP2002609	51.566	22.622	50.513	17.534	20.249	18.692	26.812	44.491
NT2RP2002618	54.802	20.530	64.541	20.957	20.177	31.222	20.834	32.080
NT2RP2002621	108.854	151.631	361.642	75.866	73.104	87.556	37.662	72.940
NT2RP2002643	79.459	49.749	159.326	32.265	31.588	30.054	50.389	48.139
NT2RP2002672	97.309	70.875	124.816	41.317	54.912	65.362	54.912	61.191
NT2RP2002673	33.731	27.367	31.454	11.741	16.225	18.592	18.872	41.668
NT2RP2002674	13.503	12.059	23.980	5.008	15.903	5.926	8.720	8.883
NT2RP2002686	45.156	22.604	57.057	22.253	22.373	30.389	27.672	13.377
NT2RP2002688	85.273	71.163	154.737	61.783	35.115	56.421	42.460	68.118
NT2RP2002695	80.865	40.613	62.941	16.213	22.197	43.453	30.540	28.172
NT2RP2002701	68.274	58.034	54.220	24.008	29.811	75.585	54.744	29.997
NT2RP2002706	66.710	49.408	147.083	42.409	25.501	40.462	31.482	31.678
NT2RP2002710	876.030	389.806	785.892	246.642	312.053	990.051	876.290	401.334
NT2RP2002721	120.344	48.897	112.902	26.906	37.076	81.599	62.600	40.801
NT2RP2002727	19.985	16.809	28.658	5.885	10.968	18.932	17.127	19.197
NT2RP2002734	84.484	81.389	244.997	57.973	45.229	35.711	33.199	39.655
NT2RP2002736	18.170	7.757	29.873	5.264	10.456	10.179	9.257	11.010
NT2RP2002740	13.219	14.424	23.343	12.863	6.975	8.152	8.795	7.772
NT2RP2002741	77.823	67.266	223.592	33.955	36.594	51.261	45.295	14.049
NT2RP2002750	140.558	111.369	512.500	99.367	68.412	72.711	76.999	72.280
NT2RP2002752	177.349	105.312	290.520	63.592	64.508	103.376	92.228	65.849
NT2RP2002753	131.824	60.851	110.980	32.981	43.667	85.850	102.908	117.429
NT2RP2002760	130.675	58.967	119.405	28.837	37.588	59.420	51.267	51.768
NT2RP2002769	19.077	14.018	32.873	14.190	12.332	10.357	15.988	25.043
NT2RP2002778	38.616	37.548	30.303	18.271	16.022	71.865	31.460	77.045
NT2RP2002791	95.319	55.458	105.096	34.190	38.076	66.995	54.639	45.519
NT2RP2002800	90.052	59.554	197.798	40.413	37.123	87.119	52.880	48.173
NT2RP2002805	14.997	12.041	9.573	4.470	8.397	5.324	5.699	14.665
NT2RP2002811	84.563	36.955	70.308	17.273	24.509	89.018	46.163	49.186
NT2RP2002824	44.392	48.364	75.269	21.980	25.621	56.385	42.073	38.118
NT2RP2002839	45.683	28.499	42.893	12.083	18.567	22.078	23.650	21.604
NT2RP2002845	46.337	22.545	45.003	11.450	16.060	6.978	26.900	14.552
NT2RP2002857	26.773	11.114	27.648	7.358	7.968	15.413	17.314	11.937
NT2RP2002862	122.430	114.903	392.000	81.893	61.001	82.758	60.301	50.334
NT2RP2002880	46.913	32.677	29.822	12.750	16.704	35.359	14.768	24.866
NT2RP2002885	24.335	26.185	27.174	10.146	19.062	54.580	55.170	22.593
NT2RP2002891	33.411	27.772	38.018	14.600	16.632	38.658	34.150	26.201
NT2RP2002907	31.117	36.465	35.948	13.227	13.010	49.335	37.225	26.747
NT2RP2002925	30.213	17.281	33.298	11.072	11.726	25.559	24.754	17.499
NT2RP2002927	21.224	35.383	40.539	21.437	7.365	35.485	14.771	39.460
NT2RP2002928	13.771	14.521	49.574	11.977	6.869	9.129	7.289	8.057
NT2RP2002929	21.741	22.530	32.027	7.934	12.601	20.143	13.573	25.568
NT2RP2002934	63.248	35.331	42.688	10.849	16.987	39.637	27.937	23.467
NT2RP2002939	53.914	30.833	62.082	15.330	19.313	35.512	35.749	26.290
NT2RP2002942	82.129	82.694	187.805	50.572	53.315	49.000	38.922	90.399
NT2RP2002954	33.490	25.335	35.779	11.591	11.217	27.293	16.672	26.618
NT2RP2002959	18.029	22.305	18.230	8.391	14.540	12.392	9.227	31.203
NT2RP2002974	34.775	17.807	29.755	6.220	18.382	28.562	36.888	41.144
NT2RP2002976	7.266	6.893	13.152	2.886	5.205	17.007	6.657	17.861
NT2RP2002979	156.906	139.229	395.529	82.939	71.144	104.220	76.074	81.377
NT2RP2002980	98.467	79.422	285.396	49.557	40.675	57.510	33.004	50.480
NT2RP2002986	210.452	66.962	105.842	25.570	34.404	156.863	99.482	35.944
NT2RP2002987	170.131	130.848	355.987	114.067	85.014	125.562	105.241	119.400
NT2RP2002988	35.092	33.804	42.437	7.516	22.093	78.216	26.257	53.462
NT2RP2002993	41.408	20.150	29.978	8.083	13.951	19.869	17.068	17.776
NT2RP2003000	91.683	72.701	265.303	52.674	45.922	52.225	38.486	61.960
NT2RP2003008	19.429	42.300	26.458	14.959	11.323	22.796	23.430	31.344
NT2RP2003020	146.283	83.102	231.026	31.287	198.298	95.120	89.298	74.362
NT2RP2003032	42.858	35.052	46.187	15.872	16.376	25.572	24.460	29.698
NT2RP2003034	97.685	100.455	302.158	45.216	40.853	44.346	20.833	60.360
NT2RP2003042	32.097	30.146	30.859	9.131	14.406	14.312	25.483	23.898
NT2RP2003050	43.965	23.480	42.356	12.150	15.913	20.938	29.611	20.940
NT2RP2003060	43.467	23.385	32.696	13.554	17.473	48.442	37.686	31.235
NT2RP2003073	90.622	74.038	305.973	46.484	45.555	68.737	36.287	64.071

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Table 88

NT2RP2003099	69.980	61.964	197.831	28.962	29.485	52.756	36.145	46.753
NT2RP2003108	22.037	23.450	29.734	12.784	12.243	25.414	19.582	14.441
NT2RP2003115	175.202	76.490	219.003	26.090	53.025	89.403	96.086	53.165
NT2RP2003117	132.572	135.106	428.449	65.631	66.802	77.649	41.504	75.169
NT2RP2003121	77.521	49.860	42.009	15.143	26.745	31.652	32.041	27.916
NT2RP2003125	35.377	29.656	27.135	9.957	16.383	12.805	20.265	8.252
NT2RP2003127	29.566	16.867	20.397	5.212	10.531	18.240	19.752	7.540
NT2RP2003129	50.461	54.112	157.477	25.025	29.892	16.686	23.103	33.770
NT2RP2003137	8.001	18.759	14.140	10.321	7.469	15.281	5.429	3.225
NT2RP2003138	52.296	44.278	85.267	21.446	22.368	30.612	24.709	34.031
NT2RP2003146	55.329	37.398	52.403	14.492	12.222	29.608	23.329	32.663
NT2RP2003148	150.386	104.523	330.270	60.524	70.523	90.836	76.602	100.291
NT2RP2003150	26.432	11.157	23.761	15.678	11.132	36.468	7.133	18.954
NT2RP2003157	58.172	46.518	64.963	42.288	23.422	50.314	42.129	48.145
NT2RP2003158	44.248	20.906	37.740	8.136	17.954	27.119	19.062	38.471
NT2RP2003161	19.274	11.968	16.062	2.701	7.578	17.086	7.441	31.024
NT2RP2003164	49.401	19.110	28.830	12.219	12.819	22.155	19.787	34.090
NT2RP2003165	89.985	65.955	218.487	37.132	35.205	34.406	24.887	33.303
NT2RP2003177	43.596	22.142	51.196	11.148	3.934	15.303	13.349	69.154
NT2RP2003179	69.718	46.328	169.618	30.883	22.456	37.444	43.967	45.776
NT2RP2003194	144.137	17.980	22.293	13.420	10.852	20.144	19.065	43.611
NT2RP2003206	7.840	5.369	10.850	6.014	4.029	11.290	7.725	3.709
NT2RP2003210	51.322	21.586	38.521	12.974	17.884	37.608	30.477	29.805
NT2RP2003227	42.906	18.716	24.162	17.143	9.513	37.425	15.949	23.165
NT2RP2003228	58.612	29.572	62.903	22.926	28.577	30.449	37.367	63.378
NT2RP2003230	5.885	10.431	148.181	5.253	9.252	9.617	6.228	22.492
NT2RP2003231	69.197	41.691	59.459	34.789	15.272	58.827	33.617	37.859
NT2RP2003237	30.563	38.860	123.572	28.832	11.050	15.189	9.580	23.097
NT2RP2003239	33.469	21.053	50.845	20.348	11.513	25.692	7.484	35.924
NT2RP2003243	145.467	34.182	76.360	17.705	28.702	66.482	55.093	28.921
NT2RP2003265	29.516	23.976	32.673	9.710	15.918	17.608	20.157	14.165
NT2RP2003267	65.087	29.515	67.969	24.282	21.518	34.797	27.241	43.679
NT2RP2003272	41.457	22.351	19.055	27.076	19.762	28.028	26.982	45.977
NT2RP2003277	107.913	82.634	92.986	31.633	32.424	67.812	26.460	53.116
NT2RP2003280	19.151	14.918	20.689	11.633	7.567	43.338	5.070	12.961
NT2RP2003286	21.848	17.740	29.829	11.104	6.965	28.110	26.734	26.233
NT2RP2003293	94.719	83.407	364.260	76.134	56.105	78.539	44.376	97.047
NT2RP2003295	17.874	16.886	18.717	18.256	19.625	15.088	25.617	16.166
NT2RP2003297	9.592	10.816	15.547	2.211	5.615	8.461	10.162	5.662
NT2RP2003300	15.144	16.953	26.519	10.354	14.045	6.847	8.974	11.058
NT2RP2003302	22.071	15.550	64.210	26.397	10.289	12.880	11.722	68.523
NT2RP2003307	22.086	9.418	17.120	5.220	6.112	15.691	17.396	7.096
NT2RP2003308	17.436	24.315	20.930	11.886	7.814	20.422	12.860	31.766
NT2RP2003311	22.001	9.144	13.842	5.360	10.074	18.616	5.176	21.146
NT2RP2003329	44.872	14.471	19.961	10.976	13.401	22.292	12.093	14.770
NT2RP2003339	20.422	19.625	85.412	16.458	12.443	17.818	9.125	13.152
NT2RP2003345	23.118	8.297	17.237	4.695	8.379	12.952	12.259	23.215
NT2RP2003347	12.389	4.636	9.822	7.720	7.500	12.461	7.182	16.011
NT2RP2003367	10.794	19.368	21.160	7.884	14.120	12.142	14.419	13.409
NT2RP2003369	41.141	18.327	38.318	11.072	14.356	33.971	28.126	19.613
NT2RP2003383	55.891	32.218	76.058	21.558	27.536	76.861	50.564	36.175
NT2RP2003390	73.620	57.765	91.034	41.124	35.539	63.744	46.234	42.766
NT2RP2003391	241.564	161.239	277.051	75.828	95.432	220.668	152.546	143.981
NT2RP2003393	11.758	13.507	20.112	4.687	11.809	12.940	19.991	21.749
NT2RP2003394	7.323	9.816	9.506	2.871	10.713	1.307	6.346	14.753
NT2RP2003401	25.259	3.938	8.376	2.832	4.096	7.246	16.169	7.442
NT2RP2003403	31.239	26.205	109.072	18.680	14.206	9.380	14.946	8.745
NT2RP2003433	79.603	33.408	70.460	19.431	29.526	42.730	34.783	28.629
NT2RP2003445	38.525	33.248	95.090	23.648	21.333	27.951	21.347	33.662
NT2RP2003446	67.228	39.971	49.302	18.878	21.829	54.339	39.113	29.464
NT2RP2003456	1.902	13.833	10.178	7.437	1.522	5.049	1.410	3.486
NT2RP2003466	72.001	27.022	47.862	12.506	26.814	66.543	51.004	41.515
NT2RP2003469	35.915	29.791	90.766	19.558	17.254	24.857	16.952	39.575
NT2RP2003470	20.820	31.916	84.744	64.680	20.126	61.522	22.215	98.657

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Table 89

NT2RP2003471	7.424	5.547	6.488	7.037	5.447	6.505	7.782	10.212
NT2RP2003480	78.094	65.408	137.798	31.787	40.594	58.633	37.776	39.678
NT2RP2003495	15.982	11.924	14.233	7.870	5.725	11.076	8.329	14.404
NT2RP2003499	55.449	13.382	25.597	4.229	14.517	54.430	36.252	15.105
NT2RP2003505	55.425	27.024	46.996	11.964	7.933	31.002	31.997	27.989
NT2RP2003506	29.029	19.815	26.696	9.949	12.205	23.185	12.152	24.906
NT2RP2003511	85.237	37.479	50.383	22.212	25.152	50.854	41.079	36.551
NT2RP2003513	2.085	4.521	4.122	3.531	5.027	3.740	2.918	7.377
NT2RP2003517	37.834	17.587	35.502	11.597	12.069	30.516	43.651	39.873
NT2RP2003522	24.832	37.794	30.938	13.985	21.613	21.384	15.975	15.713
NT2RP2003525	112.839	77.947	318.616	53.968	64.300	64.511	45.220	44.281
NT2RP2003533	95.494	87.932	267.080	44.833	35.543	46.891	33.401	37.402
NT2RP2003541	59.237	40.256	51.598	18.653	24.451	41.018	38.504	56.566
NT2RP2003543	60.456	24.016	25.862	11.661	16.145	17.623	31.288	25.312
NT2RP2003545	5.111	9.859	11.338	12.197	5.950	2.774	8.060	34.030
NT2RP2003559	26.905	22.287	37.874	13.292	12.911	24.477	17.350	31.685
NT2RP2003564	29.146	18.045	64.896	13.749	13.213	15.703	17.055	25.744
NT2RP2003565	71.340	106.907	131.344	34.826	44.614	78.728	62.826	61.650
NT2RP2003567	70.892	54.381	72.715	19.440	21.968	61.162	50.325	46.459
NT2RP2003575	8.045	11.848	16.656	3.697	4.227	5.271	7.753	9.628
NT2RP2003576	94.175	119.128	189.789	159.528	39.210	94.530	84.153	280.017
NT2RP2003579	55.985	110.923	72.170	19.865	32.853	121.326	99.589	58.803
NT2RP2003581	72.231	34.935	63.218	15.922	25.161	44.829	45.801	38.825
NT2RP2003587	109.102	46.403	76.235	20.483	28.667	127.344	62.139	47.892
NT2RP2003590	27.361	26.330	26.653	9.837	5.016	24.313	17.397	36.147
NT2RP2003593	98.848	66.189	91.401	17.565	31.030	61.583	54.982	56.233
NT2RP2003596	20.156	17.830	46.567	15.376	7.364	8.849	10.462	35.925
NT2RP2003599	99.163	72.506	53.708	30.551	33.831	64.394	76.259	72.122
NT2RP2003600	39.566	25.200	27.397	13.373	16.019	22.567	30.947	25.783
NT2RP2003604	30.188	48.497	24.769	15.941	13.513	20.832	18.908	35.739
NT2RP2003629	12.593	10.012	13.520	5.134	7.235	8.896	12.558	21.197
NT2RP2003630	55.769	31.553	55.456	13.290	24.270	37.506	32.166	28.383
NT2RP2003643	20.532	14.638	38.212	9.363	17.760	18.713	18.506	19.629
NT2RP2003655	46.795	29.612	38.397	10.145	18.688	20.220	24.997	18.685
NT2RP2003664	23.372	28.188	21.831	11.981	11.047	39.022	14.701	15.715
NT2RP2003668	98.074	77.678	215.011	48.838	58.733	45.358	46.022	49.968
NT2RP2003687	36.469	27.937	30.101	11.600	12.659	14.676	15.349	16.155
NT2RP2003691	57.166	66.814	140.266	28.579	24.877	10.915	18.651	30.704
NT2RP2003702	77.231	74.259	157.835	37.740	29.269	33.935	36.174	35.262
NT2RP2003704	33.958	19.273	90.406	13.087	15.614	12.526	13.208	27.631
NT2RP2003706	15.581	9.802	10.782	1.905	1.888	20.850	8.045	6.106
NT2RP2003713	16.960	13.155	19.058	12.333	6.597	11.248	12.533	12.834
NT2RP2003714	58.106	48.190	156.974	28.216	25.935	21.990	15.804	26.140
NT2RP2003727	16.878	30.048	11.471	24.840	10.360	26.581	2.051	18.209
NT2RP2003737	35.097	27.626	24.696	15.279	8.490	48.230	26.577	18.778
NT2RP2003751	24.927	12.926	14.285	5.654	5.362	15.115	11.036	11.385
NT2RP2003760	61.964	14.851	34.689	31.937	11.912	70.013	35.412	50.086
NT2RP2003764	70.923	28.030	49.140	23.190	33.253	31.845	28.042	21.978
NT2RP2003769	42.617	20.886	27.599	7.054	10.396	11.852	16.178	10.912
NT2RP2003770	137.506	66.296	82.283	29.001	19.657	59.586	43.465	55.063
NT2RP2003777	79.392	37.432	49.453	21.542	23.944	31.481	38.443	30.003
NT2RP2003781	113.598	78.822	248.846	43.005	41.064	65.158	51.558	43.936
NT2RP2003785	39.008	38.895	81.842	23.800	81.398	60.210	21.078	32.965
NT2RP2003793	29.403	32.842	38.373	11.279	11.070	27.094	13.519	16.114
NT2RP2003806	141.377	86.683	300.547	56.391	57.427	54.142	52.055	74.576
NT2RP2003825	200.861	142.661	421.147	81.431	83.143	96.953	65.464	115.589
NT2RP2003840	100.905	61.436	80.952	27.801	38.812	73.708	55.685	43.672
NT2RP2003857	135.915	99.087	88.444	48.707	32.982	109.107	66.696	63.138
NT2RP2003859	112.898	91.670	144.716	35.434	18.445	66.240	39.367	23.246
NT2RP2003871	16.891	14.873	18.946	20.075	9.742	10.433	6.276	13.332
NT2RP2003876	20.553	18.667	33.132	17.736	9.744	22.067	11.629	10.917
NT2RP2003878	10.935	24.440	15.728	7.186	11.534	5.285	2.003	13.835
NT2RP2003885	86.861	91.093	40.636	9.621	12.995	23.247	25.798	7.129
NT2RP2003898	42.684	30.561	43.471	13.576	37.187	19.007	22.509	33.529

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Table 90

NT2RP2003902	147.643	124.985	109.475	45.984	48.594	124.353	51.962	58.344
NT2RP2003912	125.311	242.124	511.945	129.243	109.998	129.880	47.537	95.222
NT2RP2003931	26.887	8.179	6.459	2.307	5.260	8.153	1.858	3.142
NT2RP2003940	186.397	64.618	262.034	55.607	30.649	41.635	23.343	65.087
NT2RP2003950	36.158	19.195	49.413	13.592	20.939	19.343	26.770	21.989
NT2RP2003952	15.955	17.931	35.750	13.974	12.406	27.300	20.083	13.016
NT2RP2003968	45.877	22.833	13.459	11.361	12.355	12.353	12.010	25.113
NT2RP2003976	37.958	44.808	95.495	38.986	28.544	21.209	8.325	15.117
NT2RP2003981	38.654	43.006	57.657	15.338	29.345	30.659	23.563	25.867
NT2RP2003984	132.353	65.644	60.516	16.394	44.914	84.097	45.289	33.280
NT2RP2003986	186.062	146.313	421.324	109.891	71.468	70.656	43.927	53.945
NT2RP2003988	112.131	82.329	348.163	81.784	60.909	64.387	44.174	58.384
NT2RP2004013	35.821	31.054	41.104	24.447	20.809	33.899	21.394	38.113
NT2RP2004014	51.068	77.076	125.407	38.647	29.948	34.055	26.943	33.783
NT2RP2004036	34.592	12.491	12.862	9.166	7.965	9.771	12.722	18.319
NT2RP2004041	61.828	31.728	66.443	16.578	28.668	39.049	31.113	30.197
NT2RP2004042	95.416	34.628	56.458	18.193	31.581	50.180	28.757	19.510
NT2RP2004049	30.836	31.163	33.858	10.780	19.423	28.518	29.763	8.339
NT2RP2004060	33.939	22.080	47.086	13.117	10.598	29.819	24.922	24.074
NT2RP2004066	36.939	51.977	61.500	23.281	20.470	26.729	15.403	25.483
NT2RP2004069	29.217	33.889	47.332	22.168	14.676	23.715	30.550	18.563
NT2RP2004076	9.020	12.153	35.232	4.198	9.970	5.069	6.316	20.634
NT2RP2004080	23.022	8.835	21.995	4.309	8.489	27.512	5.327	10.188
NT2RP2004081	38.786	30.091	83.806	31.063	33.602	10.431	18.338	56.090
NT2RP2004098	47.764	21.424	36.354	14.003	22.548	26.497	22.648	13.621
NT2RP2004108	28.744	38.559	67.714	34.947	23.442	39.884	20.636	48.103
NT2RP2004124	43.031	24.659	37.232	12.008	12.194	23.487	10.186	21.361
NT2RP2004130	62.738	36.522	73.772	37.407	24.390	44.094	20.478	34.479
NT2RP2004133	163.939	56.278	112.008	40.808	61.092	157.167	95.384	52.343
NT2RP2004141	49.570	22.611	50.916	9.793	20.924	53.203	22.033	30.466
NT2RP2004142	34.850	23.492	33.078	17.102	15.132	27.703	11.237	17.601
NT2RP2004152	14.256	11.207	21.943	19.655	8.860	14.997	12.981	8.353
NT2RP2004165	147.447	92.813	238.228	40.497	54.357	70.413	30.081	44.940
NT2RP2004170	107.111	64.978	194.673	41.028	56.020	66.291	58.470	56.553
NT2RP2004172	22.440	15.213	19.562	6.795	12.099	15.400	14.334	12.024
NT2RP2004176	120.902	23.723	54.734	12.552	24.966	70.512	39.664	28.280
NT2RP2004179	72.406	30.327	45.178	12.821	11.733	33.905	35.842	30.011
NT2RP2004187	25.235	21.870	33.704	11.364	19.908	8.982	12.208	16.442
NT2RP2004190	33.406	32.037	37.882	8.251	10.063	16.897	16.826	36.649
NT2RP2004194	84.064	81.541	54.017	35.398	25.386	70.700	59.372	84.014
NT2RP2004196	105.711	65.320	61.236	35.178	35.795	83.939	40.164	46.168
NT2RP2004205	144.445	71.761	300.198	38.897	46.886	102.336	55.538	55.936
NT2RP2004207	34.894	12.571	14.703	6.333	7.074	34.908	17.403	14.550
NT2RP2004226	63.802	26.160	69.559	17.665	24.160	72.242	27.469	21.672
NT2RP2004232	19.053	14.404	25.695	7.555	9.877	15.593	12.523	32.679
NT2RP2004239	49.739	30.594	47.640	22.915	18.596	31.416	32.672	84.520
NT2RP2004240	43.946	56.977	36.742	39.656	38.450	39.881	22.758	41.302
NT2RP2004242	24.272	10.675	24.496	11.743	14.023	31.038	18.900	15.124
NT2RP2004245	18.673	23.813	15.945	12.936	16.016	18.326	7.178	10.903
NT2RP2004270	234.182	227.894	511.563	104.046	110.474	124.225	90.436	89.248
NT2RP2004300	59.573	43.407	77.768	15.466	13.124	34.892	25.094	19.570
NT2RP2004304	30.539	31.035	68.652	13.187	14.829	18.430	12.663	17.214
NT2RP2004313	52.639	26.629	35.836	12.439	13.307	42.833	29.621	25.693
NT2RP2004316	7.937	6.053	8.996	2.798	3.869	5.139	1.817	5.009
NT2RP2004321	16.873	18.267	25.584	5.327	9.905	12.235	12.417	6.754
NT2RP2004336	27.640	16.775	31.426	5.804	11.702	19.152	18.808	17.712
NT2RP2004339	253.896	255.780	749.568	115.658	151.722	126.261	70.845	110.855
NT2RP2004347	39.311	42.402	63.341	12.445	14.095	30.534	11.378	12.471
NT2RP2004364	71.148	60.019	167.378	28.894	26.652	36.565	22.223	23.600
NT2RP2004365	27.548	25.940	29.162	10.909	8.661	13.199	18.665	18.356
NT2RP2004368	34.341	34.055	33.525	8.555	14.786	3.641	15.740	27.122
NT2RP2004373	28.456	29.195	22.244	7.193	17.101	34.007	21.569	14.963
NT2RP2004375	22.258	23.633	23.795	24.768	8.964	14.617	11.807	28.153
NT2RP2004389	26.163	41.878	17.940	11.246	10.837	22.718	14.078	16.693

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Table 91

NT2RP2004392	80.969	136.238	185.407	107.306	71.728	98.742	40.421	94.207
NT2RP2004396	74.685	55.569	232.453	39.577	40.329	51.827	19.795	36.180
NT2RP2004399	60.880	42.455	62.661	13.504	14.626	15.041	17.402	11.134
NT2RP2004400	48.188	46.127	127.225	31.390	26.256	16.692	21.998	27.979
NT2RP2004404	94.197	59.189	80.085	33.584	39.340	32.995	41.822	41.552
NT2RP2004410	42.321	76.331	55.926	19.723	73.546	51.855	24.894	53.454
NT2RP2004412	13.609	18.755	18.039	11.352	6.207	29.062	12.037	4.016
NT2RP2004414	14.966	13.344	29.690	8.080	8.676	35.340	12.897	8.527
NT2RP2004425	15.759	4.692	13.145	5.794	4.150	4.256	11.714	5.665
NT2RP2004447	42.510	30.709	103.682	26.465	17.475	15.766	15.563	25.352
NT2RP2004463	64.696	47.400	81.626	29.385	29.125	65.475	55.192	37.759
NT2RP2004476	27.281	77.743	30.875	42.538	9.672	26.270	24.224	25.991
NT2RP2004488	22.602	16.334	32.445	12.940	12.612	19.801	12.795	25.305
NT2RP2004490	108.056	33.325	36.585	11.778	28.608	83.898	48.408	47.844
NT2RP2004495	24.445	8.305	18.686	11.202	4.044	24.630	15.828	7.643
NT2RP2004512	4.285	7.813	16.614	6.915	11.355	6.603	2.640	14.259
NT2RP2004523	100.195	69.639	192.670	43.236	39.566	47.481	28.357	44.602
NT2RP2004524	44.944	32.536	60.310	17.428	15.331	26.455	22.167	50.697
NT2RP2004536	61.814	19.213	31.957	8.029	18.302	52.061	24.818	16.740
NT2RP2004538	844.732	696.798	1443.610	422.320	403.488	580.281	434.455	470.608
NT2RP2004548	81.639	84.667	179.445	54.320	34.612	101.391	35.028	58.770
NT2RP2004551	20.101	20.257	8.701	5.567	6.509	4.732	2.996	4.857
NT2RP2004556	186.686	124.741	397.345	91.884	102.226	91.039	70.486	107.235
NT2RP2004568	92.661	117.910	131.215	47.958	44.000	46.192	45.819	146.073
NT2RP2004580	117.798	112.312	308.956	61.075	41.911	54.139	28.004	55.832
NT2RP2004585	88.489	51.782	72.459	31.850	12.237	75.503	38.854	53.952
NT2RP2004587	9.681	12.544	13.758	5.129	6.286	5.708	2.284	3.479
NT2RP2004594	17.013	7.543	15.550	11.674	7.962	3.168	5.020	19.533
NT2RP2004600	24.043	10.196	26.881	6.520	4.919	5.752	8.192	20.142
NT2RP2004602	123.606	61.805	80.505	32.526	37.163	36.752	6.232	35.380
NT2RP2004606	95.195	78.770	115.775	31.102	36.965	58.545	65.119	56.082
NT2RP2004614	88.734	53.501	57.570	36.772	25.720	49.230	34.724	39.520
NT2RP2004648	20.700	23.018	14.031	14.391	8.537	50.158	15.799	9.179
NT2RP2004655	15.547	12.030	20.925	7.353	6.707	24.083	10.703	5.977
NT2RP2004664	115.653	30.969	45.941	18.159	33.692	93.784	43.213	29.634
NT2RP2004670	37.342	20.435	29.733	8.337	17.064	23.260	22.585	18.670
NT2RP2004675	90.376	87.838	277.252	52.918	33.597	43.245	31.102	40.195
NT2RP2004681	80.974	41.493	71.220	24.851	34.241	54.143	45.414	29.175
NT2RP2004689	15.361	6.449	9.318	5.269	6.188	5.655	17.368	7.173
NT2RP2004709	76.835	57.745	96.083	23.386	38.263	34.748	18.462	31.462
NT2RP2004710	55.266	57.910	39.262	18.404	10.078	36.682	30.725	36.367
NT2RP2004721	326.635	50.412	98.334	21.234	65.676	230.530	162.452	35.853
NT2RP2004736	151.717	95.950	265.487	84.638	82.942	67.704	64.264	123.565
NT2RP2004743	34.118	25.149	128.802	17.805	15.041	28.540	44.641	29.720
NT2RP2004750	83.958	75.396	199.356	68.993	52.468	133.541	50.743	56.041
NT2RP2004755	31.604	24.450	46.432	13.888	69.303	26.643	15.757	22.713
NT2RP2004767	79.661	59.962	217.503	30.858	29.576	29.740	25.153	35.482
NT2RP2004788	13.287	13.098	19.823	9.173	5.193	3.545	2.323	8.664
NT2RP2004775	10.197	8.827	40.973	5.720	4.909	3.010	5.098	1.954
NT2RP2004791	68.964	37.186	133.612	23.163	25.209	12.978	21.406	22.080
NT2RP2004794	230.935	115.789	236.516	45.963	115.577	229.430	167.093	66.975
NT2RP2004795	38.086	12.315	42.332	9.762	10.237	23.540	30.190	27.839
NT2RP2004799	32.524	12.267	12.671	2.945	22.824	24.117	5.268	5.775
NT2RP2004802	10.030	10.579	12.121	10.897	8.541	5.714	8.012	10.032
NT2RP2004810	42.256	25.180	28.300	12.413	6.788	15.976	14.419	10.508
NT2RP2004816	30.283	32.534	22.857	17.849	20.763	23.062	16.143	21.647
NT2RP2004837	247.337	65.232	133.432	34.923	121.558	220.470	155.775	58.119
NT2RP2004841	18.863	23.561	19.087	12.969	6.680	26.241	6.007	27.597
NT2RP2004847	273.546	127.737	198.598	82.212	76.886	209.860	173.790	137.505
NT2RP2004851	39.358	31.567	90.952	21.161	16.051	19.568	16.014	16.274
NT2RP2004887	15.367	22.365	32.446	11.399	17.811	26.917	58.022	46.071
NT2RP2004932	183.953	95.539	145.469	60.038	97.052	126.042	109.623	90.071
NT2RP2004933	18.660	21.000	61.644	10.893	8.184	31.855	24.143	11.593
NT2RP2004936	10.618	16.165	27.376	5.543	8.959	13.920	6.220	8.621

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Table 92

NT2RP2004951	30.413	16.712	16.279	18.835	12.085	15.888	11.101	14.477
NT2RP2004959	7.613	10.358	13.406	5.314	5.926	11.986	2.543	5.752
NT2RP2004961	42.335	32.379	69.235	34.253	21.447	34.663	18.456	42.255
NT2RP2004962	30.669	30.353	89.154	14.113	9.384	17.622	8.128	20.787
NT2RP2004966	42.472	14.720	27.864	9.661	13.817	26.018	22.899	25.847
NT2RP2004967	57.426	40.541	179.390	31.892	23.923	31.052	16.791	43.678
NT2RP2004974	31.596	11.054	27.118	11.874	12.196	35.458	18.873	24.149
NT2RP2004978	92.366	58.297	58.744	11.187	26.598	42.390	34.073	15.958
NT2RP2004982	2.062	5.171	6.063	2.288	3.775	3.554	3.062	0.000
NT2RP2004985	87.939	67.149	78.678	45.629	27.293	69.956	48.241	62.719
NT2RP2004999	54.349	44.327	160.162	26.886	23.352	26.240	26.943	41.559
NT2RP2005000	26.080	14.589	21.728	7.864	8.002	19.702	12.179	15.480
NT2RP2005001	26.862	13.183	23.055	6.161	9.633	14.650	18.615	13.447
NT2RP2005003	69.867	63.795	165.289	39.371	25.182	33.952	24.278	47.013
NT2RP2005012	30.982	21.105	42.355	15.018	14.157	41.891	24.522	29.434
NT2RP2005018	111.833	49.415	78.251	22.107	42.271	59.226	38.060	18.699
NT2RP2005020	60.906	32.923	38.225	11.918	20.379	16.776	20.985	35.434
NT2RP2005022	44.931	25.614	37.383	8.777	13.169	17.643	25.803	22.979
NT2RP2005027	57.511	85.851	98.132	22.401	17.117	35.304	31.116	36.532
NT2RP2005031	14.601	8.758	14.468	5.468	5.699	7.564	8.732	3.246
NT2RP2005035	61.937	41.750	49.801	22.387	27.920	58.127	29.585	39.144
NT2RP2005037	27.745	16.434	26.221	9.584	20.837	24.795	26.368	30.429
NT2RP2005038	13.976	3.551	12.702	3.787	6.660	9.747	35.202	5.795
NT2RP2005048	55.851	47.103	55.038	22.550	27.846	30.149	28.713	25.891
NT2RP2005069	89.645	160.853	309.743	119.361	135.285	158.356	127.275	142.122
NT2RP2005073	28.642	24.071	29.062	8.191	14.897	17.052	25.028	53.376
NT2RP2005097	17.446	11.744	11.103	4.196	6.885	7.430	12.482	11.248
NT2RP2005108	22.062	6.419	8.005	4.736	8.210	16.355	10.080	48.380
NT2RP2005116	161.700	67.851	96.374	39.093	51.697	82.025	122.651	68.891
NT2RP2005126	24.712	30.925	25.757	24.268	22.706	35.722	14.976	36.438
NT2RP2005135	38.054	16.075	22.834	7.220	8.729	26.814	9.825	8.452
NT2RP2005139	25.339	21.341	24.789	9.299	9.331	10.389	15.907	13.632
NT2RP2005140	25.302	14.152	18.762	7.827	14.629	21.623	15.226	7.661
NT2RP2005144	57.910	24.627	35.294	9.403	20.129	22.753	25.702	14.422
NT2RP2005147	35.344	15.053	40.777	7.320	13.980	7.943	9.818	7.040
NT2RP2005148	71.460	50.351	93.151	24.862	24.403	40.037	28.927	30.934
NT2RP2005159	32.863	9.249	11.688	11.160	6.240	11.164	8.584	7.623
NT2RP2005162	33.677	20.731	31.783	9.893	9.733	6.520	16.473	12.891
NT2RP2005163	406.419	245.982	312.290	125.386	135.331	256.832	253.752	198.401
NT2RP2005168	44.795	9.276	16.080	8.798	9.082	15.704	20.783	14.247
NT2RP2005181	58.670	24.911	19.589	19.590	10.885	16.528	28.301	18.946
NT2RP2005204	61.862	36.997	48.257	21.014	21.820	26.400	20.001	33.933
NT2RP2005219	118.951	44.601	71.232	24.297	39.166	94.145	83.743	57.016
NT2RP2005227	63.985	85.586	198.792	37.680	26.287	29.966	35.172	44.374
NT2RP2005237	95.186	85.568	117.090	33.460	57.400	91.954	81.365	194.934
NT2RP2005239	45.116	20.823	33.169	16.031	8.498	11.991	27.107	20.678
NT2RP2005247	55.177	33.524	91.868	28.505	25.628	27.978	38.659	30.388
NT2RP2005254	67.776	32.943	35.931	20.251	16.723	35.298	24.338	25.348
NT2RP2005270	36.792	20.989	23.940	12.941	20.407	34.731	24.269	12.424
NT2RP2005276	34.791	50.008	19.917	15.429	19.430	30.784	9.484	44.820
NT2RP2005287	75.555	49.491	25.557	16.229	7.738	23.753	21.837	56.655
NT2RP2005288	84.486	30.764	16.471	9.015	8.671	29.745	15.169	27.020
NT2RP2005289	74.343	79.614	195.975	30.937	28.926	33.261	20.112	23.154
NT2RP2005293	32.574	17.527	13.426	14.326	12.226	25.911	15.734	9.085
NT2RP2005315	30.488	58.065	52.471	14.353	24.658	23.599	29.610	56.840
NT2RP2005322	54.278	66.487	69.926	39.640	44.675	56.756	45.067	30.738
NT2RP2005325	244.369	45.065	114.652	20.676	66.949	180.520	130.512	46.096
NT2RP2005336	118.767	75.218	151.013	52.856	19.178	13.614	34.194	55.755
NT2RP2005343	83.426	71.474	185.631	30.816	16.652	38.395	18.655	27.604
NT2RP2005344	13.456	15.006	16.224	6.558	7.385	8.086	8.800	3.847
NT2RP2005347	29.998	29.498	40.925	17.105	11.916	12.479	19.200	17.201
NT2RP2005354	200.810	179.788	410.980	73.329	74.840	81.380	48.521	65.973
NT2RP2005358	51.404	44.153	60.127	16.579	25.468	31.822	38.900	37.828
NT2RP2005360	73.041	47.709	39.257	21.144	21.993	56.153	28.537	28.347

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Table 93

NT2RP2005378	276.722	60.663	120.794	35.912	75.334	165.512	90.853	98.444
NT2RP2005391	150.127	47.813	76.113	25.253	31.400	92.500	35.776	47.335
NT2RP2005393	70.899	55.424	140.116	29.969	28.518	49.057	25.746	34.105
NT2RP2005407	49.576	20.202	38.801	8.339	17.993	20.349	19.728	11.408
NT2RP2005419	14.831	11.867	19.565	9.795	8.679	10.513	8.946	8.857
NT2RP2005425	18.167	59.599	35.636	25.050	15.104	8.153	9.614	51.727
NT2RP2005429	59.197	19.497	39.350	10.173	18.944	57.213	14.988	13.492
NT2RP2005436	79.164	77.083	60.113	36.736	34.134	54.347	21.339	40.541
NT2RP2005441	13.042	15.338	15.762	8.369	12.826	20.597	9.547	15.936
NT2RP2005442	38.553	25.938	32.259	17.285	15.576	32.634	33.798	38.091
NT2RP2005444	71.342	49.614	44.203	32.335	34.594	66.817	40.260	65.040
NT2RP2005453	14.907	15.128	11.162	5.959	22.081	9.421	11.234	15.739
NT2RP2005457	140.563	70.504	365.826	82.692	104.746	121.659	116.087	102.686
NT2RP2005458	20.125	11.007	11.247	8.652	9.030	17.490	6.559	3.649
NT2RP2005463	33.251	29.837	73.818	20.532	31.448	29.345	25.049	51.072
NT2RP2005464	15.800	16.043	35.864	14.911	13.341	13.525	14.209	18.361
NT2RP2005465	14.668	18.280	26.584	6.257	10.356	14.681	6.572	9.479
NT2RP2005472	16.851	25.760	9.199	8.686	4.966	40.418	42.443	7.644
NT2RP2005476	46.416	52.525,	104.203	20.584	20.782	24.546	5.316	32.360
NT2RP2005490	61.983	24.419	28.345	12.864	15.040	12.501	22.637	19.383
NT2RP2005491	374.811	74.888	145.408	24.336	165.612	317.177	231.269	69.296
NT2RP2005495	31.802	17.805	29.680	11.830	10.557	8.912	14.827	34.592
NT2RP2005496	148.755	112.441	375.031	47.535	53.667	47.282	40.191	44.995
NT2RP2005498	44.735	18.772	34.164	9.402	20.468	26.500	17.998	17.049
NT2RP2005501	40.853	37.008	48.454	14.020	18.699	36.333	14.886	19.992
NT2RP2005506	90.354	86.896	75.939	25.611	32.147	174.626	79.478	131.787
NT2RP2005509	49.249	30.854	40.983	21.945	13.500	50.085	24.330	36.909
NT2RP2005514	27.107	19.658	27.479	12.890	10.652	12.518	18.695	17.325
NT2RP2005520	17.919	21.654	27.300	18.855	10.163	12.223	7.568	30.261
NT2RP2005525	39.486	38.604	46.862	28.621	21.332	32.985	26.679	36.176
NT2RP2005531	14.400	12.033	22.722	7.730	9.380	14.414	16.744	11.422
NT2RP2005535	101.541	107.605	200.015	82.259	60.740	56.504	51.248	118.559
NT2RP2005539	66.664	29.346	46.698	21.888	19.870	64.043	30.246	26.001
NT2RP2005540	20.513	15.829	14.697	8.223	3.931	49.149	7.536	29.160
NT2RP2005541	64.709	41.297	53.989	27.868	23.974	31.435	25.336	31.933
NT2RP2005549	32.008	17.222	22.169	5.861	8.219	16.966	10.809	20.882
NT2RP2005555	32.893	26.046	65.848	10.597	20.624	14.475	13.940	32.764
NT2RP2005557	17.758	22.321	31.949	8.994	15.581	5.592	13.074	7.963
NT2RP2005581	90.896	89.844	311.596	54.248	36.454	51.670	42.717	57.487
NT2RP2005586	15.319	12.081	23.020	7.054	4.455	13.988	9.947	14.644
NT2RP2005597	70.922	36.752	50.127	12.506	18.474	43.281	28.038	27.738
NT2RP2005600	57.039	36.730	42.297	19.089	22.952	20.349	26.429	35.687
NT2RP2005605	89.117	41.403	109.938	32.943	40.472	75.058	52.177	50.487
NT2RP2005614	7.627	7.626	13.603	2.603	13.051	6.276	5.809	8.317
NT2RP2005620	42.734	21.553	33.023	9.850	14.899	31.978	27.521	25.649
NT2RP2005622	17.770	22.460	29.124	15.992	11.139	27.623	9.965	36.314
NT2RP2005632	14.999	31.771	43.031	12.307	17.618	13.899	11.335	15.678
NT2RP2005635	49.456	30.521	47.412	10.091	23.056	33.511	25.653	30.736
NT2RP2005637	12.810	11.271	23.258	10.723	0.000	8.150	7.172	12.007
NT2RP2005640	4.097	3.653	9.894	0.840	1.980	8.957	6.220	1.795
NT2RP2005645	20.889	32.389	36.306	18.400	17.660	5.119	17.090	35.045
NT2RP2005651	73.019	20.719	36.098	13.026	13.892	30.207	30.624	40.618
NT2RP2005654	39.235	27.889	43.919	18.330	15.864	16.064	25.659	25.595
NT2RP2005666	62.014	31.370	41.680	13.597	18.813	69.986	43.533	15.230
NT2RP2005669	64.432	53.672	65.910	23.933	25.429	55.388	61.239	61.894
NT2RP2005670	37.363	15.333	17.547	8.556	14.756	36.642	25.697	14.161
NT2RP2005671	43.306	44.120	31.058	10.830	17.143	63.049	30.396	23.799
NT2RP2005675	142.194	57.967	69.677	20.463	42.418	100.132	100.664	78.669
NT2RP2005683	25.353	27.395	30.738	14.852	10.519	19.049	11.915	16.611
NT2RP2005690	15.846	16.544	27.961	9.000	6.927	4.338	11.115	16.932
NT2RP2005694	76.694	67.508	146.549	25.507	24.945	11.950	27.362	28.108
NT2RP2005701	423.656	185.579	226.672	116.197	135.844	350.114	247.379	185.727
NT2RP2005712	27.492	13.221	17.195	4.214	6.957	24.369	21.985	16.350
NT2RP2005719	10.978	10.918	15.474	8.156	13.142	16.466	10.245	5.368

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Table 94

NT2RP2005722	34.666	61.425	70.544	51.843	34.010	57.142	30.735	84.009
NT2RP2005723	37.670	25.612	103.399	9.672	11.861	29.530	9.230	34.076
NT2RP2005726	84.115	36.206	48.072	11.996	17.484	39.045	38.061	22.448
NT2RP2005729	58.884	54.269	60.427	19.257	22.993	12.151	26.199	35.691
NT2RP2005731	17.800	7.316	9.355	4.076	7.122	6.849	10.218	6.724
NT2RP2005732	135.853	80.248	89.882	31.905	49.498	82.876	94.937	95.379
NT2RP2005737	185.624	120.622	192.481	48.397	56.581	148.601	144.906	98.588
NT2RP2005741	46.137	31.647	35.369	13.164	19.315	12.578	24.931	17.774
NT2RP2005748	37.338	25.300	30.354	12.292	9.999	24.185	17.843	16.711
NT2RP2005752	83.285	59.855	77.223	35.613	43.031	39.000	35.985	52.873
NT2RP2005753	420.897	246.480	444.538	136.522	121.988	399.581	356.877	181.575
NT2RP2005763	20.019	6.095	33.705	10.540	9.232	5.201	14.128	11.843
NT2RP2005767	46.813	15.583	33.205	10.684	15.614	27.907	23.447	10.054
NT2RP2005773	291.831	182.413	441.247	117.268	110.788	192.144	163.936	144.244
NT2RP2005774	55.239	48.822	145.962	59.822	22.432	33.644	24.248	66.283
NT2RP2005775	30.878	18.336	17.192	11.176	0.000	19.156	17.205	15.094
NT2RP2005781	56.648	31.034	24.498	10.923	17.115	16.751	30.579	26.075
NT2RP2005784	153.655	51.631	100.244	26.389	25.452	104.958	92.590	20.477
NT2RP2005788	74.249	51.916	68.043	24.721	19.271	60.694	30.122	14.401
NT2RP2005799	71.863	10.045	12.797	6.316	3.181	47.328	6.050	3.897
NT2RP2005804	52.496	43.561	70.286	25.906	16.838	25.088	23.482	31.711
NT2RP2005812	49.420	17.666	27.165	8.036	15.484	13.521	16.634	20.990
NT2RP2005815	27.570	20.859	32.235	11.501	9.452	14.728	19.248	36.742
NT2RP2005835	112.785	78.188	150.766	35.828	53.880	99.576	62.221	32.500
NT2RP2005841	41.693	18.145	43.677	15.477	18.203	8.667	17.036	33.652
NT2RP2005853	70.296	52.756	205.381	30.242	23.198	54.689	16.871	24.992
NT2RP2005857	23.173	20.068	18.329	34.075	5.778	4.049	6.163	12.771
NT2RP2005859	33.168	17.202	37.200	12.544	13.483	19.950	9.659	26.739
NT2RP2005860	31.260	19.609	26.277	8.837	10.871	17.943	20.399	13.975
NT2RP2005863	21.267	29.851	26.528	17.209	15.572	12.614	18.527	11.789
NT2RP2005868	39.601	30.998	45.149	22.672	23.499	19.410	12.734	17.486
NT2RP2005876	182.087	242.226	222.167	16.258	31.298	2198.108	17.529	20.489
NT2RP2005878	91.078	63.689	193.261	46.963	36.817	19.789	29.099	39.512
NT2RP2005883	20.941	23.594	20.782	9.131	19.950	18.957	6.938	12.667
NT2RP2005886	39.296	39.439	60.317	47.352	18.027	22.441	30.721	46.169
NT2RP2005887	57.014	35.877	88.514	16.318	48.626	59.669	24.351	36.393
NT2RP2005890	1.467	3.944	6.429	8.930	1.110	0.000	0.985	1.454
NT2RP2005901	20.981	6.590	21.187	2.036	7.367	5.299	7.158	4.126
NT2RP2005902	20.393	16.947	32.820	8.084	22.093	14.130	8.168	6.766
NT2RP2005908	151.932	107.992	314.719	54.159	56.994	88.516	49.539	55.664
NT2RP2005927	44.735	18.407	16.648	7.455	11.632	30.787	17.918	15.966
NT2RP2005933	9.824	12.141	12.068	9.453	13.104	26.904	7.543	21.967
NT2RP2005941	212.014	56.163	125.056	30.940	64.307	146.736	115.114	49.381
NT2RP2005942	18.504	15.139	25.696	8.924	13.074	17.417	7.750	20.426
NT2RP2005946	9.728	10.356	21.222	6.005	9.750	8.251	6.713	15.168
NT2RP2005970	270.432	161.716	481.318	122.569	121.562	121.380	132.328	127.095
NT2RP2005980	46.492	47.170	116.755	26.037	32.671	22.244	18.314	24.318
NT2RP2005994	24.926	29.869	28.280	11.011	14.761	16.126	15.547	12.085
NT2RP2006004	33.199	22.482	40.736	2.254	13.327	15.670	22.705	28.705
NT2RP2006013	37.195	30.477	49.417	14.196	16.611	24.253	14.883	27.870
NT2RP2006023	352.327	279.775	760.112	199.154	108.052	252.378	165.286	194.967
NT2RP2006028	16.154	16.322	9.466	8.482	6.921	16.415	12.189	19.676
NT2RP2006038	0.000	0.000	0.000	2.022	0.000	0.000	2.750	0.000
NT2RP2006042	171.799	43.226	84.802	30.749	34.076	105.581	87.203	50.321
NT2RP2006043	42.853	34.278	46.615	31.083	20.581	20.396	21.562	24.255
NT2RP2006052	81.736	38.197	32.678	22.263	18.783	11.840	20.855	18.722
NT2RP2006057	10.366	16.636	17.971	3.253	8.817	19.481	5.521	4.099
NT2RP2006064	49.505	48.411	44.958	10.467	13.976	35.690	11.141	42.302
NT2RP2006068	32.753	25.167	31.742	12.673	13.801	29.984	17.006	20.716
NT2RP2006069	5.168	1.476	0.000	0.885	3.204	1.811	3.399	1.150
NT2RP2006071	44.047	28.636	40.383	20.021	15.376	32.715	25.050	58.869
NT2RP2006080	36.345	15.495	26.707	7.612	10.138	27.073	18.729	16.094
NT2RP2006092	26.028	24.133	41.028	12.793	22.737	20.714	23.958	24.611
NT2RP2006097	26.828	35.230	63.866	22.123	14.392	27.780	13.780	24.430

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Table 95

NT2RP2006098	9.221	8.862	15.825	1.548	7.695	2.607	2.890	5.114
NT2RP2006099	36.984	26.268	76.849	17.513	9.927	22.657	13.432	24.422
NT2RP2006100	6.166	9.812	13.286	1.403	7.183	10.053	6.143	24.935
NT2RP2006103	61.199	24.990	32.481	5.365	8.444	14.474	6.643	15.554
NT2RP2006106	160.473	47.046	79.073	14.926	42.304	95.141	66.256	54.310
NT2RP2006127	299.049	72.341	157.315	35.299	69.360	160.904	129.470	82.790
NT2RP2006134	7.925	6.856	14.868	7.190	5.404	8.696	12.032	8.793
NT2RP2006141	34.209	25.853	25.279	11.925	12.291	24.288	16.957	12.817
NT2RP2006166	145.927	143.316	390.446	53.472	49.950	70.158	31.362	36.423
NT2RP2006176	38.237	32.296	48.672	13.808	41.752	37.097	22.363	19.576
NT2RP2006181	7.938	2.562	3.108	2.599	3.019	2.533	2.693	7.338
NT2RP2006184	427.733	164.565	311.744	90.540	136.553	294.751	209.379	191.687
NT2RP2006186	9.611	7.571	10.891	2.107	7.906	2.215	13.759	17.231
NT2RP2006196	64.570	46.625	187.805	24.294	26.945	31.212	13.067	38.607
NT2RP2006199	32.521	17.361	28.888	10.561	7.708	21.719	25.552	11.042
NT2RP2006200	45.197	30.904	68.326	12.637	20.289	14.015	24.697	16.848
NT2RP2006210	13.063	42.759	41.239	76.812	21.527	21.342	4.951	46.272
NT2RP2006219	19.770	12.088	17.232	4.165	9.125	6.702	12.944	14.193
NT2RP2006224	56.084	46.968	124.695	25.238	22.235	39.796	14.970	39.612
NT2RP2006237	23.936	13.588	29.768	8.240	8.266	24.478	15.621	12.940
NT2RP2006238	30.339	10.705	17.681	1.647	9.826	9.810	5.796	9.385
NT2RP2006258	134.594	65.669	94.583	35.749	42.774	37.896	67.144	58.117
NT2RP2006261	30.527	20.607	20.756	7.023	10.500	26.668	20.779	32.986
NT2RP2006269	273.686	190.160	282.087	75.118	88.026	221.069	173.956	143.367
NT2RP2006275	85.280	39.874	56.619	10.486	19.434	48.212	55.210	39.859
NT2RP2006282	18.372	26.364	78.637	7.247	13.037	10.134	7.395	10.427
NT2RP2006302	35.243	63.455	48.101	22.449	24.844	39.182	9.675	14.948
NT2RP2006312	65.434	60.394	81.415	26.895	27.020	35.036	41.172	38.133
NT2RP2006320	42.111	32.881	107.012	21.102	25.087	24.083	19.555	40.879
NT2RP2006321	7.504	10.403	35.594	9.608	9.770	25.528	7.823	3.899
NT2RP2006323	7.851	2.520	3.223	1.919	1.885	6.166	3.878	3.640
NT2RP2006333	30.987	16.865	28.885	6.560	9.086	8.529	9.411	9.392
NT2RP2006334	12.349	6.246	10.111	7.506	2.643	10.779	6.657	9.120
NT2RP2006338	3.452	3.965	5.603	1.571	3.999	1.378	0.000	5.658
NT2RP2006339	25.764	16.783	14.506	7.871	9.927	10.052	16.010	8.999
NT2RP2006355	20.663	13.101	11.565	6.563	7.455	7.126	9.386	6.085
NT2RP2006365	4.545	5.794	3.527	6.016	4.317	2.172	4.635	2.088
NT2RP2006374	411.795	181.700	244.772	88.732	81.469	224.300	186.562	160.290
NT2RP2006393	49.201	46.271	138.242	24.009	21.170	18.558	17.331	21.921
NT2RP2006394	28.334	29.547	20.558	4.570	13.741	24.300	15.936	15.737
NT2RP2006400	24.921	12.448	22.520	10.436	6.781	12.164	12.987	14.072
NT2RP2006411	170.083	45.848	109.486	76.812	50.885	136.021	80.417	46.178
NT2RP2006429	17.592	22.689	50.747	10.696	17.317	23.371	18.641	17.956
NT2RP2006435	55.611	34.885	57.426	16.304	26.895	37.137	39.774	37.506
NT2RP2006436	152.017	117.923	294.214	79.789	75.537	107.196	47.063	35.486
NT2RP2006441	24.518	19.297	41.744	27.285	33.736	14.991	17.341	13.076
NT2RP2006447	13.367	6.103	5.701	2.225	4.629	8.175	4.129	2.450
NT2RP2006454	12.135	6.375	11.243	2.681	0.000	18.444	3.071	5.464
NT2RP2006455	11.895	17.452	13.837	6.890	6.158	14.783	6.071	8.830
NT2RP2006456	38.021	19.288	35.373	9.022	12.219	34.935	12.195	8.454
NT2RP2006464	65.475	59.218	64.107	23.982	11.975	46.736	45.415	26.468
NT2RP2006467	182.556	82.534	110.746	33.773	58.531	134.845	89.415	79.911
NT2RP2006472	52.035	81.984	49.222	27.110	22.246	58.236	23.092	21.013
NT2RP2006474	87.750	59.508	90.991	40.960	68.884	46.386	41.819	43.544
NT2RP2006475	31.939	25.175	56.713	5.942	98.476	222.460	20.356	7.479
NT2RP2006476	21.072	30.518	25.064	26.064	6.000	10.383	11.027	21.451
NT2RP2006501	49.705	32.865	29.408	27.184	4.907	32.045	10.526	22.257
NT2RP2006512	27.180	32.082	24.613	26.192	14.264	30.488	12.111	19.931
NT2RP2006528	1.990	16.410	1.143	0.714	1.146	0.000	1.142	0.000
NT2RP2006527	89.786	37.810	65.465	19.956	29.390	58.611	41.655	42.817
NT2RP2006534	12.307	17.082	25.981	7.920	10.780	7.152	5.503	7.803
NT2RP2006537	152.141	97.164	238.317	56.113	45.970	66.047	31.701	24.076
NT2RP2006543	41.814	17.923	95.586	6.904	6.956	16.769	11.226	15.747
NT2RP2006554	5.859	5.374	21.959	8.776	3.884	8.154	5.595	4.909

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Table 96

NT2RP2006565	8.167	7.704	24.371	5.814	14.320	10.696	2.358	4.111
NT2RP2006571	279.311	52.710	116.641	23.676	53.970	199.457	130.143	46.164
NT2RP2006573	14.833	9.728	14.833	10.165	4.273	12.181	5.836	11.189
NT2RP2006598	50.217	58.672	84.436	36.450	20.183	47.448	27.628	33.428
NT2RP2006601	363.326	80.354	103.722	48.729	76.933	194.071	89.671	34.186
NT2RP3000002	54.787	35.587	138.409	14.410	15.645	42.782	17.893	13.809
NT2RP3000011	86.241	70.778	179.249	26.157	23.114	44.263	20.905	26.577
NT2RP3000014	13.859	16.745	34.145	13.964	62.052	11.790	6.030	23.999
NT2RP3000016	37.105	33.786	44.744	13.554	18.247	35.947	22.381	14.827
NT2RP3000022	94.200	21.219	43.091	11.156	18.896	66.602	28.935	18.892
NT2RP3000024	7.842	17.722	80.534	57.536	15.195	28.526	14.924	31.215
NT2RP3000031	40.539	15.466	45.699	14.680	16.043	21.658	37.591	14.624
NT2RP3000034	47.041	16.354	46.033	9.722	17.283	27.871	22.418	14.394
NT2RP3000037	207.077	121.888	344.732	90.995	100.871	120.707	93.233	68.047
NT2RP3000040	19.046	21.059	10.120	5.362	4.717	7.751	13.678	12.858
NT2RP3000041	52.107	45.044	152.312	40.210	22.300	35.890	26.992	49.633
NT2RP3000045	66.472	44.521	156.649	32.533	24.374	70.316	23.701	21.537
NT2RP3000047	67.673	24.262	49.113	15.475	21.518	33.173	30.093	27.627
NT2RP3000049	48.739	25.122,	91.910	30.451	29.572	32.060	28.583	20.154
NT2RP3000050	26.074	40.719	88.636	24.767	22.328	23.604	11.688	48.303
NT2RP3000051	66.710	26.569	41.823	15.685	23.009	34.385	30.860	29.647
NT2RP3000054	102.785	62.230	100.267	27.596	31.738	71.470	53.863	44.388
NT2RP3000055	75.199	57.387	100.976	32.041	39.402	46.743	33.378	38.034
NT2RP3000056	39.543	22.913	30.865	6.902	18.029	31.675	21.577	18.143
NT2RP3000059	37.238	25.053	41.439	8.975	11.901	30.284	16.708	27.602
NT2RP3000063	185.029	52.340	95.324	25.648	51.543	102.170	98.453	32.215
NT2RP3000068	31.037	24.156	26.439	9.761	13.197	30.638	22.295	20.840
NT2RP3000069	10.170	17.834	29.064	3.122	10.074	26.020	12.191	15.438
NT2RP3000072	14.842	17.988	11.379	7.153	9.559	10.360	3.475	9.404
NT2RP3000080	324.225	127.554	363.840	79.623	88.104	197.811	132.385	96.818
NT2RP3000085	51.661	29.771	37.844	10.819	18.134	39.828	23.587	17.525
NT2RP3000087	17.091	10.622	46.219	24.865	22.511	28.404	15.603	41.935
NT2RP3000092	35.685	15.980	24.034	8.335	8.477	12.472	10.082	10.611
NT2RP3000109	18.561	16.632	14.110	13.437	4.116	20.790	11.884	10.865
NT2RP3000119	77.508	36.674	39.664	14.435	17.248	54.174	31.225	36.072
NT2RP3000125	73.603	69.403	81.547	42.247	34.639	56.907	38.200	46.977
NT2RP3000131	120.919	64.403	90.654	35.148	31.692	68.253	45.665	51.614
NT2RP3000134	112.388	83.404	239.571	43.058	33.667	26.549	37.483	34.264
NT2RP3000137	62.456	42.787	44.389	14.934	21.465	33.205	29.974	26.136
NT2RP3000142	26.473	48.731	52.053	38.739	20.973	36.445	18.076	21.664
NT2RP3000148	63.507	22.034	36.823	8.026	12.884	44.451	23.171	18.256
NT2RP3000149	97.776	30.350	50.788	16.701	25.676	64.729	43.962	43.994
NT2RP3000163	26.802	19.938	31.411	6.275	9.088	20.951	21.878	23.068
NT2RP3000168	795.144	114.786	283.898	44.650	145.359	605.075	401.513	129.011
NT2RP3000169	24.676	16.941	26.930	10.017	9.998	22.440	17.412	12.677
NT2RP3000171	98.370	112.386	277.503	71.994	84.185	92.446	72.076	90.890
NT2RP3000172	61.369	27.571	34.375	12.627	22.318	30.658	22.317	17.859
NT2RP3000188	94.000	91.952	162.821	37.334	35.006	23.969	28.600	28.365
NT2RP3000197	73.123	35.617	164.002	24.125	21.785	35.486	29.445	24.978
NT2RP3000201	102.553	70.806	142.754	44.107	29.649	62.714	48.605	33.413
NT2RP3000204	18.200	14.164	20.111	7.985	6.811	22.398	6.414	16.458
NT2RP3000207	156.781	36.850	65.015	12.469	27.276	91.928	59.198	23.678
NT2RP3000216	198.806	79.206	109.849	21.139	46.927	98.763	89.370	46.993
NT2RP3000220	41.042	21.189	35.304	10.343	13.834	34.368	22.050	8.817
NT2RP3000221	14.840	11.900	19.520	9.467	7.825	20.185	21.420	5.118
NT2RP3000232	27.369	22.973	47.647	25.604	26.475	26.635	21.694	58.778
NT2RP3000233	29.604	18.166	20.836	7.062	10.046	10.901	14.488	13.964
NT2RP3000234	81.664	54.616	83.379	20.000	23.342	34.772	28.379	31.629
NT2RP3000235	83.990	44.388	63.809	18.177	16.009	48.324	46.171	18.108
NT2RP3000238	37.735	37.968	34.913	18.056	20.915	38.341	15.352	39.089
NT2RP3000247	39.588	21.300	20.867	8.851	13.233	20.777	17.822	10.760
NT2RP3000251	113.350	59.317	72.549	22.848	36.203	92.438	60.767	66.928
NT2RP3000252	60.796	43.494	58.311	14.499	17.495	33.029	20.185	17.559
NT2RP3000255	70.857	30.714	38.046	8.728	10.951	35.304	33.779	15.636

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Table 97

NT2RP3000262	12.216	24.325	22.227	10.435	13.784	14.416	11.609	16.866
NT2RP3000266	60.888	57.736	67.209	20.988	24.591	38.289	23.653	41.422
NT2RP3000267	44.661	37.513	25.280	10.160	9.316	10.177	21.121	21.341
NT2RP3000271	83.084	46.052	52.186	20.876	28.139	32.541	43.838	26.269
NT2RP3000278	32.035	43.936	47.584	38.351	21.589	32.926	27.054	36.075
NT2RP3000281	90.519	61.619	132.576	27.694	29.002	49.528	37.903	38.324
NT2RP3000292	3.966	10.376	3.409	3.495	2.695	5.631	11.626	1.198
NT2RP3000299	59.244	17.953	32.272	11.088	19.017	25.398	24.814	30.991
NT2RP3000304	112.022	42.176	44.039	17.256	21.312	68.495	41.001	11.248
NT2RP3000310	51.923	40.371	23.866	18.763	12.225	17.033	12.288	8.239
NT2RP3000312	53.784	42.298	111.962	28.662	28.499	47.636	21.749	17.055
NT2RP3000320	207.335	105.256	82.557	32.315	34.370	306.433	171.177	16.257
NT2RP3000322	58.959	145.034	68.676	49.667	43.457	53.749	59.223	53.805
NT2RP3000324	48.873	14.767	34.844	16.823	13.446	25.783	30.738	24.781
NT2RP3000326	65.235	51.932	107.139	28.709	7.123	38.932	21.519	21.276
NT2RP3000329	93.768	78.384	210.960	64.677	30.715	47.282	30.786	30.002
NT2RP3000330	24.642	49.689	27.966	9.468	6.970	26.195	18.445	15.597
NT2RP3000333	6.551	4.474	6.490	3.373	1.210	8.119	6.219	2.641
NT2RP3000341	105.554	78.685,	292.105	48.172	44.341	47.850	37.664	24.434
NT2RP3000344	21.848	16.348	18.737	15.208	14.171	11.842	9.663	8.826
NT2RP3000345	13.615	4.231	8.891	4.341	4.244	9.519	7.200	2.442
NT2RP3000348	215.751	824.234	231.063	124.822	216.289	288.551	206.453	397.251
NT2RP3000350	75.031	53.082	54.573	26.912	16.935	64.380	20.038	26.035
NT2RP3000359	60.599	28.652	25.133	36.113	16.097	67.120	56.693	48.617
NT2RP3000361	97.227	40.753	62.678	25.399	25.559	78.478	40.608	39.929
NT2RP3000366	29.933	23.388	51.997	16.575	24.680	39.191	19.302	20.995
NT2RP3000378	36.122	36.646	53.425	29.190	18.810	14.993	29.540	12.427
NT2RP3000384	94.244	64.810	247.061	65.250	53.993	55.586	28.548	35.998
NT2RP3000389	145.164	130.566	88.715	60.458	59.767	126.866	46.046	46.304
NT2RP3000393	34.304	26.482	38.672	12.816	10.966	53.247	23.028	22.722
NT2RP3000395	130.734	261.655	185.074	139.360	67.626	191.905	113.593	356.673
NT2RP3000397	23.796	14.400	15.115	8.197	10.685	19.437	11.865	15.686
NT2RP3000398	53.315	53.724	168.232	39.457	13.432	46.057	24.302	28.636
NT2RP3000403	57.006	49.114	63.081	38.685	24.406	48.333	25.226	24.101
NT2RP3000418	50.531	48.172	170.356	32.562	26.123	10.592	29.707	10.604
NT2RP3000424	63.365	21.340	38.478	16.563	16.925	53.214	30.826	17.735
NT2RP3000427	62.721	39.857	128.557	24.313	28.283	29.359	22.716	18.652
NT2RP3000431	16.834	8.211	12.394	7.692	12.872	8.065	13.418	13.114
NT2RP3000433	50.616	79.462	104.236	42.090	39.902	42.064	33.371	38.488
NT2RP3000436	16.242	16.422	40.709	16.813	6.539	20.516	10.885	17.733
NT2RP3000439	71.848	23.969	40.354	14.754	15.239	53.741	31.396	8.363
NT2RP3000441	11.212	9.002	12.696	5.044	10.679	13.013	5.428	5.597
NT2RP3000444	22.933	18.685	29.664	9.645	13.646	17.025	18.757	13.305
NT2RP3000448	33.060	20.309	55.374	17.566	24.368	22.687	16.155	11.895
NT2RP3000449	6.959	23.459	17.422	10.472	7.118	8.871	9.364	3.475
NT2RP3000451	125.446	62.063	59.005	22.337	34.264	60.126	41.591	27.148
NT2RP3000456	88.916	43.502	69.366	17.277	29.249	56.726	42.776	41.151
NT2RP3000460	53.276	27.765	47.239	14.257	14.152	40.035	29.749	13.869
NT2RP3000471	120.686	35.942	65.409	19.114	21.966	84.016	40.300	40.267
NT2RP3000477	135.254	69.833	123.785	56.384	66.460	143.732	64.962	29.801
NT2RP3000478	29.313	21.768	61.753	10.082	21.998	33.287	14.477	44.282
NT2RP3000481	10.750	3.732	5.456	0.726	2.539	11.124	6.047	2.438
NT2RP3000484	37.552	21.006	28.635	15.721	14.002	24.786	24.639	18.179
NT2RP3000487	57.292	37.922	107.654	33.349	33.101	34.015	30.560	34.378
NT2RP3000512	40.012	21.185	25.342	10.503	13.140	44.846	27.137	10.397
NT2RP3000523	99.365	56.104	57.485	32.088	34.445	78.588	42.509	36.741
NT2RP3000526	45.488	30.104	53.085	16.516	10.374	24.429	16.363	12.300
NT2RP3000527	44.308	22.761	18.000	7.682	12.301	36.809	24.394	15.830
NT2RP3000531	317.473	170.480	234.934	104.005	126.165	204.346	175.754	116.929
NT2RP3000532	69.884	23.745	36.210	16.034	19.464	37.931	28.117	30.722
NT2RP3000542	53.226	27.049	115.161	42.422	30.182	44.442	28.283	44.087
NT2RP3000554	46.760	48.740	47.313	22.048	25.077	32.396	21.710	28.087
NT2RP3000561	34.700	20.076	36.509	11.166	12.551	31.072	12.335	21.743
NT2RP3000562	61.916	30.119	37.119	14.204	15.849	36.832	26.415	21.173

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Table 98

NT2RP3000578	15.402	10.162	16.063	7.228	4.718	6.130	9.838	13.311
NT2RP3000582	39.271	21.923	38.385	15.003	10.964	17.246	14.457	23.415
NT2RP3000584	50.928	29.642	70.817	14.592	15.938	25.450	18.096	13.886
NT2RP3000586	104.429	33.153	41.205	15.381	26.618	56.849	60.938	32.115
NT2RP3000590	26.385	19.138	20.258	7.852	11.948	19.961	17.171	14.281
NT2RP3000592	38.458	13.253	18.849	6.663	11.214	15.506	10.347	13.365
NT2RP3000596	97.160	124.897	111.320	54.127	55.968	95.489	58.183	68.801
NT2RP3000598	27.723	23.836	21.699	6.517	10.630	24.268	12.753	5.443
NT2RP3000603	58.661	36.820	44.037	20.279	17.695	42.330	42.704	30.254
NT2RP3000605	28.480	12.057	23.849	6.629	7.081	16.695	13.635	14.891
NT2RP3000607	24.868	40.289	21.827	5.879	13.852	13.642	13.588	19.173
NT2RP3000616	13.295	18.170	13.744	4.297	8.368	12.637	6.395	3.593
NT2RP3000621	32.066	35.204	40.136	10.823	13.912	32.917	35.694	30.496
NT2RP3000622	77.250	48.804	56.101	26.510	26.964	60.270	33.756	35.001
NT2RP3000624	69.148	40.431	50.570	17.495	18.274	44.392	30.661	19.154
NT2RP3000628	101.279	78.344	315.194	66.794	47.806	62.753	39.571	65.891
NT2RP3000631	83.274	57.931	64.862	38.915	26.193	49.662	32.548	66.985
NT2RP3000632	75.512	46.888	137.791	36.803	25.072	37.533	39.161	39.835
NT2RP3000638	42.585	33.637	37.613	14.925	17.500	33.937	31.430	24.095
NT2RP3000644	165.984	142.937	393.193	71.526	75.904	86.493	86.017	83.257
NT2RP3000645	406.046	291.113	353.711	137.438	154.952	264.140	265.679	203.054
NT2RP3000652	27.913	38.545	66.305	53.070	30.592	38.016	20.919	70.560
NT2RP3000658	119.274	49.302	84.139	19.097	26.904	41.744	58.038	42.209
NT2RP3000660	154.015	93.717	291.388	47.970	61.811	77.378	54.638	32.448
NT2RP3000661	61.960	37.363	58.907	19.857	23.806	34.888	27.236	22.377
NT2RP3000665	36.030	11.500	21.945	7.361	8.773	16.187	15.502	4.205
NT2RP3000676	93.465	71.379	82.472	34.775	44.271	57.208	63.670	56.415
NT2RP3000677	112.363	32.537	52.925	14.666	38.145	49.852	47.252	14.122
NT2RP3000681	36.511	66.476	75.231	35.416	18.401	37.570	41.478	66.253
NT2RP3000683	58.416	64.592	97.551	38.537	29.638	37.665	22.530	57.162
NT2RP3000685	114.973	74.466	133.468	30.843	36.634	44.885	43.642	44.225
NT2RP3000690	44.317	22.720	28.586	11.755	16.142	19.525	23.913	12.295
NT2RP3000698	67.409	29.101	27.424	12.677	18.813	30.558	35.120	22.330
NT2RP3000708	69.762	31.242	34.468	18.438	17.109	25.677	35.649	27.340
NT2RP3000719	101.619	37.708	40.561	16.843	22.310	30.132	41.665	29.714
NT2RP3000721	62.292	33.883	41.328	20.719	17.808	29.864	31.483	34.754
NT2RP3000728	15.781	13.248	15.483	9.343	7.806	5.356	8.199	8.869
NT2RP3000730	16.503	10.183	12.261	4.259	5.390	10.857	12.834	7.121
NT2RP3000733	55.476	33.770	134.994	26.531	11.886	24.025	14.564	29.631
NT2RP3000735	21.669	7.407	9.693	5.816	9.383	28.210	2.497	11.449
NT2RP3000736	44.789	26.680	38.153	13.731	16.809	30.640	25.306	25.557
NT2RP3000739	206.032	42.295	130.965	26.071	58.557	146.191	92.971	37.396
NT2RP3000742	348.588	140.896	195.591	50.032	81.126	190.392	158.586	73.831
NT2RP3000753	62.272	31.221	40.211	20.489	20.282	94.033	25.801	41.475
NT2RP3000759	29.716	22.350	32.951	18.751	26.712	22.364	11.768	12.157
NT2RP3000789	39.203	42.612	22.684	12.737	16.316	24.563	14.289	8.744
NT2RP3000815	81.211	54.520	145.901	29.707	22.766	48.640	24.152	22.295
NT2RP3000818	77.152	41.510	81.608	27.176	30.804	51.380	29.052	28.761
NT2RP3000820	76.041	118.421	231.975	55.326	38.009	77.248	35.255	64.172
NT2RP3000821	125.957	64.013	112.255	27.822	47.320	81.799	57.688	32.892
NT2RP3000825	4.611	0.000	4.828	2.088	0.000	3.614	3.042	11.736
NT2RP3000828	143.292	64.787	162.627	46.686	56.407	101.167	61.127	46.725
NT2RP3000836	83.974	80.423	210.942	45.858	32.214	23.251	37.753	44.587
NT2RP3000838	199.574	535.714	166.498	90.546	149.924	216.645	161.565	295.666
NT2RP3000839	16.488	6.477	7.238	3.037	1.517	11.754	5.693	6.807
NT2RP3000841	43.065	36.679	115.803	21.240	15.592	30.244	12.610	21.751
NT2RP3000845	98.566	28.826	47.444	11.595	21.815	115.944	48.273	28.363
NT2RP3000847	102.018	59.230	140.484	36.275	34.261	46.634	43.858	48.553
NT2RP3000848	43.608	33.763	54.299	20.531	16.249	35.936	17.881	22.982
NT2RP3000850	162.391	74.431	281.196	66.439	66.101	84.573	58.454	43.150
NT2RP3000852	20.645	19.238	19.388	15.545	10.909	11.941	10.740	8.905
NT2RP3000859	151.904	86.258	69.935	21.801	30.699	73.401	46.530	35.975
NT2RP3000861	97.656	79.986	361.968	92.325	57.527	85.858	37.902	78.976
NT2RP3000862	87.649	39.014	36.132	15.942	23.416	47.236	69.109	15.390

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Table 99

NT2RP3000865	63.270	47.853	102.873	32.472	33.487	53.656	34.278	21.893
NT2RP3000866	34.716	25.903	38.593	12.760	15.744	54.423	32.374	18.694
NT2RP3000868	85.284	61.512	85.178	31.575	34.644	53.975	41.313	22.132
NT2RP3000869	77.514	27.048	71.150	21.470	27.958	26.061	26.717	11.830
NT2RP3000871	32.339	15.895	28.790	10.764	12.347	17.382	19.415	15.477
NT2RP3000875	64.304	26.967	41.187	17.427	17.449	63.004	27.104	29.777
NT2RP3000895	37.607	26.551	21.094	10.531	9.611	39.637	23.121	22.804
NT2RP3000900	142.017	81.808	211.235	53.019	47.970	81.157	50.066	57.451
NT2RP3000901	70.807	27.339	68.215	18.628	38.633	87.435	34.055	17.677
NT2RP3000903	13.003	24.507	60.511	13.378	13.428	29.263	6.790	12.691
NT2RP3000904	52.698	18.398	31.708	12.964	16.730	32.075	26.793	6.596
NT2RP3000907	166.727	60.470	136.938	38.479	50.160	105.219	95.047	42.673
NT2RP3000913	94.023	47.327	91.333	23.378	31.301	50.434	47.912	29.311
NT2RP3000917	32.888	39.658	21.466	16.870	11.875	27.038	18.723	21.313
NT2RP3000919	94.068	33.556	46.679	16.703	24.240	78.449	55.568	30.552
NT2RP3000921	37.830	26.534	66.403	7.357	8.929	61.748	8.623	14.620
NT2RP3000942	171.953	62.500	108.369	33.025	42.178	102.140	75.932	47.639
NT2RP3000968	113.182	183.788	251.225	112.172	45.194	135.391	114.314	284.978
NT2RP3000974	31.061	18.639	28.044	11.335	13.883	20.765	19.154	8.182
NT2RP3000980	75.435	43.616	144.923	25.869	22.636	53.158	21.266	5.678
NT2RP3000984	80.420	55.909	211.662	30.046	34.753	46.023	41.008	39.028
NT2RP3000994	26.597	13.100	24.899	10.246	18.755	15.021	12.030	11.524
NT2RP3001001	41.741	14.316	24.372	9.822	11.943	20.619	21.560	7.191
NT2RP3001004	21.324	19.490	22.465	8.748	12.668	37.792	8.027	5.197
NT2RP3001007	73.322	49.966	175.492	41.711	29.860	30.759	23.563	18.521
NT2RP3001012	17.551	14.673	17.235	9.520	7.664	14.146	11.598	11.610
NT2RP3001042	56.542	31.176	40.712	11.357	21.273	42.340	30.644	16.851
NT2RP3001044	57.032	39.083	68.934	22.349	40.025	60.364	34.476	25.794
NT2RP3001048	39.639	23.540	39.473	18.858	15.279	32.436	23.205	26.116
NT2RP3001050	40.144	37.630	102.740	17.755	44.501	73.595	26.881	21.142
NT2RP3001055	36.578	21.787	34.665	11.391	15.586	44.493	17.343	39.665
NT2RP3001057	40.477	31.367	56.914	35.425	16.396	40.782	15.582	41.540
NT2RP3001061	35.545	23.074	31.908	11.906	22.306	27.393	25.460	19.287
NT2RP3001069	106.748	62.272	150.656	32.917	23.305	58.467	35.766	47.515
NT2RP3001074	14.550	14.541	22.555	7.827	16.140	15.294	11.052	4.620
NT2RP3001078	52.226	37.483	61.489	16.718	18.374	26.786	29.722	37.845
NT2RP3001081	27.544	17.926	40.857	14.999	13.731	23.258	19.326	14.022
NT2RP3001084	48.930	20.162	28.411	8.915	19.688	35.485	28.948	20.795
NT2RP3001095	5.532	7.106	9.117	1.907	1.873	1.686	4.160	6.179
NT2RP3001096	72.786	64.406	72.692	26.305	30.582	41.528	32.077	27.965
NT2RP3001097	25.257	17.811	73.704	11.171	12.488	5.176	10.401	15.261
NT2RP3001107	81.894	32.783	61.356	24.675	27.453	53.316	37.116	40.327
NT2RP3001109	29.099	23.842	24.494	12.892	16.120	14.893	15.303	18.912
NT2RP3001111	69.862	29.991	36.252	13.681	16.731	44.954	31.601	22.477
NT2RP3001112	57.507	80.536	82.448	80.792	39.380	58.111	23.819	75.560
NT2RP3001113	17.615	26.847	19.375	9.970	8.233	11.421	5.759	13.956
NT2RP3001115	21.858	18.916	28.812	7.324	4.563	13.477	9.463	11.057
NT2RP3001116	40.872	22.335	23.917	10.468	15.106	15.973	21.496	6.979
NT2RP3001119	124.291	38.911	66.173	19.498	29.478	73.564	71.005	23.217
NT2RP3001120	18.656	32.833	65.009	14.974	14.114	43.177	17.732	46.909
NT2RP3001126	37.515	26.047	38.382	9.469	16.381	17.926	22.835	12.549
NT2RP3001127	11.834	4.025	5.195	3.694	4.697	2.608	36.686	5.923
NT2RP3001133	70.288	79.857	161.425	34.123	22.428	47.625	46.500	34.323
NT2RP3001140	23.850	15.525	27.441	7.787	14.096	43.859	22.377	36.073
NT2RP3001147	41.415	23.333	25.696	7.439	15.613	27.307	21.623	12.688
NT2RP3001150	50.310	27.305	40.429	13.413	12.407	17.499	22.391	24.362
NT2RP3001152	3.974	1.479	1.712	0.807	0.788	0.915	1.821	0.000
NT2RP3001155	39.961	39.114	41.386	21.748	14.042	40.594	41.468	31.833
NT2RP3001156	31.035	17.102	23.691	6.973	9.466	31.538	17.411	9.742
NT2RP3001159	137.273	38.120	74.062	19.455	36.267	73.862	75.135	35.944
NT2RP3001170	35.615	34.235	64.722	18.272	20.302	35.625	22.021	14.394
NT2RP3001176	58.889	60.413	127.466	30.928	33.027	62.693	23.996	56.392
NT2RP3001195	72.627	47.832	119.011	16.902	19.658	15.312	25.740	27.006
NT2RP3001209	458.437	263.607	330.947	136.852	187.739	350.320	327.764	223.342

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Table 100

NT2RP3001214	15.760	24.578	18.804	10.536	12.107	7.011	7.277	12.208
NT2RP3001216	29.191	41.925	42.777	26.031	31.602	30.104	23.133	26.408
NT2RP3001221	25.240	20.176	20.644	4.858	10.770	7.315	13.513	8.946
NT2RP3001226	54.304	47.592	67.642	24.341	24.384	38.331	32.669	45.697
NT2RP3001230	23.680	20.599	27.561	11.735	11.032	25.537	13.367	12.758
NT2RP3001232	4.151	14.071	13.135	9.855	6.746	9.778	5.130	7.513
NT2RP3001236	28.593	14.443	35.687	7.512	5.884	10.789	13.692	14.135
NT2RP3001239	15.380	5.089	16.960	4.419	3.497	6.366	6.599	8.021
NT2RP3001240	17.531	13.481	30.743	12.073	14.733	12.342	22.647	11.311
NT2RP3001245	17.405	11.231	97.349	10.570	10.667	11.712	11.709	5.360
NT2RP3001253	29.416	21.939	30.308	17.125	8.767	28.879	20.229	15.732
NT2RP3001259	66.464	26.700	30.561	28.122	16.780	50.988	35.111	9.149
NT2RP3001260	15.811	4.776	8.508	3.773	11.179	5.131	7.611	6.513
NT2RP3001264	17.474	9.326	19.891	6.147	0.000	13.645	11.466	13.410
NT2RP3001268	10.917	11.531	28.253	21.540	5.251	19.724	6.886	19.730
NT2RP3001271	504.472	230.117	363.954	129.052	147.454	341.938	290.090	221.262
NT2RP3001272	53.274	65.558	170.406	46.512	25.065	49.775	25.165	40.714
NT2RP3001274	379.452	180.634	305.168	109.916	102.975	251.219	221.619	125.753
NT2RP3001275	69.350	44.463	39.465	12.598	20.694	29.868	27.346	15.608
NT2RP3001280	84.373	66.148	58.661	22.588	41.962	35.792	31.005	24.067
NT2RP3001281	108.112	65.094	147.713	26.972	40.778	44.735	37.860	23.491
NT2RP3001288	37.247	71.613	48.891	21.593	34.714	52.211	28.610	57.051
NT2RP3001297	74.827	48.767	64.601	33.081	24.851	55.981	45.160	38.893
NT2RP3001300	97.287	54.906	120.465	40.784	42.784	70.008	44.204	40.196
NT2RP3001301	11.093	5.654	18.227	4.517	6.710	15.021	4.763	1.496
NT2RP3001307	61.481	16.300	67.269	13.678	18.372	43.312	26.354	11.694
NT2RP3001310	25.947	50.116	44.928	47.746	27.742	21.494	12.532	23.321
NT2RP3001318	2.615	3.369	14.422	2.026	3.965	19.407	1.976	0.653
NT2RP3001322	23.311	16.139	27.515	12.075	11.630	21.825	11.372	27.956
NT2RP3001325	22.066	21.492	31.828	22.944	8.193	35.016	13.134	12.706
NT2RP3001338	267.619	127.929	200.245	81.462	81.219	191.701	160.006	129.805
NT2RP3001339	55.924	18.296	23.218	9.542	15.077	30.484	15.924	10.368
NT2RP3001340	298.177	147.842	242.840	118.851	106.391	255.313	197.733	160.604
NT2RP3001341	23.654	19.357	26.001	10.758	14.654	8.713	20.669	6.157
NT2RP3001354	87.315	79.863	264.818	54.210	48.577	53.865	34.407	62.241
NT2RP3001355	42.549	24.220	47.797	11.284	26.805	23.247	21.876	15.122
NT2RP3001356	34.895	26.366	50.692	16.458	11.954	15.544	17.696	14.918
NT2RP3001359	69.545	40.643	64.520	10.543	19.486	38.410	36.229	16.040
NT2RP3001364	52.551	18.103	37.863	13.181	12.916	34.493	28.810	10.544
NT2RP3001373	92.853	21.226	65.327	12.110	28.221	75.073	40.142	19.775
NT2RP3001374	18.587	16.153	13.874	9.085	8.007	19.729	12.896	13.227
NT2RP3001383	35.886	15.749	32.731	12.969	13.335	20.056	21.243	6.300
NT2RP3001384	48.057	31.309	50.523	17.718	21.014	25.468	27.812	18.039
NT2RP3001388	55.759	50.699	117.391	21.210	51.970	52.288	26.887	29.189
NT2RP3001392	21.410	21.933	25.706	8.332	7.588	8.588	10.071	8.795
NT2RP3001396	15.219	8.348	19.141	7.594	10.677	11.741	7.988	10.281
NT2RP3001398	232.068	78.008	227.136	38.826	59.027	175.527	102.665	51.488
NT2RP3001399	92.466	61.566	193.463	33.588	29.343	44.058	36.467	18.064
NT2RP3001402	26.552	22.030	30.054	10.244	16.784	15.120	12.991	23.925
NT2RP3001407	18.523	26.250	28.873	22.708	11.616	32.784	12.119	9.034
NT2RP3001416	46.040	28.810	36.947	10.094	15.710	31.887	29.218	27.952
NT2RP3001420	39.104	40.226	112.497	29.782	17.944	17.648	21.378	24.813
NT2RP3001425	39.881	24.233	38.220	17.938	17.233	24.809	27.932	23.131
NT2RP3001426	93.587	58.250	74.483	29.242	37.668	70.217	46.545	43.211
NT2RP3001427	42.182	35.278	33.424	18.910	17.612	29.923	26.039	24.764
NT2RP3001428	59.474	65.787	162.966	40.062	19.191	22.870	32.859	22.870
NT2RP3001429	35.365	23.903	90.012	12.419	8.727	11.508	11.358	8.026
NT2RP3001432	42.083	23.762	67.215	13.740	8.729	9.061	7.315	14.038
NT2RP3001439	136.789	39.813	81.846	20.164	30.564	96.253	70.005	58.770
NT2RP3001441	38.061	24.064	25.139	12.626	14.885	31.263	17.597	19.725
NT2RP3001446	20.584	15.857	21.782	11.500	7.326	13.920	17.301	7.485
NT2RP3001447	104.606	70.020	154.062	30.513	35.791	54.330	36.473	40.409
NT2RP3001449	10.642	11.657	12.517	5.248	3.069	9.786	3.931	5.883
NT2RP3001453	87.023	43.788	114.632	22.536	14.076	36.685	26.653	35.481

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Table 101

NT2RP3001457	57.656	31.667	38.475	9.474	16.537	32.375	23.383	23.793
NT2RP3001459	60.291	21.305	34.270	9.400	12.047	30.246	18.427	13.216
NT2RP3001463	37.349	24.189	26.737	11.241	16.712	12.719	16.251	18.600
NT2RP3001466	3.829	2.179	4.207	1.152	6.985	7.668	4.907	8.467
NT2RP3001472	42.523	90.955	71.226	30.689	20.551	29.208	32.709	50.536
NT2RP3001475	78.059	60.351	58.086	17.203	25.592	46.882	39.257	36.666
NT2RP3001479	51.578	39.412	55.653	11.108	26.361	52.488	31.590	18.401
NT2RP3001490	9.839	19.316	39.150	6.364	17.825	19.656	7.865	7.287
NT2RP3001492	26.968	22.905	24.652	26.603	12.384	24.009	18.581	38.062
NT2RP3001495	42.340	19.294	36.741	7.565	17.241	28.985	27.157	19.314
NT2RP3001497	32.950	17.434	21.044	7.024	15.546	10.180	19.393	11.452
NT2RP3001501	49.067	12.638	47.469	8.720	17.879	41.926	36.474	34.151
NT2RP3001527	128.120	106.243	244.961	55.672	47.467	62.628	70.008	82.431
NT2RP3001529	126.912	81.307	206.759	36.211	39.398	67.609	39.145	62.778
NT2RP3001538	88.926	38.255	69.884	13.233	24.804	68.411	33.275	32.991
NT2RP3001539	81.817	43.540	51.302	22.808	20.905	63.546	26.220	38.541
NT2RP3001542	11.704	7.892	19.344	6.489	4.478	17.599	4.710	7.688
NT2RP3001549	60.840	55.102	62.218	28.542	25.159	35.315	25.069	26.210
NT2RP3001554	63.142	38.335	57.520	12.016	24.143	31.920	38.546	16.779
NT2RP3001560	31.508	10.439	17.431	4.171	2.833	51.650	11.927	4.890
NT2RP3001561	63.493	90.177	97.829	34.619	16.230	73.893	63.557	42.901
NT2RP3001564	24.224	31.924	65.851	31.318	22.874	32.192	22.750	54.688
NT2RP3001568	67.785	39.398	77.618	15.998	21.374	60.561	47.360	27.334
NT2RP3001575	158.363	105.187	188.761	35.371	49.236	104.929	66.520	52.127
NT2RP3001580	22.928	24.103	27.902	11.308	13.846	10.773	15.209	6.535
NT2RP3001587	30.882	46.805	32.389	23.716	21.127	18.550	19.430	26.668
NT2RP3001589	87.238	55.913	140.234	21.405	30.269	16.502	28.129	10.227
NT2RP3001592	47.242	30.596	31.040	13.899	18.557	41.892	35.638	42.607
NT2RP3001607	16.545	13.286	20.677	4.980	9.882	24.464	11.354	5.914
NT2RP3001608	107.899	35.856	58.646	18.572	27.828	41.340	38.549	32.556
NT2RP3001613	181.447	52.790	94.058	22.958	35.402	79.493	85.597	41.703
NT2RP3001619	37.170	25.761	28.424	19.581	14.720	20.892	19.236	19.461
NT2RP3001621	25.051	25.597	20.759	20.248	14.008	11.806	23.506	15.754
NT2RP3001629	42.495	29.023	21.485	11.692	14.221	12.517	24.496	15.072
NT2RP3001630	55.203	33.318	32.380	8.398	13.075	15.299	24.396	22.471
NT2RP3001631	44.095	28.385	25.774	21.960	8.104	12.247	12.424	22.548
NT2RP3001634	49.389	31.519	50.276	17.438	9.120	14.725	16.971	25.097
NT2RP3001642	58.384	63.135	64.537	32.197	35.654	40.765	40.711	48.812
NT2RP3001646	46.102	25.499	30.071	11.012	13.561	30.364	19.040	15.478
NT2RP3001650	24.560	13.692	28.286	3.177	10.587	18.321	16.939	9.216
NT2RP3001667	25.379	40.979	30.084	11.709	14.158	32.432	17.482	25.227
NT2RP3001671	51.796	35.962	30.710	14.900	16.883	48.652	22.108	17.635
NT2RP3001672	125.298	47.766	73.324	32.053	41.587	103.311	68.493	24.949
NT2RP3001676	44.058	36.932	114.623	30.805	23.379	25.887	17.997	8.670
NT2RP3001678	48.527	41.805	54.658	14.292	18.855	29.685	32.419	36.221
NT2RP3001679	56.508	35.021	81.826	15.299	18.731	40.182	31.070	17.889
NT2RP3001682	33.136	20.214	19.464	8.314	10.046	16.063	14.268	5.567
NT2RP3001685	95.365	62.809	194.220	24.485	21.045	38.439	16.225	11.304
NT2RP3001688	122.935	103.280	232.690	54.732	41.328	31.580	55.067	32.257
NT2RP3001690	48.596	45.935	42.137	20.012	17.447	39.119	24.083	18.809
NT2RP3001693	76.315	27.860	52.551	37.607	26.960	72.114	45.231	19.480
NT2RP3001696	35.875	28.246	35.927	21.333	60.841	9.615	24.315	9.560
NT2RP3001698	43.726	102.017	42.229	16.546	27.452	36.516	25.269	42.349
NT2RP3001708	36.121	26.604	23.161	16.082	1.714	11.104	2.885	20.780
NT2RP3001712	113.609	129.822	366.565	126.311	59.689	78.525	41.638	61.807
NT2RP3001716	9.845	7.608	13.734	5.525	8.563	23.994	5.143	4.152
NT2RP3001724	43.121	23.040	32.820	19.574	11.027	20.906	11.708	5.732
NT2RP3001727	72.718	46.280	190.324	43.096	41.722	61.017	47.265	36.342
NT2RP3001729	10.639	10.707	8.428	17.052	3.948	3.216	64.178	7.190
NT2RP3001730	63.737	67.851	122.541	39.916	31.307	27.433	31.876	23.118
NT2RP3001733	40.642	8.190	17.849	8.778	11.778	26.030	18.334	5.155
NT2RP3001737	106.767	31.997	40.871	23.282	26.905	36.357	25.210	18.710
NT2RP3001738	174.651	37.341	91.532	33.803	49.232	87.359	90.833	19.024
NT2RP3001739	119.404	43.837	72.501	19.331	38.072	77.999	61.245	24.127

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Table 102

NT2RP3001742	58.731	59.672	86.234	43.100	39.678	62.316	23.594	32.745
NT2RP3001751	48.631	34.876	158.212	47.830	31.536	36.350	15.916	18.927
NT2RP3001752	94.578	61.575	307.338	43.572	55.894	46.187	9.168	38.702
NT2RP3001753	23.594	18.268	28.874	16.113	17.103	13.403	14.360	7.574
NT2RP3001754	257.019	147.414	145.593	48.124	69.378	138.023	89.833	70.678
NT2RP3001756	106.542	23.060	11.890	3.761	12.461	39.172	8.157	5.587
NT2RP3001764	97.616	41.097	57.216	18.829	29.263	46.634	32.748	8.673
NT2RP3001771	89.626	20.149	49.519	15.739	25.796	66.030	41.963	10.077
NT2RP3001777	58.067	26.504	49.752	19.057	29.401	31.279	31.451	13.675
NT2RP3001782	78.349	53.349	189.787	42.036	31.814	40.007	32.537	31.265
NT2RP3001792	116.784	33.273	79.277	30.838	34.190	79.914	66.384	24.845
NT2RP3001799	56.002	33.221	58.797	25.754	26.042	47.831	44.737	16.237
NT2RP3001819	99.523	31.676	64.535	11.784	27.979	48.855	30.729	15.920
NT2RP3001829	73.466	107.350	119.232	72.609	47.731	75.897	53.911	85.472
NT2RP3001836	24.805	27.404	43.716	32.034	20.484	30.135	10.824	26.221
NT2RP3001839	65.164	48.291	49.763	22.383	28.432	53.489	36.072	27.184
NT2RP3001844	66.622	61.308	123.313	25.118	28.657	41.010	27.431	29.936
NT2RP3001848	155.399	71.963	136.546	46.040	30.799	64.847	88.349	81.167
NT2RP3001854	27.874	31.416	19.202	25.627	11.291	39.721	17.078	15.781
NT2RP3001855	27.658	6.272	33.869	13.508	8.116	5.497	12.706	16.492
NT2RP3001857	56.318	28.077	35.198	13.759	19.378	31.136	31.027	10.998
NT2RP3001858	54.103	24.171	29.092	13.284	15.411	32.167	36.372	11.561
NT2RP3001861	63.497	29.741	57.635	20.968	28.106	45.119	47.585	13.999
NT2RP3001866	10.249	12.382	19.920	12.616	11.772	42.626	11.074	7.998
NT2RP3001871	12.631	15.883	25.471	6.868	6.207	12.620	4.571	4.517
NT2RP3001874	11.507	11.103	18.203	4.856	8.061	6.546	18.725	3.916
NT2RP3001878	18.465	9.045	11.792	9.332	8.403	9.161	9.699	4.707
NT2RP3001885	96.791	37.635	150.137	59.749	39.678	65.282	51.265	28.873
NT2RP3001896	32.191	20.738	27.405	6.654	24.453	44.306	22.893	9.765
NT2RP3001898	78.914	42.917	61.453	15.826	29.295	67.204	51.298	17.212
NT2RP3001899	41.343	15.205	21.780	9.260	12.053	26.711	26.329	25.656
NT2RP3001901	66.535	31.714	47.183	21.483	19.792	40.418	25.763	53.079
NT2RP3001915	13.485	9.383	12.294	10.822	7.631	16.078	5.131	7.213
NT2RP3001926	6.261	3.066	9.593	3.684	3.576	9.671	11.215	1.684
NT2RP3001929	60.492	34.768	142.251	36.157	39.929	21.055	30.245	40.792
NT2RP3001931	61.641	53.696	67.258	14.577	19.384	29.503	29.562	27.881
NT2RP3001938	40.274	25.723	28.062	7.496	13.890	31.768	21.367	10.885
NT2RP3001943	28.287	39.405	55.585	15.302	25.639	35.454	26.626	14.424
NT2RP3001944	73.315	27.407	47.229	18.622	23.648	23.459	28.532	14.827
NT2RP3001945	34.740	226.973	44.000	46.158	19.151	46.315	28.688	17.572
NT2RP3001947	116.378	37.593	58.570	24.995	34.634	68.127	58.533	46.304
NT2RP3001949	21.954	11.535	33.877	4.860	16.683	22.117	14.558	17.598
NT2RP3001952	143.519	121.088	53.648	50.889	37.440	105.617	83.380	63.243
NT2RP3001954	62.996	26.992	48.377	12.537	20.542	32.191	29.976	25.668
NT2RP3001958	129.978	158.142	151.322	123.162	62.713	92.406	67.282	100.024
NT2RP3001967	93.636	55.466	88.272	10.572	29.097	36.626	46.055	17.092
NT2RP3001969	34.479	21.534	19.898	9.167	5.399	15.105	15.158	2.531
NT2RP3001976	37.230	23.786	60.518	23.795	22.136	24.440	19.911	25.309
NT2RP3001988	24.216	19.727	27.547	10.801	12.852	13.805	18.920	10.726
NT2RP3001989	1.471	1.909	7.536	0.621	1.861	0.578	0.269	1.159
NT2RP3002002	86.258	90.727	227.536	60.750	55.252	43.279	35.961	27.250
NT2RP3002004	19.703	13.852	27.972	4.752	16.286	18.094	19.787	7.343
NT2RP3002007	23.474	20.861	30.086	11.557	12.246	16.556	11.639	9.539
NT2RP3002014	73.272	44.064	105.038	21.583	22.923	30.079	37.416	19.158
NT2RP3002015	45.650	25.353	31.414	12.464	11.588	23.493	22.893	14.440
NT2RP3002033	7.919	7.838	6.105	2.217	2.555	1.242	5.234	1.639
NT2RP3002045	21.618	5.917	11.205	1.926	3.123	8.022	6.419	4.266
NT2RP3002054	12.875	15.125	21.352	7.162	14.499	15.344	8.332	4.770
NT2RP3002058	15.165	25.056	14.776	16.349	11.179	12.472	5.599	27.199
NT2RP3002057	34.454	21.088	18.683	15.978	12.035	23.460	21.618	18.390
NT2RP3002061	35.549	24.492	34.009	18.402	15.138	21.477	15.115	17.613
NT2RP3002062	30.631	13.014	52.221	11.461	16.044	21.886	8.319	7.954
NT2RP3002063	23.330	22.063	18.919	7.923	12.276	13.149	10.874	7.143
NT2RP3002064	108.343	49.219	61.758	11.778	26.355	47.256	44.374	26.732

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Table 103

NT2RP3002071	18.641	8.678	10.550	3.877	8.890	15.118	11.681	9.986
NT2RP3002073	21.421	28.270	17.244	8.390	7.984	14.893	9.734	12.810
NT2RP3002074	58.380	28.105	42.899	18.734	20.881	18.721	29.611	19.857
NT2RP3002075	59.306	37.344	42.700	25.078	27.978	35.950	33.241	20.022
NT2RP3002077	120.301	28.839	29.039	10.364	16.319	40.212	29.213	9.478
NT2RP3002081	26.831	15.778	21.982	12.572	10.820	14.083	12.614	11.083
NT2RP3002086	87.926	53.777	142.446	48.023	26.542	32.148	26.246	52.677
NT2RP3002094	33.062	35.549	57.575	42.152	21.321	27.615	18.554	12.485
NT2RP3002096	49.540	22.516	39.610	9.388	18.743	33.193	33.700	12.017
NT2RP3002097	26.334	27.838	34.989	21.007	14.939	24.394	20.920	11.430
NT2RP3002098	44.592	23.806	37.622	21.688	21.108	22.573	24.025	31.657
NT2RP3002102	79.033	86.261	164.477	46.235	35.252	56.190	33.162	43.258
NT2RP3002106	77.525	71.059	239.471	34.504	16.297	23.309	16.557	32.205
NT2RP3002108	44.613	18.028	23.167	12.003	9.700	17.108	11.361	8.970
NT2RP3002109	48.832	54.217	110.537	30.507	53.885	32.217	28.672	32.057
NT2RP3002110	89.630	210.042	214.246	193.998	55.568	79.385	66.216	96.572
NT2RP3002113	56.372	35.313	57.256	20.790	24.151	40.633	31.916	21.890
NT2RP3002120	29.242	37.086	18.529	14.039	12.431	13.596	15.152	8.244
NT2RP3002121	16.794	22.468	34.546	15.934	19.042	18.137	15.462	9.151
NT2RP3002126	41.432	79.714	33.116	16.398	35.960	52.883	34.750	31.846
NT2RP3002128	181.295	79.422	107.432	30.207	38.340	110.226	72.274	55.110
NT2RP3002130	146.473	43.354	77.922	29.452	37.242	74.976	38.796	20.167
NT2RP3002133	57.753	91.578	70.347	18.863	21.214	49.924	14.482	21.057
NT2RP3002138	43.801	49.959	66.820	35.859	53.999	51.027	15.709	17.711
NT2RP3002140	64.973	38.168	59.056	29.445	31.803	46.421	49.899	13.225
NT2RP3002142	132.430	135.567	308.150	95.713	104.450	105.460	76.193	111.169
NT2RP3002145	110.073	69.842	274.145	50.104	54.554	46.952	38.770	22.003
NT2RP3002147	79.974	78.251	76.290	23.131	32.938	49.028	36.864	20.569
NT2RP3002151	28.317	56.044	35.024	31.238	13.466	19.730	29.531	21.213
NT2RP3002155	113.358	59.837	83.053	31.667	33.044	85.787	59.718	11.547
NT2RP3002156	18.567	17.466	43.089	11.697	14.283	20.150	19.476	8.599
NT2RP3002160	45.470	32.287	51.148	8.537	17.337	18.576	19.383	9.987
NT2RP3002163	58.319	76.385	85.220	36.452	25.979	54.323	41.118	65.634
NT2RP3002165	99.653	52.118	87.449	32.574	44.305	65.099	54.567	25.366
NT2RP3002166	37.449	18.398	38.523	7.973	18.270	16.300	16.573	5.836
NT2RP3002173	138.293	67.332	233.564	25.504	39.519	46.406	22.234	32.147
NT2RP3002174	34.983	25.592	20.612	10.322	10.075	33.100	18.166	8.352
NT2RP3002181	25.553	17.452	12.477	15.521	6.186	13.861	17.883	5.289
NT2RP3002185	130.901	22.501	42.897	20.805	18.996	58.093	23.439	7.852
NT2RP3002193	48.914	35.893	57.402	12.166	28.331	65.610	51.617	21.157
NT2RP3002204	25.437	16.825	30.602	6.124	18.001	26.166	12.479	21.873
NT2RP3002244	49.842	27.141	57.904	22.937	24.682	26.606	32.340	22.561
NT2RP3002248	86.580	63.454	102.977	40.434	37.198	51.108	39.002	34.672
NT2RP3002253	55.575	9.382	8.780	13.506	12.566	16.080	15.217	3.963
NT2RP3002255	35.015	68.339	52.684	56.744	24.356	32.145	25.739	37.424
NT2RP3002264	55.986	34.735	59.125	27.856	26.745	42.746	33.939	8.983
NT2RP3002267	80.099	23.461	44.639	24.189	20.404	52.393	26.915	33.436
NT2RP3002273	112.221	85.604	140.868	66.160	58.014	79.427	50.417	36.059
NT2RP3002276	62.303	48.041	50.683	13.361	24.974	43.308	34.452	31.732
NT2RP3002281	40.333	19.037	24.587	16.378	13.790	21.545	20.931	8.966
NT2RP3002286	27.525	24.696	32.519	15.907	12.207	12.167	13.138	14.040
NT2RP3002297	184.330	104.754	239.133	101.492	75.626	106.831	74.738	83.240
NT2RP3002301	53.311	19.361	38.416	18.640	28.458	40.874	31.521	16.259
NT2RP3002303	151.906	66.595	108.440	41.097	41.354	98.439	62.889	20.317
NT2RP3002304	9.712	7.368	13.268	9.520	3.566	6.387	8.272	2.623
NT2RP3002309	34.656	9.379	19.868	19.687	8.915	31.244	28.005	8.625
NT2RP3002311	44.224	21.425	31.676	9.614	15.336	23.060	17.155	24.047
NT2RP3002315	60.149	39.087	49.728	29.239	27.551	69.218	44.550	30.664
NT2RP3002319	29.909	14.381	39.512	12.835	8.358	20.152	26.375	28.658
NT2RP3002324	84.644	48.794	79.950	26.759	38.717	55.982	49.196	49.374
NT2RP3002330	40.225	35.781	41.419	18.069	24.353	43.432	29.047	24.194
NT2RP3002333	739.604	109.838	247.248	63.516	145.604	638.213	368.164	89.849
NT2RP3002337	12.429	9.488	14.787	4.435	5.777	6.399	6.548	8.159
NT2RP3002342	18.485	16.965	24.764	8.272	19.656	13.221	7.806	10.971

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Table 104

NT2RP3002343	98.077	41.393	159.033	34.235	37.461	51.737	39.000	34.837
NT2RP3002351	11.568	8.544	17.447	8.504	7.516	10.032	16.378	11.298
NT2RP3002352	61.768	50.393	66.786	25.296	17.190	34.146	31.668	29.346
NT2RP3002353	84.753	66.818	124.498	39.521	45.715	83.255	42.335	39.394
NT2RP3002362	147.017	77.918	101.793	33.659	48.293	105.808	93.191	47.902
NT2RP3002363	51.360	22.194	27.308	16.354	18.149	41.241	27.368	9.958
NT2RP3002377	22.585	15.479	26.241	11.831	11.702	22.164	19.250	14.688
NT2RP3002383	36.652	26.590	37.776	12.961	18.317	29.595	32.435	19.372
NT2RP3002388	41.759	29.432	82.187	16.223	19.758	13.702	16.544	34.308
NT2RP3002394	64.877	31.565	40.945	18.641	23.109	44.424	35.200	24.054
NT2RP3002398	344.708	216.589	379.846	153.561	145.584	244.214	334.003	155.648
NT2RP3002399	120.898	118.841	123.581	92.322	61.939	76.458	34.837	92.415
NT2RP3002402	52.959	35.232	68.571	16.571	20.492	53.151	21.545	24.518
NT2RP3002409	167.688	37.697	100.184	25.069	35.882	114.827	88.945	40.800
NT2RP3002410	144.081	109.377	101.178	45.575	39.226	71.259	45.433	41.401
NT2RP3002411	93.030	33.468	50.254	10.997	27.600	27.023	23.738	15.047
NT2RP3002429	43.781	19.997	33.403	9.720	14.797	31.472	21.609	8.498
NT2RP3002448	18.505	12.378	25.831	8.000	12.388	14.483	16.180	11.704
NT2RP3002454	22.834	27.433	27.109	11.518	12.679	23.830	18.696	7.724
NT2RP3002455	42.267	39.024	48.252	18.078	25.184	40.843	26.300	25.891
NT2RP3002456	63.618	62.895	132.023	60.865	48.457	47.502	34.943	107.915
NT2RP3002462	81.232	66.732	75.545	22.706	28.463	63.509	41.976	23.685
NT2RP3002469	31.281	25.018	41.900	16.283	18.312	31.313	22.887	8.884
NT2RP3002470	394.179	240.381	344.971	150.134	156.904	226.629	242.639	129.974
NT2RP3002484	119.962	120.572	179.767	55.590	78.186	80.561	80.333	27.126
NT2RP3002491	20.237	11.861	12.690	4.614	6.231	7.954	11.431	9.537
NT2RP3002494	102.258	227.475	73.714	31.409	28.100	91.250	58.572	81.116
NT2RP3002497	111.163	46.894	64.415	16.949	25.888	83.935	42.893	24.093
NT2RP3002500	77.111	26.529	42.337	12.959	16.485	30.996	37.915	22.524
NT2RP3002501	53.661	44.526	44.009	16.212	22.884	27.120	37.461	16.746
NT2RP3002512	63.608	44.357	40.061	20.054	21.830	23.291	29.988	18.925
NT2RP3002529	45.341	43.112	48.262	25.498	22.514	23.399	23.938	31.672
NT2RP3002533	94.195	65.870	61.041	18.300	73.412	49.543	39.779	31.520
NT2RP3002539	48.864	37.046	54.572	30.194	21.685	26.897	29.822	42.332
NT2RP3002540	30.794	21.358	37.383	11.560	13.724	17.298	19.581	11.502
NT2RP3002543	223.940	110.144	120.839	52.219	64.994	144.657	115.227	76.872
NT2RP3002545	15.100	41.894	32.270	19.423	32.049	13.151	11.195	10.417
NT2RP3002549	28.199	14.150	27.495	13.528	19.671	17.420	11.163	7.548
NT2RP3002552	47.064	17.945	25.504	12.370	13.372	28.220	22.837	14.570
NT2RP3002558	61.923	30.846	56.966	17.185	28.359	33.407	22.300	21.755
NT2RP3002565	62.350	42.196	107.270	25.722	27.937	33.279	27.380	20.262
NT2RP3002566	54.275	39.776	49.593	22.587	24.849	18.616	38.067	25.776
NT2RP3002571	16.476	11.788	20.308	3.165	5.305	12.738	11.591	7.492
NT2RP3002572	65.635	36.206	37.772	17.526	23.615	29.016	17.205	16.571
NT2RP3002573	104.009	83.178	49.387	56.147	11.324	27.549	32.818	43.821
NT2RP3002577	52.884	22.337	33.591	12.529	6.690	22.718	19.368	7.491
NT2RP3002579	71.729	30.291	36.007	21.690	15.920	21.971	21.241	10.888
NT2RP3002582	81.979	51.167	67.043	31.231	41.904	56.964	46.155	37.227
NT2RP3002587	26.087	32.407	69.922	18.487	19.982	21.677	19.805	12.145
NT2RP3002590	7.512	8.105	10.729	21.190	15.305	8.973	7.009	4.548
NT2RP3002602	47.775	17.298	29.784	12.271	15.119	25.375	31.820	9.770
NT2RP3002603	161.708	183.767	216.650	65.839	78.955	109.597	71.485	115.706
NT2RP3002621	119.248	24.598	40.553	16.479	9.925	62.060	30.435	25.390
NT2RP3002622	69.767	50.020	145.390	29.140	21.618	41.045	15.163	15.918
NT2RP3002624	1.393	5.920	0.000	0.942	2.232	1.299	2.998	1.562
NT2RP3002628	9.999	8.708	17.715	17.122	8.351	14.530	9.109	5.659
NT2RP3002629	249.675	59.767	98.304	56.623	88.848	134.353	115.158	40.132
NT2RP3002631	0.595	0.000	0.000	0.000	0.000	0.000	0.000	0.000
NT2RP3002647	30.462	15.046	27.336	16.536	12.777	15.918	14.630	14.888
NT2RP3002649	120.351	83.386	89.024	51.631	33.853	77.229	31.648	30.637
NT2RP3002650	78.123	37.371	55.575	21.740	26.972	61.290	42.009	51.110
NT2RP3002652	40.736	15.102	33.402	15.021	16.044	39.523	34.502	10.676
NT2RP3002654	32.673	14.185	26.107	12.823	19.846	18.421	24.175	8.617
NT2RP3002657	79.710	86.415	129.177	41.769	103.657	80.846	59.737	46.192

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Table 105·

NT2RP3002659	18.914	12.170	24.486	6.353	13.890	36.308	7.922	9.590
NT2RP3002660	64.465	53.376	119.655	42.835	35.909	41.916	10.430	27.532
NT2RP3002663	30.048	20.813	29.457	13.786	13.557	15.463	15.414	13.216
NT2RP3002664	14.659	18.990	23.494	8.867	10.564	9.625	5.085	4.798
NT2RP3002667	15.216	16.234	11.286	11.809	8.647	8.484	26.055	18.907
NT2RP3002671	39.495	26.960	28.177	15.153	12.285	24.589	13.809	14.654
NT2RP3002682	11.347	14.990	21.206	28.999	14.002	9.455	16.128	33.677
NT2RP3002684	13.722	11.697	16.858	8.392	12.676	7.181	5.777	4.503
NT2RP3002687	2.560	4.651	10.162	1.691	1.917	2.141	3.706	3.397
NT2RP3002688	15.864	2.884	22.879	1.260	13.309	20.413	8.939	1.088
NT2RP3002698	28.485	12.350	29.970	11.179	18.339	22.012	15.073	59.183
NT2RP3002701	144.580	68.552	65.738	22.713	47.971	117.171	58.063	64.453
NT2RP3002705	50.811	34.865	76.689	77.242	38.688	84.791	28.441	54.479
NT2RP3002708	107.193	25.745	48.335	10.739	20.147	29.081	22.130	32.554
NT2RP3002711	38.410	19.460	31.129	24.261	21.934	31.711	19.413	9.154
NT2RP3002712	127.597	337.217	172.297	85.410	157.291	209.750	71.600	90.235
NT2RP3002713	25.722	12.997	26.653	9.930	11.236	16.757	16.310	18.652
NT2RP3002721	48.039	15.327	24.924	23.105	19.153	24.353	19.280	10.413
NT2RP3002722	421.087	147.659,	338.772	115.647	164.233	259.199	308.668	136.618
NT2RP3002723	43.086	95.012	67.010	38.528	35.204	150.941	121.373	45.387
NT2RP3002737	71.494	27.672	52.178	22.716	32.049	58.862	47.802	16.795
NT2RP3002738	47.542	16.654	36.964	9.362	16.223	38.458	25.360	23.198
NT2RP3002742	81.782	149.322	102.776	54.228	44.909	105.384	127.394	33.680
NT2RP3002744	2.263	4.168	21.735	2.015	3.502	1.976	2.225	0.560
NT2RP3002756	22.619	12.182	21.840	8.009	10.135	11.380	12.917	4.838
NT2RP3002757	113.772	65.294	69.951	34.431	19.743	281.518	37.409	82.637
NT2RP3002758	60.176	82.911	68.360	23.774	51.197	81.519	55.695	20.674
NT2RP3002762	70.007	62.402	96.808	44.296	70.524	111.844	35.008	61.053
NT2RP3002763	65.632	38.286	93.384	42.890	27.102	55.601	31.878	35.587
NT2RP3002770	35.381	13.511	35.913	7.950	10.042	24.469	17.980	11.225
NT2RP3002771	40.863	23.186	29.004	13.976	35.897	25.254	18.920	17.572
NT2RP3002785	13.960	5.890	4.173	2.677	2.677	9.071	5.889	5.289
NT2RP3002790	34.782	20.599	28.673	15.987	14.483	19.288	18.105	19.768
NT2RP3002799	39.751	31.026	83.485	29.150	23.866	22.566	21.257	45.619
NT2RP3002801	47.659	26.163	128.555	31.073	22.498	26.337	24.586	24.190
NT2RP3002802	146.487	73.131	121.221	33.066	38.992	67.510	59.237	21.826
NT2RP3002810	10.160	45.362	22.360	7.561	8.729	7.648	14.315	7.654
NT2RP3002818	4.667	6.464	10.095	3.200	6.216	4.871	5.874	11.969
NT2RP3002821	76.117	34.802	53.630	32.950	28.735	58.082	41.128	16.704
NT2RP3002823	11.784	13.818	14.562	1.977	7.384	12.328	6.617	11.325
NT2RP3002825	51.146	13.354	18.612	8.300	12.766	20.235	20.838	24.852
NT2RP3002829	35.187	38.250	97.142	25.989	24.214	26.885	16.084	21.503
NT2RP3002831	66.496	27.156	68.213	17.668	23.336	61.962	46.206	37.479
NT2RP3002836	130.172	72.920	90.667	20.404	36.995	100.291	59.703	56.686
NT2RP3002845	64.337	22.726	40.173	14.166	18.291	22.445	10.215	12.196
NT2RP3002852	38.556	19.001	25.493	7.993	8.490	26.043	16.609	7.989
NT2RP3002861	2.544	8.478	5.538	2.371	1.076	11.828	8.852	2.388
NT2RP3002869	119.363	36.492	65.104	27.751	37.200	48.198	61.052	17.114
NT2RP3002874	24.807	10.169	15.126	5.983	8.446	11.486	15.977	17.599
NT2RP3002876	64.967	22.806	49.911	23.937	25.658	54.137	50.714	12.582
NT2RP3002877	86.753	69.686	258.276	48.444	44.144	53.777	36.801	48.742
NT2RP3002887	32.513	9.192	16.424	15.590	7.085	25.821	19.262	5.065
NT2RP3002900	17.592	22.036	56.235	9.751	17.946	18.936	16.030	15.494
NT2RP3002902	77.119	87.651	99.208	65.469	23.869	49.857	35.525	68.682
NT2RP3002909	651.498	271.044	348.888	147.447	159.876	403.448	375.523	192.134
NT2RP3002911	18.365	31.404	29.903	8.152	11.463	10.299	14.454	11.143
NT2RP3002948	31.554	19.471	22.058	5.625	13.560	11.821	12.470	4.969
NT2RP3002953	86.292	18.063	24.427	6.969	18.812	14.379	32.470	9.777
NT2RP3002955	19.801	7.571	12.412	9.001	5.316	8.726	8.912	8.536
NT2RP3002958	41.536	22.160	22.741	5.690	11.415	41.119	17.410	12.258
NT2RP3002969	37.280	28.189	25.925	9.002	18.977	16.248	14.471	9.514
NT2RP3002972	22.208	18.736	16.171	2.364	9.532	9.859	13.526	7.568
NT2RP3002978	17.816	15.240	32.009	15.003	9.596	5.319	8.999	3.049
NT2RP3002983	7.404	5.940	7.102	1.188	7.742	3.489	6.275	6.214

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Table 106

NT2RP3002985	54.322	20.945	33.398	9.562	18.165	28.438	25.968	20.623
NT2RP3002988	17.700	17.268	27.888	13.345	13.104	15.971	19.252	22.620
NT2RP3003000	76.725	68.978	102.455	35.327	36.878	75.681	73.309	47.982
NT2RP3003008	40.397	31.290	39.838	8.641	14.630	27.543	20.015	10.881
NT2RP3003012	14.280	14.189	33.526	7.156	11.442	14.530	6.941	4.141
NT2RP3003015	54.108	13.725	29.619	7.455	12.688	24.800	30.124	11.125
NT2RP3003018	10.045	6.127	17.611	6.653	9.081	19.649	6.155	2.761
NT2RP3003028	75.625	33.179	39.416	26.480	25.319	7.487	13.397	10.834
NT2RP3003029	86.986	50.846	63.900	15.149	20.126	31.780	36.530	32.637
NT2RP3003032	136.276	96.942	314.984	60.769	68.889	66.630	49.952	17.929
NT2RP3003041	0.774	0.000	0.000	0.000	0.000	0.000	1.309	0.000
NT2RP3003044	58.906	34.057	37.901	33.307	16.940	40.357	27.766	20.617
NT2RP3003047	299.110	142.539	196.643	84.285	77.718	179.257	155.007	76.424
NT2RP3003050	109.372	50.507	141.571	31.797	25.077	71.052	48.869	21.064
NT2RP3003053	274.051	115.298	324.746	103.977	94.331	152.747	122.042	87.952
NT2RP3003059	2.357	7.346	12.467	3.194	4.084	5.560	5.012	5.335
NT2RP3003061	73.691	33.582	61.169	13.328	36.122	45.965	43.431	12.628
NT2RP3003068	37.384	20.186	32.010	15.417	17.562	24.065	18.951	10.008
NT2RP3003071	67.292	86.945	86.857	82.004	27.275	45.183	35.965	42.507
NT2RP3003076	416.323	202.004	220.395	107.162	152.849	340.664	234.319	136.293
NT2RP3003078	71.012	26.534	49.393	29.939	5.761	38.583	27.416	13.913
NT2RP3003081	19.188	18.554	20.891	20.934	9.794	13.502	9.853	16.047
NT2RP3003090	24.820	15.196	39.751	22.524	18.155	24.073	18.075	11.570
NT2RP3003097	40.069	29.407	79.380	21.495	17.378	23.253	27.673	8.566
NT2RP3003098	13.217	23.032	48.998	16.354	11.329	10.279	11.069	6.398
NT2RP3003101	39.920	30.326	45.276	16.850	23.417	25.447	16.056	8.843
NT2RP3003109	119.924	108.927	295.233	59.830	51.482	54.674	35.646	24.366
NT2RP3003121	2393.421	71.299	32.543	7.629	41.587	873.484	227.334	18.974
NT2RP3003133	11.661	5.814	23.481	8.926	17.718	13.665	11.081	14.402
NT2RP3003137	68.371	27.614	38.170	18.316	18.742	45.822	36.054	10.575
NT2RP3003138	44.343	32.139	50.171	17.889	22.092	27.827	31.428	9.428
NT2RP3003139	32.937	37.068	127.432	21.947	22.860	33.577	10.762	15.124
NT2RP3003145	64.875	32.258	72.318	22.546	31.586	50.878	56.040	16.059
NT2RP3003150	42.321	27.108	62.590	18.416	21.031	25.656	29.781	16.540
NT2RP3003157	188.220	140.662	506.895	130.211	104.053	100.283	60.660	81.294
NT2RP3003185	35.909	24.691	42.997	16.452	17.320	37.070	32.807	25.906
NT2RP3003193	48.750	36.867	108.147	41.546	24.503	37.327	24.359	47.838
NT2RP3003197	43.343	21.902	29.083	20.464	12.340	28.720	23.116	10.543
NT2RP3003203	153.994	40.417	93.798	29.132	49.066	119.739	77.380	29.340
NT2RP3003204	52.532	32.770	132.406	37.419	35.096	33.072	28.607	12.176
NT2RP3003210	47.284	47.257	92.480	28.382	35.162	29.885	33.588	22.928
NT2RP3003212	51.752	32.358	143.629	28.494	28.759	34.382	24.899	16.702
NT2RP3003213	50.864	21.698	54.368	14.258	27.197	21.835	26.272	24.633
NT2RP3003224	13.983	12.957	12.821	7.212	9.704	11.616	6.674	9.347
NT2RP3003226	16.228	18.549	16.359	5.465	13.435	9.616	13.939	5.004
NT2RP3003230	31.730	19.544	37.790	12.117	10.448	26.264	14.491	4.525
NT2RP3003235	49.021	57.135	135.476	23.077	25.398	43.447	24.772	17.016
NT2RP3003242	16.643	9.743	12.011	3.953	5.705	9.943	7.847	1.564
NT2RP3003251	105.227	79.924	206.051	45.598	38.945	39.441	42.132	48.708
NT2RP3003252	72.597	32.121	56.052	21.016	24.060	43.414	42.743	34.203
NT2RP3003258	161.647	70.976	113.824	51.504	62.130	87.395	113.828	62.410
NT2RP3003260	114.060	56.574	37.258	44.299	21.435	88.808	31.572	22.039
NT2RP3003264	67.795	44.399	153.011	36.137	30.168	47.695	22.285	16.139
NT2RP3003273	11.164	9.672	10.474	15.421	5.945	12.757	7.385	3.145
NT2RP3003278	21.149	2.696	5.589	11.708	2.774	13.626	10.155	3.221
NT2RP3003280	27.159	20.262	31.552	13.961	13.568	10.944	21.479	28.154
NT2RP3003282	46.749	20.720	28.508	11.886	15.656	31.511	27.454	26.077
NT2RP3003290	149.162	75.603	249.880	57.514	56.137	81.416	57.703	30.573
NT2RP3003301	52.258	34.467	128.126	22.579	18.873	27.921	26.294	25.862
NT2RP3003302	46.288	23.690	92.158	17.983	15.001	23.542	18.752	19.610
NT2RP3003311	4.124	7.411	10.651	6.453	14.885	11.665	3.658	3.020
NT2RP3003312	14.814	8.617	14.507	5.774	2.403	16.774	9.193	8.645
NT2RP3003313	15.411	6.290	9.374	4.661	3.186	10.303	5.674	15.392
NT2RP3003327	48.258	39.473	117.218	19.521	16.192	24.164	15.226	21.848

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Table 107

NT2RP3003330	29.506	12.597	10.896	8.585	8.115	8.559	6.939	9.940
NT2RP3003344	29.694	14.023	28.467	10.446	14.551	23.190	14.110	21.136
NT2RP3003345	105.530	66.425	241.668	37.233	38.412	50.911	50.114	35.893
NT2RP3003349	20.318	21.037	19.247	6.025	8.572	15.104	15.004	13.774
NT2RP3003353	10.529	10.306	3.139	3.872	5.195	16.793	3.277	2.796
NT2RP3003354	481.127	242.462	577.215	170.336	177.749	307.555	235.179	214.175
NT2RP3003368	47.684	23.833	38.838	12.045	15.329	29.997	27.654	13.096
NT2RP3003375	9.531	13.959	20.610	8.653	7.770	15.597	5.760	11.087
NT2RP3003377	166.751	42.971	84.536	25.743	44.033	73.870	73.821	25.200
NT2RP3003384	44.335	23.396	37.902	18.516	20.006	33.001	24.969	18.065
NT2RP3003385	94.843	42.782	74.715	20.456	31.187	68.473	67.072	48.712
NT2RP3003396	33.482	30.352	33.756	14.143	15.615	30.475	16.101	16.251
NT2RP3003403	53.313	37.215	59.716	18.488	19.630	41.023	7.020	14.203
NT2RP3003409	34.343	23.644	29.939	10.044	13.315	26.899	23.574	10.007
NT2RP3003411	79.480	70.920	90.615	61.424	39.065	48.593	32.903	26.101
NT2RP3003420	61.545	52.479	134.682	28.549	32.168	25.103	23.751	18.844
NT2RP3003425	28.870	18.577	22.890	8.071	10.241	21.558	25.924	11.363
NT2RP3003426	126.098	63.120	93.804	24.452	32.319	90.461	44.692	26.808
NT2RP3003427	53.936	61.645	67.284	18.467	14.098	40.426	41.425	24.813
NT2RP3003433	97.022	87.577	196.547	46.930	103.713	35.421	49.581	51.308
NT2RP3003437	70.471	90.341	101.893	38.490	90.843	65.265	43.848	39.524
NT2RP3003448	166.318	99.558	171.792	33.106	57.030	82.442	40.878	33.734
NT2RP3003455	98.805	99.945	87.828	44.898	40.079	47.665	54.700	42.051
NT2RP3003462	42.184	21.903	23.018	11.812	14.369	18.994	22.972	14.965
NT2RP3003464	20.285	19.800	20.515	13.066	11.398	11.185	9.509	8.151
NT2RP3003469	63.020	31.314	45.443	12.277	22.567	43.698	25.742	22.878
NT2RP3003473	49.194	61.265	73.244	52.029	33.239	49.762	41.082	60.344
NT2RP3003474	25.607	8.816	7.783	3.674	4.629	13.456	6.864	6.240
NT2RP3003475	68.962	28.799	37.252	11.016	19.936	32.908	31.492	21.824
NT2RP3003490	20.464	20.731	22.026	3.717	16.041	3.738	7.208	8.419
NT2RP3003491	10.282	25.486	15.580	15.193	6.202	6.287	6.927	9.848
NT2RP3003493	225.729	58.149	69.338	48.207	44.647	93.915	53.796	47.878
NT2RP3003500	16.211	21.791	23.783	12.174	8.905	10.384	6.189	9.984
NT2RP3003527	35.235	13.032	16.125	4.540	9.823	21.336	14.921	8.623
NT2RP3003532	35.952	35.805	89.452	21.080	32.372	12.131	23.670	14.186
NT2RP3003535	30.511	17.215	16.247	3.432	9.615	14.199	11.449	7.658
NT2RP3003536	35.415	11.045	31.565	10.484	18.265	21.717	21.923	38.703
NT2RP3003543	69.871	52.348	78.481	28.057	40.066	19.654	56.835	72.031
NT2RP3003549	42.025	14.802	50.570	18.842	33.282	15.787	31.229	23.611
NT2RP3003552	4.529	4.296	2.807	0.000	4.647	10.319	2.766	9.014
NT2RP3003555	57.410	40.350	57.743	40.386	32.961	12.721	42.457	36.766
NT2RP3003559	20.066	11.398	15.254	4.806	6.892	5.159	6.000	8.501
NT2RP3003564	66.462	28.214	41.863	14.294	13.568	36.338	25.239	22.138
NT2RP3003572	50.882	28.277	31.870	11.128	15.322	36.904	28.134	19.912
NT2RP3003576	236.584	162.700	666.955	119.960	79.895	90.587	262.925	105.267
NT2RP3003587	34.277	96.685	36.352	13.214	15.718	5.529	28.863	23.236
NT2RP3003589	69.284	86.270	72.517	19.025	34.071	58.468	35.012	42.995
NT2RP3003592	93.627	36.255	60.268	26.747	38.599	27.570	31.962	29.013
NT2RP3003593	64.187	68.925	34.760	5.259	11.913	10.024	11.351	30.666
NT2RP3003614	202.651	80.341	135.229	42.309	52.562	65.826	104.861	77.771
NT2RP3003621	15.164	13.030	15.710	5.347	0.000	7.392	5.209	11.686
NT2RP3003625	131.346	86.625	204.034	32.075	25.952	35.395	31.357	56.208
NT2RP3003627	95.853	64.906	113.102	24.418	43.349	33.276	48.816	77.820
NT2RP3003636	87.887	33.546	51.644	14.475	38.157	18.067	40.566	25.499
NT2RP3003642	33.158	29.959	62.265	29.745	29.841	31.737	24.361	56.869
NT2RP3003645	42.276	23.456	37.015	12.651	15.281	37.561	21.220	15.411
NT2RP3003648	53.111	36.625	54.165	13.954	21.371	20.753	30.160	30.265
NT2RP3003649	13.907	1.465	7.845	4.909	3.500	3.731	3.722	21.889
NT2RP3003650	70.844	54.077	30.996	32.103	41.741	11.885	4.037	9.110
NT2RP3003656	60.131	39.399	21.967	19.082	28.005	21.521	5.926	6.462
NT2RP3003659	60.751	25.453	29.389	28.617	49.090	33.702	21.321	11.457
NT2RP3003662	44.735	45.811	57.204	18.032	8.625	30.812	16.749	60.144
NT2RP3003664	31.481	40.038	50.322	14.238	24.609	25.151	18.244	27.693
NT2RP3003665	9.682	7.431	10.792	3.210	5.228	8.900	22.769	15.662

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Table 108

NT2RP3003671	19.991	16.142	32.517	10.512	26.620	6.813	15.367	4.134
NT2RP3003672	59.637	70.861	52.702	21.219	42.465	28.220	33.602	25.472
NT2RP3003673	22.381	26.615	29.196	8.319	9.184	13.218	19.475	8.663
NT2RP3003679	210.406	183.454	88.575	68.184	55.109	70.199	47.217	161.678
NT2RP3003680	36.432	9.726	11.980	2.868	17.580	10.982	9.675	4.489
NT2RP3003686	23.300	18.187	60.813	12.758	15.373	14.321	13.248	18.094
NT2RP3003689	16.292	10.228	7.344	18.943	22.892	23.049	1.755	14.648
NT2RP3003697	18.041	18.889	23.041	11.465	5.304	14.646	14.387	27.765
NT2RP3003701	23.411	19.362	26.737	5.128	15.953	19.109	21.561	12.363
NT2RP3003704	83.293	69.818	227.532	48.512	34.531	23.793	34.747	31.728
NT2RP3003714	27.845	26.701	35.031	16.071	7.707	11.396	10.568	7.157
NT2RP3003716	23.382	29.412	32.116	1.957	10.013	19.271	16.236	6.862
NT2RP3003721	47.677	30.191	49.197	16.267	34.684	31.096	35.668	28.013
NT2RP3003722	23.636	24.625	30.510	14.691	14.255	9.224	6.260	18.801
NT2RP3003726	71.518	25.344	63.123	17.350	34.451	43.109	46.483	33.548
NT2RP3003729	48.252	22.558	41.664	11.182	23.933	14.940	29.613	40.648
NT2RP3003731	117.126	53.921	150.601	44.104	59.737	67.883	52.971	70.102
NT2RP3003740	95.127	38.608	55.360	23.461	31.988	57.694	54.566	25.167
NT2RP3003746	16.191	12.220,	16.980	7.510	13.596	12.664	8.103	4.718
NT2RP3003749	0.000	0.000	0.000	0.603	0.000	2.487	2.557	3.945
NT2RP3003754	15.865	21.394	19.162	12.449	13.299	26.475	9.854	18.648
NT2RP3003759	0.000	0.000	0.000	1.040	0.228	0.000	0.000	0.000
NT2RP3003764	83.938	66.804	64.694	34.845	35.239	58.222	58.654	59.695
NT2RP3003766	65.630	30.349	55.241	12.627	24.046	19.839	39.865	29.001
NT2RP3003767	70.910	69.657	250.723	42.998	34.723	31.166	25.595	43.641
NT2RP3003778	131.825	86.793	385.771	86.755	57.514	68.379	54.893	62.981
NT2RP3003779	109.510	79.471	82.764	30.193	42.973	68.003	45.497	45.498
NT2RP3003783	20.728	49.548	65.851	31.076	42.337	19.891	30.990	36.938
NT2RP3003787	52.420	24.376	34.398	5.999	3.586	110.807	52.440	37.987
NT2RP3003789	49.434	35.220	51.425	19.152	23.911	36.130	35.358	51.169
NT2RP3003795	35.141	27.549	49.460	9.850	9.646	24.082	23.805	22.055
NT2RP3003799	43.365	13.905	22.874	6.981	14.894	24.044	24.707	15.462
NT2RP3003800	33.918	17.363	27.230	9.216	12.645	25.354	23.431	31.197
NT2RP3003805	63.293	44.084	37.398	25.212	22.134	20.827	35.180	33.836
NT2RP3003809	31.815	50.351	23.357	8.497	6.068	18.501	12.588	23.610
NT2RP3003819	524.121	195.245	386.972	66.656	124.750	204.320	163.951	105.623
NT2RP3003824	23.645	17.797	34.795	9.543	22.963	19.518	18.840	18.478
NT2RP3003825	100.544	64.212	102.915	27.816	51.197	72.544	46.338	78.067
NT2RP3003828	13.857	3.284	8.953	5.968	12.172	6.483	4.696	6.839
NT2RP3003831	58.812	63.105	141.638	36.763	42.372	35.689	36.027	61.956
NT2RP3003833	37.263	25.079	32.114	16.395	15.132	21.745	17.267	29.782
NT2RP3003836	139.979	72.806	102.049	51.574	60.838	71.273	62.037	67.712
NT2RP3003842	173.727	172.520	421.266	66.791	82.994	67.844	51.328	70.400
NT2RP3003843	40.446	57.570	27.866	10.205	61.585	12.265	18.777	39.377
NT2RP3003844	71.843	59.271	53.342	25.835	23.638	29.874	45.658	29.555
NT2RP3003846	9.016	12.338	29.501	8.508	8.017	9.155	11.844	13.878
NT2RP3003849	59.374	29.253	45.642	15.609	18.400	31.563	24.824	35.683
NT2RP3003862	28.859	32.198	37.516	7.219	14.207	16.311	10.540	19.157
NT2RP3003870	163.978	56.534	97.566	27.696	45.763	66.418	66.181	41.207
NT2RP3003874	25.106	64.501	32.262	14.095	20.034	22.879	79.189	8.302
NT2RP3003876	57.365	29.873	42.814	12.716	37.174	19.085	11.236	26.223
NT2RP3003880	46.503	23.356	32.742	9.926	15.723	26.939	26.220	22.845
NT2RP3003889	7.749	87.132	0.000	4.141	0.000	9.987	0.000	44.372
NT2RP3003891	25.663	16.659	18.188	7.572	4.310	18.561	10.999	21.695
NT2RP3003914	84.860	63.645	125.797	31.137	33.556	38.079	39.405	63.562
NT2RP3003916	24.657	11.712	30.742	7.298	10.691	17.859	22.731	9.083
NT2RP3003918	73.118	28.378	32.082	12.218	25.015	44.211	27.234	26.810
NT2RP3003920	52.911	76.524	182.384	22.589	23.248	24.928	25.551	47.359
NT2RP3003924	42.265	34.488	91.378	12.690	20.859	21.272	23.509	18.187
NT2RP3003932	43.906	36.677	103.580	18.902	39.162	15.130	39.334	27.069
NT2RP3003939	45.015	23.114	34.980	14.860	22.109	22.574	16.204	23.960
NT2RP3003940	73.958	53.552	60.719	18.245	37.229	44.476	29.223	32.163
NT2RP3003943	76.185	17.072	23.043	7.858	34.360	21.195	34.259	44.238
NT2RP3003959	33.097	24.518	31.719	13.955	19.977	24.442	23.073	22.296

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Table 109

NT2RP3003963	225.975	65.265	81.733	29.808	52.069	80.205	81.146	44.991
NT2RP3003965	116.328	148.769	160.481	123.378	65.718	64.058	36.726	123.379
NT2RP3003972	178.647	135.585	147.168	34.841	77.695	106.673	70.941	52.120
NT2RP3003973	62.806	37.262	47.172	25.442	23.541	30.764	27.857	45.075
NT2RP3003979	42.205	32.192	109.653	39.966	32.734	35.850	18.262	64.857
NT2RP3003980	43.589	24.631	26.030	11.906	6.253	21.641	13.122	23.086
NT2RP3003982	12.297	22.386	11.608	2.387	11.030	5.747	12.456	34.995
NT2RP3003989	17.308	4.219	22.495	7.718	11.234	3.600	3.546	106.880
NT2RP3003992	38.217	23.384	39.566	7.169	21.356	24.091	21.385	25.954
NT2RP3004000	14.260	12.046	9.623	3.141	15.292	10.563	26.334	5.687
NT2RP3004001	15.524	17.005	53.914	11.406	10.314	27.264	13.462	16.712
NT2RP3004005	9.869	9.263	84.786	19.372	0.000	4.857	1.497	9.756
NT2RP3004013	14.485	12.461	42.406	11.492	13.049	8.125	6.478	17.758
NT2RP3004016	26.353	20.174	14.242	8.659	7.098	11.464	20.928	17.553
NT2RP3004025	60.555	22.329	39.729	22.559	18.276	23.525	24.555	35.771
NT2RP3004030	612.399	230.471	834.283	175.098	230.371	417.549	400.971	300.584
NT2RP3004041	35.758	19.204	29.889	17.016	20.612	23.674	15.019	17.667
NT2RP3004042	212.341	150.283	197.509	53.931	78.902	164.218	126.411	98.212
NT2RP3004044	72.252	110.791	51.482	17.239	26.945	24.143	30.198	21.882
NT2RP3004051	152.863	73.839	142.232	35.932	51.071	43.163	38.869	49.345
NT2RP3004052	121.021	59.192	74.633	29.148	35.481	72.900	21.817	40.892
NT2RP3004053	98.068	91.523	277.692	61.036	78.666	68.730	38.992	75.069
NT2RP3004055	94.456	63.815	20.623	13.216	5.886	21.414	72.807	7.926
NT2RP3004059	26.860	40.017	21.750	33.539	23.030	10.773	12.908	18.849
NT2RP3004063	18.643	7.895	20.299	7.097	24.752	5.609	24.116	30.966
NT2RP3004067	252.237	73.282	95.895	48.083	19.941	65.794	83.498	20.778
NT2RP3004070	48.573	60.633	86.573	21.957	33.015	28.191	23.513	30.233
NT2RP3004075	38.601	29.096	32.376	11.710	25.118	31.470	27.043	31.641
NT2RP3004078	123.241	42.946	72.005	18.027	27.424	76.975	68.265	35.076
NT2RP3004083	44.275	15.592	19.299	10.656	16.243	25.486	10.927	25.077
NT2RP3004084	20.841	11.260	17.316	13.491	18.285	6.670	5.617	3.170
NT2RP3004087	61.884	66.963	88.119	34.544	41.231	18.188	46.470	43.578
NT2RP3004090	36.365	32.568	40.579	21.173	17.529	18.879	17.880	26.579
NT2RP3004093	161.528	139.905	344.325	50.577	97.795	88.393	53.404	59.593
NT2RP3004095	200.143	125.167	292.455	60.637	74.060	107.607	74.457	93.441
NT2RP3004102	189.415	73.338	84.114	25.857	52.758	90.150	84.260	44.710
NT2RP3004110	147.625	133.897	357.078	89.105	74.491	121.974	73.119	123.538
NT2RP3004119	104.164	75.262	197.706	41.776	44.915	38.873	58.991	47.932
NT2RP3004125	312.772	144.655	288.945	81.440	117.997	203.963	194.543	177.494
NT2RP3004129	32.046	25.525	80.210	15.236	13.862	6.399	91.521	13.988
NT2RP3004130	49.467	45.820	69.122	17.019	28.933	35.035	32.730	28.345
NT2RP3004133	55.970	58.961	100.212	16.731	9.248	33.261	34.485	27.866
NT2RP3004145	105.806	51.341	52.276	13.000	30.673	49.189	43.159	26.374
NT2RP3004148	206.658	51.505	96.093	26.557	47.130	133.546	97.568	36.471
NT2RP3004155	65.340	68.555	193.114	35.382	55.725	47.245	42.482	35.181
NT2RP3004165	31.599	44.217	34.859	21.674	20.207	39.412	7.182	33.175
NT2RP3004179	35.856	20.632	34.990	9.754	16.663	24.234	26.890	25.902
NT2RP3004185	32.929	15.710	25.847	5.595	13.361	12.464	17.866	14.309
NT2RP3004188	125.817	53.211	66.560	31.419	32.369	61.530	53.134	39.182
NT2RP3004189	71.207	30.246	39.386	13.328	16.496	45.470	27.774	13.851
NT2RP3004190	23.559	32.253	43.574	9.312	53.269	16.769	14.567	17.553
NT2RP3004191	83.281	88.775	164.178	69.201	36.600	55.079	55.128	50.378
NT2RP3004202	65.428	24.275	29.745	9.879	16.541	26.270	30.799	19.098
NT2RP3004205	85.092	47.734	63.971	13.089	27.925	58.672	54.078	34.998
NT2RP3004206	14.256	29.344	64.128	15.347	7.707	19.033	11.635	31.827
NT2RP3004207	43.461	19.436	50.653	17.280	18.710	28.637	29.185	24.442
NT2RP3004209	25.959	24.203	39.564	19.865	19.485	19.029	15.259	22.310
NT2RP3004215	31.701	16.545	24.589	8.189	19.140	22.457	12.156	6.928
NT2RP3004219	155.994	82.391	96.342	22.107	51.385	131.790	96.886	48.658
NT2RP3004242	24.137	26.975	34.382	16.270	12.213	15.115	13.723	32.886
NT2RP3004246	77.637	61.572	206.426	50.779	31.994	42.306	32.830	60.878
NT2RP3004253	33.041	24.223	39.674	7.658	22.082	33.370	29.632	32.520
NT2RP3004258	33.065	42.534	65.365	25.376	34.541	29.550	19.844	49.800
NT2RP3004262	71.434	29.972	47.060	12.020	24.614	35.849	39.562	57.434

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Table 110

NT2RP3004275	98.699	36.290	83.006	24.540	22.746	61.823	54.050	37.950
NT2RP3004282	220.789	134.052	178.061	49.657	96.836	146.266	106.109	47.357
NT2RP3004289	15.745	32.192	24.193	7.292	8.756	13.882	7.956	36.428
NT2RP3004294	60.266	26.724	26.421	11.149	5.484	19.565	13.721	12.117
NT2RP3004298	132.592	61.132	108.061	41.028	51.835	81.222	91.861	86.967
NT2RP3004309	144.028	38.007	72.661	18.449	49.804	89.984	72.157	51.104
NT2RP3004321	231.684	53.180	108.237	29.746	51.266	130.535	104.335	90.745
NT2RP3004322	37.875	23.343	26.724	12.249	19.668	22.470	23.599	36.486
NT2RP3004332	106.333	91.471	249.231	44.955	55.341	76.389	72.376	107.059
NT2RP3004334	68.850	32.416	38.730	9.752	18.775	14.058	18.048	16.320
NT2RP3004336	51.294	59.827	77.110	20.736	37.630	26.664	34.386	34.983
NT2RP3004338	18.622	16.241	17.569	3.872	10.946	14.386	14.110	86.362
NT2RP3004341	19.200	20.230	19.614	6.657	8.502	12.520	6.268	32.744
NT2RP3004345	23.625	19.497	30.403	9.060	9.720	11.640	14.563	16.985
NT2RP3004348	152.635	117.901	359.204	67.822	108.792	59.212	48.175	79.425
NT2RP3004349	156.222	104.964	468.032	69.388	77.765	53.467	43.103	73.727
NT2RP3004355	58.395	30.712	72.395	19.596	16.476	48.617	127.957	121.148
NT2RP3004356	110.831	61.735	75.603	20.147	52.762	88.239	65.266	48.103
NT2RP3004360	41.674	35.467	41.306	19.910	12.453	15.566	22.989	27.326
NT2RP3004361	46.996	33.404	30.049	14.201	14.577	23.509	11.195	14.723
NT2RP3004374	95.389	57.120	48.566	15.283	39.161	43.002	46.264	23.628
NT2RP3004378	58.764	49.662	50.107	18.157	38.127	30.939	38.526	49.716
NT2RP3004399	16.800	27.122	23.992	18.781	27.937	12.441	19.782	23.253
NT2RP3004405	76.975	42.401	68.536	14.461	40.127	30.855	27.361	25.603
NT2RP3004406	59.371	18.451	36.531	9.936	27.693	43.690	31.470	25.327
NT2RP3004411	92.442	48.901	74.904	12.415	33.625	61.907	28.318	22.563
NT2RP3004424	40.886	26.604	29.952	10.559	13.320	23.158	18.753	13.677
NT2RP3004428	141.707	50.415	59.329	18.251	39.655	61.213	57.747	33.647
NT2RP3004432	26.049	27.127	235.751	18.465	175.041	22.755	14.727	14.260
NT2RP3004434	146.690	70.435	71.916	32.310	42.640	67.791	64.267	46.448
NT2RP3004446	27.192	19.189	44.272	8.673	16.147	5.257	19.506	10.316
NT2RP3004451	45.826	26.986	81.355	14.858	17.991	15.972	19.748	17.124
NT2RP3004454	13.596	21.506	24.434	5.907	6.024	8.062	8.872	9.047
NT2RP3004466	267.157	127.933	175.917	65.272	67.867	153.148	173.844	118.891
NT2RP3004470	150.361	134.643	271.527	54.812	70.601	50.612	49.084	95.231
NT2RP3004472	13.995	10.444	6.945	8.463	7.742	9.150	3.258	25.525
NT2RP3004475	89.313	39.845	56.364	22.197	34.071	46.397	52.228	36.349
NT2RP3004480	27.508	23.946	28.297	14.978	36.756	18.216	23.949	28.732
NT2RP3004481	31.506	22.386	32.532	15.846	17.215	13.188	11.393	75.655
NT2RP3004490	5.922	2.592	0.000	0.000	0.000	0.000	8.285	6.621
NT2RP3004496	24.027	28.908	28.749	24.196	13.349	15.561	11.595	12.252
NT2RP3004498	109.432	51.964	126.945	23.368	34.097	43.928	34.988	37.439
NT2RP3004503	162.798	115.770	489.798	56.760	66.406	56.670	46.593	74.722
NT2RP3004504	62.371	28.837	57.527	18.389	15.784	30.245	70.081	29.325
NT2RP3004505	25.650	46.920	38.179	15.593	11.983	15.997	28.823	36.454
NT2RP3004507	50.531	32.594	47.091	13.176	25.414	16.514	34.107	31.896
NT2RP3004519	38.355	14.576	23.652	7.881	25.541	10.577	6.345	25.622
NT2RP3004524	38.228	27.009	84.901	19.528	13.759	17.664	33.496	24.924
NT2RP3004527	27.651	20.933	12.117	3.539	15.253	9.821	3.786	15.761
NT2RP3004534	33.516	8.840	42.395	18.636	0.000	23.692	5.434	9.045
NT2RP3004539	100.285	63.233	118.931	33.763	38.717	95.714	53.713	73.442
NT2RP3004541	36.828	14.720	43.013	5.166	8.200	26.251	15.421	12.869
NT2RP3004544	52.885	38.258	53.085	39.055	11.567	35.154	22.436	94.341
NT2RP3004551	26.759	17.006	33.344	4.740	15.511	10.082	17.450	14.870
NT2RP3004552	100.028	33.585	57.413	16.213	39.101	26.011	44.497	30.764
NT2RP3004557	44.768	30.470	33.284	14.695	20.775	13.301	18.512	22.802
NT2RP3004561	103.770	34.283	58.620	21.128	33.914	22.418	32.255	61.361
NT2RP3004566	99.005	43.108	55.789	20.777	24.049	34.687	45.052	36.253
NT2RP3004569	94.551	49.341	39.943	22.787	36.432	39.608	53.015	37.001
NT2RP3004572	55.491	23.041	40.509	14.634	14.847	45.626	30.377	41.143
NT2RP3004578	38.321	36.168	39.762	17.939	20.596	29.096	32.099	23.011
NT2RP3004584	62.502	25.851	65.773	21.818	32.015	37.561	47.268	25.404
NT2RP3004588	88.255	39.095	216.247	40.330	34.231	51.647	25.258	19.672
NT2RP3004594	46.177	56.747	57.402	32.610	13.065	12.913	32.945	25.495

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Table 111

NT2RP3004603	78.679	80.544	62.737	47.277	28.549	51.397	38.270	98.212
NT2RP3004612	74.014	32.975	30.756	11.218	37.649	29.374	13.820	21.608
NT2RP3004617	34.514	16.958	15.437	7.541	9.813	10.362	13.498	6.437
NT2RP3004618	45.654	67.084	24.650	10.899	12.856	27.696	15.781	34.862
NT2RP3004625	75.276	30.663	96.644	20.740	43.066	82.423	59.145	28.086
NT2RP3004635	67.742	53.096	56.701	30.583	29.960	46.122	44.888	61.643
NT2RP3004640	89.717	58.380	202.476	49.309	45.610	45.215	57.393	54.691
NT2RP3004642	173.246	73.060	118.760	36.694	65.566	113.287	76.702	49.519
NT2RP3004647	101.143	79.944	113.136	52.874	50.982	53.766	48.670	44.858
NT2RP3004652	203.591	158.366	434.477	72.065	120.412	63.735	70.579	53.556
NT2RP3004669	83.602	70.489	66.421	12.848	23.192	58.448	88.231	37.292
NT2RP3004870	193.547	128.951	178.554	73.935	102.781	166.902	107.905	94.007
NT2RP4000008	19.767	47.505	24.109	17.304	29.354	55.419	33.855	34.432
NT2RP4000018	56.348	39.769	80.074	15.072	26.721	42.484	38.619	43.517
NT2RP4000023	53.022	17.753	34.758	10.911	23.301	26.391	19.092	19.833
NT2RP4000025	45.646	56.593	72.466	8.582	83.053	47.152	45.373	52.951
NT2RP4000035	119.584	72.523	321.911	40.713	60.319	94.350	45.943	45.399
NT2RP4000041	186.503	56.255	41.691	8.801	47.224	60.208	34.302	31.401
NT2RP4000049	47.651	27.923	39.552	7.903	6.803	18.769	24.059	13.748
NT2RP4000050	46.861	18.274	33.191	8.103	13.428	12.029	13.779	7.279
NT2RP4000051	40.843	29.142	32.303	10.190	21.384	40.455	39.037	17.835
NT2RP4000063	43.284	30.034	25.813	11.605	18.431	28.262	27.310	20.178
NT2RP4000065	11.102	17.154	21.158	43.890	19.264	6.730	6.069	32.776
NT2RP4000070	59.796	43.567	133.907	34.788	23.019	47.653	20.318	14.552
NT2RP4000074	18.725	4.052	10.370	1.424	4.150	8.454	6.795	2.366
NT2RP4000078	62.113	86.532	57.818	34.813	30.151	56.743	50.257	36.799
NT2RP4000080	224.722	111.931	192.627	75.992	91.873	205.033	130.550	126.661
NT2RP4000099	321.974	219.279	1600.483	150.687	285.007	248.048	126.052	293.699
NT2RP4000102	8.753	18.572	15.774	4.228	7.806	9.573	53.928	13.964
NT2RP4000103	34.791	23.847	32.776	10.952	8.411	17.791	47.841	72.767
NT2RP4000108	62.537	43.717	44.931	25.841	148.533	28.159	30.906	35.415
NT2RP4000109	261.144	124.505	231.410	69.135	84.528	232.287	157.290	146.451
NT2RP4000111	28.240	10.956	13.276	3.790	9.951	18.128	12.668	12.698
NT2RP4000112	174.823	126.761	222.355	29.525	41.360	94.077	68.016	67.817
NT2RP4000116	104.464	46.026	87.051	17.566	38.187	78.479	43.365	44.515
NT2RP4000129	20.582	20.434	22.054	7.476	11.813	11.733	11.125	12.513
NT2RP4000137	40.931	26.333	38.192	19.805	13.933	28.819	22.933	25.032
NT2RP4000138	53.828	41.054	56.796	8.100	30.556	62.995	15.210	44.386
NT2RP4000141	62.206	42.856	27.517	15.337	27.602	16.576	20.734	34.135
NT2RP4000147	26.467	16.245	24.754	8.363	10.418	21.963	32.513	27.229
NT2RP4000150	170.729	155.621	193.591	111.407	84.297	120.085	78.831	153.213
NT2RP4000151	89.499	70.326	88.485	15.693	34.976	55.423	46.381	38.147
NT2RP4000157	374.212	306.778	1320.234	101.052	267.293	258.633	142.467	214.943
NT2RP4000159	21.294	38.510	22.222	4.978	9.029	6.726	11.020	2.839
NT2RP4000163	38.106	28.442	47.497	14.252	14.961	40.800	33.454	23.270
NT2RP4000167	20.173	26.500	23.216	7.845	5.552	5.423	7.245	14.035
NT2RP4000171	81.073	52.022	67.728	21.187	28.509	44.872	35.093	37.752
NT2RP4000175	81.743	84.274	82.433	36.175	79.980	58.585	86.742	88.556
NT2RP4000180	58.476	59.435	73.494	30.105	37.648	47.113	80.700	76.984
NT2RP4000185	92.601	101.645	150.266	44.577	77.183	75.717	60.488	85.600
NT2RP4000192	127.476	49.521	75.782	5.687	46.143	55.129	61.367	32.097
NT2RP4000194	56.167	54.180	31.757	11.553	23.917	32.670	26.241	35.726
NT2RP4000196	92.478	57.125	90.828	20.213	49.026	42.066	78.755	73.674
NT2RP4000210	488.775	304.062	484.740	166.128	178.561	369.938	361.357	310.071
NT2RP4000212	262.175	187.947	456.537	97.216	100.219	119.552	87.129	138.067
NT2RP4000214	209.094	145.483	438.818	74.480	101.385	69.191	73.163	99.829
NT2RP4000216	27.754	23.804	32.743	9.142	21.766	20.150	23.347	26.648
NT2RP4000218	116.307	61.722	177.365	25.931	25.141	34.742	29.243	62.428
NT2RP4000223	305.665	161.526	257.394	54.652	135.566	196.254	184.146	106.046
NT2RP4000243	143.570	175.090	348.917	55.746	78.966	68.882	62.393	92.330
NT2RP4000246	46.967	55.303	46.655	12.855	24.581	16.374	23.615	32.643
NT2RP4000250	53.966	193.957	78.957	33.077	29.249	79.779	38.597	115.514
NT2RP4000256	61.500	54.535	57.504	13.472	28.112	22.609	19.612	30.227
NT2RP4000257	146.739	75.562	68.081	16.986	74.826	29.177	32.953	39.299

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Table 112

NT2RP4000259	36.679	60.559	46.332	10.684	19.988	21.634	16.480	15.511
NT2RP4000261	43.317	19.258	30.162	7.462	9.311	20.800	15.617	17.669
NT2RP4000262	57.147	28.869	41.516	10.478	21.699	32.040	20.770	27.384
NT2RP4000263	26.287	13.027	49.010	13.046	27.187	12.910	17.489	13.293
NT2RP4000280	404.385	153.579	276.968	132.346	126.840	273.688	195.012	134.292
NT2RP4000286	349.970	68.061	124.456	10.943	103.023	163.664	158.229	165.646
NT2RP4000290	69.776	37.297	56.790	14.548	26.462	24.909	28.704	27.597
NT2RP4000291	92.235	210.055	87.276	110.666	29.297	73.542	109.583	151.177
NT2RP4000301	72.312	25.823	43.205	17.404	22.667	20.721	34.359	47.720
NT2RP4000312	30.600	23.813	38.345	71.709	0.000	27.976	30.543	16.077
NT2RP4000321	152.139	101.314	320.889	47.164	45.419	56.735	18.656	58.799
NT2RP4000323	37.462	25.699	95.138	15.085	11.924	10.455	5.460	17.376
NT2RP4000324	336.502	41.027	28.832	17.302	54.837	40.659	43.151	23.155
NT2RP4000334	115.354	138.505	182.550	93.928	63.038	90.617	72.433	115.991
NT2RP4000343	75.003	25.817	17.727	13.013	26.022	34.661	24.607	19.361
NT2RP4000348	56.032	12.454	12.331	15.203	15.484	6.180	3.506	18.446
NT2RP4000349	7.762	0.000	0.000	3.720	0.000	0.000	0.000	6.473
NT2RP4000355	87.546	71.121	115.193	27.548	24.554	33.248	29.345	30.833
NT2RP4000356	211.845	121.033	114.259	51.743	65.136	144.965	93.350	89.148
NT2RP4000360	70.699	38.241	86.142	10.374	34.417	19.318	20.576	39.379
NT2RP4000367	18.288	5.279	7.668	4.052	7.149	4.373	5.067	3.767
NT2RP4000370	32.692	19.934	38.747	6.510	17.936	9.489	6.000	24.412
NT2RP4000373	8.950	23.267	11.530	6.424	4.499	3.890	0.839	4.844
NT2RP4000376	35.864	18.265	19.621	12.884	15.395	5.826	23.805	21.083
NT2RP4000381	46.926	33.826	103.826	18.455	27.076	17.117	10.557	22.372
NT2RP4000388	5084.865	1317.306	2099.929	227.725	2132.319	3323.080	4907.667	1152.125
NT2RP4000390	257.545	160.161	219.816	71.826	85.442	187.036	159.581	156.149
NT2RP4000393	12.640	11.957	20.415	9.221	11.409	7.438	11.324	8.524
NT2RP4000398	17.518	22.876	62.033	33.290	29.094	38.274	16.243	64.756
NT2RP4000406	72.166	37.198	50.776	14.912	16.850	25.605	52.793	18.016
NT2RP4000407	17.281	27.203	36.363	15.988	14.182	13.109	11.945	14.661
NT2RP4000413	28.139	4.608	24.755	4.471	18.199	9.618	9.564	3.410
NT2RP4000415	52.988	28.236	62.216	11.670	19.273	18.078	30.417	40.803
NT2RP4000417	120.835	54.541	46.666	20.336	52.684	49.364	45.494	40.422
NT2RP4000423	45.442	44.179	39.359	11.506	22.404	15.869	30.636	33.860
NT2RP4000424	69.125	46.323	210.620	28.361	37.650	36.808	16.234	39.788
NT2RP4000447	43.171	50.572	84.440	39.944	38.491	45.721	39.832	64.904
NT2RP4000448	19.367	24.180	80.917	16.101	11.296	3.059	13.254	21.512
NT2RP4000449	13.620	10.795	11.538	2.925	6.616	4.388	8.988	2.997
NT2RP4000453	16.784	23.231	20.252	12.639	17.714	8.345	19.980	15.034
NT2RP4000455	24.141	9.211	25.236	8.774	21.609	10.059	20.357	12.379
NT2RP4000456	119.272	61.157	163.661	22.286	65.150	132.301	52.249	54.831
NT2RP4000457	64.206	43.798	49.492	18.495	31.270	76.065	78.938	18.719
NT2RP4000461	24.023	16.736	42.860	8.086	28.640	24.287	12.689	10.443
NT2RP4000462	61.975	32.022	55.648	25.804	23.165	20.388	41.481	46.650
NT2RP4000463	44.030	41.396	65.217	27.109	26.324	27.922	36.605	49.391
NT2RP4000471	37.502	19.098	33.476	5.338	11.489	19.044	0.000	11.363
NT2RP4000472	13.349	14.082	11.918	3.395	5.066	10.401	8.705	6.892
NT2RP4000476	8.321	93.773	34.435	13.728	23.669	4.372	15.350	7.001
NT2RP4000480	211.458	95.964	129.427	15.810	72.857	76.584	80.179	54.430
NT2RP4000481	31.888	26.600	25.630	7.943	9.597	13.290	14.597	17.385
NT2RP4000483	21.998	15.487	14.048	11.756	10.365	13.738	23.308	15.114
NT2RP4000487	60.364	31.407	22.474	11.302	12.610	14.044	7.594	9.748
NT2RP4000496	5.856	1.759	0.000	1.020	0.000	1.332	1.331	1.300
NT2RP4000497	14.222	23.785	35.435	9.191	6.838	6.266	19.870	19.909
NT2RP4000498	10.973	30.501	18.513	11.562	11.061	3.896	18.332	11.258
NT2RP4000500	28.356	22.346	29.213	6.186	20.760	15.985	16.224	7.833
NT2RP4000507	65.764	65.249	44.910	11.415	12.964	62.638	27.083	16.799
NT2RP4000515	326.302	155.582	205.890	76.678	101.826	196.853	160.500	152.025
NT2RP4000516	44.610	41.687	143.747	33.380	28.078	31.697	20.743	51.511
NT2RP4000517	43.875	14.219	143.214	16.861	8.127	16.458	9.150	20.642
NT2RP4000518	26.023	21.987	59.276	7.160	16.049	11.817	12.546	27.280
NT2RP4000519	26.153	8.810	13.853	3.109	6.990	8.139	7.151	18.564
NT2RP4000524	1.938	0.000	0.000	0.000	0.000	0.000	0.000	11.634

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Table 113

NT2RP4000528	12.526	60.186	18.819	3.919	15.244	19.800	6.732	22.213
NT2RP4000537	119.677	216.504	170.091	45.816	89.192	83.433	71.078	86.062
NT2RP4000541	106.565	47.194	70.174	11.695	21.855	33.231	40.279	26.263
NT2RP4000543	121.504	31.320	49.049	15.964	35.981	45.932	36.402	28.580
NT2RP4000545	109.666	94.098	286.924	83.348	51.684	53.797	34.347	94.961
NT2RP4000546	34.736	33.000	110.405	21.240	28.754	7.806	12.598	34.617
NT2RP4000549	27.942	60.396	16.907	8.050	24.334	25.452	36.475	51.804
NT2RP4000556	22.418	10.709	22.462	7.923	12.069	10.840	14.194	24.088
NT2RP4000557	22.285	18.841	21.106	3.617	11.430	13.950	15.418	23.701
NT2RP4000558	98.220	60.580	112.943	14.814	42.417	80.107	52.601	55.628
NT2RP4000560	145.648	126.576	198.616	29.117	67.842	111.268	88.953	88.195
NT2RP4000568	4.653	7.710	9.495	4.212	14.707	5.118	4.418	1.728
NT2RP4000583	100.314	94.610	258.628	54.914	59.898	38.219	57.364	56.537
NT2RP4000585	36.734	19.742	25.585	3.609	10.851	9.594	12.368	9.441
NT2RP4000588	24.965	28.422	24.615	3.894	8.655	9.562	10.506	9.648
NT2RP4000590	82.643	29.520	74.380	7.381	16.388	16.999	38.929	28.565
NT2RP4000599	5.134	12.959	2.254	2.300	0.000	5.232	2.076	4.437
NT2RP4000603	48.331	23.244	35.033	10.422	23.763	77.588	27.888	18.472
NT2RP4000607	43.033	46.964,	51.845	3.610	170.311	14.213	16.592	35.286
NT2RP4000614	93.469	104.724	288.948	65.946	55.948	39.332	42.871	69.619
NT2RP4000634	41.268	55.106	42.366	20.080	29.301	16.909	25.716	34.506
NT2RP4000638	38.714	37.491	60.350	10.197	20.301	7.339	21.773	11.532
NT2RP4000648	28.051	19.136	29.021	11.429	52.517	8.564	11.255	17.817
NT2RP4000657	59.641	34.960	39.531	15.723	16.922	9.859	13.485	21.954
NT2RP4000691	25.254	56.069	53.527	20.960	17.701	25.333	15.651	24.709
NT2RP4000697	41.565	23.570	47.024	8.681	17.064	41.529	26.741	15.415
NT2RP4000704	150.527	58.692	94.083	27.108	61.336	83.179	82.422	52.001
NT2RP4000710	544.068	385.881	401.163	199.745	308.821	570.526	370.976	288.408
NT2RP4000713	28.318	29.133	25.800	8.247	17.041	12.819	13.220	15.778
NT2RP4000724	15.864	37.851	33.515	4.863	0.000	12.161	11.700	21.516
NT2RP4000725	73.250	28.340	42.587	10.791	15.656	23.049	29.695	16.914
NT2RP4000728	398.420	264.734	679.544	140.230	76.304	191.521	224.945	194.628
NT2RP4000737	10.955	3.270	11.232	3.668	5.117	2.568	5.042	3.466
NT2RP4000739	15.887	23.255	23.005	9.500	14.336	12.603	11.904	11.565
NT2RP4000749	66.966	32.925	44.669	15.449	15.178	33.005	27.405	18.522
NT2RP4000769	65.261	48.013	75.648	22.094	24.165	36.022	30.919	26.509
NT2RP4000774	42.939	36.592	46.497	13.414	18.307	19.211	16.686	12.228
NT2RP4000781	34.651	17.546	33.740	8.360	9.849	17.872	14.911	6.625
NT2RP4000783	29.279	12.391	20.881	15.327	3.867	20.509	21.416	4.930
NT2RP4000787	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
NT2RP4000788	57.142	47.566	42.475	22.374	15.545	36.822	18.884	32.902
NT2RP4000792	26.349	10.430	22.784	9.272	0.000	13.445	11.068	16.223
NT2RP4000809	33.934	109.004	47.604	14.815	14.118	130.537	459.568	2.963
NT2RP4000817	76.682	20.256	38.151	11.596	23.415	26.562	17.001	12.542
NT2RP4000821	121.213	96.900	50.576	24.242	27.444	74.033	37.727	20.369
NT2RP4000822	140.413	82.390	238.604	35.669	42.569	28.697	55.099	10.656
NT2RP4000823	135.384	158.604	92.017	60.055	51.992	105.428	517.857	15.029
NT2RP4000831	62.896	29.385	59.567	15.141	27.742	44.635	56.751	39.831
NT2RP4000833	122.764	143.283	293.871	54.134	35.213	59.985	36.700	53.259
NT2RP4000837	96.184	62.893	85.421	24.336	12.853	108.156	63.147	18.389
NT2RP4000839	80.940	59.635	88.717	37.592	8.300	49.470	22.530	10.946
NT2RP4000848	58.077	31.507	77.224	17.876	9.450	20.275	20.877	18.662
NT2RP4000848	103.080	69.956	299.625	42.214	26.206	34.689	23.120	18.618
NT2RP4000855	34.677	17.013	12.507	9.287	13.091	8.694	28.917	11.970
NT2RP4000863	8.561	4.898	3.423	2.559	3.763	0.240	1.403	4.230
NT2RP4000865	48.035	43.964	108.504	74.371	40.824	29.915	36.035	54.061
NT2RP4000873	196.286	173.321	390.821	72.791	40.443	97.997	66.825	71.502
NT2RP4000874	114.596	38.794	67.452	24.650	26.653	63.430	52.080	41.554
NT2RP4000875	185.360	106.889	455.763	90.088	37.851	83.221	55.792	83.494
NT2RP4000878	204.507	172.927	327.443	75.171	78.099	84.553	88.900	49.029
NT2RP4000879	9.334	12.529	11.389	5.490	6.675	16.421	0.958	4.164
NT2RP4000880	38.501	38.645	67.150	20.860	34.803	27.293	40.144	14.100
NT2RP4000894	134.523	44.853	121.558	10.896	45.448	46.826	69.374	12.711
NT2RP4000899	115.121	187.401	170.218	144.109	38.964	96.487	103.728	166.562

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Table 114

NT2RP4000902	185.480	188.808	401.324	78.930	64.333	95.484	61.641	85.667
NT2RP4000906	0.305	1.603	0.000	0.000	0.170	0.372	0.278	0.771
NT2RP4000907	32.198	42.723	44.472	21.830	25.520	24.599	19.934	29.737
NT2RP4000915	46.291	15.516	19.755	9.014	17.749	25.501	19.811	5.257
NT2RP4000916	16.757	34.708	57.738	23.947	17.681	49.695	16.463	25.121
NT2RP4000918	446.948	180.459	261.903	104.431	141.078	221.658	308.724	195.950
NT2RP4000925	33.696	20.203	25.426	9.727	8.694	5.257	12.183	6.460
NT2RP4000927	32.369	2.391	13.088	3.360	6.917	9.429	12.242	9.739
NT2RP4000928	132.499	77.919	75.824	27.459	38.566	63.795	51.626	47.129
NT2RP4000929	10.454	6.358	16.205	5.348	5.657	12.035	5.522	3.568
NT2RP4000946	132.281	63.256	114.387	25.969	53.023	57.751	42.531	26.322
NT2RP4000947	2.292	0.165	0.000	0.681	0.000	0.000	0.000	0.000
NT2RP4000949	61.713	79.888	67.197	17.482	26.263	41.870	34.746	13.260
NT2RP4000955	138.011	52.132	123.547	28.823	73.259	121.259	99.293	22.957
NT2RP4000959	41.008	45.994	71.680	28.437	32.234	40.989	21.659	24.213
NT2RP4000962	18.486	6.696	26.840	19.188	7.866	19.686	12.214	6.047
NT2RP4000973	36.650	32.445	36.565	12.436	12.341	24.833	19.337	14.157
NT2RP4000975	76.542	69.291	152.889	24.672	28.007	28.454	22.694	22.187
NT2RP4000979	34.880	19.409,	37.326	20.821	11.127	35.561	8.305	14.375
NT2RP4000984	5.549	5.330	0.000	9.035	5.964	4.130	9.900	5.147
NT2RP4000986	67.644	33.142	45.802	10.889	17.544	33.261	23.729	20.835
NT2RP4000988	51.541	48.973	114.030	19.535	18.718	5.732	14.224	16.391
NT2RP4000989	59.625	24.400	48.553	14.412	13.785	30.921	35.963	28.297
NT2RP4000990	18.308	8.624	16.388	16.947	32.230	29.187	8.098	10.761
NT2RP4000994	61.619	79.591	73.376	19.693	19.056	47.138	20.380	42.869
NT2RP4000996	84.850	105.301	82.603	17.132	51.465	48.697	18.081	61.243
NT2RP4000997	67.079	54.671	60.172	84.356	34.967	41.069	18.376	96.597
NT2RP4001001	14.208	21.359	18.095	11.765	11.811	15.392	12.511	20.370
NT2RP4001004	33.229	16.130	9.361	5.116	9.588	16.002	13.550	14.012
NT2RP4001006	43.300	32.280	76.984	15.078	9.382	26.487	11.510	24.738
NT2RP4001009	18.841	26.736	22.167	10.117	15.306	18.272	18.325	18.908
NT2RP4001010	66.828	26.273	64.129	11.395	22.696	42.432	33.273	36.440
NT2RP4001013	172.600	136.757	152.076	50.579	71.395	91.790	74.989	69.214
NT2RP4001029	51.999	52.569	51.080	19.391	11.246	37.483	22.170	20.460
NT2RP4001036	50.398	28.370	38.461	20.941	14.732	21.283	16.094	22.458
NT2RP4001041	63.254	27.315	44.653	17.800	14.949	39.536	29.151	12.363
NT2RP4001042	120.393	53.507	99.807	25.727	52.624	62.242	42.161	65.349
NT2RP4001046	84.525	39.857	54.695	12.528	15.796	44.068	31.184	29.152
NT2RP4001050	23.495	16.696	14.229	3.130	7.595	15.142	37.084	15.929
NT2RP4001051	55.986	46.618	105.231	34.838	19.098	22.295	20.760	29.183
NT2RP4001057	106.673	52.182	65.933	22.523	26.382	66.537	20.457	21.945
NT2RP4001063	170.235	69.039	102.410	24.821	14.098	94.361	66.708	23.759
NT2RP4001064	89.983	57.290	64.770	15.070	12.139	42.538	37.978	28.126
NT2RP4001067	32.210	18.655	23.175	7.147	6.320	18.181	17.994	8.877
NT2RP4001078	70.346	22.808	30.478	9.119	13.915	11.118	32.316	11.554
NT2RP4001079	39.015	23.923	38.401	7.023	14.496	15.803	18.762	14.515
NT2RP4001080	14.552	29.116	54.653	6.580	5.732	7.627	7.008	8.413
NT2RP4001086	62.838	43.770	64.943	29.980	22.792	56.125	30.073	45.256
NT2RP4001095	108.108	110.235	255.542	37.781	80.702	55.098	43.809	54.938
NT2RP4001098	70.282	49.290	54.985	17.657	20.245	37.384	31.281	34.153
NT2RP4001100	197.231	163.233	346.289	64.078	75.241	107.015	69.878	66.887
NT2RP4001105	230.319	76.169	70.257	26.174	57.028	86.626	87.810	59.540
NT2RP4001110	57.855	44.336	61.199	25.702	18.898	18.716	33.736	20.912
NT2RP4001115	72.571	43.734	66.947	20.426	27.358	20.977	47.782	23.254
NT2RP4001117	53.949	26.454	27.949	9.754	12.786	27.164	23.470	15.958
NT2RP4001122	74.373	73.859	55.273	28.246	24.494	39.511	36.880	32.941
NT2RP4001123	103.600	40.395	69.670	16.738	17.045	55.106	52.069	29.553
NT2RP4001126	70.020	118.846	92.913	55.909	48.688	56.960	35.367	78.750
NT2RP4001127	17.316	17.921	16.598	4.302	4.543	7.932	6.088	3.388
NT2RP4001138	34.858	28.363	20.031	8.100	8.737	16.238	16.525	11.957
NT2RP4001143	89.870	104.250	131.882	30.154	34.329	44.010	63.462	45.180
NT2RP4001148	10.496	8.968	14.713	2.463	2.640	2.953	4.275	13.549
NT2RP4001149	121.101	16.961	36.641	6.362	14.072	27.469	27.329	17.906
NT2RP4001150	90.570	29.463	50.833	11.559	12.988	28.002	41.812	17.678

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Table 115

NT2RP4001159	38.009	23.566	30.231	13.969	15.202	22.514	8.474	15.455
NT2RP4001162	26.480	12.988	32.747	7.435	8.821	8.329	10.137	7.744
NT2RP4001170	22.282	12.703	20.500	4.074	19.879	9.183	5.871	4.037
NT2RP4001174	160.485	77.682	283.723	47.118	44.041	51.544	63.046	39.356
NT2RP4001175	105.636	84.266	237.685	56.987	37.302	44.846	49.808	28.044
NT2RP4001176	316.295	539.044	440.109	306.340	44.764	249.181	449.982	321.567
NT2RP4001184	58.252	23.348	36.224	15.108	13.298	29.737	56.984	16.700
NT2RP4001198	155.102	120.100	81.937	37.566	13.326	92.551	80.670	61.997
NT2RP4001199	22.232	18.559	25.847	3.025	0.000	22.887	29.205	23.250
NT2RP4001206	167.873	59.707	53.222	31.978	27.295	101.042	75.329	47.196
NT2RP4001207	6.816	7.800	9.463	4.474	4.601	2.301	0.915	9.232
NT2RP4001210	5.482	9.826	9.141	8.107	1.396	3.060	4.469	2.598
NT2RP4001213	18.439	21.799	46.620	26.850	14.691	14.012	16.268	14.828
NT2RP4001214	7.837	5.075	21.917	3.759	2.750	2.889	2.203	1.557
NT2RP4001219	17.372	12.922	29.465	15.168	7.172	11.232	12.740	10.296
NT2RP4001228	60.317	46.912	82.456	22.249	23.349	41.381	20.046	18.506
NT2RP4001235	70.885	42.694	74.087	20.626	11.053	41.808	8.307	26.337
NT2RP4001256	53.903	27.494	40.975	9.302	9.044	22.660	27.827	9.288
NT2RP4001257	91.093	39.253	66.828	12.871	33.167	19.549	35.715	16.676
NT2RP4001260	30.932	22.193	31.916	6.755	16.733	19.462	6.274	7.635
NT2RP4001261	203.546	343.200	241.244	94.907	116.433	194.685	126.891	64.973
NT2RP4001274	29.234	29.291	20.294	16.725	11.827	4.089	12.005	6.899
NT2RP4001276	288.394	86.186	155.256	76.171	77.526	99.724	126.975	37.044
NT2RP4001283	602.951	260.199	332.966	68.876	287.262	624.729	534.357	126.212
NT2RP4001299	44.703	49.576	35.736	19.564	12.675	15.229	13.741	18.202
NT2RP4001313	28.076	13.041	11.004	3.551	7.304	11.207	9.673	4.674
NT2RP4001315	24.647	15.443	17.362	12.324	7.639	21.010	12.223	11.809
NT2RP4001320	98.164	61.534	65.437	15.593	22.738	54.032	34.155	23.969
NT2RP4001325	144.734	90.080	132.401	61.000	64.433	99.148	198.660	71.382
NT2RP4001336	33.783	28.245	46.453	11.843	24.831	17.470	36.926	23.698
NT2RP4001339	68.525	15.937	41.646	9.764	25.036	39.624	26.253	9.570
NT2RP4001343	161.856	91.193	100.371	27.738	38.512	92.415	57.982	44.590
NT2RP4001344	144.107	58.474	66.215	21.137	22.316	72.157	71.543	28.102
NT2RP4001345	50.445	32.733	43.703	11.121	15.544	24.026	24.553	13.451
NT2RP4001351	111.802	66.455	97.136	54.896	34.425	45.604	34.545	34.491
NT2RP4001353	19.537	9.810	20.460	6.940	6.519	12.325	7.907	7.125
NT2RP4001355	43.678	23.203	33.304	7.482	15.675	24.196	21.364	10.692
NT2RP4001367	14.283	17.653	14.776	4.211	8.006	2.253	3.639	0.000
NT2RP4001372	140.185	27.600	56.900	12.537	24.364	62.204	41.922	18.450
NT2RP4001373	126.580	38.189	93.856	23.267	28.220	77.754	42.832	38.641
NT2RP4001375	62.861	32.389	48.017	13.250	23.490	43.660	31.665	13.296
NT2RP4001379	77.263	41.191	123.636	24.440	18.057	56.629	33.185	12.466
NT2RP4001381	67.146	46.036	150.720	64.411	23.477	41.258	40.245	17.295
NT2RP4001386	47.308	42.624	147.963	19.177	12.559	15.127	15.891	6.679
NT2RP4001389	32.461	38.092	48.803	17.637	14.303	29.242	28.109	24.013
NT2RP4001396	15.198	11.286	9.852	4.401	3.270	4.252	5.253	5.075
NT2RP4001407	13.731	19.546	21.832	9.379	5.846	11.131	8.899	4.678
NT2RP4001409	26.965	45.073	26.488	6.042	6.075	16.038	11.306	7.105
NT2RP4001410	111.952	58.388	89.502	31.596	42.948	111.493	177.918	34.807
NT2RP4001414	63.484	72.860	54.366	30.455	26.471	40.346	21.075	42.279
NT2RP4001424	18.505	15.050	18.180	8.353	8.456	7.908	12.261	8.200
NT2RP4001433	28.627	47.828	111.176	1.742	3.250	41.197	17.950	7.176
NT2RP4001438	93.429	51.160	63.518	28.266	34.394	39.516	76.382	59.077
NT2RP4001442	46.900	23.169	80.514	5.365	17.576	19.430	14.414	23.765
NT2RP4001447	20.522	17.746	37.089	10.313	11.549	14.801	15.207	21.970
NT2RP4001466	84.366	74.971	78.307	31.341	28.164	50.904	37.694	43.489
NT2RP4001467	15.268	25.951	20.698	4.979	5.450	12.316	14.737	10.161
NT2RP4001472	23.447	20.560	19.664	9.955	16.415	13.051	11.929	10.897
NT2RP4001474	23.982	25.100	20.243	9.361	9.008	17.381	16.055	15.142
NT2RP4001483	21.106	19.511	25.457	6.485	5.041	10.975	9.879	11.486
NT2RP4001488	27.970	20.497	49.782	9.070	13.416	14.898	20.195	30.898
NT2RP4001492	147.304	52.305	152.125	29.017	25.021	50.537	64.959	35.615
NT2RP4001498	25.282	13.660	23.919	9.033	6.316	17.644	16.153	13.136
NT2RP4001502	104.608	138.488	125.018	60.786	58.647	81.803	46.693	100.340

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Table 116

NT2RP4001503	16.918	68.637	34.943	6.221	4.744	16.123	9.930	6.312
NT2RP4001507	45.444	50.856	165.482	28.606	29.404	30.143	22.556	24.934
NT2RP4001510	32.998	28.050	63.008	35.045	3.511	13.039	13.396	31.578
NT2RP4001516	103.727	30.191	54.389	13.924	22.032	60.980	55.131	21.835
NT2RP4001520	99.702	61.159	80.454	19.076	44.823	57.892	65.886	85.758
NT2RP4001523	74.331	53.855	97.039	28.897	26.233	31.769	22.342	34.713
NT2RP4001524	63.685	43.657	79.486	31.768	17.811	34.268	61.096	32.252
NT2RP4001529	55.817	26.458	47.156	18.137	9.583	36.746	22.545	17.561
NT2RP4001531	76.426	49.034	79.547	19.985	15.454	48.895	27.165	35.500
NT2RP4001546	475.672	254.067	158.609	114.463	52.423	188.321	90.884	193.923
NT2RP4001547	35.657	46.341	75.052	22.751	21.180	18.635	16.599	17.284
NT2RP4001551	15.709	5.677	9.034	3.319	2.064	4.065	8.300	1.720
NT2RP4001555	35.187	13.947	15.040	6.049	8.613	14.562	15.505	1.914
NT2RP4001567	23.617	22.434	19.944	10.030	13.497	14.121	17.021	12.931
NT2RP4001568	656.402	328.894	456.250	169.687	176.926	432.308	269.108	137.575
NT2RP4001569	71.047	45.066	68.921	13.181	27.919	55.014	36.067	22.875
NT2RP4001571	31.048	30.838	25.301	9.879	38.867	28.423	12.829	7.326
NT2RP4001574	104.513	60.846	51.480	12.719	37.902	43.358	52.975	26.473
NT2RP4001575	99.868	54.792,	66.563	18.178	23.871	48.657	33.611	35.035
NT2RP4001578	27.146	46.286	41.253	12.060	16.868	28.516	38.747	21.566
NT2RP4001592	56.759	41.720	35.056	13.288	19.751	32.000	46.040	26.863
NT2RP4001593	34.423	36.251	40.059	19.801	27.006	22.857	28.378	30.708
NT2RP4001605	35.830	55.962	46.086	30.654	17.304	12.782	25.954	20.171
NT2RP4001606	36.059	22.836	25.785	9.780	11.049	23.731	22.906	11.246
NT2RP4001607	12.252	38.564	26.768	11.976	11.793	10.856	12.358	17.689
NT2RP4001610	41.606	26.761	24.395	9.284	13.420	18.581	25.355	17.897
NT2RP4001614	5.320	7.451	3.713	3.222	6.786	0.000	4.236	3.006
NT2RP4001623	17.761	23.809	29.296	18.722	11.464	7.465	7.749	11.940
NT2RP4001626	39.777	77.553	31.850	125.728	14.578	17.234	15.665	43.780
NT2RP4001634	42.268	33.465	29.710	15.079	5.960	12.998	22.448	22.801
NT2RP4001638	28.002	28.424	27.619	11.196	10.399	6.955	19.293	11.952
NT2RP4001644	13.937	31.012	33.018	11.442	10.696	15.844	17.103	18.814
NT2RP4001646	110.825	35.914	100.039	15.650	68.751	72.780	36.023	14.760
NT2RP4001656	113.964	57.203	81.638	25.444	41.071	67.708	57.712	34.629
NT2RP4001665	75.518	31.622	54.757	17.666	17.943	29.002	29.742	13.617
NT2RP4001670	143.248	64.754	95.837	25.903	20.467	58.425	77.751	32.776
NT2RP4001677	364.565	222.618	310.713	96.394	105.468	224.860	256.793	96.732
NT2RP4001679	225.706	136.839	407.981	82.012	82.799	62.241	83.957	50.075
NT2RP4001695	51.430	18.839	33.607	11.914	5.205	20.014	20.606	3.263
NT2RP4001696	92.139	56.306	51.701	21.125	15.829	67.642	34.335	27.080
NT2RP4001699	20.126	24.412	12.024	6.153	9.166	12.777	38.966	11.931
NT2RP4001717	104.794	22.524	47.196	16.831	10.332	44.003	28.697	10.303
NT2RP4001719	4.115	3.996	6.251	6.793	0.000	3.648	0.000	5.696
NT2RP4001725	32.499	19.952	25.192	14.409	10.172	27.215	32.425	18.951
NT2RP4001726	54.527	36.453	64.243	26.169	28.497	40.523	55.394	19.268
NT2RP4001730	12.704	4.465	10.741	6.560	6.940	4.424	3.677	4.124
NT2RP4001739	100.531	27.275	89.269	26.597	21.415	57.785	66.185	25.777
NT2RP4001741	110.382	99.274	234.294	44.252	36.564	43.056	33.008	41.898
NT2RP4001753	39.441	20.491	71.424	37.461	1.805	37.216	18.904	38.683
NT2RP4001760	14.764	11.531	4.629	15.113	4.914	5.657	5.650	2.825
NT2RP4001787	258.392	145.823	264.342	128.018	104.482	137.855	226.897	211.755
NT2RP4001790	34.934	24.033	47.502	23.049	19.224	20.959	21.785	26.319
NT2RP4001795	64.250	59.518	90.887	55.846	29.460	30.950	41.200	41.068
NT2RP4001803	30.124	17.002	33.008	12.028	5.604	11.542	8.057	8.711
NT2RP4001805	69.724	47.736	91.734	21.767	28.977	49.346	29.736	15.069
NT2RP4001809	249.052	50.599	114.889	32.414	75.066	114.744	91.752	13.588
NT2RP4001817	46.954	36.438	25.771	14.621	13.677	59.903	27.216	21.236
NT2RP4001822	177.317	48.258	102.447	19.403	35.452	81.929	51.381	28.953
NT2RP4001823	30.502	15.399	18.920	5.780	6.496	10.465	7.520	6.128
NT2RP4001827	65.786	52.243	54.585	30.666	20.071	35.276	26.036	20.301
NT2RP4001828	265.068	110.898	195.484	63.750	99.323	140.250	144.652	63.747
NT2RP4001836	136.462	50.159	118.930	24.890	59.417	39.904	29.937	18.265
NT2RP4001838	154.169	54.298	78.857	23.853	25.980	67.323	52.328	17.783
NT2RP4001841	53.995	81.543	68.608	23.556	51.873	35.401	32.437	39.023

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Table 117

NT2RP4001849	127.297	17.445	38.764	4.795	19.911	39.260	53.938	8.385
NT2RP4001861	247.889	113.986	152.565	70.140	77.706	119.545	74.993	93.651
NT2RP4001877	101.731	60.233	139.463	63.735	37.564	43.408	50.482	50.974
NT2RP4001879	52.547	46.318	81.300	25.097	20.585	42.533	33.249	30.904
NT2RP4001889	70.569	45.627	140.257	26.366	28.442	18.192	17.861	25.113
NT2RP4001893	25.380	22.592	43.017	18.499	15.138	9.424	8.376	6.982
NT2RP4001896	34.081	20.051	44.749	10.547	15.271	19.037	14.839	13.968
NT2RP4001898	214.122	125.432	418.651	67.171	53.688	119.010	53.767	70.070
NT2RP4001901	98.678	53.976	182.276	39.521	42.438	38.087	23.271	32.169
NT2RP4001910	37.857	50.894	99.896	25.518	57.751	122.391	71.018	74.327
NT2RP4001925	63.642	29.438	46.884	25.210	22.129	45.913	35.236	19.704
NT2RP4001926	21.200	13.827	24.573	7.083	11.581	7.544	10.754	9.806
NT2RP4001927	19.268	17.900	28.017	9.329	12.222	11.234	14.514	7.786
NT2RP4001931	97.433	45.715	58.255	21.472	23.167	20.695	41.852	23.242
NT2RP4001933	94.894	38.536	49.116	18.868	30.123	17.978	20.041	20.718
NT2RP4001938	286.138	121.070	279.936	37.391	35.937	120.491	73.356	57.647
NT2RP4001942	65.948	38.369	38.848	27.689	31.221	62.157	96.580	29.143
NT2RP4001945	41.368	18.714	27.898	8.014	14.644	17.772	15.860	11.677
NT2RP4001946	26.736	25.374	44.253	18.892	16.137	18.739	15.375	19.575
NT2RP4001947	3.902	6.862	18.880	3.327	6.771	2.037	3.124	8.202
NT2RP4001950	43.788	52.338	61.416	20.392	18.601	15.837	9.943	21.246
NT2RP4001953	74.594	54.521	201.576	35.155	25.200	19.900	24.690	37.538
NT2RP4001965	59.559	15.062	48.054	10.833	25.873	32.505	27.673	16.883
NT2RP4001970	250.998	97.493	91.936	22.958	56.420	113.696	71.723	47.051
NT2RP4001975	66.332	42.906	96.575	25.793	35.690	65.632	31.289	42.704
NT2RP4001988	34.115	69.980	24.419	10.144	8.048	24.865	25.619	34.649
NT2RP4001996	34.292	25.552	27.656	12.286	17.188	25.718	14.676	10.275
NT2RP4002014	96.789	141.748	123.891	28.921	44.195	55.818	35.380	37.118
NT2RP4002018	51.913	24.760	41.235	10.014	19.687	23.559	18.245	34.018
NT2RP4002035	29.954	14.435	25.087	12.863	31.601	28.211	23.642	22.189
NT2RP4002043	22.692	22.569	32.601	19.499	11.381	22.102	20.695	23.533
NT2RP4002046	96.899	76.132	55.715	18.254	26.488	53.136	30.705	25.046
NT2RP4002047	32.738	46.847	44.327	32.723	15.068	26.152	13.938	32.144
NT2RP4002052	15.972	18.197	19.425	11.638	8.069	13.935	10.066	12.588
NT2RP4002056	135.983	113.302	169.971	38.787	125.176	113.563	77.593	83.524
NT2RP4002057	84.885	34.408	60.458	17.766	21.946	77.991	75.176	47.433
NT2RP4002058	23.685	18.994	29.136	10.874	14.415	11.785	16.779	16.312
NT2RP4002064	30.635	14.897	33.490	16.524	16.922	12.258	15.014	25.572
NT2RP4002071	44.464	31.989	67.896	26.934	14.700	35.364	41.060	22.140
NT2RP4002075	12.341	23.187	23.062	7.438	8.387	13.256	7.417	9.609
NT2RP4002078	29.846	42.027	82.198	17.811	5.991	41.201	10.199	52.455
NT2RP4002081	188.987	84.568	105.808	21.123	35.926	97.846	71.564	35.425
NT2RP4002083	2.403	4.985	0.000	0.314	0.000	0.000	1.168	0.000
NT2RP4002099	78.239	28.086	39.672	11.893	30.439	25.384	40.614	18.182
NT2RP4002106	58.519	39.159	55.467	21.121	12.917	66.398	104.992	30.602
NT2RP4002111	276.429	227.374	252.398	129.656	67.040	206.459	208.212	245.585
NT2RP4002112	24.864	26.469	24.598	12.981	9.167	27.016	16.882	13.120
NT2RP4002116	43.886	61.673	98.270	42.933	38.005	36.286	25.145	12.745
NT2RP4002122	44.771	24.552	24.373	26.789	12.328	6.628	8.237	19.312
NT2RP4002126	58.138	23.058	51.469	13.176	13.341	21.828	27.785	31.381
NT2RP4002133	86.426	80.537	66.020	23.353	23.704	46.666	42.292	33.380
NT2RP4002136	84.825	38.199	57.051	14.996	23.918	31.464	46.186	26.328
NT2RP4002139	76.548	64.715	56.669	34.571	20.583	36.387	35.415	37.823
NT2RP4002174	100.223	26.806	136.927	21.487	10.831	17.747	16.730	22.815
NT2RP4002185	84.685	98.123	101.806	56.809	25.728	38.576	50.054	42.202
NT2RP4002186	76.426	104.170	270.574	75.854	79.446	47.076	41.217	75.609
NT2RP4002187	47.198	70.549	84.418	12.734	27.208	71.434	52.262	26.859
NT2RP4002188	35.383	30.278	67.328	48.848	43.711	39.200	18.696	45.047
NT2RP4002199	8.790	3.765	7.735	3.103	3.671	4.856	6.602	4.582
NT2RP4002206	65.655	41.544	56.183	14.975	16.172	23.112	30.357	19.694
NT2RP4002210	89.632	39.449	49.442	26.733	14.817	29.546	36.670	13.077
NT2RP4002222	66.188	28.126	48.518	18.433	9.476	18.229	30.855	13.676
NT2RP4002241	21.472	73.064	52.707	19.669	16.108	20.165	24.348	35.568
NT2RP4002248	89.805	44.853	53.025	15.207	28.490	47.016	40.320	26.933

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Table 118

NT2RP4002250	9.932	2.790	2.832	3.032	2.884	3.939	3.541	2.731
NT2RP4002259	98.207	83.004	106.317	27.935	22.544	53.580	27.771	28.361
NT2RP4002268	76.648	38.869	74.529	23.758	30.978	42.466	39.855	19.465
NT2RP4002288	385.663	297.805	359.839	170.051	129.643	303.550	199.320	193.830
NT2RP4002290	36.179	20.072	47.837	6.799	18.426	18.201	11.227	12.869
NT2RP4002298	36.246	17.225	18.192	23.131	9.100	14.492	16.163	9.824
NT2RP4002306	106.632	73.744	244.843	37.397	44.511	42.955	43.305	15.782
NT2RP4002308	32.611	5.236	14.575	3.239	0.000	18.399	6.762	8.392
NT2RP4002336	58.486	27.861	65.731	14.287	0.000	40.974	32.637	24.822
NT2RP4002340	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.608
NT2RP4002361	58.644	10.427	47.735	8.516	9.638	11.404	11.251	4.202
NT2RP4002367	33.403	12.467	18.470	12.044	5.048	13.606	23.450	11.551
NT2RP4002368	30.961	37.918	39.910	11.210	13.572	15.090	26.947	17.073
NT2RP4002377	54.340	43.892	116.766	38.442	20.404	44.896	56.968	37.630
NT2RP4002408	13.226	8.072	12.192	7.437	5.595	8.466	9.233	1.448
NT2RP4002425	9.657	6.220	8.381	3.685	1.438	1.029	3.019	3.646
NT2RP4002432	162.057	67.674	98.832	18.405	27.254	50.612	54.723	46.891
NT2RP4002447	38.164	33.834	62.023	30.863	14.303	29.507	8.767	8.930
NT2RP4002451	7.843	13.049,	15.746	6.677	3.617	8.815	1.747	9.433
NT2RP4002461	96.759	88.219	116.998	47.479	57.340	32.249	36.274	24.074
NT2RP4002486	134.976	61.570	83.309	71.309	46.898	61.095	41.576	21.740
NT2RP4002517	58.053	36.106	59.653	12.934	25.946	17.882	24.902	21.801
NT2RP4002556	43.020	59.649	60.047	47.543	16.113	30.397	20.361	21.390
NT2RP4002569	55.960	24.230	25.391	9.256	12.527	28.839	41.356	15.537
NT2RP4002587	66.993	24.539	29.137	12.319	10.000	27.896	26.210	13.197
NT2RP4002591	30.924	17.255	64.461	40.777	19.170	45.337	11.471	35.621
NT2RP4002607	54.314	34.936	46.019	25.502	12.780	34.916	29.754	19.269
NT2RP4002627	77.997	65.880	94.854	27.581	43.756	52.437	23.907	43.664
NT2RP4002628	21.252	24.628	31.576	38.351	13.833	13.934	20.421	19.758
NT2RP4002630	70.308	48.663	165.068	28.270	26.685	23.920	21.463	25.050
NT2RP4002639	34.573	25.557	46.433	21.541	27.552	30.947	24.555	20.118
NT2RP4002641	107.016	60.263	102.333	24.417	23.197	63.371	31.978	22.283
NT2RP4002658	49.532	66.012	31.405	43.805	11.257	29.226	40.300	36.588
NT2RP4002669	139.676	37.293	45.595	14.602	38.129	45.705	53.924	19.231
NT2RP4002677	20.241	31.667	46.092	45.042	15.952	20.098	16.586	53.152
NT2RP4002715	66.829	32.913	90.988	19.361	54.330	49.099	48.752	33.038
NT2RP4002750	74.179	34.932	56.851	17.150	20.232	23.076	29.740	18.218
NT2RP4002784	67.421	24.006	62.663	18.995	23.720	28.427	58.514	16.510
NT2RP4002791	28.944	34.248	39.645	19.520	14.437	25.409	18.682	19.866
NT2RP4002811	191.101	48.977	64.562	15.450	18.301	79.439	82.520	19.601
NT2RP4002830	105.586	49.177	76.222	25.375	47.589	45.374	21.154	24.854
NT2RP4002832	25.813	10.744	26.473	5.157	5.007	10.239	3.522	4.192
NT2RP4002850	149.082	57.743	102.303	28.532	37.913	75.770	47.566	29.262
NT2RP4002874	60.455	22.464	40.061	7.249	18.394	31.321	29.662	14.021
NT2RP4002884	143.158	172.626	226.029	43.885	40.049	72.829	100.195	80.578
NT2RP4002888	674.861	131.669	285.125	53.073	130.491	374.710	309.640	77.843
NT2RP4002891	49.251	19.998	83.408	45.255	22.748	23.519	25.198	32.282
NT2RP4002894	52.025	17.730	44.439	15.465	30.670	53.933	19.786	17.490
NT2RP4002898	62.611	29.872	36.349	8.160	14.509	32.175	23.150	9.215
NT2RP4002905	66.278	20.133	27.924	9.606	17.387	37.876	9.098	11.326
NT2RP4002907	133.109	146.263	986.435	80.359	7.640	119.281	47.532	4.835
NT2RP5003469	104.697	52.694	23.001	28.403	58.257	68.072	73.297	73.672
NT2RP5003481	13.597	25.252	19.706	20.131	10.924	4.203	12.049	16.282
NT2RP5003471	67.015	71.340	73.641	28.289	26.026	42.807	59.142	75.646
NT2RP5003477	99.313	40.896	89.264	23.215	24.470	47.291	53.314	38.937
NT2RP5003487	149.480	394.096	441.718	265.002	121.873	351.279	181.435	545.031
NT2RP5003492	121.748	38.219	55.597	23.529	23.174	61.042	47.790	32.333
NT2RP5003500	28.243	13.949	28.326	7.609	6.374	19.974	10.924	7.373
NT2RP5003508	134.622	138.997	142.784	43.006	50.574	83.904	56.185	74.393
NT2RP5003512	34.416	11.927	16.738	3.974	7.691	7.518	10.845	8.612
NT2RP5003522	70.316	37.613	44.952	19.574	25.328	22.112	21.875	28.029
NT2RP5003524	37.812	24.325	51.778	11.791	10.830	11.580	15.958	15.290
NT2RP5003527	548.452	324.151	547.100	240.290	240.483	435.490	606.993	396.820
NT2RP5003531	218.385	231.836	102.817	12.058	28.603	161.069	24.666	55.299

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Table 119

NT2RP5003534	52.710	32.028	38.558	7.019	15.506	20.156	15.510	8.979
NT2RP6000020	210.149	130.471	144.056	41.190	61.827	130.501	91.960	129.873
NT2RP6000022	21.538	14.233	20.157	9.477	8.940	8.583	13.793	19.548
NT2RP6000050	71.839	29.419	34.531	13.907	10.240	25.335	35.367	26.244
NT2RP6000063	64.066	28.604	49.917	15.400	35.731	36.275	41.783	27.262
NT2RP6000074	158.830	63.135	82.278	24.913	42.059	81.152	81.658	52.773
NT2RP6000083	77.705	50.820	78.153	25.019	26.843	53.073	63.619	37.514
NT2RP6000100	50.338	49.391	48.240	38.749	18.889	28.023	21.991	17.677
NT2RP6000123	93.881	40.481	91.240	14.231	12.925	21.554	11.762	21.172
NT2RP6000129	88.985	47.556	65.182	18.250	6.578	44.353	35.215	33.928
NT2RP6000147	92.349	57.944	378.808	14.768	31.975	24.474	24.050	25.120
NT2RP6000163	25.983	24.930	19.397	3.670	5.619	4.373	7.249	6.228
NT2RP6000181	156.005	46.707	83.042	23.577	40.609	63.752	82.227	48.686
NT2RP6000182	88.398	83.770	188.105	36.383	59.805	37.752	28.971	44.514
OVARC1000001	80.247	58.966	66.050	19.840	25.013	40.518	55.886	20.561
OVARC1000003	20.948	26.924	29.257	6.511	9.613	12.291	10.501	12.627
OVARC1000004	80.203	65.653	78.764	43.217	16.647	43.045	49.235	40.643
OVARC1000005	30.735	28.510	27.987	8.280	13.556	26.127	22.928	6.489
OVARC1000013	57.790	56.730	33.604	8.558	12.487	25.216	24.982	13.217
OVARC1000014	77.754	46.427	51.294	14.220	15.288	23.140	45.111	37.444
OVARC1000017	117.243	44.469	63.710	20.838	20.603	56.329	47.142	30.588
OVARC1000026	48.571	90.236	108.886	113.202	47.802	62.912	49.285	92.751
OVARC1000035	49.364	29.380	53.296	24.565	28.515	42.393	36.018	23.376
OVARC1000037	217.386	150.962	123.831	103.776	107.202	127.890	99.068	110.962
OVARC1000058	126.770	102.554	238.989	41.391	55.660	36.598	18.334	26.662
OVARC1000060	69.220	52.141	61.680	16.724	30.594	25.644	26.946	50.637
OVARC1000068	13.131	13.623	21.327	11.889	11.183	5.229	8.992	12.530
OVARC1000069	101.314	75.808	53.487	27.968	38.426	35.714	36.399	56.941
OVARC1000071	18.796	24.923	14.847	12.360	18.401	4.200	10.123	10.463
OVARC1000075	2485.301	555.545	463.529	172.018	1135.376	1656.344	703.861	375.646
OVARC1000083	28.000	26.575	47.619	26.281	19.723	45.186	32.169	29.140
OVARC1000085	102.017	92.945	160.004	82.480	133.814	49.366	47.840	68.991
OVARC1000086	90.269	76.669	42.857	41.659	25.286	36.964	47.871	41.838
OVARC1000087	19.951	31.052	13.384	10.950	9.727	13.579	27.946	13.255
OVARC1000090	102.718	128.317	77.866	86.960	52.554	50.587	59.255	73.796
OVARC1000091	20.738	22.588	16.835	15.147	15.944	18.317	24.472	14.038
OVARC1000092	45.388	47.278	30.923	56.969	21.795	27.471	24.142	30.390
OVARC1000105	56.618	51.625	28.040	39.250	20.320	35.440	41.724	47.581
OVARC1000106	97.264	85.498	48.102	31.853	33.621	45.854	56.254	52.554
OVARC1000109	114.256	62.904	50.032	28.577	38.160	60.871	53.325	44.146
OVARC1000113	34.168	25.308	21.666	38.682	21.936	24.745	30.026	25.837
OVARC1000114	55.942	73.163	50.779	53.005	19.962	35.869	27.590	39.625
OVARC1000133	5.433	9.465	6.445	3.599	2.421	3.824	7.063	6.210
OVARC1000137	41.293	26.211	21.220	13.873	15.408	25.975	29.535	16.677
OVARC1000139	84.491	47.729	43.252	31.553	35.336	57.357	112.486	56.571
OVARC1000145	26.915	13.800	13.435	8.493	4.736	16.675	21.906	9.604
OVARC1000148	95.785	51.946	47.706	22.802	33.066	41.883	45.597	39.685
OVARC1000151	111.083	48.761	50.667	22.177	24.840	81.184	53.839	31.939
OVARC1000157	62.383	114.029	28.960	63.914	19.555	36.685	41.200	59.747
OVARC1000162	5.118	14.000	6.832	5.603	6.337	4.543	9.793	8.590
OVARC1000168	81.607	75.614	57.301	56.633	36.377	46.771	48.149	49.790
OVARC1000169	78.957	58.791	36.013	29.258	23.912	45.597	77.117	58.589
OVARC1000178	106.533	52.682	38.525	31.101	37.430	64.424	120.686	45.081
OVARC1000182	15.786	9.753	6.250	2.924	6.078	5.238	9.722	7.079
OVARC1000186	178.795	62.303	67.117	22.063	47.239	71.323	93.931	44.381
OVARC1000188	55.199	40.588	29.176	19.785	20.797	37.219	38.548	31.660
OVARC1000191	14.885	2.691	6.015	3.796	3.482	9.072	4.942	5.421
OVARC1000198	72.128	80.950	54.486	54.117	33.922	43.403	37.363	41.179
OVARC1000208	73.832	151.668	79.809	82.075	69.383	50.018	50.296	63.159
OVARC1000209	45.018	32.401	13.771	12.070	17.681	55.006	120.917	35.627
OVARC1000212	50.452	37.867	27.931	26.874	23.195	35.446	34.851	30.436
OVARC1000216	33.528	22.596	8.224	10.405	12.069	17.504	239.036	15.017
OVARC1000240	101.692	80.568	37.390	41.065	35.961	25.139	30.705	41.984
OVARC1000241	96.730	62.529	34.963	20.886	28.711	41.611	41.876	40.107

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Table 120

OVARC1000249	61.518	33.009	33.209	13.471	15.622	30.315	31.563	26.366
OVARC1000254	86.926	108.103	77.039	42.563	81.235	81.095	78.301	85.308
OVARC1000255	60.970	39.851	26.458	25.736	26.168	36.286	39.977	34.354
OVARC1000267	99.396	106.106	72.814	56.946	76.696	67.094	68.179	55.598
OVARC1000275	1.361	3.837	0.000	0.676	1.682	4.413	19.023	14.619
OVARC1000287	32.661	22.716	11.398	11.361	9.849	19.833	62.592	48.262
OVARC1000288	82.750	57.876	28.088	21.493	23.388	32.508	34.475	29.764
OVARC1000298	23.487	30.867	16.778	9.152	10.710	22.218	12.148	15.140
OVARC1000302	29.507	43.409	20.343	19.607	16.971	18.175	10.089	15.944
OVARC1000304	45.645	44.852	33.516	20.672	15.744	39.549	33.592	42.327
OVARC1000307	24.624	30.250	26.631	15.444	18.919	21.450	27.043	23.654
OVARC1000309	50.270	38.396	29.381	16.928	23.152	40.904	33.254	20.287
OVARC1000312	54.891	39.139	41.157	12.112	22.445	49.126	63.285	25.737
OVARC1000313	62.108	49.417	23.463	16.503	20.288	43.637	40.674	39.428
OVARC1000321	38.317	91.534	39.988	16.691	58.665	36.640	32.452	40.394
OVARC1000326	58.790	34.963	27.371	25.834	24.229	32.514	31.258	28.072
OVARC1000327	79.408	45.673	47.401	27.601	25.688	51.080	44.339	24.826
OVARC1000331	67.541	33.220	28.427	25.603	24.396	42.607	52.669	29.584
OVARC1000335	12.573	16.067	12.457	10.283	12.062	15.090	16.235	11.984
OVARC1000347	10.404	19.839	9.744	14.234	10.300	11.772	15.807	14.484
OVARC1000348	104.509	53.231	29.087	28.611	27.286	49.055	59.346	36.658
OVARC1000363	23.207	29.136	17.234	17.138	22.355	12.064	14.282	17.705
OVARC1000377	24.447	20.967	8.919	11.225	9.000	9.306	12.677	10.839
OVARC1000382	43.425	38.484	25.520	12.983	19.971	27.581	24.011	20.004
OVARC1000384	39.526	33.430	34.510	29.733	34.546	26.194	23.240	27.218
OVARC1000401	19.377	21.365	10.833	14.856	8.159	13.368	15.387	15.593
OVARC1000406	246.308	104.316	212.801	47.902	275.450	229.284	231.727	63.004
OVARC1000407	37.707	28.148	15.167	29.769	18.198	20.301	24.339	24.226
OVARC1000408	176.546	182.488	168.003	92.253	152.822	131.022	104.696	123.181
OVARC1000410	132.351	71.592	33.987	19.006	47.593	63.597	105.036	45.064
OVARC1000411	24.928	46.964	21.466	16.795	18.354	16.759	17.621	24.921
OVARC1000414	53.052	80.288	77.929	45.828	64.588	36.694	43.527	34.813
OVARC1000420	210.281	97.795	116.314	65.770	48.502	138.372	122.981	79.364
OVARC1000421	126.414	65.308	43.609	41.965	30.984	66.717	77.617	43.013
OVARC1000427	85.522	76.052	61.132	54.694	43.202	55.414	85.904	58.425
OVARC1000431	29.754	43.257	31.464	59.910	40.269	33.174	24.118	40.748
OVARC1000437	101.746	108.759	36.433	33.368	38.706	67.360	68.627	59.999
OVARC1000439	55.100	39.820	23.665	17.682	26.837	27.173	37.589	27.642
OVARC1000440	9.304	16.390	4.607	5.910	7.569	12.799	5.759	8.778
OVARC1000442	71.954	97.290	60.169	48.043	50.925	49.780	49.452	49.132
OVARC1000443	23.336	24.854	21.466	6.313	14.231	15.300	17.929	17.277
OVARC1000461	38.961	27.338	30.933	18.801	25.228	29.577	31.675	33.815
OVARC1000465	24.244	26.635	23.588	15.988	16.431	17.245	18.033	20.237
OVARC1000466	78.845	45.309	35.183	22.710	29.028	42.270	78.325	34.551
OVARC1000467	68.457	41.646	26.636	17.995	24.535	32.636	50.520	33.453
OVARC1000470	79.505	66.390	34.473	51.974	38.874	30.248	35.482	44.070
OVARC1000473	104.626	46.950	38.060	19.545	49.878	53.144	60.639	36.861
OVARC1000479	13.043	22.838	18.446	27.648	14.611	11.592	14.222	14.645
OVARC1000484	81.135	119.477	61.550	71.199	61.618	42.186	32.384	37.475
OVARC1000485	43.060	37.552	15.873	26.931	21.970	20.014	12.533	17.483
OVARC1000496	6.894	5.795	2.024	9.550	5.845	4.482	5.597	6.952
OVARC1000520	10.944	13.261	5.969	10.975	8.640	4.681	5.177	7.377
OVARC1000522	57.377	36.524	49.921	34.183	62.162	27.574	36.847	42.071
OVARC1000526	89.641	108.239	58.125	65.691	63.235	45.200	63.148	66.145
OVARC1000528	57.424	54.050	21.682	25.091	30.072	29.592	53.851	44.743
OVARC1000533	259.058	92.210	92.325	54.816	108.661	158.123	180.752	58.313
OVARC1000543	9.147	20.003	8.468	14.598	10.808	7.160	7.656	9.778
OVARC1000550	51.120	35.681	19.454	19.769	24.341	23.780	29.758	19.911
OVARC1000553	106.477	109.455	53.476	65.549	62.372	43.081	54.040	60.551
OVARC1000556	84.636	47.645	29.302	13.010	36.300	34.811	56.871	26.716
OVARC1000557	30.381	33.997	15.138	26.106	16.920	12.137	18.672	18.092
OVARC1000561	130.212	131.086	62.529	70.306	56.212	50.615	66.315	60.071
OVARC1000564	43.577	60.550	30.136	18.864	19.300	44.661	34.156	37.974
OVARC1000573	74.996	71.429	42.493	41.906	33.040	35.765	29.517	39.465

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Table 121

OVARC1000576	322.369	178.635	134.897	63.583	61.558	195.012	191.660	126.973
OVARC1000578	41.245	47.399	27.512	62.221	23.000	19.402	20.991	28.222
OVARC1000581	19.381	18.054	16.597	12.946	10.926	16.921	23.687	17.958
OVARC1000586	58.760	84.513	39.858	53.327	17.530	41.985	63.279	95.673
OVARC1000588	52.736	46.547	28.747	35.144	19.236	20.189	27.881	28.239
OVARC1000605	25.011	21.584	16.038	16.026	12.949	28.632	20.949	12.415
OVARC1000622	236.401	229.625	142.634	146.619	111.039	103.900	84.581	117.758
OVARC1000636	62.041	58.870	30.872	26.680	23.116	39.517	52.845	27.699
OVARC1000640	37.774	40.454	27.435	25.421	14.327	20.971	27.326	24.570
OVARC1000649	119.925	80.531	59.932	34.951	42.653	66.545	126.333	64.422
OVARC1000661	91.942	47.731	46.674	29.765	29.826	53.562	68.611	41.478
OVARC1000677	47.303	42.727	39.478	18.654	17.990	29.788	33.925	31.139
OVARC1000678	53.878	40.134	32.060	37.092	23.552	26.846	42.330	32.378
OVARC1000679	25.552	33.892	27.236	13.826	12.729	13.248	18.589	22.125
OVARC1000681	64.996	39.676	33.010	23.036	25.157	35.864	32.183	28.963
OVARC1000682	89.453	46.031	48.073	26.181	22.664	56.539	67.656	36.205
OVARC1000689	40.766	43.141	31.489	16.450	18.494	36.522	52.050	30.362
OVARC1000700	65.661	65.260	46.443	51.382	36.724	40.865	31.889	43.299
OVARC1000703	68.421	67.574	44.166	43.328	32.848	43.707	34.063	33.710
OVARC1000722	90.588	55.674	40.426	28.083	33.617	39.059	84.669	53.295
OVARC1000726	223.039	61.254	64.375	36.671	46.678	62.745	120.014	59.080
OVARC1000727	101.498	52.857	32.778	21.030	24.747	45.216	39.732	28.241
OVARC1000730	32.092	36.451	14.144	26.825	11.752	14.326	24.052	21.653
OVARC1000741	93.409	52.169	37.001	21.498	22.633	47.358	43.609	24.156
OVARC1000746	18.880	20.011	11.250	10.152	10.039	12.336	11.833	14.185
OVARC1000764	94.412	66.494	49.103	37.950	38.405	57.102	51.799	45.024
OVARC1000769	61.249	87.994	63.412	48.573	49.372	46.621	37.596	54.747
OVARC1000771	17.704	22.392	12.731	11.680	15.094	14.537	11.734	13.386
OVARC1000773	309.712	63.691	128.640	93.505	135.643	247.891	47.762	56.423
OVARC1000775	39.822	40.473	19.087	17.945	17.047	20.931	22.217	24.299
OVARC1000778	57.819	40.229	23.354	27.887	19.703	25.351	15.434	16.858
OVARC1000779	13.359	9.700	3.596	4.604	3.376	6.590	5.881	4.469
OVARC1000781	28.426	18.324	19.364	8.066	2.533	18.289	13.313	9.987
OVARC1000787	57.756	46.552	31.436	36.327	24.660	31.315	26.423	26.916
OVARC1000789	56.045	42.830	21.343	32.278	26.180	29.815	35.483	31.401
OVARC1000800	152.906	115.192	91.456	100.625	80.665	74.709	72.586	83.426
OVARC1000802	56.307	41.592	29.261	21.865	29.614	38.004	29.144	37.338
OVARC1000810	117.305	73.073	45.217	47.024	30.840	54.331	22.585	30.212
OVARC1000811	24.376	21.125	12.822	10.066	8.476	14.818	12.129	13.407
OVARC1000814	109.717	173.696	116.374	110.400	99.820	81.598	52.542	70.043
OVARC1000816	38.942	32.627	29.109	10.508	18.910	26.961	43.388	30.931
OVARC1000817	7.152	7.754	5.073	4.922	1.435	3.770	5.107	7.052
OVARC1000834	52.593	59.148	30.623	25.871	27.698	43.601	43.333	33.619
OVARC1000846	128.045	121.550	80.555	82.014	63.814	79.270	47.279	73.330
OVARC1000850	63.194	47.834	24.998	22.731	23.832	31.759	43.348	29.789
OVARC1000853	47.482	127.726	57.523	25.369	55.048	41.556	32.136	37.576
OVARC1000862	31.255	26.218	21.640	13.240	25.873	16.507	16.932	8.079
OVARC1000873	59.654	49.105	31.649	32.533	37.513	39.866	44.461	30.226
OVARC1000875	178.627	94.134	92.359	64.818	79.244	116.581	163.150	75.514
OVARC1000876	8.798	15.017	5.566	12.799	6.112	8.158	8.444	16.825
OVARC1000883	44.435	33.208	17.857	33.562	21.585	25.327	28.768	27.716
OVARC1000885	11.029	16.263	7.277	16.699	8.434	58.765	18.303	13.712
OVARC1000886	41.813	40.086	18.851	13.178	22.604	30.692	35.601	21.522
OVARC1000890	216.895	167.860	92.458	66.405	70.562	97.108	128.741	96.438
OVARC1000891	20.905	24.028	19.790	8.818	7.749	13.015	11.884	12.875
OVARC1000897	9.048	31.172	6.976	6.993	2.984	7.384	6.185	9.271
OVARC1000912	15.809	11.325	6.349	14.551	6.939	9.404	13.732	9.946
OVARC1000914	26.259	35.138	27.276	22.701	17.946	18.401	14.325	19.336
OVARC1000915	75.637	70.430	44.897	67.623	39.966	40.708	37.700	37.607
OVARC1000916	51.456	41.509	29.511	22.182	21.453	30.494	39.766	29.531
OVARC1000924	31.774	26.872	12.891	6.378	16.342	20.449	32.562	22.496
OVARC1000928	36.954	58.011	21.195	13.024	27.684	15.057	30.125	17.883
OVARC1000936	22.358	30.709	22.132	20.757	13.382	30.025	17.362	22.497
OVARC1000937	50.958	48.239	37.559	26.648	23.630	35.710	37.949	33.063

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Table 122

OVARC1000945	72.670	66.756	35.734	31.061	28.439	44.288	57.299	34.609
OVARC1000948	13.138	9.821	6.873	5.701	6.145	7.947	8.485	6.560
OVARC1000956	53.521	35.128	27.412	25.007	31.512	30.356	47.794	38.003
OVARC1000959	73.657	56.906	34.594	53.936	29.777	37.237	43.699	40.734
OVARC1000960	336.284	304.478	264.514	301.674	301.925	170.334	206.868	211.921
OVARC1000964	109.457	89.334	92.736	42.962	107.425	66.304	100.429	104.440
OVARC1000971	23.347	22.555	11.767	9.454	10.751	11.968	14.346	9.949
OVARC1000975	38.653	41.668	22.926	16.702	21.947	23.016	30.329	22.999
OVARC1000976	5.549	11.344	5.097	7.562	6.992	4.915	5.760	8.357
OVARC1000981	38.051	38.818	23.473	34.246	24.179	25.155	27.878	49.594
OVARC1000982	18.237	20.180	8.868	15.397	12.870	12.622	17.681	16.489
OVARC1000984	64.280	32.461	21.258	21.860	23.534	26.715	40.246	32.960
OVARC1000995	98.670	98.801	50.363	66.552	60.125	43.967	46.967	67.398
OVARC1000996	23.461	22.409	9.648	11.387	13.424	14.277	20.244	19.657
OVARC1000999	142.766	147.956	91.391	112.389	86.587	72.322	63.450	71.881
OVARC1001000	196.742	223.698	123.240	137.198	124.411	96.923	91.581	110.353
OVARC1001004	15.837	24.777	8.416	6.761	11.301	5.392	7.712	7.076
OVARC1001010	20.746	21.844	10.176	13.214	12.974	9.756	20.656	11.492
OVARC1001011	56.262	49.134	31.219	40.269	29.627	26.821	32.007	29.717
OVARC1001030	267.698	257.417	369.890	123.083	481.589	213.259	236.252	156.604
OVARC1001032	25.684	32.175	13.978	17.255	17.403	12.728	21.746	22.424
OVARC1001034	26.408	30.129	18.682	14.209	24.225	14.437	22.093	19.148
OVARC1001038	38.346	41.992	24.957	24.612	28.412	29.918	36.871	30.300
OVARC1001040	98.109	163.189	57.680	96.342	37.120	36.870	51.690	65.780
OVARC1001041	93.629	176.563	45.646	73.484	59.177	42.401	48.353	76.436
OVARC1001044	29.011	33.627	14.802	21.262	17.318	16.763	22.227	22.829
OVARC1001049	156.011	131.461	99.014	60.845	95.518	95.243	124.468	83.710
OVARC1001051	180.769	195.784	75.946	127.551	72.219	104.988	166.021	161.466
OVARC1001054	44.196	25.475	14.270	15.193	14.800	17.493	25.623	19.511
OVARC1001055	49.946	52.425	26.074	16.256	16.038	22.736	26.492	26.988
OVARC1001062	9.764	52.550	13.991	22.860	14.380	12.344	7.304	17.143
OVARC1001065	20.300	19.807	20.195	9.804	10.947	15.910	27.631	19.975
OVARC1001068	56.993	44.653	31.867	20.677	17.254	28.843	44.829	31.704
OVARC1001072	156.343	67.114	52.898	30.164	30.884	59.064	66.747	40.238
OVARC1001073	34.815	40.406	29.440	33.203	20.617	29.525	38.538	21.374
OVARC1001074	18.735	18.807	6.927	9.591	8.229	12.569	22.029	15.581
OVARC1001078	170.789	81.144	63.392	42.879	41.437	60.250	97.102	51.664
OVARC1001085	48.583	37.562	22.446	18.020	16.558	51.666	25.272	24.844
OVARC1001086	94.509	38.291	23.565	18.437	19.838	42.555	39.613	26.858
OVARC1001091	59.024	54.767	39.117	31.558	15.085	41.685	65.548	38.043
OVARC1001092	78.369	48.366	35.270	24.652	27.135	48.099	68.542	28.251
OVARC1001104	9.822	12.079	8.053	6.860	3.025	6.895	13.769	8.849
OVARC1001107	132.584	59.642	57.112	32.997	46.497	103.685	120.752	61.479
OVARC1001113	35.730	35.073	29.872	25.624	16.230	24.132	39.291	35.356
OVARC1001117	91.761	65.878	42.978	55.698	23.367	45.042	42.492	38.455
OVARC1001118	78.150	72.874	45.679	47.079	35.711	49.123	35.261	47.146
OVARC1001125	19.282	29.524	14.882	30.810	6.474	16.234	19.586	21.569
OVARC1001129	26.932	18.386	14.691	12.212	8.606	16.751	19.030	7.081
OVARC1001132	7.132	10.388	7.883	7.540	6.168	4.130	6.582	8.385
OVARC1001138	308.799	242.318	123.419	77.068	99.486	165.174	159.386	99.862
OVARC1001141	48.972	28.503	23.912	13.741	19.193	23.582	30.980	24.417
OVARC1001154	66.885	91.460	43.947	37.042	36.702	48.431	80.339	79.168
OVARC1001161	71.634	56.342	31.340	42.482	14.597	25.244	28.686	26.648
OVARC1001162	80.697	81.514	58.697	43.494	34.028	46.796	40.262	50.829
OVARC1001163	170.857	43.068	59.424	17.764	29.289	91.606	90.481	55.488
OVARC1001167	77.273	85.145	46.746	44.768	32.264	35.631	32.410	29.958
OVARC1001169	10.634	15.674	9.302	5.674	5.124	9.510	12.220	9.744
OVARC1001170	48.257	49.203	32.879	28.366	23.146	21.439	43.645	39.076
OVARC1001171	71.425	65.035	38.595	39.746	29.129	40.964	39.089	54.225
OVARC1001173	116.007	101.332	67.406	103.307	65.939	60.129	54.280	60.387
OVARC1001176	245.124	107.908	82.421	85.014	77.976	145.459	105.359	82.551
OVARC1001180	195.252	157.056	72.136	68.290	69.367	72.299	67.658	67.806
OVARC1001188	63.149	49.538	32.804	26.683	20.348	25.538	21.817	24.241
OVARC1001200	21.549	27.975	18.502	11.241	24.300	13.472	12.226	12.568

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Table 123

OVARC1001202	122.810	79.160	74.976	45.179	34.305	57.752	54.521	52.075
OVARC1001206	42.615	25.397	25.932	13.326	28.104	29.089	32.918	22.690
OVARC1001209	72.876	58.366	36.700	24.151	40.859	38.440	59.191	47.601
OVARC1001219	33.632	13.311	13.625	12.687	15.459	16.636	29.651	23.801
OVARC1001222	32.786	21.648	10.686	9.886	10.225	25.581	20.058	17.564
OVARC1001232	117.540	87.613	50.146	34.554	30.246	57.933	49.208	37.950
OVARC1001240	75.374	60.625	38.831	32.204	26.238	32.631	20.938	29.225
OVARC1001243	9.543	16.485	6.223	5.619	1.978	7.592	11.212	9.204
OVARC1001244	169.003	111.321	69.720	46.121	39.223	93.281	105.487	89.348
OVARC1001245	102.652	232.219	202.228	159.295	307.379	168.939	66.384	180.606
OVARC1001247	51.814	49.398	25.400	17.972	24.516	29.579	38.406	32.633
OVARC1001260	53.551	100.419	29.364	25.020	34.864	30.489	28.556	34.131
OVARC1001261	48.536	42.267	28.153	13.070	26.118	36.641	37.660	22.612
OVARC1001268	51.904	118.717	47.463	24.361	63.661	38.492	51.108	43.123
OVARC1001270	20.955	18.655	11.209	10.629	7.297	10.404	10.615	9.730
OVARC1001271	82.087	105.253	59.789	67.369	40.952	49.040	49.902	56.550
OVARC1001282	2.151	7.862	2.074	5.144	2.146	4.070	1.658	4.939
OVARC1001296	11.865	15.267	7.897	10.844	6.153	11.518	15.515	10.296
OVARC1001306	25.532	50.725	28.628	24.049	17.847	22.716	24.404	32.492
OVARC1001314	12.995	19.789	11.346	14.481	11.454	16.041	17.642	15.122
OVARC1001316	14.093	43.453	9.049	9.287	10.402	12.676	9.571	8.634
OVARC1001329	236.298	224.291	230.056	140.553	147.173	134.506	88.940	124.623
OVARC1001330	34.063	30.737	21.299	12.416	9.409	18.781	21.774	14.306
OVARC1001336	64.433	86.449	37.979	30.312	22.554	34.649	46.151	36.127
OVARC1001338	29.434	27.732	16.123	16.132	16.945	20.146	25.217	26.946
OVARC1001339	32.829	42.256	31.603	10.158	27.332	21.573	35.452	25.220
OVARC1001340	27.630	18.361	12.822	7.427	6.739	12.500	23.923	14.457
OVARC1001341	95.252	81.979	52.630	68.282	53.071	55.813	59.589	60.054
OVARC1001342	100.966	252.091	51.417	202.538	60.427	87.325	80.221	137.940
OVARC1001344	103.513	107.791	75.126	75.888	55.791	47.394	56.015	68.157
OVARC1001357	10.771	20.444	6.064	5.959	2.545	8.202	6.654	9.212
OVARC1001359	74.406	41.612	39.409	39.521	22.602	47.817	49.919	41.248
OVARC1001360	12.963	15.729	5.865	8.162	5.343	8.344	7.449	5.231
OVARC1001369	30.741	30.024	17.593	14.376	15.376	19.395	28.970	17.236
OVARC1001372	47.372	31.878	28.420	22.363	23.533	27.224	35.738	26.351
OVARC1001376	65.628	113.295	43.890	78.146	52.979	38.758	43.990	55.762
OVARC1001381	115.063	118.072	70.088	92.127	69.013	60.845	53.880	62.779
OVARC1001391	39.498	37.024	30.883	12.771	21.036	26.802	26.851	18.964
OVARC1001392	17.841	35.639	29.498	12.487	18.354	13.407	13.843	15.944
OVARC1001399	43.831	87.706	37.282	44.533	34.853	26.357	28.943	38.749
OVARC1001417	26.403	24.005	20.041	15.997	12.488	15.218	23.379	13.202
OVARC1001419	102.361	46.760	47.763	31.720	43.416	60.531	66.782	40.700
OVARC1001425	36.511	32.857	19.181	27.837	18.684	27.353	39.805	22.560
OVARC1001436	56.321	33.132	21.728	19.600	24.952	23.512	43.382	21.101
OVARC1001442	85.715	36.595	24.645	21.266	30.507	37.805	58.999	27.499
OVARC1001451	34.303	30.697	30.804	34.477	24.521	23.798	19.177	24.423
OVARC1001452	53.317	30.445	17.186	12.444	18.765	27.539	29.572	22.163
OVARC1001453	16.620	33.383	8.673	8.363	7.911	7.294	15.113	10.726
OVARC1001476	23.408	34.646	23.709	17.349	17.688	17.078	15.241	27.167
OVARC1001486	69.410	32.323	28.385	21.037	14.968	36.453	52.487	28.092
OVARC1001489	10.998	9.249	5.028	7.129	6.338	4.046	10.274	9.908
OVARC1001493	55.166	55.346	14.849	9.601	15.915	27.767	38.065	22.112
OVARC1001496	85.220	65.108	29.250	24.050	41.730	36.194	61.219	38.523
OVARC1001499	27.560	27.910	16.669	16.239	20.204	20.989	35.173	22.472
OVARC1001508	67.326	60.488	43.800	30.337	35.006	34.184	46.403	31.327
OVARC1001509	45.793	56.347	29.884	32.079	26.485	23.100	23.398	18.605
OVARC1001510	14.065	17.712	12.458	11.811	11.932	6.535	17.532	9.275
OVARC1001516	64.781	44.167	26.084	28.410	30.019	33.509	55.926	34.068
OVARC1001525	8.675	10.658	6.559	6.011	4.611	3.863	6.484	5.884
OVARC1001542	34.447	36.452	18.588	20.569	17.086	20.034	32.156	28.167
OVARC1001544	97.739	98.662	46.751	55.837	47.415	35.307	53.917	51.833
OVARC1001546	40.692	24.215	14.449	9.924	10.317	17.393	21.638	34.075
OVARC1001547	4.108	6.476	2.931	4.799	7.154	5.168	4.549	5.293
OVARC1001555	48.644	45.769	33.072	18.823	21.553	30.921	53.633	33.664

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Table 124

OVARC1001560	9.995	11.616	22.248	5.899	8.179	16.185	10.151	7.957
OVARC1001569	40.746	31.448	15.414	17.742	13.831	32.806	32.162	24.321
OVARC1001570	45.828	32.466	28.804	16.797	17.223	29.282	50.455	32.827
OVARC1001577	18.703	19.196	13.453	17.108	9.651	14.718	23.685	24.544
OVARC1001578	4.894	1.347	3.487	1.668	2.647	3.022	0.000	0.000
OVARC1001596	84.296	49.737	31.737	18.041	23.005	61.151	47.274	34.947
OVARC1001600	54.416	43.232	24.561	22.726	16.594	23.734	27.443	19.377
OVARC1001607	21.077	19.469	15.218	12.687	5.720	14.273	22.223	16.907
OVARC1001610	22.320	13.445	7.606	4.839	6.723	8.590	14.535	14.413
OVARC1001611	10.788	15.290	11.190	3.816	6.271	10.248	18.405	10.394
OVARC1001615	83.171	33.856	33.256	23.489	27.385	39.578	60.842	26.422
OVARC1001636	19.126	18.265	9.929	10.903	5.896	14.319	20.083	11.921
OVARC1001668	184.639	178.409	101.057	130.922	77.578	71.883	78.800	99.902
OVARC1001702	74.853	43.682	37.735	17.471	24.833	47.858	40.347	30.531
OVARC1001703	20.271	16.866	19.593	10.314	12.106	14.193	17.305	11.237
OVARC1001710	104.705	53.627	46.081	22.841	30.909	61.922	57.754	30.671
OVARC1001711	38.919	48.731	30.797	20.615	17.927	29.742	29.051	30.493
OVARC1001713	58.871	50.075	38.715	24.728	28.026	37.714	59.338	46.137
OVARC1001725	12.462	6.462	9.161	5.766	5.579	7.643	12.283	11.952
OVARC1001726	60.846	30.421	22.951	16.102	17.141	25.341	40.000	23.764
OVARC1001727	12.749	6.695	1.629	3.384	2.943	5.347	11.864	5.882
OVARC1001731	417.237	296.389	159.879	90.412	79.927	104.739	112.601	182.645
OVARC1001735	29.333	21.981	13.004	10.850	7.779	19.246	25.926	9.776
OVARC1001741	62.439	80.254	36.924	40.754	30.175	31.693	40.353	35.965
OVARC1001745	105.943	90.392	54.073	48.385	29.915	42.496	52.805	40.912
OVARC1001759	6.344	6.101	7.549	5.672	5.285	7.629	4.284	16.699
OVARC1001762	15.752	20.242	8.966	13.129	12.132	11.198	17.879	12.812
OVARC1001766	50.421	44.814	32.524	34.416	32.044	28.483	26.974	25.134
OVARC1001767	12.694	11.424	7.232	4.392	4.561	7.783	6.753	3.775
OVARC1001768	30.851	32.866	18.111	12.623	14.716	15.800	18.499	17.641
OVARC1001770	99.967	29.814	24.915	16.646	18.553	49.766	33.065	24.957
OVARC1001776	84.733	66.614	35.351	18.038	20.855	40.357	40.259	38.765
OVARC1001791	82.228	59.107	38.878	27.000	19.647	41.210	58.352	34.508
OVARC1001795	35.170	31.032	19.091	14.053	19.096	16.818	23.677	24.540
OVARC1001798	113.936	95.099	73.266	84.613	71.384	61.440	58.197	68.677
OVARC1001802	125.877	98.941	72.747	75.225	59.196	77.683	67.227	71.441
OVARC1001805	10.464	10.835	12.686	8.980	8.339	13.601	7.696	8.902
OVARC1001807	135.513	172.138	42.410	25.456	42.245	77.908	59.683	39.476
OVARC1001809	118.235	105.836	62.430	46.885	49.795	56.085	64.919	59.018
OVARC1001812	67.287	48.010	53.706	41.376	36.383	38.322	38.347	31.540
OVARC1001813	69.943	84.621	53.953	56.458	42.844	41.002	32.364	36.514
OVARC1001820	52.381	53.833	35.503	41.319	24.742	28.840	25.646	28.845
OVARC1001828	8.200	10.217	4.364	9.812	6.280	8.885	6.886	8.407
OVARC1001833	86.833	60.894	37.693	22.705	29.730	50.489	52.516	40.092
OVARC1001839	39.140	38.162	14.245	19.805	17.227	23.521	26.722	22.628
OVARC1001846	14.794	24.500	15.503	10.407	8.977	15.603	9.900	14.219
OVARC1001849	73.011	60.883	43.536	39.792	33.900	30.397	28.153	30.952
OVARC1001861	63.938	43.449	26.931	16.558	17.111	24.800	36.196	21.959
OVARC1001873	37.219	38.842	19.844	22.293	20.314	24.148	34.160	26.819
OVARC1001879	76.088	51.361	39.655	29.363	28.800	45.644	47.894	29.618
OVARC1001880	135.860	84.254	58.296	66.680	55.691	73.306	83.823	57.413
OVARC1001883	81.852	74.425	52.983	53.494	55.481	39.665	45.082	50.587
OVARC1001900	55.149	42.744	20.659	17.501	28.891	25.216	36.722	27.567
OVARC1001901	35.402	43.250	19.139	18.068	14.966	16.860	28.327	21.865
OVARC1001911	26.676	31.540	16.048	15.000	9.189	16.480	16.595	14.072
OVARC1001916	57.008	57.583	30.437	33.497	24.346	38.467	49.017	28.751
OVARC1001928	11.760	11.451	9.871	8.924	3.218	9.310	7.928	8.861
OVARC1001937	41.094	331.797	26.182	31.807	18.612	29.201	28.632	31.167
OVARC1001940	31.671	25.633	19.059	18.927	15.166	24.914	25.701	31.361
OVARC1001942	30.967	37.334	26.741	17.951	21.439	17.640	29.921	25.107
OVARC1001943	85.434	52.979	27.869	23.583	35.086	45.562	49.703	36.562
OVARC1001949	27.732	45.197	29.233	33.177	22.996	24.826	26.681	54.991
OVARC1001950	114.630	90.867	57.193	51.930	43.996	70.058	71.925	46.593
OVARC1001952	140.095	114.529	76.000	76.812	57.544	76.600	127.024	117.497

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Table 125

OVARC1001954	38.148	34.154	24.826	18.570	18.070	29.136	28.466	23.093
OVARC1001963	70.685	73.510	38.247	43.880	39.594	41.763	47.995	42.856
OVARC1001983	103.819	85.974	83.133	104.971	53.259	65.630	60.001	74.940
OVARC1001987	55.904	47.294	16.298	23.921	28.833	28.724	72.176	33.793
OVARC1001989	126.786	123.408	98.472	101.800	109.717	72.479	80.807	76.628
OVARC1001991	106.789	61.566	52.852	26.772	46.555	61.290	57.420	50.807
OVARC1002005	43.909	50.446	52.235	34.217	36.792	22.115	37.361	38.275
OVARC1002044	68.989	92.088	47.242	60.982	37.959	40.246	32.518	39.591
OVARC1002046	142.697	103.646	61.978	48.709	50.959	89.078	107.957	65.922
OVARC1002050	150.418	79.832	52.259	30.717	50.113	74.307	95.763	52.005
OVARC1002058	31.725	28.126	16.056	14.204	10.314	24.705	25.418	21.662
OVARC1002066	22.845	30.065	5.783	10.572	14.029	17.339	17.127	29.452
OVARC1002082	142.891	132.300	69.068	83.947	73.662	57.050	101.160	85.803
OVARC1002091	49.223	46.691	28.357	26.618	29.431	30.906	42.116	35.122
OVARC1002092	16.502	13.069	11.455	8.986	10.442	10.939	11.841	11.658
OVARC1002093	206.510	229.583	94.978	52.679	65.398	105.804	108.886	66.303
OVARC1002094	57.983	70.842	22.175	21.837	26.392	25.855	44.104	28.562
OVARC1002107	81.163	81.383	51.719	88.540	57.860	40.826	46.289	44.621
OVARC1002112	71.336	80.431	40.320	85.579	47.248	39.907	60.603	67.156
OVARC1002126	114.239	87.851	47.175	35.010	40.692	63.760	106.294	65.520
OVARC1002127	55.311	43.006	22.728	10.831	21.021	26.217	51.525	32.857
OVARC1002138	8.951	13.827	3.935	7.856	8.359	7.853	10.350	10.188
OVARC1002143	46.546	34.713	16.666	15.769	19.276	24.331	31.142	20.410
OVARC1002156	12.544	23.040	10.035	15.363	8.291	12.374	13.614	15.810
OVARC1002158	56.221	28.255	18.260	10.748	16.251	20.791	31.215	19.064
OVARC1002165	101.989	143.172	84.011	82.086	75.946	58.837	85.203	75.063
OVARC1002175	207.395	83.881	84.413	54.135	104.278	114.458	134.235	69.297
OVARC1002178	17.313	27.443	12.750	10.705	15.530	12.936	23.362	17.872
OVARC1002182	40.283	37.762	18.779	11.770	18.311	21.416	34.402	24.309
OVARC1002185	36.278	33.563	17.925	17.394	20.095	28.241	45.498	31.989
PLACE1000004	41.829	37.799	18.473	16.218	12.661	20.372	25.010	22.000
PLACE1000005	33.315	36.712	26.079	24.859	17.404	25.038	28.162	24.028
PLACE1000008	48.081	38.647	24.284	19.081	18.255	32.116	54.951	30.255
PLACE1000007	24.221	25.983	17.339	11.998	16.921	17.706	46.581	21.338
PLACE1000014	57.292	49.432	36.234	32.812	25.276	24.815	35.655	32.759
PLACE1000031	42.309	61.878	50.107	46.094	37.373	29.757	38.437	47.194
PLACE1000033	7.856	22.257	8.411	7.606	9.169	11.609	12.768	10.286
PLACE1000040	36.717	30.479	20.358	21.457	23.948	12.296	22.459	20.099
PLACE1000048	32.105	28.302	21.619	18.209	13.458	16.364	16.026	12.244
PLACE1000050	33.955	41.358	21.915	18.172	15.208	24.691	30.515	22.038
PLACE1000061	159.492	228.723	82.722	177.569	132.119	143.553	116.181	188.103
PLACE1000066	59.266	55.710	42.829	38.851	46.700	47.171	50.185	56.938
PLACE1000075	15.690	15.994	12.949	6.500	11.914	10.574	6.929	11.391
PLACE1000078	46.952	57.637	52.225	42.480	22.126	28.527	38.463	41.033
PLACE1000081	75.884	63.282	38.644	23.924	29.174	30.920	50.546	41.886
PLACE1000086	85.184	67.162	52.586	27.421	38.070	64.488	55.431	42.640
PLACE1000094	49.828	42.276	20.226	10.189	9.355	21.041	19.625	8.506
PLACE1000101	10.188	23.449	16.699	19.362	17.073	11.091	13.623	19.675
PLACE1000121	56.678	34.412	30.070	13.506	19.044	31.104	40.290	25.078
PLACE1000133	39.057	29.915	23.128	29.843	20.718	24.672	26.803	39.107
PLACE1000142	59.811	47.628	31.984	14.740	21.065	43.454	61.693	35.205
PLACE1000146	68.834	62.270	34.321	47.131	27.243	17.729	39.001	47.833
PLACE1000163	102.015	87.206	45.923	38.164	45.943	62.968	120.625	52.326
PLACE1000172	9.508	23.847	6.470	9.595	10.491	12.594	4.745	20.625
PLACE1000181	51.412	36.469	31.628	23.060	30.850	23.966	21.392	24.437
PLACE1000184	16.961	3.226	6.684	2.195	8.764	24.786	5.246	4.794
PLACE1000185	62.981	45.178	41.261	26.145	25.092	35.082	37.231	52.199
PLACE1000198	34.090	28.795	19.770	10.196	14.083	15.181	22.504	21.227
PLACE1000213	29.427	38.826	20.161	17.037	20.362	61.122	55.368	17.891
PLACE1000214	8.728	14.768	9.733	11.456	12.426	6.184	8.011	2.408
PLACE1000220	35.035	36.902	22.387	16.421	20.597	25.167	26.274	20.792
PLACE1000231	348.135	182.545	114.755	86.687	95.201	164.292	106.589	98.294
PLACE1000236	79.604	63.001	31.919	29.088	25.550	32.712	26.593	31.426
PLACE1000245	86.867	78.966	48.398	55.441	30.699	45.854	59.148	58.356

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Table 126

PLACE1000246	63.620	60.061	23.370	26.968	16.702	28.102	27.116	50.991
PLACE1000258	107.386	86.542	60.892	92.906	67.210	62.207	74.824	84.168
PLACE1000288	61.904	530.859	32.390	151.291	33.764	52.872	47.184	566.824
PLACE1000292	134.374	107.978	64.652	76.783	64.315	53.082	46.786	64.840
PLACE1000302	36.212	31.351	48.891	8.192	73.167	20.044	16.870	23.303
PLACE1000304	77.695	50.861	24.615	19.705	21.314	32.791	44.370	34.969
PLACE1000308	13.844	18.591	10.915	15.228	13.497	11.170	8.490	10.525
PLACE1000309	171.086	79.282	53.477	30.661	44.221	99.582	89.605	51.438
PLACE1000312	25.013	29.701	14.081	15.125	7.699	11.121	12.364	24.742
PLACE1000330	29.657	13.102	12.306	10.127	9.659	16.951	19.395	12.431
PLACE1000332	13.294	6.752	7.366	6.938	4.823	5.141	7.821	8.302
PLACE1000347	46.531	37.378	19.406	17.234	19.477	19.786	29.460	24.427
PLACE1000351	93.299	56.437	40.461	27.466	26.428	44.784	56.685	47.749
PLACE1000374	89.871	66.668	53.557	66.616	45.909	45.689	49.979	76.296
PLACE1000380	22.012	21.037	15.351	9.985	12.229	7.428	19.713	17.050
PLACE1000383	29.005	24.752	16.349	15.183	11.959	16.827	29.293	19.713
PLACE1000397	35.368	26.208	19.042	6.636	9.008	19.143	19.667	12.826
PLACE1000401	121.012	77.115	91.986	73.017	85.204	77.263	97.740	89.014
PLACE1000406	43.944	37.883	20.305	20.530	17.412	26.601	31.601	28.177
PLACE1000412	14.283	24.094	8.322	10.240	8.659	9.837	13.298	15.409
PLACE1000420	95.364	99.949	57.598	50.129	39.257	39.215	34.611	48.196
PLACE1000421	59.754	60.388	52.953	37.350	31.433	40.619	40.095	47.679
PLACE1000423	49.130	51.837	22.800	9.952	21.218	55.558	49.895	90.332
PLACE1000424	57.584	46.928	23.243	25.445	11.122	23.277	21.409	24.420
PLACE1000430	9.008	14.497	9.324	6.648	12.506	3.176	4.529	9.751
PLACE1000433	61.817	33.422	22.755	10.220	12.877	30.460	38.040	20.834
PLACE1000435	58.251	49.033	24.534	33.925	25.131	18.878	26.453	33.894
PLACE1000437	37.691	42.505	19.354	13.578	22.936	27.017	52.788	24.766
PLACE1000442	28.959	53.891	36.443	45.883	36.218	29.092	28.915	59.563
PLACE1000444	222.629	268.192	164.724	178.057	143.884	113.247	125.051	157.345
PLACE1000453	60.912	56.717	45.737	28.913	34.374	46.491	47.877	46.094
PLACE1000466	59.850	55.649	26.148	10.788	16.900	32.811	31.014	25.102
PLACE1000485	63.781	32.184	28.609	22.813	15.851	25.834	76.172	29.680
PLACE1000481	117.442	55.048	43.008	40.607	39.135	57.771	62.403	44.241
PLACE1000492	85.199	42.804	28.200	13.820	16.493	35.818	62.470	37.299
PLACE1000508	48.116	30.697	17.662	19.193	14.645	26.367	39.846	23.454
PLACE1000512	23.066	37.331	52.438	15.899	43.633	17.392	16.605	25.441
PLACE1000540	6.354	22.237	6.827	9.533	6.338	8.582	5.690	8.570
PLACE1000541	139.592	95.891	62.856	44.350	48.779	102.808	118.737	83.454
PLACE1000546	24.434	15.843	9.813	13.003	8.921	13.653	21.807	14.697
PLACE1000547	138.587	72.254	64.656	57.672	49.694	71.928	84.849	56.997
PLACE1000560	39.727	25.726	19.961	10.708	14.907	22.472	42.419	29.563
PLACE1000562	74.380	77.139	35.608	44.686	31.444	29.868	26.773	50.026
PLACE1000564	45.712	39.050	20.165	14.663	19.526	22.670	43.140	35.028
PLACE1000583	122.345	132.820	73.526	90.516	75.343	62.557	52.925	95.075
PLACE1000587	99.842	63.364	42.075	55.988	38.170	36.599	30.062	36.245
PLACE1000588	86.166	135.917	34.894	41.374	26.506	42.479	60.642	72.805
PLACE1000598	49.265	55.996	23.832	26.469	29.318	57.681	28.073	35.812
PLACE1000599	79.259	72.325	37.975	49.064	36.704	32.501	40.446	38.539
PLACE1000605	46.938	54.185	20.654	19.011	15.275	25.549	73.210	37.742
PLACE1000610	45.555	31.108	16.017	11.318	13.984	22.493	36.775	27.839
PLACE1000611	83.806	72.237	34.984	19.496	31.956	36.823	73.743	37.315
PLACE1000626	25.444	20.294	26.796	13.307	42.252	20.623	23.163	24.644
PLACE1000633	51.819	72.312	34.517	36.919	35.957	28.726	32.601	40.217
PLACE1000636	19.979	28.179	10.228	15.590	13.380	12.707	24.141	13.996
PLACE1000653	19.174	29.774	9.902	11.497	12.647	8.885	20.791	11.318
PLACE1000656	207.889	68.319	57.763	33.548	59.611	78.748	110.176	49.086
PLACE1000663	27.908	22.175	79.442	9.906	106.232	14.462	23.389	15.120
PLACE1000706	283.571	94.948	65.754	40.790	70.486	112.748	210.569	73.830
PLACE1000712	61.631	49.744	23.617	15.665	21.178	14.931	57.877	39.148
PLACE1000716	26.011	26.336	15.816	9.969	11.091	19.128	22.664	15.949
PLACE1000740	34.490	32.481	19.323	13.899	13.528	23.824	29.403	19.851
PLACE1000748	8.182	18.702	8.763	10.496	2.952	8.739	11.227	11.219
PLACE1000749	246.155	158.647	101.055	70.317	70.301	173.879	198.491	125.375

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Table 127

PLACE1000751	8.591	28.632	6.888	6.628	8.859	7.678	7.926	11.115
PLACE1000755	22.080	22.789	11.946	14.166	9.125	11.761	20.466	14.904
PLACE1000769	16.024	19.119	15.504	12.207	5.547	12.731	21.034	18.074
PLACE1000778	109.940	168.867	46.116	36.217	54.573	33.450	40.021	61.410
PLACE1000785	54.501	35.590	19.231	21.344	11.939	17.233	19.818	30.628
PLACE1000786	63.401	34.818	26.260	25.783	21.236	33.236	29.738	24.419
PLACE1000793	48.092	49.470	31.204	14.276	17.894	36.450	38.082	31.337
PLACE1000795	38.178	43.688	29.889	21.674	10.765	21.955	41.921	41.550
PLACE1000798	31.236	40.770	22.606	25.191	17.921	17.856	21.782	21.758
PLACE1000812	24.169	23.549	17.121	14.965	8.140	11.726	13.094	25.608
PLACE1000823	81.457	78.801	40.416	88.702	37.795	36.623	32.882	44.655
PLACE1000825	72.220	107.715	51.491	134.346	31.956	47.353	61.449	155.007
PLACE1000838	44.642	81.659	25.304	15.146	16.808	62.951	59.936	33.016
PLACE1000841	19.731	9.168	3.325	14.206	7.817	19.073	12.783	10.985
PLACE1000843	23.326	27.970	19.816	10.746	10.401	15.372	21.004	17.198
PLACE1000849	171.333	62.539	65.353	38.857	44.284	93.732	118.022	61.526
PLACE1000856	36.302	20.267	19.938	11.857	16.559	18.275	24.314	14.524
PLACE1000863	61.947	24.729	17.318	10.548	32.356	45.071	40.695	26.491
PLACE1000876	79.589	41.303	31.803	27.682	30.566	41.161	58.457	35.801
PLACE1000899	36.028	54.514	19.200	14.563	23.816	17.191	23.052	18.916
PLACE1000907	34.468	58.737	45.762	53.355	33.953	45.837	23.987	112.516
PLACE1000909	17.260	18.289	7.853	7.770	4.100	9.541	11.860	5.411
PLACE1000912	72.300	41.738	29.873	18.579	21.304	47.829	47.423	31.816
PLACE1000914	34.274	20.778	16.170	8.631	12.137	13.771	20.247	22.212
PLACE1000918	6.646	24.953	6.298	21.039	6.076	8.001	14.538	7.614
PLACE1000927	28.004	62.278	11.519	25.240	15.288	27.303	24.639	36.302
PLACE1000931	60.013	70.374	41.114	48.090	31.983	37.593	35.750	38.045
PLACE1000944	15.469	20.100	11.329	9.583	11.301	10.496	10.907	13.479
PLACE1000948	32.119	174.384	19.147	11.561	8.864	13.716	16.344	23.012
PLACE1000958	24.559	28.912	20.683	12.101	15.980	17.758	18.551	16.227
PLACE1000972	120.934	92.640	56.098	49.344	42.043	64.933	66.648	83.486
PLACE1000977	5.160	23.071	5.930	7.450	7.265	6.795	7.348	13.664
PLACE1000979	36.518	36.872	31.314	43.863	34.967	34.693	38.011	58.543
PLACE1000986	39.462	32.248	17.759	9.962	10.922	17.210	20.134	11.670
PLACE1000987	85.543	56.030	33.710	26.097	53.247	35.833	43.907	42.264
PLACE1001000	15.969	18.182	11.199	15.991	10.697	10.336	15.117	15.657
PLACE1001007	41.857	48.683	23.082	21.556	18.037	24.959	24.887	38.857
PLACE1001010	29.468	27.943	26.350	21.964	14.359	16.726	17.763	18.489
PLACE1001015	20.540	30.643	18.387	20.211	7.569	13.946	8.904	23.581
PLACE1001016	77.787	62.441	29.862	30.282	22.094	36.963	57.898	62.858
PLACE1001022	33.101	30.827	19.383	11.100	14.872	22.156	23.755	20.499
PLACE1001024	86.274	27.421	25.662	12.087	19.171	38.266	41.922	20.735
PLACE1001036	80.642	165.022	64.983	46.681	67.747	121.474	402.289	252.956
PLACE1001038	452.345	139.825	89.101	67.372	64.392	122.656	119.479	107.665
PLACE1001048	49.948	49.581	16.660	14.592	10.687	24.644	36.889	36.435
PLACE1001054	134.306	67.365	61.474	36.835	33.520	69.944	111.570	67.974
PLACE1001062	74.158	88.783	52.589	64.589	49.941	41.816	51.497	54.685
PLACE1001063	10.880	13.653	8.862	9.859	6.427	6.510	8.010	9.447
PLACE1001078	14.575	15.670	12.223	5.950	12.881	9.910	15.204	12.067
PLACE1001081	12.530	13.285	8.314	5.016	4.852	19.472	31.441	10.426
PLACE1001088	25.759	16.332	10.811	9.362	11.628	15.207	22.359	14.210
PLACE1001092	15.938	44.121	18.940	15.854	15.358	18.646	27.718	25.006
PLACE1001098	51.863	74.664	44.477	36.802	35.002	36.534	40.789	44.072
PLACE1001100	69.984	61.458	42.513	37.432	21.199	38.215	39.752	36.621
PLACE1001104	37.879	43.589	22.459	19.257	15.200	22.158	23.976	24.947
PLACE1001114	50.995	43.129	28.583	41.340	23.689	22.370	24.583	26.608
PLACE1001118	55.858	39.536	30.416	29.284	13.566	35.583	35.042	61.564
PLACE1001123	30.236	32.692	12.932	16.066	9.901	19.213	20.910	28.778
PLACE1001136	127.205	106.279	47.874	46.520	45.126	54.639	67.043	60.071
PLACE1001144	59.577	74.773	33.377	21.823	38.443	32.412	40.190	39.315
PLACE1001147	59.813	42.869	27.085	20.092	30.181	39.398	45.339	34.463
PLACE1001148	37.059	29.368	18.220	13.240	14.014	19.609	42.976	28.919
PLACE1001159	23.780	18.761	10.274	9.929	12.302	17.285	19.282	17.753
PLACE1001168	26.768	24.323	12.289	8.468	8.558	14.711	22.168	20.921

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Table 128

PLACE1001171	37.609	26.312	19.416	9.788	11.645	20.994	34.674	26.387
PLACE1001183	48.472	34.255	16.988	12.402	13.998	24.043	41.590	34.736
PLACE1001185	98.156	72.026	33.520	17.455	34.874	41.246	78.451	45.433
PLACE1001201	20.710	28.202	14.832	19.137	16.156	11.504	21.093	18.878
PLACE1001229	33.202	50.727	25.432	24.039	19.810	29.842	30.368	33.000
PLACE1001231	28.893	32.022	21.470	16.244	15.489	23.482	30.611	22.184
PLACE1001238	67.072	60.114	37.423	43.278	30.120	34.706	41.011	38.313
PLACE1001241	21.610	25.407	7.984	17.578	8.443	14.781	31.035	14.575
PLACE1001242	45.592	69.441	28.266	26.878	24.774	29.386	68.093	55.636
PLACE1001247	14.525	18.387	7.186	6.906	8.128	9.488	6.808	15.989
PLACE1001250	49.114	30.049	15.521	12.388	20.092	23.448	40.190	18.900
PLACE1001257	62.294	83.027	38.705	44.550	45.672	38.236	37.267	51.354
PLACE1001272	63.255	35.776	22.716	18.567	23.479	28.934	54.496	33.742
PLACE1001279	20.477	21.478	8.935	8.448	12.817	12.013	16.223	11.151
PLACE1001280	68.512	56.354	46.699	32.609	50.557	37.478	30.514	34.496
PLACE1001294	16.622	36.699	12.414	23.498	22.103	14.441	14.208	23.363
PLACE1001295	158.866	63.791	43.310	26.850	56.659	72.706	110.093	39.852
PLACE1001300	64.491	33.466	14.714	9.167	18.136	13.210	28.528	23.798
PLACE1001304	70.999	60.035	54.352	72.569	49.765	40.745	55.843	97.914
PLACE1001311	77.711	67.514	37.479	36.657	50.824	35.191	38.273	47.028
PLACE1001323	85.671	92.960	47.002	40.309	44.877	41.038	46.429	45.578
PLACE1001325	63.854	83.048	40.238	34.763	38.177	31.146	36.745	54.898
PLACE1001340	50.316	43.105	32.357	18.188	41.779	27.080	44.703	34.275
PLACE1001344	21.096	20.141	12.901	11.211	11.242	13.229	17.699	15.374
PLACE1001351	21.665	30.334	17.172	16.561	21.087	13.674	23.521	25.699
PLACE1001366	51.121	41.493	20.763	22.794	22.644	20.945	39.950	30.512
PLACE1001377	17.643	7.950	8.199	6.636	10.878	8.266	14.816	8.211
PLACE1001383	19.371	31.320	12.152	16.238	10.327	18.369	19.779	20.881
PLACE1001384	12.523	28.763	17.012	8.145	10.197	11.093	21.749	13.042
PLACE1001387	74.695	38.816	24.690	18.993	17.630	44.878	42.628	24.984
PLACE1001396	16.685	20.986	21.294	11.232	11.885	13.388	11.627	17.398
PLACE1001399	226.500	168.857	120.411	105.668	74.590	106.559	109.855	113.693
PLACE1001401	7.198	22.276	6.559	8.709	5.336	6.428	17.374	13.590
PLACE1001407	36.871	35.435	20.290	26.813	14.205	17.551	44.441	18.269
PLACE1001412	37.695	27.537	14.076	15.165	12.728	15.789	38.368	22.732
PLACE1001414	217.145	130.533	105.385	81.994	74.062	115.387	103.177	72.729
PLACE1001416	35.223	39.103	34.029	25.498	14.222	24.743	21.597	25.005
PLACE1001433	145.429	164.813	104.366	153.159	55.364	82.221	118.995	143.644
PLACE1001440	58.228	39.255	26.807	18.655	18.643	29.783	43.995	27.882
PLACE1001456	45.774	64.005	62.545	47.264	46.872	43.771	53.047	50.036
PLACE1001464	14.904	12.569	12.016	7.606	7.643	10.634	21.002	14.923
PLACE1001468	12.628	13.185	11.183	8.049	10.407	10.393	17.688	12.134
PLACE1001484	111.986	88.704	61.951	103.045	57.131	47.838	72.549	64.633
PLACE1001500	112.534	66.487	40.149	29.195	31.131	66.175	52.403	47.197
PLACE1001502	111.530	51.123	42.187	21.773	27.041	52.421	55.175	32.016
PLACE1001503	104.144	79.570	47.845	42.970	37.990	50.872	57.729	52.788
PLACE1001505	20.479	27.535	13.492	15.526	12.841	22.000	19.770	21.944
PLACE1001513	30.859	24.448	21.001	14.991	10.141	18.450	24.882	26.311
PLACE1001516	133.217	89.711	99.042	58.879	78.064	73.719	71.012	63.994
PLACE1001517	69.164	42.110	28.024	23.097	19.564	24.584	39.431	31.706
PLACE1001523	44.322	26.222	15.440	33.292	16.685	26.064	28.195	35.152
PLACE1001526	12.214	48.804	32.938	18.497	27.271	29.631	19.107	33.278
PLACE1001534	14.278	14.916	17.792	13.675	17.033	22.739	18.831	18.893
PLACE1001536	25.937	21.827	14.716	13.316	8.319	14.594	19.891	10.823
PLACE1001545	81.173	118.411	60.729	57.604	60.102	55.719	62.273	73.495
PLACE1001551	29.258	24.058	15.777	17.582	14.381	14.773	23.849	25.399
PLACE1001564	12.683	21.942	10.266	7.274	6.981	12.704	27.781	11.258
PLACE1001570	10.554	41.593	5.601	19.923	9.421	18.406	16.691	18.288
PLACE1001571	127.122	86.608	38.342	58.413	34.598	53.965	49.652	34.301
PLACE1001595	116.778	213.788	32.313	32.498	34.618	50.204	34.174	37.047
PLACE1001602	23.415	17.913	9.921	11.848	9.736	11.310	8.437	13.830
PLACE1001603	49.559	59.889	39.368	29.795	29.035	28.595	39.306	37.052
PLACE1001608	26.740	49.685	21.856	26.287	32.997	19.418	12.572	39.795
PLACE1001610	103.785	116.714	78.094	80.451	74.242	57.490	65.946	70.900

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Table 129

PLACE1001611	58.972	40.610	21.168	17.897	20.458	26.980	37.282	29.415
PLACE1001629	23.692	21.349	10.779	11.703	9.654	17.389	16.943	17.712
PLACE1001632	56.162	39.917	28.058	32.960	30.608	36.189	37.819	50.929
PLACE1001634	18.018	22.871	12.492	5.629	10.744	11.917	13.604	13.552
PLACE1001637	61.890	34.286	23.149	18.271	16.901	31.188	43.749	17.679
PLACE1001640	80.631	63.007	32.766	49.291	29.961	30.898	32.648	42.726
PLACE1001655	29.386	40.949	10.818	14.407	12.505	8.704	14.876	16.268
PLACE1001672	34.615	40.370	24.145	16.896	19.193	20.408	30.495	28.727
PLACE1001678	10.323	5.349	4.889	7.928	5.142	5.752	4.884	4.020
PLACE1001683	99.245	101.853	51.020	46.928	31.257	45.917	57.578	71.255
PLACE1001691	55.061	48.826	32.495	70.656	37.287	27.851	24.285	45.922
PLACE1001692	50.688	45.778	29.336	31.751	20.230	23.603	23.387	30.475
PLACE1001705	54.991	45.920	32.949	30.739	23.884	24.736	21.290	26.568
PLACE1001716	19.961	39.584	17.983	14.122	11.592	15.645	26.052	30.073
PLACE1001720	45.804	36.576	23.337	13.159	14.367	26.395	38.216	23.892
PLACE1001728	25.294	12.023	10.018	4.500	6.969	13.369	17.313	10.651
PLACE1001729	54.474	30.538	23.378	14.206	12.538	34.643	36.119	24.025
PLACE1001739	72.181	46.505	32.326	17.618	26.461	46.354	57.211	33.755
PLACE1001740	44.321	37.300	20.706	23.395	18.627	20.277	22.849	29.188
PLACE1001745	88.492	59.243	42.077	24.655	33.811	52.589	78.154	41.999
PLACE1001746	34.637	42.251	39.371	25.196	29.098	20.925	24.039	30.103
PLACE1001748	68.976	42.569	32.885	20.301	21.057	36.582	50.459	30.910
PLACE1001753	49.985	45.870	23.560	22.075	3.690	25.936	41.529	38.920
PLACE1001756	58.884	78.676	32.148	72.106	23.706	32.912	52.816	82.360
PLACE1001761	80.396	70.047	114.350	98.694	126.278	53.735	66.182	112.998
PLACE1001767	101.474	95.179	45.516	33.144	52.766	54.932	101.273	76.611
PLACE1001771	19.712	26.759	20.057	12.622	18.385	16.780	19.880	23.194
PLACE1001775	4.588	40.521	8.311	6.556	7.390	9.035	9.683	17.408
PLACE1001777	61.261	31.312	29.820	13.022	17.840	32.541	34.897	21.794
PLACE1001781	16.525	17.889	7.311	9.028	3.652	9.892	13.994	12.461
PLACE1001783	82.003	24.962	30.707	19.043	16.757	38.137	43.807	19.485
PLACE1001786	24.406	20.572	9.992	12.368	9.648	12.063	27.946	22.791
PLACE1001788	39.981	29.419	23.164	10.091	15.084	30.627	38.055	36.556
PLACE1001795	36.820	39.618	20.098	14.057	16.433	21.056	32.809	26.943
PLACE1001799	128.712	38.515	26.836	13.466	28.718	51.074	76.434	36.462
PLACE1001810	14.418	17.039	10.361	10.109	9.092	9.695	10.813	10.585
PLACE1001817	30.913	22.601	33.584	11.211	34.814	38.481	19.140	20.248
PLACE1001821	44.377	41.515	23.006	22.091	25.640	19.095	24.750	27.083
PLACE1001836	51.521	27.558	20.807	7.935	23.084	27.957	36.704	21.625
PLACE1001844	29.459	29.744	21.870	21.220	18.464	14.961	23.954	18.459
PLACE1001845	33.946	36.421	18.233	14.133	19.354	20.298	32.062	33.894
PLACE1001858	36.762	28.558	15.393	27.399	23.094	20.179	32.496	27.946
PLACE1001869	41.811	29.631	16.671	13.297	14.417	29.644	49.283	21.491
PLACE1001890	21.015	19.216	7.813	9.785	8.947	7.055	22.588	20.287
PLACE1001897	41.587	43.503	18.203	17.788	18.625	34.484	37.521	38.175
PLACE1001902	33.879	86.444	26.521	77.375	23.800	40.850	29.474	82.496
PLACE1001904	42.359	28.323	18.415	13.316	15.185	24.027	48.664	25.843
PLACE1001907	99.999	94.157	52.221	54.031	60.482	55.231	87.790	65.770
PLACE1001910	76.138	126.370	33.663	25.331	33.103	39.045	66.245	37.978
PLACE1001912	72.652	96.989	43.604	44.098	51.566	44.297	53.061	61.895
PLACE1001918	59.029	60.982	33.789	30.466	29.328	46.949	78.822	51.365
PLACE1001920	9.437	24.354	8.429	22.027	10.009	15.594	8.844	29.435
PLACE1001928	20.462	35.914	14.995	17.670	10.114	16.420	22.437	22.775
PLACE1001930	16.268	28.124	18.470	13.279	15.554	13.919	22.090	19.274
PLACE1001949	23.830	22.587	13.269	10.049	11.377	14.909	26.537	9.643
PLACE1001959	40.952	30.344	15.913	13.328	24.661	21.015	37.170	18.763
PLACE1001965	12.458	20.205	14.372	15.468	10.543	9.561	13.870	16.621
PLACE1001974	21.533	45.767	37.839	18.194	36.382	18.154	19.101	21.180
PLACE1001981	37.122	27.300	20.961	8.701	16.875	15.523	25.093	21.729
PLACE1001983	84.898	45.469	30.920	16.864	17.046	41.287	52.042	28.458
PLACE1001989	47.501	59.400	30.952	30.644	23.359	33.328	33.521	32.148
PLACE1002004	96.924	138.468	70.255	74.069	44.965	61.641	60.598	60.144
PLACE1002008	67.655	101.031	63.838	57.207	53.740	50.343	63.192	74.655
PLACE1002015	48.810	48.095	25.042	26.422	28.835	36.724	35.174	29.389

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Table 130

PLACE1002044	15.432	19.617	12.298	7.674	10.740	14.882	16.986	23.255
PLACE1002046	35.129	24.586	16.894	16.958	15.796	25.488	45.998	25.557
PLACE1002052	13.131	11.184	10.040	6.082	7.542	10.153	10.668	10.355
PLACE1002066	77.695	109.726	92.490	79.876	58.443	57.230	64.889	69.207
PLACE1002072	97.971	90.711	48.605	48.732	39.945	44.244	40.362	47.906
PLACE1002073	48.101	39.394	30.681	27.085	15.219	30.451	35.202	22.863
PLACE1002080	147.011	90.983	77.089	67.438	53.419	83.047	71.583	70.087
PLACE1002081	6.752	13.958	11.761	8.303	6.211	11.142	11.382	8.460
PLACE1002090	19.854	27.734	20.058	14.085	36.381	18.780	21.857	42.680
PLACE1002095	60.336	45.829	29.642	33.247	26.663	24.615	34.539	41.411
PLACE1002102	164.050	58.094	40.254	32.448	30.279	73.576	158.991	75.372
PLACE1002109	45.221	57.996	53.572	43.855	38.839	41.641	47.534	53.651
PLACE1002115	9.512	11.954	8.778	7.248	4.013	7.023	5.912	6.295
PLACE1002119	36.430	58.455	53.047	27.115	43.709	26.254	23.542	33.029
PLACE1002140	48.179	44.018	31.256	17.883	20.743	30.803	35.802	31.498
PLACE1002150	14.549	14.324	13.952	8.635	12.089	7.434	7.940	13.111
PLACE1002153	99.975	52.998	35.156	18.899	19.864	38.034	40.428	32.754
PLACE1002157	55.938	35.819	25.050	31.682	30.081	23.109	34.931	28.217
PLACE1002163	57.219	47.664	19.449	22.757	26.545	33.066	43.744	29.963
PLACE1002168	30.977	46.777	30.115	44.322	21.088	30.717	33.746	25.283
PLACE1002170	68.838	22.754	23.239	11.296	13.008	21.765	31.640	17.540
PLACE1002171	23.819	23.126	16.254	25.334	9.191	13.358	14.604	12.880
PLACE1002180	18.621	18.513	11.924	11.799	15.091	9.384	14.450	16.442
PLACE1002184	11.237	16.438	6.314	6.973	5.890	7.372	15.552	5.123
PLACE1002200	41.279	32.645	19.848	12.160	14.612	26.495	24.978	18.652
PLACE1002205	8.060	8.833	8.840	5.678	9.502	7.453	5.919	5.027
PLACE1002213	132.823	94.631	54.268	62.752	37.757	66.436	72.589	61.367
PLACE1002219	28.945	25.808	12.888	18.583	11.494	15.981	15.553	12.757
PLACE1002227	82.051	55.700	42.058	32.436	34.199	39.449	33.444	40.762
PLACE1002253	58.857	21.589	23.552	8.315	9.457	21.335	22.438	14.348
PLACE1002256	11.668	27.097	12.608	15.320	10.327	9.326	7.247	18.657
PLACE1002259	12.944	16.713	14.115	16.119	13.177	10.814	8.343	7.436
PLACE1002285	12.935	14.107	10.661	5.670	8.397	8.906	13.661	8.898
PLACE1002301	40.882	61.873	38.880	19.138	39.970	34.344	28.064	32.685
PLACE1002310	16.971	21.006	23.836	10.651	24.965	17.853	17.328	20.350
PLACE1002311	32.060	30.946	17.177	14.219	10.905	20.580	20.767	19.139
PLACE1002319	21.289	17.105	17.384	12.607	9.953	15.052	12.933	13.930
PLACE1002329	41.607	28.970	16.757	13.513	9.723	19.282	28.768	18.428
PLACE1002333	10.233	17.705	5.802	5.259	5.108	7.829	11.050	8.546
PLACE1002342	48.414	46.073	26.203	18.031	31.808	29.119	31.805	35.900
PLACE1002343	38.774	31.024	21.839	9.918	13.209	21.177	28.826	23.746
PLACE1002355	37.547	27.979	16.049	8.792	11.795	19.972	18.057	19.576
PLACE1002358	48.964	52.954	25.597	17.560	25.248	26.885	39.078	44.650
PLACE1002359	70.702	60.072	41.768	24.857	27.424	38.617	51.234	48.247
PLACE1002374	119.415	70.407	40.003	52.366	27.254	71.202	86.975	59.999
PLACE1002376	76.607	80.189	66.224	38.374	30.440	43.752	57.781	47.015
PLACE1002379	46.960	37.677	24.324	15.686	8.747	27.687	38.031	38.157
PLACE1002386	34.135	56.039	21.956	15.130	13.263	40.392	20.988	18.948
PLACE1002395	50.771	34.342	21.705	12.792	17.447	30.904	41.999	26.921
PLACE1002398	26.369	26.554	11.941	11.546	12.821	16.487	21.773	21.163
PLACE1002407	24.383	13.800	14.460	6.932	17.857	10.390	8.160	9.349
PLACE1002433	48.909	60.537	30.096	33.352	22.856	24.152	49.419	48.535
PLACE1002437	41.702	30.287	21.358	10.885	8.866	22.078	29.556	17.959
PLACE1002438	13.555	11.187	8.617	6.781	2.684	9.005	7.945	7.896
PLACE1002446	21.605	27.628	11.792	11.569	10.494	11.830	17.464	16.893
PLACE1002447	35.206	16.567	12.839	7.714	16.646	21.325	23.151	14.505
PLACE1002450	7.279	19.248	9.887	11.951	10.923	5.788	16.070	16.657
PLACE1002462	28.126	22.054	9.073	8.084	9.639	12.889	28.071	18.658
PLACE1002465	50.708	38.829	28.583	22.053	22.627	24.578	37.561	35.602
PLACE1002474	42.838	48.831	28.190	20.034	25.208	37.936	39.355	29.560
PLACE1002477	68.476	88.049	43.373	49.594	28.828	30.662	33.024	45.912
PLACE1002493	20.932	15.425	14.743	9.609	5.982	13.112	18.554	13.289
PLACE1002497	62.857	26.623	15.819	9.997	10.197	19.095	23.320	14.788
PLACE1002499	25.484	35.975	17.658	12.207	20.785	19.603	26.553	24.711

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Table 131

PLACE1002500	61.430	52.592	20.851	20.792	20.608	26.596	35.837	25.000
PLACE1002514	57.950	34.821	25.761	14.063	20.170	29.748	38.465	28.873
PLACE1002518	33.229	41.213	15.047	27.600	25.421	15.108	39.619	19.093
PLACE1002529	20.589	17.020	8.550	4.795	6.064	5.232	8.483	8.689
PLACE1002532	228.966	81.188	71.766	41.993	49.408	124.500	121.100	70.493
PLACE1002536	54.940	104.532	50.236	37.932	32.704	37.719	49.674	44.065
PLACE1002537	50.443	35.983	26.347	14.124	16.394	28.846	22.586	18.551
PLACE1002539	43.269	40.064	22.458	15.887	20.345	19.917	47.789	34.032
PLACE1002547	56.046	40.874	34.045	20.245	32.445	28.657	42.402	32.824
PLACE1002571	22.915	18.915	20.884	11.040	19.304	18.369	20.827	18.977
PLACE1002578	110.554	134.909	53.782	65.675	56.576	47.716	58.650	75.950
PLACE1002583	10.726	15.813	12.765	12.655	12.171	11.770	8.242	11.466
PLACE1002591	30.958	26.809	17.781	9.878	19.760	16.773	24.345	16.337
PLACE1002598	14.446	16.092	4.386	12.890	11.213	8.112	5.827	10.365
PLACE1002604	31.921	44.779	19.490	23.538	18.247	17.300	19.554	24.344
PLACE1002612	55.401	62.901	26.650	24.921	30.069	38.235	60.295	44.841
PLACE1002625	23.240	23.910	6.945	6.719	8.340	13.804	18.338	-12.847
PLACE1002638	47.938	43.765	20.041	12.130	17.684	35.619	30.109	30.357
PLACE1002655	99.112	95.019	46.543	45.871	43.682	48.343	74.802	60.920
PLACE1002665	56.436	48.910	34.541	41.310	34.121	40.016	45.653	42.518
PLACE1002685	125.131	56.394	32.422	13.563	38.268	66.967	86.419	50.297
PLACE1002692	132.787	228.548	52.995	46.294	48.882	52.021	80.560	61.182
PLACE1002714	44.319	53.609	23.573	28.126	20.794	16.095	44.240	36.632
PLACE1002721	48.707	45.968	24.879	33.949	24.596	24.407	47.991	34.094
PLACE1002722	51.611	20.165	11.297	10.959	22.220	21.294	29.351	14.502
PLACE1002726	125.645	66.983	41.963	24.383	43.077	52.449	71.534	49.750
PLACE1002756	76.684	90.401	34.602	33.347	35.450	32.003	38.085	37.112
PLACE1002768	37.065	34.695	22.471	18.473	10.495	27.644	30.569	9.688
PLACE1002772	19.381	21.230	12.133	12.530	9.455	11.715	18.808	10.755
PLACE1002775	215.958	171.561	119.480	99.390	61.339	134.546	191.663	118.381
PLACE1002780	176.781	287.195	23.632	43.077	19.593	82.890	72.700	18.752
PLACE1002782	27.818	23.226	15.927	9.468	12.050	16.476	22.237	15.411
PLACE1002794	34.691	31.569	16.222	15.221	8.616	19.358	32.122	23.951
PLACE1002795	34.772	50.236	36.000	40.363	13.011	24.050	29.340	37.202
PLACE1002811	40.778	28.219	23.615	10.194	9.406	18.249	26.914	13.705
PLACE1002815	32.688	27.116	17.000	9.929	13.556	19.575	20.271	16.079
PLACE1002816	121.530	77.053	58.292	56.734	32.151	78.899	64.752	42.913
PLACE1002822	35.773	43.718	34.305	25.631	11.831	23.639	48.755	30.733
PLACE1002833	24.398	36.649	16.262	14.271	19.041	21.708	18.804	12.550
PLACE1002834	20.377	29.028	18.884	38.505	26.786	19.706	15.958	54.212
PLACE1002835	104.711	48.012	49.299	39.789	40.131	89.778	70.476	54.471
PLACE1002839	22.756	19.064	13.353	10.924	8.604	13.987	21.043	11.363
PLACE1002851	22.576	22.474	16.954	12.287	11.607	17.683	15.934	14.373
PLACE1002853	34.418	31.665	25.145	13.903	16.657	15.712	10.771	9.732
PLACE1002881	102.976	97.917	70.514	87.830	61.598	50.758	41.241	42.291
PLACE1002901	71.648	63.698	66.555	29.645	45.140	59.208	76.206	45.691
PLACE1002904	6.345	11.408	5.948	6.331	4.476	4.773	15.458	10.017
PLACE1002905	43.777	43.201	24.460	25.880	14.443	21.261	27.020	24.149
PLACE1002908	38.273	28.688	19.809	11.922	14.762	22.711	23.772	25.263
PLACE1002911	280.363	142.219	110.578	86.148	94.746	116.830	190.264	121.060
PLACE1002941	45.141	51.204	25.368	25.127	21.749	21.182	28.172	23.976
PLACE1002950	22.227	42.383	28.848	18.964	13.679	40.551	30.415	27.392
PLACE1002955	118.340	126.144	74.949	61.222	67.700	127.593	138.479	103.622
PLACE1002958	42.823	73.248	29.043	43.999	21.046	30.246	30.209	53.696
PLACE1002962	7.154	11.720	8.629	3.908	11.152	5.236	10.848	10.215
PLACE1002967	62.925	77.879	33.266	40.761	36.265	24.991	35.749	78.774
PLACE1002968	73.792	79.691	34.647	36.303	26.835	30.815	23.266	26.721
PLACE1002976	24.111	38.815	16.069	23.739	17.440	20.322	26.434	27.217
PLACE1002991	83.434	88.462	43.928	55.219	35.522	33.200	32.513	44.550
PLACE1002993	62.886	51.207	37.983	33.434	28.969	27.082	27.450	28.611
PLACE1002996	19.729	20.547	14.273	16.278	5.760	11.996	16.766	16.581
PLACE1003010	240.363	125.220	98.211	60.019	42.226	129.379	119.840	90.413
PLACE1003025	68.787	25.412	19.967	14.489	16.064	28.852	59.970	29.353
PLACE1003027	22.588	27.019	12.986	10.960	16.947	17.092	18.805	11.735

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Table 132

PLACE1003044	14.108	16.171	12.882	10.168	11.272	11.173	13.588	13.162
PLACE1003045	9.931	13.537	6.830	5.366	4.210	11.198	8.884	10.489
PLACE1003052	44.591	46.375	21.677	18.989	17.471	26.652	30.614	25.422
PLACE1003083	20.536	22.159	9.236	10.342	7.370	10.043	10.531	9.741
PLACE1003085	24.408	20.399	11.964	14.547	6.525	15.327	21.584	12.854
PLACE1003092	12.637	30.662	12.298	17.303	9.545	11.397	14.192	24.648
PLACE1003097	21.163	28.352	8.618	7.565	3.855	8.878	9.083	12.625
PLACE1003100	43.307	32.855	19.035	17.015	15.982	50.024	32.500	18.851
PLACE1003108	58.475	45.704	33.791	31.380	26.209	26.815	25.220	26.126
PLACE1003115	143.932	81.794	76.879	39.097	80.354	68.496	127.480	88.406
PLACE1003120	100.979	101.665	82.247	77.470	49.512	53.513	62.113	89.513
PLACE1003135	6.556	10.790	5.392	16.841	4.741	6.451	6.382	9.459
PLACE1003136	55.512	44.451	32.908	30.362	21.310	28.720	24.260	37.347
PLACE1003141	7.159	13.191	10.628	9.244	4.399	6.923	11.238	10.791
PLACE1003145	37.746	12.816	10.773	3.856	7.578	23.487	24.678	15.744
PLACE1003147	15.381	13.149	11.750	9.884	10.068	7.642	10.640	10.362
PLACE1003153	70.554	49.471	30.621	42.667	28.210	30.997	31.700	41.448
PLACE1003163	37.733	16.360	12.470	5.123	13.824	40.304	50.483	17.288
PLACE1003172	223.164	104.257	83.462	50.706	45.640	123.594	116.341	107.613
PLACE1003174	6.847	14.478	8.537	6.465	6.249	8.629	8.998	9.029
PLACE1003176	12.670	10.690	9.875	9.192	3.516	6.864	12.376	12.198
PLACE1003181	11.687	8.674	6.252	6.507	4.411	6.989	5.948	7.466
PLACE1003184	23.604	20.100	15.005	12.717	8.845	11.973	22.555	14.655
PLACE1003190	12.444	5.722	6.366	11.024	5.871	14.481	12.229	12.369
PLACE1003200	4.994	7.575	2.794	1.074	2.399	1.597	1.208	4.980
PLACE1003205	156.027	157.191	53.553	83.830	63.878	61.050	52.411	61.365
PLACE1003209	19.507	25.938	12.603	10.839	9.269	15.181	16.630	15.534
PLACE1003214	38.350	83.164	20.591	69.513	15.776	19.528	39.872	125.749
PLACE1003229	49.722	43.024	29.429	25.068	15.677	21.087	17.077	23.421
PLACE1003238	17.754	10.174	7.246	3.501	3.841	9.069	7.319	5.314
PLACE1003249	51.840	53.347	30.500	32.695	22.004	24.099	28.567	28.591
PLACE1003256	348.304	244.002	177.910	180.405	124.873	188.558	160.554	142.541
PLACE1003258	11.993	6.155	2.063	1.279	4.364	5.665	7.306	7.153
PLACE1003279	141.943	126.197	62.494	87.403	63.808	59.323	70.538	91.072
PLACE1003294	61.234	50.989	24.331	20.131	23.485	28.680	40.974	34.169
PLACE1003296	41.072	45.050	21.216	19.875	16.935	42.888	30.941	33.241
PLACE1003297	21.895	44.307	20.050	21.456	14.465	22.409	27.850	28.987
PLACE1003302	11.776	33.428	28.663	42.408	24.581	29.862	17.565	71.757
PLACE1003334	28.230	35.424	22.095	24.742	15.104	19.475	23.808	27.587
PLACE1003337	7.957	26.706	3.267	14.838	4.774	19.084	12.500	28.263
PLACE1003342	45.708	24.591	13.442	10.821	11.910	22.698	29.220	24.007
PLACE1003343	17.266	13.753	6.616	6.894	8.198	9.061	13.065	7.734
PLACE1003344	323.950	233.808	153.566	133.460	157.350	204.264	266.356	264.565
PLACE1003353	53.698	66.145	26.553	32.701	25.639	48.208	44.219	57.187
PLACE1003361	84.141	102.796	46.744	55.344	40.194	47.082	41.263	49.755
PLACE1003366	87.834	63.858	27.862	28.427	27.117	31.747	33.446	27.075
PLACE1003369	47.071	39.619	16.521	17.558	18.957	16.856	24.902	19.932
PLACE1003372	24.973	37.849	16.679	21.014	16.249	20.971	27.530	18.337
PLACE1003373	94.491	102.178	34.895	57.049	44.893	39.537	40.009	45.753
PLACE1003375	36.319	27.954	14.531	8.317	18.694	17.347	38.060	21.672
PLACE1003378	10.936	9.134	3.801	3.628	4.293	9.302	10.181	37.634
PLACE1003383	23.472	30.580	11.017	13.956	16.293	19.925	21.999	14.820
PLACE1003394	32.582	51.968	30.162	18.863	25.768	26.807	51.214	29.166
PLACE1003401	24.258	20.812	11.820	9.448	8.493	7.409	11.371	10.841
PLACE1003405	200.792	69.910	68.877	50.446	73.544	91.798	149.248	62.838
PLACE1003407	150.376	60.878	43.383	28.913	48.667	65.167	94.258	52.526
PLACE1003420	68.281	66.140	34.814	35.102	35.617	32.390	42.536	52.238
PLACE1003428	34.299	47.479	25.133	24.448	23.830	14.848	52.937	29.065
PLACE1003432	42.089	50.659	29.613	35.048	15.118	31.218	32.711	33.577
PLACE1003438	140.387	63.379	51.749	27.965	32.257	72.208	70.053	46.148
PLACE1003452	19.655	37.426	19.169	15.047	11.209	15.772	25.014	15.196
PLACE1003454	126.775	72.771	50.122	30.788	40.364	92.647	99.924	32.089
PLACE1003455	241.296	81.923	63.513	47.555	58.375	109.875	96.270	58.596
PLACE1003458	118.238	97.468	61.858	80.667	54.057	56.681	53.136	61.523

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Table 133

PLACE1003460	102.833	81.573	50.363	49.760	31.621	74.863	91.750	61.493
PLACE1003478	40.947	22.624	17.515	11.339	9.308	17.242	28.787	13.341
PLACE1003484	93.925	88.475	99.487	63.575	89.873	53.034	49.889	59.266
PLACE1003493	268.545	164.272	115.044	85.931	75.866	116.655	174.628	103.683
PLACE1003503	73.547	147.014	62.133	98.370	49.594	72.492	61.425	119.480
PLACE1003505	22.557	36.343	17.315	10.863	10.402	19.193	31.835	20.526
PLACE1003516	28.486	21.226	19.003	17.714	12.254	12.104	19.556	13.167
PLACE1003519	139.419	169.111	84.259	142.580	98.798	125.181	74.459	170.077
PLACE1003520	122.960	94.921	139.217	91.721	132.495	50.021	63.727	115.192
PLACE1003521	17.223	38.437	23.494	26.093	12.149	17.512	27.072	33.729
PLACE1003525	175.790	102.294	111.400	74.179	68.238	165.232	232.487	100.600
PLACE1003528	295.594	306.633	154.188	294.409	135.971	193.013	253.930	588.036
PLACE1003529	198.617	81.732	80.067	39.906	48.188	118.411	106.875	72.890
PLACE1003537	25.845	23.817	16.068	12.471	8.856	18.413	24.516	16.865
PLACE1003549	39.079	30.714	21.959	18.378	20.930	26.350	37.243	23.667
PLACE1003553	44.809	34.386	16.950	14.206	12.373	13.162	26.918	17.820
PLACE1003566	108.286	89.542	60.257	82.707	41.128	52.437	55.865	54.986
PLACE1003568	19.139	24.013	10.812	8.744	6.874	6.665	12.296	6.869
PLACE1003573	28.529	30.963	16.094	16.508	11.491	20.438	20.129	16.769
PLACE1003575	69.620	62.783	42.283	48.323	24.844	28.963	18.823	28.675
PLACE1003583	13.478	10.930	8.008	6.298	3.054	6.089	10.292	7.945
PLACE1003584	42.140	46.380	30.421	29.764	19.273	18.780	16.951	29.274
PLACE1003592	98.964	131.059	76.620	85.120	70.369	47.996	51.112	68.235
PLACE1003593	2.455	7.069	2.213	8.879	4.615	4.374	3.167	7.202
PLACE1003594	22.619	21.370	12.280	14.568	22.143	26.231	42.506	19.308
PLACE1003596	21.737	41.627	16.247	20.950	11.333	20.528	17.988	29.793
PLACE1003598	197.107	100.809	87.842	57.151	53.833	101.281	103.552	70.110
PLACE1003602	27.633	19.867	12.883	13.595	7.853	15.616	14.765	13.631
PLACE1003605	13.132	30.464	12.191	29.665	9.628	29.537	19.949	40.233
PLACE1003611	37.261	46.658	40.208	40.687	21.349	29.193	33.706	37.181
PLACE1003618	22.786	32.124	18.870	19.849	15.708	16.877	16.986	14.810
PLACE1003625	16.924	16.778	13.947	11.520	16.451	12.566	11.487	11.026
PLACE1003626	94.235	146.631	108.588	90.620	68.485	68.227	76.568	114.286
PLACE1003630	66.350	38.194	46.810	34.410	25.790	40.498	47.259	42.273
PLACE1003635	16.711	14.910	11.010	9.614	7.598	11.425	11.967	16.224
PLACE1003638	42.833	38.250	23.900	33.007	18.162	21.521	20.597	26.688
PLACE1003644	32.340	47.319	50.856	35.086	25.956	21.602	39.503	41.265
PLACE1003654	8.702	11.750	4.857	7.626	4.620	4.783	6.412	11.622
PLACE1003658	13.584	9.710	6.305	3.192	2.939	12.859	10.981	8.367
PLACE1003660	48.712	57.359	34.700	32.321	18.997	26.256	31.653	37.509
PLACE1003669	18.575	20.941	11.934	7.933	11.712	11.416	9.244	12.275
PLACE1003670	208.802	92.009	91.713	62.162	57.129	95.305	111.081	86.224
PLACE1003671	86.484	44.662	34.415	21.211	22.436	39.601	73.903	47.170
PLACE1003697	20.072	30.957	22.381	12.263	12.054	18.778	27.550	30.714
PLACE1003704	37.863	72.473	31.653	35.394	19.396	26.513	28.063	51.598
PLACE1003709	2.009	0.961	4.994	3.081	0.994	2.151	2.305	18.174
PLACE1003711	69.991	36.386	26.693	20.921	22.954	36.509	43.017	28.963
PLACE1003723	64.751	56.292	26.163	27.145	23.419	26.594	37.972	40.416
PLACE1003724	108.825	79.454	49.180	55.077	46.271	43.499	54.124	55.073
PLACE1003737	13.653	29.915	11.983	5.933	6.965	11.338	19.286	17.493
PLACE1003738	55.859	28.082	23.047	12.820	11.647	24.406	34.244	18.965
PLACE1003742	45.939	34.288	20.111	23.290	11.889	14.690	17.236	19.752
PLACE1003744	133.197	117.135	50.274	33.621	26.974	59.212	81.540	51.429
PLACE1003758	38.274	21.475	16.086	7.215	7.692	19.346	23.882	14.658
PLACE1003760	26.760	76.015	54.262	18.973	62.442	50.339	24.164	38.587
PLACE1003762	49.564	49.023	28.238	25.452	24.491	29.452	34.554	31.123
PLACE1003765	85.304	73.829	31.423	19.820	32.647	27.644	30.190	31.980
PLACE1003768	44.313	74.709	35.890	37.486	26.457	32.675	31.043	35.883
PLACE1003771	21.353	25.511	22.664	14.067	11.332	17.660	19.140	20.831
PLACE1003772	15.300	89.280	10.876	29.963	10.651	30.651	32.442	57.246
PLACE1003783	21.327	19.915	8.008	6.790	10.404	11.752	17.155	9.593
PLACE1003784	14.398	17.600	9.155	10.940	7.089	6.528	9.014	11.598
PLACE1003788	17.074	15.719	6.961	5.352	7.010	9.378	16.965	9.723
PLACE1003795	47.580	49.926	26.154	21.194	19.200	30.157	37.011	26.330

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Table 134

PLACE1003827	65.231	45.890	25.681	25.602	26.890	38.750	51.689	32.624
PLACE1003833	108.277	73.312	42.599	42.885	36.400	47.382	71.347	50.389
PLACE1003839	58.333	54.929	43.243	27.226	31.205	43.659	43.726	50.779
PLACE1003845	57.999	40.351	25.022	12.391	22.439	35.548	37.628	22.735
PLACE1003850	127.357	63.517	33.460	23.365	30.954	53.921	59.726	38.279
PLACE1003852	31.154	57.883	11.655	9.912	13.233	18.435	22.723	22.101
PLACE1003858	41.915	20.593	18.192	8.183	16.756	18.529	28.232	22.273
PLACE1003861	58.968	44.111	19.141	13.711	17.998	21.832	39.228	39.849
PLACE1003864	22.459	38.407	12.279	15.595	10.850	13.808	20.707	23.670
PLACE1003870	101.899	127.451	62.650	94.009	74.206	51.275	57.946	89.658
PLACE1003885	60.423	33.558	22.851	16.758	22.675	33.025	39.475	20.419
PLACE1003886	59.008	70.715	28.043	22.294	24.099	36.534	39.216	36.502
PLACE1003888	31.386	33.156	12.296	8.686	9.487	8.891	17.821	19.193
PLACE1003892	9.030	10.854	5.434	3.842	5.628	6.081	11.548	5.474
PLACE1003900	56.299	34.490	17.726	16.257	24.111	27.255	40.929	21.927
PLACE1003902	13.429	29.453	12.159	9.597	16.000	7.119	13.508	10.317
PLACE1003903	42.879	27.988	14.980	9.315	15.918	18.933	45.780	18.960
PLACE1003915	12.145	27.163	12.885	10.567	14.419	14.179	19.072	14.872
PLACE1003918	19.087	26.774	21.996	28.560	16.673	17.769	20.733	39.272
PLACE1003923	17.938	14.010	16.114	10.428	12.304	11.045	13.677	13.626
PLACE1003932	12.148	25.177	11.239	11.640	9.027	11.609	13.946	10.585
PLACE1003936	98.915	71.254	54.545	43.722	60.900	44.493	55.944	33.641
PLACE1003966	9.602	25.105	6.373	20.612	8.000	8.156	16.577	22.580
PLACE1003968	155.632	59.259	61.976	41.239	67.653	64.474	101.806	78.393
PLACE1004018	54.312	58.203	24.249	21.023	23.896	22.724	51.031	32.530
PLACE1004020	83.348	98.787	59.310	57.638	36.190	62.304	66.390	82.643
PLACE1004028	24.781	24.415	11.783	9.512	7.540	20.059	22.302	17.720
PLACE1004034	17.910	20.422	11.915	15.479	8.400	11.398	19.335	11.027
PLACE1004042	56.266	68.516	27.953	28.385	23.656	36.706	42.138	31.854
PLACE1004078	55.853	64.437	45.957	50.360	28.188	33.762	44.473	44.379
PLACE1004103	82.183	108.065	67.258	73.844	58.609	52.188	48.497	62.546
PLACE1004104	28.527	25.472	19.215	14.931	10.266	14.257	42.824	30.092
PLACE1004113	88.762	79.179	40.847	46.070	24.179	32.925	49.556	52.027
PLACE1004114	34.482	51.070	24.001	25.218	13.524	23.678	16.143	24.982
PLACE1004118	7.959	17.781	10.600	6.021	5.716	7.170	22.166	12.479
PLACE1004128	157.419	76.024	59.277	39.964	32.057	70.811	86.636	81.153
PLACE1004130	12.810	19.897	10.691	14.553	5.947	9.537	14.197	13.183
PLACE1004149	389.247	289.561	187.336	173.146	139.349	219.176	218.135	176.125
PLACE1004156	154.127	148.253	89.024	112.406	77.253	73.380	83.983	73.719
PLACE1004160	380.298	97.742	180.381	64.718	155.863	307.172	350.794	93.857
PLACE1004161	169.005	53.952	58.840	40.858	55.087	99.826	113.689	55.889
PLACE1004166	34.880	53.232	25.983	22.633	19.476	13.270	20.643	32.986
PLACE1004168	60.294	31.301	30.139	19.493	14.214	37.430	32.263	32.104
PLACE1004170	20.591	14.931	15.171	7.631	5.880	13.252	14.579	12.294
PLACE1004178	15.161	17.955	94.893	8.136	138.324	12.187	13.182	8.196
PLACE1004183	82.644	31.272	45.235	14.851	34.570	64.117	65.703	24.241
PLACE1004197	16.554	15.430	12.063	9.295	4.620	10.632	9.453	14.626
PLACE1004199	105.771	35.874	42.409	13.689	33.976	72.635	99.795	29.738
PLACE1004203	97.622	38.875	29.121	21.384	27.473	49.790	59.416	36.062
PLACE1004242	76.021	94.358	69.979	49.223	46.887	46.304	63.046	50.392
PLACE1004249	57.692	54.868	42.542	29.091	28.894	31.370	30.144	27.719
PLACE1004255	7.624	6.797	5.218	3.278	3.974	5.853	8.367	4.680
PLACE1004256	27.907	27.196	30.222	10.195	51.103	28.629	16.493	16.024
PLACE1004257	23.879	16.029	12.630	21.613	22.449	22.658	10.030	25.329
PLACE1004258	25.963	21.667	16.937	13.963	16.737	16.892	20.871	16.224
PLACE1004270	72.433	34.960	27.059	31.207	28.043	44.279	50.286	21.577
PLACE1004272	21.378	17.600	17.337	7.701	21.982	15.067	15.410	15.983
PLACE1004273	40.856	173.858	38.516	140.311	31.529	139.986	91.578	179.424
PLACE1004274	30.795	11.771	7.313	6.800	6.612	8.810	12.741	9.115
PLACE1004277	43.258	37.923	22.392	22.375	12.191	32.785	30.462	29.403
PLACE1004279	66.082	58.555	62.441	58.027	41.289	37.682	41.595	57.510
PLACE1004282	40.317	23.357	16.305	12.448	7.975	25.489	24.710	19.388
PLACE1004284	8.514	16.033	16.324	4.991	19.954	16.281	10.800	11.690
PLACE1004289	57.838	64.819	44.685	56.740	38.403	41.069	27.562	40.271

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Table 135

PLACE1004299	72.960	55.550	24.647	14.840	20.355	39.409	46.267	40.773
PLACE1004302	0.000	2.283	0.000	2.351	1.896	0.000	0.000	2.398
PLACE1004305	48.425	22.731	21.012	11.875	13.056	23.176	27.227	16.060
PLACE1004316	13.028	20.460	9.292	6.569	6.425	10.734	13.111	14.995
PLACE1004322	5.597	14.420	3.361	13.438	2.427	2.862	15.463	30.143
PLACE1004325	210.567	142.328	97.326	76.987	66.867	109.387	137.359	89.195
PLACE1004332	20.898	80.056	11.714	95.127	6.945	10.855	19.856	120.861
PLACE1004336	162.448	109.014	85.745	88.818	74.380	88.121	64.528	76.583
PLACE1004346	33.011	29.261	14.760	16.784	13.075	16.208	18.604	15.045
PLACE1004358	303.987	155.290	114.636	79.890	97.745	151.939	184.597	122.929
PLACE1004376	26.954	55.450	24.865	32.727	18.065	20.930	21.337	31.788
PLACE1004384	41.561	34.784	24.877	26.743	16.820	18.362	17.481	21.709
PLACE1004385	2.815	8.008	1.116	0.789	0.276	1.941	4.609	1.615
PLACE1004388	9.428	16.190	11.060	5.000	14.211	5.122	9.688	9.607
PLACE1004405	8.173	12.654	5.345	1.830	0.933	5.888	9.305	5.124
PLACE1004407	29.905	23.442	14.979	13.177	16.639	25.030	34.013	28.941
PLACE1004424	10.514	15.521	10.255	7.446	7.421	9.255	10.500	10.362
PLACE1004425	19.759	20.897	10.508	10.323	4.107	7.623	8.354	13.395
PLACE1004427	27.135	16.966,	10.908	6.848	6.240	12.886	13.355	13.321
PLACE1004428	57.419	64.170	30.987	36.844	18.316	25.562	30.009	32.786
PLACE1004433	14.267	16.470	9.620	5.755	5.704	9.109	18.352	17.362
PLACE1004435	17.934	21.109	25.397	11.056	16.381	15.263	11.508	12.972
PLACE1004437	80.263	28.301	25.518	11.113	18.894	28.285	48.525	32.402
PLACE1004441	54.134	47.973	28.455	25.980	23.238	32.602	42.800	31.312
PLACE1004446	21.816	51.429	12.869	9.278	14.108	22.134	27.233	19.664
PLACE1004450	7.462	10.131	7.421	5.906	3.377	6.452	10.209	8.066
PLACE1004451	20.207	31.572	19.505	19.989	13.665	10.206	15.250	18.302
PLACE1004456	53.328	61.854	40.178	40.750	22.994	32.386	43.215	51.423
PLACE1004458	11.625	26.331	11.664	5.811	6.713	7.889	9.892	25.194
PLACE1004460	14.565	10.490	5.224	4.840	4.848	10.082	10.381	9.064
PLACE1004467	55.048	46.934	30.599	25.322	18.898	22.765	24.523	37.228
PLACE1004471	79.809	63.442	37.258	59.178	37.277	29.527	32.628	61.028
PLACE1004473	11.959	24.287	10.007	12.507	6.941	16.855	16.517	14.312
PLACE1004475	28.089	59.714	31.110	18.183	27.680	29.310	26.516	47.243
PLACE1004482	25.293	47.010	16.830	16.111	11.400	30.429	30.968	35.155
PLACE1004491	1.664	6.234	6.646	3.270	2.102	2.892	5.873	2.357
PLACE1004492	28.976	64.765	17.444	33.197	14.425	13.718	15.087	46.827
PLACE1004506	115.632	78.203	46.045	35.757	41.896	69.416	85.790	78.043
PLACE1004507	19.324	9.642	5.560	5.074	6.375	9.835	14.279	13.049
PLACE1004510	68.938	32.074	18.477	12.138	20.444	31.944	40.037	21.097
PLACE1004516	12.480	28.346	11.965	12.861	14.262	12.534	22.486	21.487
PLACE1004518	113.615	41.314	32.970	20.351	31.552	61.934	56.694	31.846
PLACE1004519	17.977	18.444	5.463	12.802	4.820	7.889	17.402	10.594
PLACE1004520	151.375	60.884	33.949	19.465	34.865	66.695	80.040	24.602
PLACE1004530	43.149	50.004	13.982	11.859	13.432	25.111	26.818	14.729
PLACE1004545	10.167	15.345	7.071	4.082	3.066	9.778	48.382	17.084
PLACE1004547	23.679	18.172	11.002	9.917	9.918	8.124	14.641	11.578
PLACE1004548	65.295	50.486	25.299	24.808	18.285	24.829	25.884	36.422
PLACE1004550	26.366	18.052	12.431	9.837	11.528	18.472	24.539	12.011
PLACE1004551	36.555	34.112	16.064	11.068	19.459	22.324	30.835	27.019
PLACE1004559	7.230	9.773	4.555	3.840	5.493	5.484	6.749	3.314
PLACE1004562	28.572	30.296	23.163	8.674	27.528	15.650	14.237	9.875
PLACE1004564	36.735	40.092	17.343	20.204	19.250	16.933	27.924	22.272
PLACE1004604	0.000	12.587	0.000	0.000	0.000	0.000	0.000	19.840
PLACE1004611	146.180	120.698	55.658	62.073	72.842	61.052	49.103	61.906
PLACE1004629	33.357	43.299	24.243	20.920	25.719	18.242	25.782	34.340
PLACE1004630	115.833	50.627	40.441	11.469	40.312	43.201	76.589	27.684
PLACE1004637	93.560	57.213	41.313	29.790	25.704	57.715	75.530	37.977
PLACE1004645	73.214	93.376	36.462	56.662	22.216	68.433	63.089	99.155
PLACE1004646	46.760	48.123	29.675	17.834	15.130	24.754	48.692	22.337
PLACE1004648	350.190	101.385	110.514	45.573	70.332	215.200	161.060	64.085
PLACE1004655	89.992	149.462	51.420	99.781	32.385	132.613	125.965	155.546
PLACE1004658	116.215	50.154	45.513	37.950	33.846	45.145	68.297	39.519
PLACE1004664	17.737	19.569	14.876	12.928	9.845	14.381	22.040	15.050

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Table 136

PLACE1004672	115.072	106.617	82.206	119.303	40.425	71.021	72.226	74.522
PLACE1004674	31.963	33.509	24.678	21.646	15.932	29.638	23.353	28.211
PLACE1004681	42.868	52.263	26.896	24.625	15.862	23.571	27.757	20.193
PLACE1004686	77.947	73.361	53.514	71.286	30.833	39.791	36.511	33.040
PLACE1004690	32.648	58.935	35.179	14.534	30.457	39.275	32.277	31.724
PLACE1004691	54.201	46.001	30.198	29.746	20.988	25.836	29.486	27.807
PLACE1004693	14.777	12.312	8.393	5.596	11.162	10.119	16.032	13.442
PLACE1004701	70.824	100.375	71.192	54.004	102.558	32.216	35.594	76.510
PLACE1004705	65.005	44.191	23.752	22.321	16.770	23.327	38.083	39.081
PLACE1004708	27.110	53.686	25.099	16.995	21.305	56.740	40.801	33.150
PLACE1004716	39.167	36.771	27.872	31.814	17.418	21.095	22.468	30.805
PLACE1004722	19.479	18.949	14.424	12.942	8.398	12.638	19.361	14.771
PLACE1004736	243.492	165.849	137.412	105.409	67.657	152.337	156.408	125.947
PLACE1004737	19.476	29.675	15.699	11.243	8.873	11.625	22.792	35.249
PLACE1004740	75.304	51.308	47.454	36.445	39.722	39.387	38.438	45.080
PLACE1004743	68.266	20.761	16.980	15.277	16.469	24.996	43.820	20.166
PLACE1004751	52.682	43.427	21.010	38.514	12.476	20.526	37.750	28.532
PLACE1004757	64.866	62.789	28.623	23.370	20.456	30.243	39.909	29.888
PLACE1004761	26.949	16.825	13.926	8.696	8.320	11.691	16.318	12.117
PLACE1004773	54.251	32.451	26.443	19.663	14.012	23.566	35.213	33.476
PLACE1004775	0.000	0.417	0.000	0.196	0.000	0.000	0.000	0.000
PLACE1004777	23.178	24.645	17.477	11.418	17.912	15.186	20.914	17.641
PLACE1004793	10.099	9.825	8.108	2.235	6.900	9.166	12.992	9.524
PLACE1004796	188.258	55.088	53.995	32.705	46.720	104.831	97.648	39.050
PLACE1004804	47.571	38.570	28.854	17.511	18.650	30.285	28.014	30.229
PLACE1004813	13.617	19.594	9.102	9.930	7.091	9.407	7.283	12.102
PLACE1004814	41.930	105.336	65.246	82.329	68.081	42.266	24.121	54.793
PLACE1004815	11.260	11.968	10.846	11.794	7.165	7.448	6.082	10.511
PLACE1004816	16.128	75.555	15.363	11.777	8.852	11.495	48.534	15.257
PLACE1004824	104.392	119.714	59.183	79.068	52.724	50.466	50.930	68.338
PLACE1004827	36.438	26.140	22.831	30.150	21.998	23.534	21.266	27.294
PLACE1004836	31.163	22.975	17.358	12.887	15.510	26.557	30.452	21.872
PLACE1004838	51.513	33.252	27.542	18.538	19.154	26.439	33.316	30.452
PLACE1004840	6.312	14.806	6.440	5.491	4.111	4.374	5.846	7.493
PLACE1004842	36.592	16.317	15.880	3.917	12.485	19.399	19.475	15.636
PLACE1004850	49.730	32.337	19.817	10.970	14.421	24.250	37.921	22.827
PLACE1004868	12.619	15.190	6.828	7.862	5.213	6.832	14.431	11.456
PLACE1004885	47.128	43.214	27.198	28.397	13.325	24.000	19.111	27.465
PLACE1004886	8.456	11.696	9.985	10.337	6.285	8.607	7.712	8.362
PLACE1004887	25.379	95.649	19.675	41.800	19.005	29.704	27.795	64.943
PLACE1004896	15.949	20.476	11.823	11.627	11.685	16.543	32.352	19.012
PLACE1004900	156.735	97.505	60.889	55.961	42.544	67.669	87.798	52.760
PLACE1004902	34.587	45.710	25.541	18.321	13.921	16.696	14.779	18.931
PLACE1004904	13.083	9.418	10.864	6.532	3.426	12.069	11.291	11.270
PLACE1004911	9.050	2.555	6.611	0.560	18.979	5.276	77.886	87.866
PLACE1004913	5.777	13.239	7.908	7.304	5.359	5.827	5.467	4.992
PLACE1004918	7.297	6.323	2.714	3.829	2.441	5.039	6.811	7.534
PLACE1004930	13.399	20.023	7.288	16.589	5.485	9.041	11.559	29.767
PLACE1004934	23.550	42.322	19.288	14.581	15.341	18.403	23.466	22.456
PLACE1004937	62.000	36.002	39.437	12.652	29.690	26.536	31.417	16.660
PLACE1004949	54.760	253.300	30.259	54.618	16.463	68.966	58.166	114.761
PLACE1004969	34.833	23.924	16.977	12.453	10.087	19.834	24.891	18.488
PLACE1004970	0.656	0.020	0.000	0.313	0.000	0.298	0.381	0.000
PLACE1004972	6.558	13.022	6.101	7.857	5.753	5.710	11.774	11.235
PLACE1004974	11.126	11.290	3.841	6.990	3.694	5.403	9.800	10.261
PLACE1004975	80.214	39.082	26.710	22.285	23.842	39.120	65.032	40.567
PLACE1004979	152.165	104.604	79.308	83.496	72.355	66.036	91.372	96.121
PLACE1004982	31.283	43.568	24.303	20.310	19.273	22.947	20.250	25.778
PLACE1004985	27.380	21.550	10.343	7.433	6.839	10.865	15.730	9.181
PLACE1005003	13.462	10.074	3.185	3.847	4.249	8.207	9.511	7.821
PLACE1005004	14.310	19.771	9.570	8.293	4.301	13.694	14.781	11.577
PLACE1005005	68.568	52.286	38.586	41.076	30.307	32.858	34.815	41.036
PLACE1005011	44.494	36.131	20.623	8.452	15.065	19.701	49.060	34.432
PLACE1005026	15.741	9.737	2.380	4.186	5.033	9.113	16.290	8.131

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Table 137

PLACE1005027	96.103	120.663	38.137	45.870	39.089	34.870	44.104	36.457
PLACE1005031	53.784	60.972	22.926	20.892	23.652	30.271	33.677	36.405
PLACE1005036	59.627	65.001	32.797	39.527	17.608	26.473	31.634	38.146
PLACE1005041	4.261	12.290	6.164	5.522	7.108	4.000	7.035	4.518
PLACE1005046	87.532	76.016	48.856	61.696	38.790	39.618	40.595	41.016
PLACE1005047	46.051	25.735	13.704	11.855	15.156	16.153	36.409	23.815
PLACE1005052	46.575	28.140	12.015	12.780	14.059	19.834	31.197	29.860
PLACE1005055	8.158	27.571	18.813	20.078	22.643	10.820	20.439	26.659
PLACE1005066	42.175	53.415	23.566	15.565	25.138	25.274	51.837	39.544
PLACE1005077	24.309	28.659	13.050	14.623	12.679	15.734	21.504	21.488
PLACE1005085	92.222	93.468	34.255	47.138	34.582	40.497	36.255	38.289
PLACE1005086	102.289	115.876	53.702	57.228	50.800	42.000	46.257	54.679
PLACE1005088	544.154	104.456	118.967	73.371	168.988	196.566	151.442	82.439
PLACE1005089	15.670	20.631	11.122	11.637	9.823	8.077	15.337	12.098
PLACE1005101	240.793	118.635	90.799	64.835	74.093	133.434	208.569	89.985
PLACE1005102	211.056	131.745	94.963	67.285	83.058	115.827	185.343	115.880
PLACE1005108	106.691	120.848	45.131	39.846	39.785	42.063	67.557	51.335
PLACE1005110	44.564	38.347	24.937	14.829	19.447	30.115	34.784	22.848
PLACE1005111	23.753	40.474	14.465	9.594	18.283	14.066	20.594	18.691
PLACE1005123	59.496	91.632	49.521	37.074	43.380	35.861	40.754	46.181
PLACE1005124	40.401	51.742	18.340	18.486	14.709	15.661	58.570	27.105
PLACE1005128	204.940	150.075	112.018	69.631	91.526	103.298	146.254	123.511
PLACE1005130	60.815	73.959	31.043	64.232	33.067	33.874	55.788	78.228
PLACE1005141	31.384	66.806	13.194	14.252	14.502	14.628	19.090	38.173
PLACE1005146	41.144	50.277	22.100	13.293	17.449	21.199	50.528	27.607
PLACE1005152	24.085	22.701	12.226	17.968	9.903	11.357	15.172	18.599
PLACE1005157	12.965	19.465	14.891	8.624	4.456	13.395	11.532	13.083
PLACE1005162	36.700	33.286	16.285	22.399	12.111	12.771	17.199	19.584
PLACE1005170	10.498	22.471	9.375	11.193	6.555	8.512	31.001	12.095
PLACE1005176	14.622	9.067	7.477	7.780	4.490	12.946	17.364	10.281
PLACE1005181	6.793	9.688	13.589	5.174	11.314	5.046	10.911	5.455
PLACE1005184	45.108	51.852	28.259	28.577	14.895	17.723	18.400	25.953
PLACE1005186	44.227	18.348	9.815	8.521	7.622	25.120	58.044	15.795
PLACE1005187	35.399	20.464	13.526	17.276	12.357	24.314	23.687	19.988
PLACE1005189	22.364	32.597	20.000	13.876	11.241	20.988	33.066	19.839
PLACE1005193	49.047	80.518	24.364	25.042	13.468	27.467	43.397	28.759
PLACE1005200	33.619	67.147	18.122	26.564	10.723	25.057	36.262	35.781
PLACE1005208	7.546	16.382	8.064	9.582	7.561	2.781	8.835	9.588
PLACE1005216	12.005	12.262	6.329	7.983	11.377	8.113	19.335	10.996
PLACE1005223	61.568	52.800	42.403	50.792	22.094	32.500	31.112	40.207
PLACE1005225	56.429	68.319	36.647	41.380	13.973	38.303	34.273	26.689
PLACE1005232	167.040	125.455	69.019	54.944	48.079	58.072	51.258	47.854
PLACE1005239	39.974	13.868	24.220	12.450	8.314	22.398	17.024	10.214
PLACE1005243	44.314	40.194	24.574	15.713	15.164	30.409	32.149	27.769
PLACE1005250	16.580	27.491	8.463	9.418	9.886	6.064	14.623	19.833
PLACE1005261	13.408	16.822	8.222	5.682	5.972	7.195	10.054	11.287
PLACE1005266	20.535	27.721	31.380	28.026	16.734	16.639	19.888	14.312
PLACE1005271	93.263	83.479	52.747	61.756	25.077	54.250	44.786	57.870
PLACE1005277	49.402	22.460	14.621	13.425	7.075	14.242	10.306	12.244
PLACE1005287	22.199	38.345	37.586	27.355	20.932	23.076	24.235	32.916
PLACE1005299	103.926	106.254	44.038	32.012	31.443	51.044	46.947	40.737
PLACE1005305	31.910	44.987	25.573	14.702	9.928	36.933	23.937	7.784
PLACE1005307	8.172	12.030	16.098	3.745	9.584	6.781	7.722	11.443
PLACE1005308	40.902	25.016	19.027	14.696	9.927	17.505	29.543	18.123
PLACE1005313	39.342	24.175	12.571	9.132	10.374	15.637	19.991	21.756
PLACE1005320	11.271	17.455	5.231	8.538	6.936	8.957	11.506	3.500
PLACE1005327	17.688	40.290	17.575	16.817	11.658	12.028	22.217	11.328
PLACE1005331	53.315	18.698	8.600	7.329	10.301	14.685	21.018	30.181
PLACE1005335	77.870	63.026	41.750	23.138	24.128	41.168	47.208	30.379
PLACE1005336	21.324	20.435	19.530	20.249	15.524	17.918	9.870	18.733
PLACE1005351	322.456	95.522	98.703	40.129	88.620	198.287	224.069	67.745
PLACE1005366	43.968	40.039	29.574	12.918	26.291	12.458	22.106	17.170
PLACE1005373	45.621	33.656	36.861	29.023	24.691	30.472	35.702	32.653
PLACE1005374	65.634	77.534	33.162	35.300	28.763	35.173	31.282	34.469

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Table 138

PLACE1005383	192.459	99.179	41.513	26.019	36.659	74.701	68.796	45.274
PLACE1005388	13.492	3.669	17.165	2.620	2.702	5.416	5.640	1.066
PLACE1005409	90.786	74.023	54.915	55.853	33.620	40.200	37.456	42.420
PLACE1005410	46.290	42.715	17.237	13.377	5.674	22.632	23.974	18.471
PLACE1005426	91.681	34.075	23.696	8.178	19.395	33.771	55.787	18.201
PLACE1005431	31.798	52.111	24.865	17.489	30.465	29.753	21.758	27.288
PLACE1005453	73.901	79.686	50.868	59.367	41.772	40.635	21.743	44.958
PLACE1005467	53.538	58.699	26.287	26.884	22.037	19.003	24.688	36.491
PLACE1005471	14.111	22.568	10.718	9.783	3.667	5.561	7.986	9.066
PLACE1005476	19.213	15.401	6.820	10.474	5.214	8.066	10.246	12.895
PLACE1005477	44.904	32.541	21.171	12.649	22.905	16.973	12.374	11.640
PLACE1005480	15.176	15.907	13.557	7.819	5.374	9.674	14.794	13.766
PLACE1005481	38.954	28.423	22.694	20.287	10.897	21.409	20.874	20.662
PLACE1005494	3.769	10.339	4.444	0.960	2.290	3.620	3.635	4.680
PLACE1005495	66.611	51.739	18.659	10.826	24.448	36.783	41.876	19.394
PLACE1005497	225.229	70.178	56.698	22.970	70.611	95.227	102.253	52.394
PLACE1005499	34.460	64.292	20.603	24.590	10.840	16.074	28.756	44.984
PLACE1005502	23.366	16.975	25.072	11.122	8.644	11.079	6.947	13.065
PLACE1005513	9.578	9.101	6.647	6.693	5.372	7.954	6.929	7.661
PLACE1005515	26.055	17.913	14.409	7.630	7.031	15.665	20.130	18.654
PLACE1005519	3.105	10.749	5.162	20.785	2.814	7.220	6.981	11.525
PLACE1005526	20.332	17.208	9.755	7.461	4.693	10.134	18.343	11.671
PLACE1005528	135.917	114.261	73.561	90.213	64.605	69.074	53.101	76.549
PLACE1005530	57.987	54.808	31.774	14.143	29.079	35.603	50.048	45.019
PLACE1005536	46.147	63.002	37.450	8.267	20.956	24.988	38.856	33.023
PLACE1005539	124.764	33.255	11.994	7.356	5.220	14.637	17.879	10.020
PLACE1005543	44.082	34.128	18.253	25.879	12.291	14.141	13.931	20.699
PLACE1005544	74.900	40.457	28.887	25.245	13.758	39.328	41.210	26.735
PLACE1005550	6.022	18.709	6.562	8.947	5.166	11.247	11.859	13.763
PLACE1005554	12.467	3.872	4.316	3.594	5.956	4.592	6.885	7.371
PLACE1005557	38.341	19.894	13.342	7.004	10.123	21.314	24.623	20.113
PLACE1005563	49.466	30.178	12.647	9.014	15.593	21.940	32.864	20.002
PLACE1005569	45.144	91.673	20.105	17.832	17.112	30.056	27.968	27.306
PLACE1005574	10.326	17.415	23.239	15.035	8.433	11.642	6.292	7.748
PLACE1005584	1.575	8.124	2.743	4.127	1.246	5.392	10.776	8.407
PLACE1005590	24.799	17.304	10.072	5.828	8.195	75.095	45.627	11.276
PLACE1005596	23.048	17.414	15.297	11.536	9.204	8.707	25.759	17.524
PLACE1005601	19.725	11.146	9.146	9.258	6.390	6.373	13.351	11.411
PLACE1005603	14.600	11.398	6.074	3.038	7.570	5.089	9.929	9.078
PLACE1005604	41.213	46.409	18.486	29.843	23.139	24.076	25.335	30.827
PLACE1005611	8.443	24.450	16.274	16.607	8.553	5.155	7.288	14.586
PLACE1005622	16.882	8.675	10.537	8.137	6.368	11.349	12.772	6.731
PLACE1005623	14.421	31.080	6.381	15.139	12.715	20.665	16.500	16.140
PLACE1005630	85.952	39.001	28.845	20.191	32.625	41.980	48.174	23.375
PLACE1005639	15.544	15.138	6.500	11.153	7.691	5.800	12.445	10.861
PLACE1005646	77.577	49.170	33.499	22.814	34.067	36.568	56.286	41.027
PLACE1005647	24.882	24.864	4.274	2.435	2.081	11.277	81.858	11.666
PLACE1005648	132.845	151.402	77.779	90.885	75.286	60.577	62.598	76.522
PLACE1005653	54.214	52.101	51.513	45.050	58.871	26.470	27.046	42.423
PLACE1005656	10.886	10.384	4.581	6.961	7.146	4.012	9.841	4.680
PLACE1005659	66.511	28.923	22.280	14.717	20.121	25.706	37.588	18.352
PLACE1005660	33.206	32.856	16.502	12.470	13.584	17.875	18.205	12.323
PLACE1005664	111.456	61.079	40.142	92.126	42.582	52.037	69.703	37.257
PLACE1005666	38.297	57.391	31.059	37.247	32.602	19.836	29.982	27.528
PLACE1005669	21.571	38.576	14.288	21.325	13.912	15.528	26.157	24.222
PLACE1005682	20.262	22.261	10.868	8.411	10.729	18.322	24.974	10.469
PLACE1005698	30.653	32.169	14.400	9.396	8.522	24.009	33.881	18.345
PLACE1005706	70.622	71.219	28.705	19.111	20.312	39.593	64.431	43.104
PLACE1005725	37.970	40.199	18.153	10.564	8.703	16.434	20.139	15.072
PLACE1005727	10.738	20.546	10.306	14.533	4.877	13.636	6.798	18.026
PLACE1005730	31.961	20.066	19.504	9.010	12.411	18.589	28.621	15.178
PLACE1005736	66.424	61.842	32.233	33.306	29.857	36.600	35.215	42.162
PLACE1005739	28.978	27.513	14.370	8.219	7.550	14.009	24.000	20.049
PLACE1005745	11.469	35.015	10.673	20.167	15.864	28.058	24.092	16.469

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Table 139

PLACE1005752	90.237	41.210	18.989	8.672	12.425	46.493	43.056	16.151
PLACE1005755	1.539	0.000	4.104	1.918	1.510	0.000	5.784	2.632
PLACE1005756	66.572	57.026	70.208	18.341	53.529	53.169	52.915	28.510
PLACE1005760	79.900	86.243	41.942	41.317	39.086	38.946	63.248	58.527
PLACE1005763	63.990	62.996	38.725	43.819	27.604	32.835	26.439	25.813
PLACE1005768	118.359	72.826	49.483	36.802	35.749	50.090	71.856	51.056
PLACE1005771	79.421	64.882	40.953	41.897	27.292	23.749	34.685	36.527
PLACE1005783	37.668	31.896	17.523	15.262	12.345	17.985	18.238	19.301
PLACE1005799	72.863	40.078	21.736	13.084	14.828	29.177	22.331	19.278
PLACE1005802	6.212	17.722	27.131	6.099	7.894	19.213	7.798	5.528
PLACE1005803	191.336	61.152	58.464	27.079	34.644	91.079	90.094	47.378
PLACE1005804	16.294	18.066	10.826	10.126	8.393	9.317	16.782	14.973
PLACE1005813	75.551	91.851	75.766	52.294	39.477	54.790	85.201	93.066
PLACE1005815	83.027	75.307	35.260	46.938	32.810	18.119	30.803	97.615
PLACE1005828	62.100	41.315	31.342	51.062	32.258	19.627	15.080	24.684
PLACE1005833	15.481	278.446	15.416	31.374	13.721	24.043	14.331	47.385
PLACE1005834	3.601	10.543	9.859	8.251	9.385	7.823	3.972	10.785
PLACE1005835	28.240	44.997	17.530	13.182	10.234	18.255	20.661	15.389
PLACE1005836	48.952	28.464	13.401	6.803	8.041	17.572	26.265	12.222
PLACE1005845	6.922	14.049	6.527	5.977	6.557	8.274	10.956	10.665
PLACE1005850	60.537	40.486	33.654	29.867	33.148	24.454	29.715	24.623
PLACE1005851	5.255	8.502	7.076	7.967	6.349	5.105	3.396	5.059
PLACE1005856	31.514	23.792	11.829	9.889	15.184	17.753	16.532	9.402
PLACE1005875	18.708	26.502	13.111	7.247	11.323	7.852	8.071	10.929
PLACE1005876	11.863	17.117	12.588	7.705	10.029	6.736	10.292	10.926
PLACE1005878	88.082	38.409	33.471	15.538	10.872	40.432	40.415	25.582
PLACE1005880	13.768	23.162	13.625	7.279	4.396	7.444	9.160	8.620
PLACE1005884	6.339	23.822	4.633	5.084	1.983	6.912	6.877	7.772
PLACE1005890	4.217	7.720	4.562	7.386	4.165	6.206	4.379	6.062
PLACE1005898	49.218	42.891	38.186	23.065	31.910	31.010	30.359	26.109
PLACE1005913	88.451	79.521	44.625	46.998	40.516	45.668	41.888	48.362
PLACE1005921	142.054	144.941	38.273	52.037	39.062	61.467	47.211	132.279
PLACE1005923	63.053	60.900	27.149	27.188	17.336	25.033	14.933	34.055
PLACE1005925	48.607	40.199	37.807	26.165	30.660	26.958	27.906	18.684
PLACE1005927	55.705	38.194	28.923	20.495	16.164	33.843	28.337	44.414
PLACE1005932	9.087	16.013	5.744	4.478	1.709	3.696	5.067	7.086
PLACE1005934	77.293	56.236	26.301	30.736	24.397	28.352	30.917	30.023
PLACE1005936	14.496	14.255	9.508	3.415	8.672	4.033	8.619	9.076
PLACE1005939	123.849	544.154	42.334	146.300	50.110	131.268	94.038	701.375
PLACE1005951	30.248	32.418	15.242	18.690	12.128	15.271	23.652	24.588
PLACE1005953	19.693	12.970	10.718	9.877	7.414	11.462	12.609	10.525
PLACE1005955	28.767	19.227	16.323	8.434	5.041	17.159	19.002	18.594
PLACE1005966	12.530	5.651	4.425	4.128	2.034	2.562	6.043	9.634
PLACE1005968	72.025	41.312	41.089	21.486	26.270	41.994	52.960	35.566
PLACE1005975	25.485	32.376	26.520	59.431	24.469	21.685	13.392	59.446
PLACE1005990	28.041	21.763	14.040	6.899	9.815	14.633	20.007	16.121
PLACE1005997	164.708	330.084	53.780	239.364	63.798	139.506	181.530	287.794
PLACE1006002	107.705	119.425	99.629	95.897	48.384	50.827	42.380	62.761
PLACE1006003	17.046	17.747	14.438	8.154	10.541	11.696	8.091	13.582
PLACE1006011	45.672	38.018	30.702	13.512	12.435	21.558	24.215	22.424
PLACE1006017	45.647	36.734	21.158	25.570	11.110	18.839	15.505	19.245
PLACE1006037	16.896	39.112	14.980	27.384	13.578	19.303	24.570	28.170
PLACE1006040	46.354	36.477	13.887	24.327	21.931	28.327	32.651	26.980
PLACE1006063	93.783	71.598	45.048	18.263	32.191	49.881	45.260	38.790
PLACE1006071	21.534	36.297	13.892	8.687	12.019	30.377	49.850	20.945
PLACE1006073	53.828	57.305	30.172	24.545	29.043	23.961	31.954	27.041
PLACE1006074	20.455	27.006	16.076	13.730	10.251	15.582	20.631	17.603
PLACE1006076	34.364	32.791	16.508	20.008	10.320	9.947	9.203	13.977
PLACE1006079	121.353	38.429	26.815	12.301	21.503	45.204	56.632	21.554
PLACE1006093	19.742	15.385	13.757	9.509	7.004	12.267	13.690	14.363
PLACE1006116	35.931	6.904	15.512	3.533	7.677	15.676	16.048	10.524
PLACE1006119	20.068	12.984	12.327	11.130	22.090	9.808	10.787	12.644
PLACE1006129	48.539	31.749	9.463	11.635	17.430	20.020	41.668	19.917
PLACE1006139	91.126	109.499	54.407	53.695	49.471	92.100	63.259	79.774

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Table 140

PLACE1006143	46.098	37.379	20.702	25.574	15.236	19.435	15.116	22.985
PLACE1006157	13.931	16.377	3.826	8.200	5.712	12.370	15.306	9.581
PLACE1006159	9.858	20.502	51.646	6.722	44.269	12.185	22.648	13.267
PLACE1006164	16.798	16.274	7.126	6.999	8.372	7.194	8.960	10.950
PLACE1006167	167.052	67.298	52.083	32.075	42.820	71.882	95.636	56.466
PLACE1006170	53.027	29.665	19.393	10.419	17.774	25.072	30.851	21.127
PLACE1006181	18.281	16.157	7.996	5.350	25.260	14.174	22.113	14.042
PLACE1006187	8.548	3.516	0.000	6.682	4.886	7.985	6.385	7.927
PLACE1006195	29.846	28.480	17.352	16.886	13.459	17.228	26.763	6.398
PLACE1006196	61.991	49.016	26.372	19.718	27.710	39.072	35.118	29.050
PLACE1006197	54.536	37.860	28.958	22.575	23.293	25.482	39.927	23.557
PLACE1006198	28.596	28.607	16.575	17.769	13.452	15.976	27.459	22.547
PLACE1006205	6.745	7.609	4.565	5.214	6.572	2.590	4.973	5.687
PLACE1006208	27.187	27.254	9.873	14.328	12.512	21.992	19.863	18.823
PLACE1006211	51.907	59.414	30.208	13.725	28.133	32.360	44.159	27.440
PLACE1006219	23.493	24.408	16.455	9.362	17.274	26.290	25.586	21.714
PLACE1006223	68.934	18.764	11.909	9.616	10.504	6.495	11.267	10.706
PLACE1006225	11.501	12.439	4.415	6.582	6.792	8.314	14.745	11.878
PLACE1006236	6.977	12.900	5.853	11.342	12.529	5.324	7.920	11.191
PLACE1006239	22.381	23.765	14.765	10.878	15.210	13.043	19.412	11.809
PLACE1006245	22.376	34.520	10.634	11.051	12.665	11.374	19.724	21.305
PLACE1006246	7.382	13.028	11.301	7.187	12.507	7.382	11.506	12.804
PLACE1006248	26.428	39.894	16.473	21.809	14.977	13.745	20.862	22.348
PLACE1006262	31.261	23.190	19.574	15.195	26.025	14.627	19.352	15.266
PLACE1006269	24.853	29.569	14.626	9.583	8.703	14.129	23.157	18.545
PLACE1006275	102.949	70.174	48.183	23.852	33.229	45.824	59.434	33.371
PLACE1006277	48.240	62.171	21.255	16.104	9.445	23.300	38.264	21.261
PLACE1006288	70.893	32.184	31.657	17.185	23.905	32.558	35.514	20.818
PLACE1006290	10.445	14.155	12.302	10.566	8.624	8.747	18.914	10.719
PLACE1006298	31.578	46.118	32.460	28.976	15.993	23.096	26.422	37.543
PLACE1006311	10.845	53.957	4.561	9.947	4.631	5.498	6.778	11.014
PLACE1006318	58.445	16.244	19.191	15.551	8.313	29.532	32.903	13.674
PLACE1006325	22.893	33.926	3.989	1.894	3.728	40.444	14.737	21.889
PLACE1006331	8.939	11.370	13.783	13.776	7.560	9.956	11.998	18.468
PLACE1006335	32.529	28.387	14.713	11.425	11.019	17.865	33.894	21.152
PLACE1006357	3.825	9.950	6.210	4.159	6.022	6.747	7.754	5.087
PLACE1006360	14.089	16.595	24.796	8.248	22.949	14.298	13.022	11.859
PLACE1006364	50.974	44.777	21.918	23.821	14.219	27.483	47.224	26.302
PLACE1006365	13.302	9.969	13.635	9.061	14.422	9.214	21.696	7.466
PLACE1006368	46.065	73.155	26.650	24.050	13.240	24.936	34.207	27.153
PLACE1006371	34.894	28.248	11.313	5.383	9.407	18.791	14.801	7.990
PLACE1006373	37.194	28.331	21.043	14.199	14.482	19.388	19.815	15.474
PLACE1006382	21.094	19.698	15.454	9.638	8.482	4.374	23.912	14.924
PLACE1006385	81.993	38.251	25.850	13.853	17.987	36.061	46.518	25.400
PLACE1006391	24.937	39.657	15.251	12.115	12.857	15.718	29.802	21.518
PLACE1006412	92.185	81.544	52.558	67.133	44.434	40.171	51.400	52.505
PLACE1006414	22.869	15.684	6.974	8.725	2.933	4.693	8.944	10.166
PLACE1006419	61.800	27.143	19.239	15.038	20.825	26.734	24.227	27.471
PLACE1006438	82.798	38.554	34.340	20.259	23.756	34.334	48.209	27.402
PLACE1006443	215.537	110.762	106.123	67.312	72.074	128.015	104.908	86.500
PLACE1006445	11.757	18.560	10.002	8.147	6.187	5.719	13.324	13.219
PLACE1006447	27.394	37.610	21.247	25.976	17.672	52.681	107.122	22.397
PLACE1006466	16.826	15.029	9.777	6.348	6.589	37.897	68.487	10.963
PLACE1006469	114.915	41.384	25.605	23.261	24.572	43.598	56.094	27.697
PLACE1006470	55.482	77.949	32.199	34.721	19.002	28.695	34.080	43.083
PLACE1006472	28.012	90.945	17.951	34.982	34.443	50.263	43.401	25.783
PLACE1006476	82.952	54.658	25.673	33.003	18.685	19.667	20.505	28.511
PLACE1006482	37.848	28.214	30.184	15.252	21.907	16.121	16.707	16.335
PLACE1006488	97.835	75.446	33.550	35.911	33.400	45.132	55.401	62.770
PLACE1006492	97.220	112.335	55.156	47.821	45.198	37.895	64.975	45.897
PLACE1006506	10.034	13.735	10.029	17.741	10.467	11.563	6.929	9.994
PLACE1006515	8.615	13.662	12.057	16.818	11.489	8.981	15.280	14.480
PLACE1006516	30.098	17.795	12.792	10.123	12.004	10.884	13.079	19.137
PLACE1006520	38.963	54.680	36.238	25.639	24.822	21.437	19.311	31.254

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Table 141

PLACE1006521	75.538	103.128	42.948	44.567	33.031	39.882	33.174	40.181
PLACE1006529	53.118	57.618	37.171	32.693	19.830	30.529	24.356	58.315
PLACE1006531	40.054	29.614	19.743	13.919	11.061	28.487	25.077	22.594
PLACE1006534	14.806	14.541	8.631	12.208	7.086	10.456	12.140	35.132
PLACE1006540	111.144	85.745	65.687	62.909	47.508	47.210	44.007	49.020
PLACE1006549	105.750	35.667	33.934	19.913	34.720	68.368	52.699	40.656
PLACE1006550	53.734	37.476	23.619	17.863	13.277	25.245	30.050	25.681
PLACE1006552	36.731	63.851	24.515	30.033	16.150	29.038	26.902	30.874
PLACE1006557	59.138	32.373	20.742	27.767	14.998	53.010	66.775	24.301
PLACE1006563	12.150	25.131	12.554	16.291	12.325	21.067	6.774	21.632
PLACE1006579	42.172	33.427	19.515	12.744	11.202	30.323	25.161	17.624
PLACE1006594	21.308	62.751	8.959	11.953	18.053	24.751	10.056	19.854
PLACE1006598	38.010	39.953	22.806	22.256	14.136	17.359	14.218	22.463
PLACE1006607	29.363	43.175	35.099	25.311	27.168	25.817	24.362	33.010
PLACE1006610	70.554	56.140	32.568	26.861	32.156	41.824	78.456	52.641
PLACE1006615	66.799	84.729	48.211	42.137	41.400	36.165	33.872	68.891
PLACE1006617	46.945	34.203	20.650	24.016	10.809	19.146	13.632	19.570
PLACE1006618	12.467	22.675	10.936	4.988	6.177	12.939	14.170	17.583
PLACE1006626	28.824	22.724	12.096	14.424	6.491	15.673	20.994	16.846
PLACE1006629	20.658	24.647	17.715	14.296	9.444	12.543	13.794	16.993
PLACE1006637	66.078	44.385	28.310	36.165	26.370	22.102	23.886	38.003
PLACE1006640	1.906	3.182	1.497	1.860	2.901	12.736	2.835	3.364
PLACE1006644	47.828	33.193	17.215	13.059	19.569	23.838	40.050	24.555
PLACE1006657	19.786	8.124	12.247	4.403	6.268	5.198	7.763	6.121
PLACE1006673	45.242	43.900	31.743	33.164	17.416	21.697	21.275	29.264
PLACE1006678	16.105	18.660	7.229	6.676	2.905	9.955	9.738	6.953
PLACE1006682	108.821	86.487	64.876	54.439	35.908	50.796	60.748	73.192
PLACE1006684	12.327	5.526	1.745	4.542	2.823	4.669	8.079	6.963
PLACE1006698	35.079	26.331	16.481	11.898	16.188	18.313	21.757	18.483
PLACE1006704	86.472	27.708	22.553	11.168	23.040	31.772	42.206	22.041
PLACE1006708	63.065	64.979	29.269	36.158	32.310	29.740	35.534	34.620
PLACE1006711	83.669	46.735	36.469	20.073	24.293	44.745	40.284	31.562
PLACE1006714	24.897	21.232	19.709	9.911	12.634	19.601	15.694	11.421
PLACE1006716	43.488	17.230	9.950	6.619	9.686	25.065	16.540	13.432
PLACE1006731	28.782	29.180	22.410	16.665	26.985	19.586	12.657	19.367
PLACE1006754	36.921	20.331	16.512	14.887	10.304	20.093	26.461	37.338
PLACE1006760	37.757	42.174	22.283	15.705	21.554	21.150	17.013	41.393
PLACE1006779	3.647	8.616	3.016	6.280	6.191	5.298	7.122	6.796
PLACE1006782	92.507	28.870	38.409	19.483	30.410	47.327	64.324	35.890
PLACE1006783	27.858	31.732	12.496	14.567	10.900	18.396	16.357	16.765
PLACE1006786	24.498	14.495	7.472	4.210	11.343	13.380	15.312	7.438
PLACE1006792	77.449	84.545	47.367	55.539	38.143	39.428	24.476	35.695
PLACE1006795	9.133	4.460	1.737	2.793	3.353	3.139	2.968	3.320
PLACE1006800	4.005	5.373	6.293	5.585	5.488	3.372	4.355	6.632
PLACE1006805	10.412	18.118	5.886	6.406	8.461	8.216	2.942	9.555
PLACE1006809	42.846	42.011	18.294	14.933	24.393	18.264	52.680	31.248
PLACE1006815	28.382	27.387	16.127	14.696	18.598	11.836	22.066	24.307
PLACE1006819	2.234	8.095	0.000	2.742	7.006	3.430	4.844	0.000
PLACE1006820	88.654	108.172	51.115	52.886	36.795	40.511	48.278	48.233
PLACE1006826	36.400	44.215	19.975	9.428	19.371	14.819	20.833	17.598
PLACE1006829	92.548	43.863	26.240	21.591	27.592	41.457	58.358	33.442
PLACE1006853	36.698	17.968	19.226	51.037	13.795	25.742	31.212	23.318
PLACE1006860	6.034	4.924	7.203	4.039	4.197	4.808	5.604	5.225
PLACE1006867	38.603	40.857	22.938	11.226	24.586	16.186	22.604	24.184
PLACE1006875	22.250	34.942	8.578	8.800	8.892	8.348	13.170	11.720
PLACE1006878	39.239	23.697	15.013	10.894	12.955	15.847	22.292	15.804
PLACE1006883	65.288	68.499	32.894	27.525	25.683	25.744	33.055	31.151
PLACE1006898	7.500	7.894	4.988	7.018	5.096	6.810	8.442	10.343
PLACE1006901	21.369	32.566	11.362	7.983	8.638	19.295	23.630	15.803
PLACE1006904	50.887	60.723	40.359	39.241	22.863	21.440	24.218	30.368
PLACE1006917	15.269	18.119	4.506	8.871	9.082	12.291	14.762	18.898
PLACE1006932	74.387	50.295	37.532	27.777	18.687	40.241	61.634	41.770
PLACE1006935	26.622	22.255	28.033	13.044	12.097	19.289	20.081	16.451
PLACE1006956	46.862	37.348	13.802	17.258	7.757	23.631	21.753	16.324

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Table 142

PLACE1006958	24.224	20.988	2.886	4.740	6.547	12.414	18.682	11.106
PLACE1006959	18.928	26.190	17.859	8.749	10.471	20.650	31.538	10.229
PLACE1006961	117.650	81.345	44.174	45.983	28.766	40.349	60.294	45.326
PLACE1006962	45.285	44.217	26.483	25.012	20.091	22.762	20.963	25.186
PLACE1006966	28.233	14.490	13.064	8.732	12.926	14.261	20.842	9.575
PLACE1006979	17.727	17.092	9.075	8.221	7.276	14.248	14.630	10.668
PLACE1006989	32.865	52.943	17.860	11.639	7.697	14.839	32.067	28.756
PLACE1007001	63.189	31.010	16.872	11.652	13.459	33.428	28.562	26.941
PLACE1007014	92.804	49.098	38.389	21.381	19.097	50.704	38.424	25.032
PLACE1007021	32.615	23.234	9.800	10.544	10.271	12.863	18.290	11.436
PLACE1007026	6.113	17.016	5.244	5.923	5.797	4.186	5.493	10.123
PLACE1007028	32.763	23.055	16.841	11.266	15.159	13.728	15.276	14.576
PLACE1007038	326.043	1311.392	60.986	281.140	73.181	232.551	242.218	1764.485
PLACE1007040	29.591	22.423	21.374	13.642	14.126	14.427	15.726	19.822
PLACE1007045	78.257	39.847	30.671	22.858	23.390	22.928	15.061	21.566
PLACE1007048	122.391	2230.938	512.462	376.525	527.636	419.669	96.387	239.735
PLACE1007053	25.010	19.115	11.205	9.097	8.179	14.765	16.384	14.731
PLACE1007068	99.855	72.463	39.350	24.132	16.753	40.977	65.159	29.062
PLACE1007070	18.155	27.141	16.021	17.985	10.589	22.789	20.149	22.755
PLACE1007076	36.900	36.555	20.522	28.282	20.816	24.263	20.952	30.465
PLACE1007077	45.865	32.193	19.090	3.110	15.647	30.538	45.495	14.900
PLACE1007081	5.244	5.196	3.378	1.304	2.199	3.337	3.589	2.171
PLACE1007082	55.736	39.537	14.678	18.774	16.347	23.666	45.049	21.718
PLACE1007092	16.389	10.500	7.344	11.776	17.009	14.076	7.700	7.525
PLACE1007096	46.332	24.876	22.197	12.502	9.398	24.039	25.213	11.883
PLACE1007097	34.116	23.336	12.085	13.012	5.587	12.093	31.892	15.157
PLACE1007099	57.957	45.253	26.945	15.165	13.161	35.273	26.948	25.079
PLACE1007105	28.626	17.036	14.234	9.937	8.933	12.714	17.885	14.722
PLACE1007108	41.006	85.910	11.197	12.028	13.853	86.217	130.751	40.877
PLACE1007111	8.964	10.681	5.949	7.255	7.501	9.749	5.640	8.886
PLACE1007112	30.195	16.582	14.410	10.804	11.077	14.707	17.795	20.354
PLACE1007130	11.359	6.838	5.607	4.816	2.918	3.208	6.435	5.903
PLACE1007132	68.292	55.387	61.678	43.595	44.456	42.578	73.359	40.514
PLACE1007140	24.801	47.103	18.726	21.699	14.109	24.706	33.892	29.052
PLACE1007143	27.771	21.700	13.298	16.396	7.325	14.674	16.496	15.455
PLACE1007169	21.059	24.932	10.043	15.314	10.483	14.373	24.878	12.622
PLACE1007178	29.316	18.952	15.204	8.851	14.010	19.633	12.459	9.702
PLACE1007190	28.853	21.235	6.481	10.255	7.822	10.991	13.037	15.192
PLACE1007201	20.919	11.754	12.200	7.867	9.329	15.651	10.737	9.150
PLACE1007202	75.891	83.211	41.376	35.864	26.097	42.107	58.498	71.342
PLACE1007226	38.727	32.391	24.013	15.641	12.748	28.566	20.020	22.254
PLACE1007238	37.920	27.260	52.707	11.101	5.882	19.768	19.683	17.554
PLACE1007239	25.792	17.879	12.822	11.697	11.572	18.220	21.634	16.456
PLACE1007242	30.312	21.645	13.524	8.187	7.387	15.238	18.734	11.918
PLACE1007243	16.786	6.525	8.256	6.326	5.657	7.341	10.310	9.966
PLACE1007247	47.743	24.409	31.744	16.238	32.693	32.792	30.910	21.768
PLACE1007257	50.989	45.094	26.453	23.676	21.435	26.525	35.446	30.498
PLACE1007274	63.868	57.917	46.739	45.986	28.012	27.790	32.367	40.126
PLACE1007276	45.004	47.623	29.716	29.699	15.514	21.277	23.689	25.771
PLACE1007282	51.770	26.821	22.456	16.571	9.849	43.054	30.862	14.968
PLACE1007286	51.312	41.826	34.573	41.722	19.403	28.174	21.307	30.962
PLACE1007296	8.691	28.816	22.924	7.019	9.655	18.375	19.761	16.151
PLACE1007301	14.846	7.597	2.854	7.648	4.229	5.900	6.990	4.970
PLACE1007314	170.251	163.936	56.463	38.977	43.654	76.971	91.606	68.051
PLACE1007317	7.805	11.960	5.840	5.398	4.800	9.797	18.145	7.716
PLACE1007329	22.649	18.115	14.302	12.544	11.135	12.522	26.259	13.018
PLACE1007338	32.760	36.157	17.328	12.019	11.239	16.157	19.433	12.376
PLACE1007342	35.584	25.027	13.466	10.077	8.452	19.638	24.471	16.054
PLACE1007345	27.643	23.135	8.538	8.998	9.212	19.233	18.792	14.508
PLACE1007348	84.876	67.312	49.862	48.124	36.586	44.530	49.735	51.509
PLACE1007359	41.334	34.842	12.894	10.401	10.905	16.783	28.957	21.056
PLACE1007367	120.915	119.906	57.724	73.270	55.553	44.404	58.114	52.219
PLACE1007375	14.867	27.740	13.196	6.713	11.526	13.015	22.797	19.523
PLACE1007377	44.023	32.953	18.430	10.505	15.018	23.300	20.623	14.853

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Table 143

PLACE1007386	18.828	87.737	1.254	10.203	6.191	27.672	67.719	218.918
PLACE1007392	8.222	11.434	10.749	9.637	5.668	4.825	14.652	34.452
PLACE1007402	65.708	33.760	18.689	10.518	17.357	31.450	39.891	22.559
PLACE1007409	9.770	9.329	3.971	4.482	6.413	5.266	14.242	6.437
PLACE1007416	27.788	14.552	13.712	11.561	17.284	15.858	12.261	17.200
PLACE1007420	46.820	65.531	26.848	15.727	22.458	25.870	29.321	26.656
PLACE1007431	19.972	36.820	4.499	11.250	12.525	8.981	18.986	18.539
PLACE1007450	45.777	50.126	22.855	30.226	21.905	18.828	17.972	24.671
PLACE1007452	33.958	46.157	8.675	25.984	25.596	10.982	23.901	19.624
PLACE1007454	73.816	122.886	31.320	44.109	41.875	41.307	59.818	59.212
PLACE1007460	46.871	45.449	25.529	18.180	20.772	23.068	34.418	21.265
PLACE1007478	30.938	25.400	12.040	19.617	18.742	17.249	22.181	21.235
PLACE1007484	35.483	18.194	16.643	12.842	15.645	21.889	39.282	17.141
PLACE1007488	12.070	11.216	5.905	2.621	6.264	5.521	13.139	9.035
PLACE1007507	16.065	19.266	11.755	10.003	10.052	11.006	19.984	19.609
PLACE1007511	12.031	9.468	5.676	5.965	5.991	6.407	13.848	8.173
PLACE1007513	28.839	33.816	17.234	10.351	5.817	26.217	25.383	15.457
PLACE1007524	31.989	52.731	17.490	18.194	13.641	11.134	17.227	20.016
PLACE1007525	53.144	47.497	20.989	29.065	21.557	14.406	17.969	19.213
PLACE1007537	114.162	62.590	29.450	28.798	42.322	39.868	74.479	42.203
PLACE1007544	13.698	23.058	10.584	10.736	6.412	6.388	19.809	12.059
PLACE1007547	34.533	43.022	15.777	19.820	14.818	10.460	22.065	27.725
PLACE1007557	68.240	54.730	20.858	22.219	17.520	22.378	30.659	28.149
PLACE1007560	56.701	37.749	42.477	13.441	33.714	29.243	17.177	19.085
PLACE1007565	19.954	13.569	9.536	4.633	3.515	11.734	10.232	6.747
PLACE1007580	5.661	16.015	3.081	3.286	2.111	3.703	7.852	3.004
PLACE1007583	21.325	12.320	19.036	4.553	5.377	21.293	19.488	5.045
PLACE1007591	23.357	23.264	12.980	17.204	13.786	15.975	15.980	13.540
PLACE1007598	10.914	22.683	12.140	19.473	7.678	9.978	10.043	33.199
PLACE1007610	8.777	5.574	4.440	3.931	0.000	4.051	14.144	7.161
PLACE1007618	27.729	17.405	12.198	7.493	7.679	9.540	14.682	10.695
PLACE1007621	127.255	33.162	30.450	23.070	22.170	28.865	21.828	41.949
PLACE1007626	52.820	41.475	28.151	29.773	20.867	60.602	51.332	54.570
PLACE1007632	59.751	36.549	27.076	16.433	16.357	35.583	30.758	23.467
PLACE1007635	54.365	34.862	13.465	8.465	10.812	17.884	31.723	24.974
PLACE1007645	36.884	32.380	12.803	11.465	4.647	16.976	17.366	15.901
PLACE1007649	22.119	4.188	5.061	14.689	4.509	20.917	21.502	5.164
PLACE1007659	68.472	46.570	26.862	59.476	24.769	18.505	25.281	32.267
PLACE1007669	68.844	76.485	26.431	38.944	24.278	27.709	17.065	31.698
PLACE1007677	36.578	30.684	12.552	23.334	10.440	22.611	14.842	25.043
PLACE1007688	56.110	18.042	22.153	6.473	14.256	12.150	17.233	6.418
PLACE1007690	6.860	17.051	10.688	8.318	11.590	6.899	7.099	22.589
PLACE1007697	12.184	6.551	4.310	0.941	2.439	6.854	5.985	3.880
PLACE1007702	60.683	12.143	7.740	2.796	6.156	6.869	11.415	8.331
PLACE1007705	40.045	12.817	8.512	4.274	16.193	10.241	23.445	15.595
PLACE1007706	39.169	33.551	11.130	5.527	15.086	10.115	26.633	16.152
PLACE1007725	21.127	27.357	11.385	7.814	15.584	9.357	10.094	10.940
PLACE1007729	28.499	11.383	5.377	3.729	5.453	10.931	14.086	2.233
PLACE1007730	24.859	34.871	14.038	4.450	6.592	10.898	20.320	10.820
PLACE1007737	64.586	44.554	26.554	35.091	21.728	24.240	17.956	20.227
PLACE1007743	0.859	3.414	1.135	0.831	1.756	0.000	2.807	3.029
PLACE1007746	32.087	24.843	12.795	9.457	15.204	23.195	23.929	16.253
PLACE1007753	45.192	21.910	9.160	5.490	6.220	15.374	19.779	8.797
PLACE1007769	10.061	8.971	6.218	3.760	4.071	5.692	14.415	1.425
PLACE1007780	67.441	127.130	21.733	15.299	22.677	23.156	29.565	40.783
PLACE1007791	23.878	27.811	11.597	13.757	6.973	17.452	7.642	15.202
PLACE1007807	19.033	12.372	5.484	6.978	9.961	8.811	4.940	6.447
PLACE1007810	4.996	1.979	9.153	2.374	1.625	2.064	0.000	2.487
PLACE1007814	14.723	20.542	6.165	4.598	7.019	42.572	9.703	22.490
PLACE1007828	27.262	13.301	7.076	3.678	7.841	36.007	16.434	6.803
PLACE1007829	39.218	31.875	29.215	36.489	31.435	20.584	14.818	23.160
PLACE1007841	28.125	53.151	12.021	8.710	12.766	9.299	12.702	16.628
PLACE1007842	27.286	21.658	17.505	13.015	10.257	15.529	19.091	16.698
PLACE1007843	5.632	5.828	4.884	2.279	5.802	2.324	1.588	5.313

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Table 144

PLACE1007845	3.434	6.356	3.584	2.435	2.658	6.674	5.597	3.658
PLACE1007846	40.170	23.220	10.470	9.642	6.328	8.370	6.111	14.996
PLACE1007848	12.413	17.578	5.873	13.557	4.620	7.164	5.426	9.910
PLACE1007852	3.936	5.252	4.966	2.146	2.510	0.958	1.562	2.641
PLACE1007858	4.377	15.690	8.840	10.046	13.186	7.564	4.439	10.001
PLACE1007866	58.984	20.206	21.195	15.579	24.307	27.536	24.518	13.052
PLACE1007871	204.996	132.437	121.332	60.458	61.024	130.512	134.180	110.829
PLACE1007877	75.858	20.469	18.620	9.121	11.830	21.548	25.804	17.607
PLACE1007878	15.982	20.582	3.622	6.710	3.655	14.406	12.913	15.821
PLACE1007881	5.139	6.128	4.453	3.005	1.236	3.305	7.871	4.530
PLACE1007885	10.863	10.414	2.393	2.603	1.012	13.782	10.374	10.918
PLACE1007897	3.536	7.072	22.069	4.855	1.990	1.974	3.199	4.659
PLACE1007908	63.322	28.830	20.884	16.585	18.747	22.332	15.357	17.050
PLACE1007922	6.729	11.816	3.722	1.844	4.727	16.181	8.423	4.078
PLACE1007946	27.577	42.553	23.514	21.412	15.005	14.653	22.549	38.209
PLACE1007950	28.154	21.145	11.483	10.791	14.345	20.195	13.857	11.448
PLACE1007954	1.952	1.428	1.401	0.592	0.724	0.690	1.654	2.786
PLACE1007955	30.872	13.716	10.671	9.325	3.419	15.434	21.029	15.095
PLACE1007956	1.554	4.401	1.470	1.778	0.511	0.943	0.995	8.053
PLACE1007958	23.822	7.110	10.987	1.811	8.123	9.545	15.981	7.219
PLACE1007965	18.538	20.464	2.855	8.612	5.623	10.415	21.427	13.049
PLACE1007969	71.000	42.207	14.155	7.330	17.492	25.314	22.985	16.519
PLACE1007971	8.582	17.461	12.294	9.798	9.716	7.546	12.569	20.375
PLACE1007990	14.189	22.169	6.466	9.895	22.657	6.165	13.868	14.027
PLACE1008000	0.000	0.000	1.759	0.861	0.988	0.774	1.458	0.870
PLACE1008002	0.864	4.483	1.720	0.911	2.225	0.000	3.225	2.113
PLACE1008037	8.517	15.137	4.093	2.533	2.819	5.266	6.174	7.710
PLACE1008044	3.591	23.823	1.467	5.023	1.182	19.457	3.724	2.532
PLACE1008045	18.199	6.964	4.191	3.679	17.990	6.174	6.044	5.063
PLACE1008080	76.289	22.095	15.736	9.042	15.116	29.174	43.170	18.085
PLACE1008092	20.084	14.350	5.254	4.007	6.883	5.838	13.221	8.271
PLACE1008095	66.206	18.003	15.876	6.661	9.692	30.034	18.610	15.864
PLACE1008105	9.855	17.053	8.653	4.784	6.369	24.163	14.324	8.775
PLACE1008107	14.915	17.501	29.282	1.321	21.336	190.243	17.482	0.000
PLACE1008111	8.429	3.951	10.948	3.878	3.406	5.838	4.201	5.349
PLACE1008113	107.214	70.670	30.690	73.906	24.521	56.386	67.918	68.831
PLACE1008122	31.236	2.957	2.188	2.896	3.218	4.599	3.943	4.297
PLACE1008129	24.832	21.510	6.892	5.243	10.303	6.956	15.518	10.266
PLACE1008132	20.962	34.980	15.446	14.729	12.780	18.057	15.326	27.742
PLACE1008137	97.118	20.794	22.343	16.524	21.684	39.970	38.580	25.034
PLACE1008174	45.018	51.261	15.909	36.535	14.772	26.923	25.502	28.082
PLACE1008177	41.484	79.290	24.754	30.372	26.003	23.816	34.010	37.711
PLACE1008181	1.719	2.220	2.731	0.000	1.579	0.000	6.557	3.286
PLACE1008195	59.623	28.489	14.221	11.368	19.333	17.299	34.734	21.508
PLACE1008198	30.548	13.400	9.985	9.568	10.838	10.004	14.077	13.967
PLACE1008201	18.370	7.316	4.891	5.330	6.707	8.374	16.701	15.508
PLACE1008209	11.353	15.685	6.786	7.826	11.313	9.337	6.422	11.127
PLACE1008226	40.512	35.430	15.314	15.161	14.198	15.868	18.668	19.246
PLACE1008227	40.507	49.861	13.616	20.914	14.854	9.763	13.025	19.554
PLACE1008231	13.879	38.634	2.426	4.727	8.085	4.880	3.680	4.587
PLACE1008238	62.239	36.096	22.111	14.596	32.492	27.046	36.607	14.304
PLACE1008244	2.208	6.899	2.977	5.162	5.114	4.285	6.204	4.727
PLACE1008249	9.950	8.827	3.637	14.938	3.829	2.643	7.089	6.790
PLACE1008266	177.598	94.617	27.398	54.336	27.771	53.728	115.566	97.747
PLACE1008273	26.850	24.840	19.295	15.300	10.215	14.210	25.631	13.366
PLACE1008275	7.369	9.842	4.453	4.989	2.363	2.541	5.429	3.803
PLACE1008280	47.000	12.903	19.045	18.567	8.878	21.704	28.612	11.871
PLACE1008282	19.090	27.779	14.090	10.295	11.110	31.118	29.438	15.956
PLACE1008297	6.219	12.097	3.998	6.013	4.168	5.065	4.017	9.825
PLACE1008303	15.637	11.812	4.839	11.352	5.186	10.716	16.193	8.079
PLACE1008309	8.980	7.655	17.125	5.783	7.441	4.054	15.194	6.597
PLACE1008315	28.142	42.303	28.402	20.318	11.259	14.958	25.052	14.165
PLACE1008329	129.029	41.587	35.939	19.948	17.798	32.238	36.345	22.076
PLACE1008330	40.094	61.042	26.271	19.770	13.083	8.774	16.194	11.542

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Table 145

PLACE1008331	27.986	47.595	19.541	30.549	6.771	12.430	19.559	14.501
PLACE1008351	31.374	25.837	26.940	15.283	21.769	12.877	29.581	16.720
PLACE1008356	11.038	24.238	10.669	11.527	6.248	8.108	12.839	23.469
PLACE1008359	23.219	18.821	4.585	6.804	10.499	0.000	2.547	1.436
PLACE1008368	7.861	12.077	7.076	8.221	6.772	3.046	4.473	8.994
PLACE1008369	13.265	19.288	23.206	5.056	9.188	8.024	3.252	7.150
PLACE1008392	33.219	24.613	7.199	8.079	6.094	3.416	5.773	14.321
PLACE1008394	408.885	231.502	159.847	115.713	108.082	197.383	152.685	161.031
PLACE1008398	25.185	65.413	11.186	3.178	10.620	12.052	60.522	4.172
PLACE1008401	9.122	14.441	7.348	5.588	6.040	4.705	5.467	13.166
PLACE1008402	9.663	11.925	9.911	6.799	5.684	2.926	6.105	8.816
PLACE1008405	564.405	448.002	386.959	390.811	233.214	323.322	279.406	299.078
PLACE1008409	310.254	194.222	107.706	88.926	100.879	133.079	164.162	134.635
PLACE1008420	102.871	44.916	30.154	14.685	18.701	45.968	47.225	19.396
PLACE1008424	7.842	8.421	6.860	6.448	7.117	8.493	7.105	5.879
PLACE1008426	34.481	18.699	20.403	7.577	16.885	9.223	17.802	15.759
PLACE1008429	19.812	18.343	10.368	12.697	6.738	14.423	9.882	12.964
PLACE1008430	15.959	9.694	5.026	2.761	4.442	8.785	16.237	9.842
PLACE1008437	29.520	12.626	6.518	4.954	3.470	6.216	6.790	9.990
PLACE1008453	45.498	38.572	11.482	14.114	13.893	18.459	30.671	26.924
PLACE1008454	92.852	69.938	35.812	43.358	32.139	34.380	44.342	24.973
PLACE1008455	110.060	132.654	101.535	72.107	48.679	28.207	49.762	96.618
PLACE1008457	221.026	164.638	87.890	67.565	56.681	96.733	57.289	64.132
PLACE1008465	14.482	45.181	6.482	5.652	7.215	4.989	7.987	10.103
PLACE1008469	191.519	126.151	83.503	66.767	67.955	101.454	113.684	104.824
PLACE1008488	12.143	25.044	5.332	0.377	5.344	4.917	4.843	10.115
PLACE1008519	26.949	18.134	9.335	5.792	12.237	15.758	18.736	15.770
PLACE1008524	16.341	9.879	14.963	4.596	10.881	12.847	12.491	8.424
PLACE1008531	26.300	44.215	12.618	14.596	8.835	12.002	17.900	27.017
PLACE1008532	23.293	26.180	13.194	12.256	5.529	20.046	14.458	31.354
PLACE1008533	50.837	25.004	15.099	14.960	12.107	13.885	15.331	16.687
PLACE1008542	7.209	11.351	11.148	11.159	7.406	3.275	4.870	8.793
PLACE1008549	24.848	27.469	14.722	7.446	35.339	4.849	21.994	15.899
PLACE1008560	16.248	9.601	10.580	4.328	6.786	9.843	14.007	6.753
PLACE1008567	31.376	46.822	16.034	16.944	14.791	13.929	17.148	17.570
PLACE1008568	9.263	28.507	12.536	7.903	15.738	22.714	15.252	13.545
PLACE1008569	21.434	13.045	5.050	6.520	8.664	9.142	10.799	9.664
PLACE1008584	29.627	24.002	13.657	10.990	11.106	13.734	22.655	21.057
PLACE1008585	25.861	23.246	13.959	7.124	8.320	13.100	8.184	14.617
PLACE1008803	11.593	12.897	3.634	5.109	4.753	7.887	18.167	11.774
PLACE1008821	6.723	3.752	3.073	2.882	0.628	2.394	2.356	6.079
PLACE1008825	5.997	8.406	1.768	1.055	1.816	1.254	2.598	3.068
PLACE1008826	5.484	3.562	1.402	1.123	1.403	3.049	5.665	3.510
PLACE1008827	49.718	18.742	10.960	7.037	8.831	13.117	21.039	15.675
PLACE1008829	21.102	28.942	11.982	3.365	9.612	12.027	17.865	12.171
PLACE1008830	9.527	21.990	10.098	9.473	7.038	5.568	7.548	9.704
PLACE1008843	41.545	29.478	16.220	15.566	9.566	16.636	24.733	18.160
PLACE1008850	4.202	2.471	1.051	2.532	0.932	2.348	3.778	2.601
PLACE1008857	10.667	16.060	5.999	8.523	5.606	4.350	8.873	8.539
PLACE1008864	7.147	9.457	8.348	2.448	3.877	5.707	7.490	2.436
PLACE1008893	35.830	32.008	13.154	7.301	10.960	12.214	13.885	10.914
PLACE1008898	30.598	14.195	9.900	6.913	8.747	8.454	9.419	10.479
PLACE1008715	6.265	13.318	2.170	5.131	3.050	3.374	6.120	5.989
PLACE1008716	10.756	11.071	14.349	7.225	9.919	5.434	16.844	11.965
PLACE1008722	19.150	29.145	12.082	14.107	7.317	7.365	11.291	13.128
PLACE1008738	12.649	24.539	11.238	5.658	9.182	17.327	16.429	12.149
PLACE1008742	4.334	14.217	7.739	8.863	5.946	8.825	6.516	10.305
PLACE1008744	8.130	10.071	2.674	2.854	2.153	2.940	3.519	4.369
PLACE1008748	8.135	6.332	0.964	1.850	7.331	2.772	2.033	6.870
PLACE1008757	0.000	1.927	1.248	0.983	2.427	2.818	1.135	1.993
PLACE1008766	4.606	24.202	3.622	1.672	4.576	4.758	5.053	2.617
PLACE1008785	84.472	51.726	24.136	25.096	17.140	24.917	15.172	19.772
PLACE1008790	31.403	25.252	14.095	12.995	13.157	12.786	21.229	14.549
PLACE1008798	3.470	1.735	2.715	1.244	2.837	1.268	3.684	4.700

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Table 146

PLACE1008807	11.746	9.388	7.010	3.398	4.152	5.286	9.954	7.993
PLACE1008808	10.497	2.010	1.832	1.724	2.154	0.000	2.960	3.938
PLACE1008813	43.335	8.124	3.170	3.472	6.648	0.000	5.265	5.081
PLACE1008836	13.208	30.377	8.014	11.550	8.774	9.700	18.296	15.156
PLACE1008851	35.131	44.912	12.581	38.594	17.658	12.467	22.869	17.982
PLACE1008854	5.882	9.135	0.000	4.861	5.302	11.675	6.631	8.631
PLACE1008864	48.984	42.179	18.396	30.397	21.064	16.595	22.139	23.902
PLACE1008867	12.377	56.824	11.324	9.452	18.933	14.620	10.186	16.826
PLACE1008876	49.946	97.258	18.984	54.608	14.811	25.438	23.529	37.995
PLACE1008887	26.489	38.089	16.208	16.042	20.811	10.479	15.115	15.164
PLACE1008902	22.685	13.678	2.921	7.383	19.625	2.141	5.762	6.510
PLACE1008911	9.060	33.193	12.197	13.856	16.972	6.042	11.666	13.828
PLACE1008917	42.217	35.405	16.607	7.160	18.874	11.592	41.024	22.806
PLACE1008920	32.162	3.225	1.754	3.766	3.590	9.067	6.073	2.425
PLACE1008925	13.417	17.966	5.400	5.416	6.761	6.566	12.223	7.803
PLACE1008930	15.886	28.504	9.408	9.552	6.095	6.477	16.830	11.057
PLACE1008934	23.769	18.548	12.356	6.943	12.662	6.117	11.146	9.917
PLACE1008941	8.316	9.677	5.776	9.338	9.104	5.758	12.723	13.555
PLACE1008947	150.057	83.432	44.128	33.278	56.786	59.699	86.640	63.955
PLACE1008984	8.712	10.873	4.711	5.382	2.608	4.656	10.459	7.929
PLACE1008985	25.866	40.327	13.608	7.899	8.177	11.454	23.995	16.883
PLACE1008994	18.162	8.786	5.711	2.403	2.775	3.796	8.332	3.014
PLACE1009020	11.578	10.784	5.965	4.614	3.880	6.161	11.355	7.439
PLACE1009027	21.125	15.947	4.623	2.459	3.520	11.909	6.684	4.839
PLACE1009039	8.664	10.154	6.735	2.521	7.750	11.874	23.006	4.885
PLACE1009045	23.977	20.675	6.979	7.407	4.810	5.799	35.292	9.408
PLACE1009048	5.091	10.171	2.268	5.954	4.362	0.000	5.318	6.521
PLACE1009050	3.470	5.590	9.098	4.708	3.880	0.000	4.164	8.669
PLACE1009060	34.280	32.398	9.016	17.646	9.108	20.791	23.124	21.665
PLACE1009067	55.833	32.552	13.821	5.577	11.693	36.606	50.944	44.507
PLACE1009071	137.113	72.622	42.839	42.259	33.328	32.445	60.967	59.816
PLACE1009090	30.957	25.567	12.139	8.147	11.883	22.624	22.381	10.572
PLACE1009091	42.486	15.715	10.526	6.902	14.110	5.159	15.660	17.580
PLACE1009094	21.335	70.138	13.676	8.271	10.714	16.361	21.919	17.604
PLACE1009099	7.525	13.610	8.280	12.776	8.281	12.542	10.801	31.093
PLACE1009110	13.415	6.006	4.409	1.648	2.849	4.580	4.965	5.369
PLACE1009111	67.629	16.954	11.182	7.515	0.000	7.804	15.142	12.395
PLACE1009113	10.615	8.546	4.331	4.640	5.385	6.432	5.643	10.147
PLACE1009130	6.901	19.609	23.895	6.686	2.762	2.544	1.446	3.744
PLACE1009150	13.031	20.426	5.736	7.683	3.673	7.990	4.988	8.429
PLACE1009155	72.157	61.300	57.610	55.149	41.987	39.328	50.150	57.022
PLACE1009158	28.497	16.235	13.335	10.201	11.626	14.318	26.507	16.570
PLACE1009166	58.030	29.706	24.997	22.721	18.028	18.384	27.587	24.065
PLACE1009172	16.222	19.005	7.161	4.843	6.408	6.734	8.370	6.017
PLACE1009174	50.892	48.998	32.343	28.578	23.381	21.627	24.363	21.250
PLACE1009183	61.545	60.739	14.751	35.658	16.796	15.529	13.831	15.373
PLACE1009186	5.029	11.552	6.154	4.372	2.812	8.067	6.126	4.542
PLACE1009190	0.112	1.383	2.215	1.077	0.922	0.000	0.000	0.879
PLACE1009196	15.938	15.069	6.337	11.235	5.301	4.199	8.229	7.836
PLACE1009200	56.062	49.582	26.621	32.612	20.016	13.451	19.592	29.814
PLACE1009217	9.045	7.250	3.382	10.839	3.645	4.062	6.924	17.092
PLACE1009230	35.137	34.356	13.699	21.015	16.141	8.394	19.789	7.528
PLACE1009236	34.867	17.528	8.326	7.770	9.004	12.493	27.327	9.172
PLACE1009246	51.787	71.164	28.320	15.835	21.078	9.019	29.697	24.935
PLACE1009265	92.450	36.053	21.026	11.424	10.085	43.325	58.877	30.908
PLACE1009279	25.174	8.294	11.814	5.069	6.771	10.155	13.253	6.328
PLACE1009288	28.708	18.088	16.943	10.646	14.479	14.708	8.886	9.738
PLACE1009308	175.031	34.217	34.842	16.711	32.150	62.967	72.179	28.297
PLACE1009319	21.209	35.386	7.874	8.898	7.493	12.353	8.009	11.881
PLACE1009328	34.584	30.370	22.052	20.297	22.536	16.474	11.081	13.533
PLACE1009335	3.869	10.615	12.941	6.343	1.756	4.228	4.162	27.779
PLACE1009338	4.629	13.280	7.145	2.945	5.427	8.953	7.332	6.665
PLACE1009344	33.854	26.440	7.150	7.043	5.231	9.005	17.883	10.752
PLACE1009355	10.104	50.509	4.034	2.919	3.153	6.227	6.669	19.235

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Table 147

PLACE1009368	42.051	14.861	10.631	6.209	7.101	7.025	15.596	9.443
PLACE1009375	19.461	10.862	1.937	2.161	5.975	8.807	9.665	4.779
PLACE1009388	41.922	22.694	9.119	6.828	8.777	12.117	12.174	12.815
PLACE1009398	9.410	16.113	10.077	14.136	8.930	7.363	10.053	24.623
PLACE1009404	27.332	38.221	8.577	12.742	8.050	15.604	26.279	8.093
PLACE1009410	9.672	6.807	2.954	3.849	2.292	2.641	6.326	4.231
PLACE1009417	11.321	13.342	11.760	7.745	9.842	13.265	12.016	15.150
PLACE1009424	143.874	161.949	83.678	44.296	55.295	145.780	98.718	82.459
PLACE1009434	3.639	9.793	2.953	4.133	3.385	3.038	6.041	7.934
PLACE1009443	10.126	5.900	2.564	1.418	3.826	4.205	6.190	3.051
PLACE1009444	75.456	51.672	32.690	29.162	27.896	35.657	35.401	25.671
PLACE1009459	110.550	32.136	23.433	13.124	19.500	46.330	49.514	27.422
PLACE1009460	7.804	18.196	5.042	1.388	3.715	11.334	3.840	5.965
PLACE1009488	24.940	28.488	14.998	8.351	9.763	9.596	31.733	20.845
PLACE1009476	18.955	12.973	6.635	5.700	3.950	6.971	12.745	5.157
PLACE1009477	28.528	28.026	14.306	21.520	9.248	17.462	14.475	15.028
PLACE1009493	9.706	13.481	2.399	3.953	1.914	6.774	6.193	9.481
PLACE1009502	3.768	2.155	2.938	0.891	2.166	5.093	2.120	1.962
PLACE1009524	41.369	7.099	18.781	3.777	7.184	16.229	19.248	12.391
PLACE1009527	41.383	14.310	8.219	3.634	8.710	15.448	19.901	11.203
PLACE1009531	43.331	29.448	11.293	13.089	12.741	23.938	26.244	25.592
PLACE1009535	11.347	16.999	7.257	9.551	6.031	5.821	7.459	13.160
PLACE1009539	27.355	33.924	17.760	19.107	12.625	17.181	18.261	21.706
PLACE1009540	26.063	18.180	18.706	13.776	10.936	19.307	24.429	16.284
PLACE1009542	32.314	9.517	6.333	8.159	7.348	18.062	22.235	9.384
PLACE1009546	12.399	7.380	5.625	1.298	3.320	4.724	8.207	4.406
PLACE1009556	13.954	15.082	5.948	1.391	6.465	10.966	16.358	19.196
PLACE1009569	22.909	21.209	6.670	12.434	5.803	8.233	9.438	12.507
PLACE1009571	13.458	10.535	6.868	4.758	5.027	9.733	7.553	9.107
PLACE1009573	16.235	9.693	6.699	13.447	6.873	4.277	8.380	12.992
PLACE1009576	4.851	10.697	8.157	4.542	2.949	3.677	5.201	5.143
PLACE1009580	35.237	47.578	24.938	26.636	15.366	25.243	27.920	23.541
PLACE1009581	30.483	8.604	7.654	6.565	7.711	16.692	24.706	13.168
PLACE1009587	3.476	3.868	5.230	3.387	4.099	4.838	6.514	5.783
PLACE1009593	7.424	8.043	3.949	5.143	4.859	7.848	5.031	4.525
PLACE1009595	63.588	58.749	27.289	26.946	25.118	25.486	32.674	29.915
PLACE1009596	10.136	8.803	2.554	6.077	10.559	3.608	12.421	11.189
PLACE1009600	15.391	21.884	10.853	7.573	11.964	20.158	11.161	14.987
PLACE1009604	32.270	9.947	13.494	11.363	10.658	9.443	19.197	18.000
PLACE1009607	75.364	85.156	35.035	26.439	26.445	29.568	26.168	30.122
PLACE1009613	4.353	6.164	2.640	5.243	1.911	2.792	2.408	6.068
PLACE1009621	29.001	49.946	14.693	13.116	18.138	23.193	22.997	15.101
PLACE1009622	27.300	10.327	8.159	5.651	12.385	9.234	15.408	7.132
PLACE1009624	27.426	19.103	3.360	2.878	7.125	4.125	12.179	7.539
PLACE1009637	5.028	13.109	5.041	2.366	9.802	4.190	6.416	4.450
PLACE1009639	9.956	16.237	4.056	3.880	8.587	3.660	14.640	27.577
PLACE1009654	29.616	69.766	58.647	5.371	50.183	22.307	21.782	12.466
PLACE1009659	10.143	12.022	13.185	10.544	15.157	2.883	7.467	4.763
PLACE1009665	19.662	15.718	10.263	8.654	15.968	3.947	7.286	5.058
PLACE1009669	74.335	65.299	22.539	17.666	23.035	36.889	47.853	26.094
PLACE1009670	48.759	30.681	15.505	15.680	13.512	21.863	46.277	13.806
PLACE1009708	9.584	14.533	5.232	5.640	7.390	7.392	11.586	7.014
PLACE1009721	0.000	5.965	1.997	1.030	1.425	4.841	5.611	3.780
PLACE1009731	31.531	29.697	5.222	13.383	9.274	42.308	14.822	16.604
PLACE1009735	24.842	17.444	8.225	8.391	3.900	11.001	10.728	17.147
PLACE1009737	20.121	19.390	12.614	11.682	4.987	10.582	13.461	11.206
PLACE1009741	3.834	48.256	3.058	11.965	12.402	22.656	1.749	4.187
PLACE1009752	37.588	360.319	9.532	24.594	5.279	91.807	22.992	435.143
PLACE1009763	15.243	3.785	8.458	12.043	11.844	8.197	7.432	17.382
PLACE1009765	15.481	13.821	10.168	12.459	8.733	9.416	11.841	13.177
PLACE1009772	25.177	13.697	7.336	5.603	5.178	8.892	12.233	6.915
PLACE1009782	8.994	6.560	6.371	4.141	13.633	6.484	6.993	16.851
PLACE1009784	16.900	14.024	7.950	9.013	5.083	18.417	17.171	7.465
PLACE1009788	16.321	14.039	13.398	11.317	4.355	4.228	6.535	7.202

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Table 148

PLACE1009845	15.220	4.333	2.997	5.329	2.393	2.613	22.333	11.323
PLACE1009849	44.946	194.619	17.197	64.071	16.467	30.251	38.997	341.202
PLACE1009857	21.842	11.784	14.813	9.010	7.686	17.560	23.505	10.157
PLACE1009861	55.060	52.334	22.982	38.531	21.999	12.526	21.181	42.147
PLACE1009872	42.867	65.398	11.814	72.397	19.845	26.217	21.062	57.158
PLACE1009877	144.154	73.771	52.613	35.986	26.345	12.461	20.382	36.147
PLACE1009879	31.357	19.333	43.105	15.026	16.781	19.583	20.282	9.265
PLACE1009886	3.579	8.567	2.869	1.043	1.021	1.571	2.025	1.893
PLACE1009888	10.362	6.906	3.541	1.720	7.325	6.831	7.680	6.285
PLACE1009908	16.750	13.979	9.123	6.093	6.107	7.524	13.900	10.848
PLACE1009919	25.958	16.368	12.802	7.838	12.682	8.032	7.157	13.099
PLACE1009921	5.294	5.301	2.647	2.379	6.669	1.694	6.864	1.626
PLACE1009923	7.666	10.700	2.427	3.962	7.335	13.971	11.821	6.627
PLACE1009924	26.023	5.683	3.961	1.712	2.571	0.000	6.021	12.826
PLACE1009925	3.609	1.404	0.882	1.882	0.508	7.012	3.169	2.473
PLACE1009931	37.980	53.080	21.843	35.590	14.645	25.179	18.163	39.695
PLACE1009935	7.854	3.468	2.666	1.324	0.764	2.382	4.922	3.501
PLACE1009947	44.482	21.773	17.615	11.373	13.359	12.852	18.329	12.383
PLACE1009961	3.264	4.537,	3.780	2.246	7.199	6.513	3.962	22.636
PLACE1009971	24.201	14.113	8.964	9.558	7.736	13.999	13.695	8.124
PLACE1009982	90.204	37.402	17.490	17.226	11.857	37.703	32.523	24.126
PLACE1009992	32.659	8.657	9.454	6.512	5.980	18.389	18.358	10.327
PLACE1009995	21.779	25.489	20.929	6.918	15.829	28.418	28.296	25.865
PLACE1009997	39.778	25.957	22.163	18.804	12.955	27.052	15.574	19.395
PLACE1010002	7.208	6.675	2.154	3.335	4.711	2.649	6.047	4.825
PLACE1010011	15.700	11.002	2.148	0.691	4.571	3.619	16.561	3.132
PLACE1010013	18.169	7.231	5.446	11.205	1.374	6.028	15.057	9.751
PLACE1010021	9.423	11.541	8.788	5.901	5.744	6.434	11.142	6.794
PLACE1010023	48.546	20.475	6.683	8.439	7.872	6.849	14.748	19.147
PLACE1010031	23.253	23.746	12.677	11.119	9.178	23.991	11.578	15.444
PLACE1010039	8.216	5.363	3.410	2.754	3.443	3.809	2.994	3.074
PLACE1010045	28.520	20.935	14.936	23.387	11.939	11.927	10.256	27.268
PLACE1010053	11.420	12.399	2.211	6.506	4.422	6.813	4.552	6.626
PLACE1010060	61.784	35.230	25.530	15.116	15.866	30.074	32.753	19.303
PLACE1010069	13.551	3.560	5.924	2.419	1.178	3.632	7.745	6.202
PLACE1010070	12.192	12.514	5.728	3.839	6.386	6.674	3.922	9.645
PLACE1010074	58.736	80.938	44.955	39.497	35.506	33.481	44.710	58.097
PLACE1010076	241.223	62.057	77.062	19.863	59.519	134.094	156.661	51.913
PLACE1010078	85.849	26.937	22.479	14.142	12.854	44.885	40.845	17.940
PLACE1010081	0.000	6.981	0.000	1.962	0.000	0.000	11.595	5.593
PLACE1010083	27.240	20.600	7.478	2.813	3.550	9.386	8.886	8.608
PLACE1010089	10.050	12.122	5.452	5.275	8.073	1.380	4.234	6.582
PLACE1010096	15.851	23.598	8.484	14.576	6.620	5.621	14.446	21.698
PLACE1010102	15.331	13.251	7.699	9.155	10.558	11.564	11.290	13.860
PLACE1010105	35.995	25.802	14.804	18.971	17.745	14.276	23.241	18.148
PLACE1010106	22.316	26.718	22.970	12.204	19.261	13.790	13.444	18.632
PLACE1010130	31.537	88.713	10.371	13.604	10.772	19.911	32.607	24.027
PLACE1010132	29.236	14.753	8.315	9.764	5.570	12.883	10.934	9.482
PLACE1010134	33.947	28.665	5.982	9.693	7.730	13.218	17.164	12.265
PLACE1010139	598.413	110.617	200.038	45.054	206.627	352.839	448.388	104.360
PLACE1010148	3.132	9.532	1.538	2.877	4.356	4.931	4.453	19.512
PLACE1010152	26.445	18.485	7.969	6.590	11.687	7.409	13.853	10.964
PLACE1010155	373.743	33.940	13.008	13.408	13.152	17.546	25.269	21.191
PLACE1010156	9.490	17.391	7.147	7.886	7.386	11.491	14.395	7.290
PLACE1010161	7.529	6.461	2.530	5.962	1.287	0.909	1.586	4.349
PLACE1010181	5.294	9.629	5.205	7.060	6.824	6.992	9.982	8.729
PLACE1010194	26.462	22.224	13.684	8.402	9.391	9.241	14.823	14.726
PLACE1010202	26.629	9.694	8.534	7.610	6.545	10.843	19.488	6.553
PLACE1010231	15.631	7.185	2.841	1.402	3.191	5.438	5.656	7.547
PLACE1010235	35.597	8.667	2.389	6.163	3.875	2.142	6.961	3.884
PLACE1010237	16.260	14.226	7.088	7.064	6.169	13.483	1580.612	9.264
PLACE1010251	22.207	49.596	11.643	9.801	49.122	9.288	17.391	23.237
PLACE1010261	9.199	12.479	6.658	4.050	3.058	2.869	4.685	3.866
PLACE1010270	3.528	2.564	2.884	1.612	2.378	5.332	5.567	4.920

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Table 149

PLACE1010273	18.198	10.799	5.456	7.563	10.408	11.696	11.805	8.650
PLACE1010274	20.202	18.193	10.486	9.941	13.997	14.739	14.496	20.193
PLACE1010277	8.937	117.446	5.398	3.512	4.011	1.815	8.164	10.102
PLACE1010293	60.036	62.516	18.939	20.260	11.120	8.879	14.863	20.261
PLACE1010297	10.456	6.185	4.720	3.674	4.733	7.175	13.007	16.488
PLACE1010300	17.008	24.187	7.187	17.501	12.198	7.801	13.650	16.733
PLACE1010310	413.605	200.863	167.599	97.554	142.759	225.854	230.002	179.252
PLACE1010321	36.500	65.804	16.701	11.196	12.716	16.372	17.343	18.872
PLACE1010324	0.000	8.637	3.654	1.998	3.447	3.169	4.956	2.116
PLACE1010329	30.906	39.387	9.407	14.862	11.246	12.390	12.923	13.038
PLACE1010330	182.247	52.788	42.842	20.272	46.381	81.215	103.997	33.527
PLACE1010335	20.429	27.007	19.301	14.056	19.661	14.766	38.945	16.803
PLACE1010341	15.512	16.397	5.370	6.587	7.213	4.477	8.264	8.294
PLACE1010342	5.485	5.818	1.359	2.968	2.444	1.600	5.664	2.119
PLACE1010346	27.509	31.551	11.234	16.701	10.972	11.936	17.866	16.679
PLACE1010362	37.800	42.341	20.410	19.994	20.516	14.039	23.979	21.826
PLACE1010364	3.637	7.688	4.890	1.792	3.344	6.491	9.839	7.931
PLACE1010368	160.448	94.255	69.658	48.395	60.226	64.663	105.004	71.078
PLACE1010373	50.531	36.656	15.978	12.876	19.197	22.390	35.216	29.763
PLACE1010383	60.222	42.672	28.248	34.317	29.853	11.968	26.253	22.869
PLACE1010385	0.000	3.211	0.000	1.653	2.697	0.000	3.102	0.000
PLACE1010389	45.010	32.965	23.673	18.734	15.387	31.864	30.482	22.113
PLACE1010401	12.554	12.082	7.358	3.809	4.486	9.049	11.163	8.023
PLACE1010410	46.622	19.531	23.525	15.038	12.094	26.576	30.580	20.641
PLACE1010418	63.170	54.185	47.245	53.690	29.885	39.952	35.428	40.754
PLACE1010425	8.496	10.271	8.511	8.469	6.845	60.372	16.883	14.750
PLACE1010443	139.820	68.717	76.495	49.901	31.535	91.673	163.084	100.340
PLACE1010445	55.230	63.853	40.195	41.679	24.598	29.543	39.397	42.435
PLACE1010481	25.071	14.236	12.932	6.994	7.811	11.242	18.708	11.397
PLACE1010482	62.044	30.485	12.054	12.510	7.434	27.561	32.378	14.322
PLACE1010491	6.692	11.769	7.835	7.107	2.403	7.772	8.897	7.016
PLACE1010492	8.815	25.244	14.396	11.795	10.757	10.883	11.758	14.039
PLACE1010509	8.728	8.603	9.041	7.620	3.097	8.537	33.229	11.438
PLACE1010518	53.737	47.379	37.510	43.651	35.422	32.152	29.681	41.839
PLACE1010522	74.460	121.326	35.701	24.026	30.767	37.996	82.263	44.005
PLACE1010529	13.116	47.273	16.874	13.123	11.833	10.805	15.047	19.475
PLACE1010547	10.791	15.015	13.620	12.464	6.861	9.050	12.611	9.113
PLACE1010560	36.084	24.074	20.254	16.291	7.397	21.958	19.638	14.752
PLACE1010562	21.600	13.040	13.412	10.004	8.160	11.786	18.067	7.693
PLACE1010578	5.809	7.166	3.015	3.108	2.173	6.175	8.453	8.370
PLACE1010580	50.738	35.579	19.709	14.021	14.505	33.521	41.838	28.526
PLACE1010599	22.697	6.399	6.660	7.383	6.210	12.163	6.932	13.134
PLACE1010606	17.463	9.467	5.119	4.737	13.966	8.754	6.341	10.710
PLACE1010616	16.337	36.535	10.492	11.411	9.645	7.170	14.986	17.679
PLACE1010622	30.437	14.238	13.526	5.708	14.881	22.701	23.807	13.849
PLACE1010624	25.823	18.627	12.823	9.811	10.874	16.364	11.721	14.514
PLACE1010628	13.901	8.075	8.420	7.978	5.728	9.596	13.922	11.287
PLACE1010629	27.634	40.133	12.859	11.330	8.045	9.191	14.370	10.210
PLACE1010630	12.405	13.949	22.021	11.675	24.752	13.736	15.999	18.920
PLACE1010631	19.768	3.918	10.504	6.454	14.638	11.915	14.522	11.552
PLACE1010651	61.423	22.948	13.549	11.707	15.050	34.204	25.544	13.578
PLACE1010661	34.409	28.267	21.006	15.010	15.022	20.249	46.492	15.719
PLACE1010662	26.892	31.410	14.036	11.805	9.079	11.854	20.418	11.826
PLACE1010668	48.769	42.753	31.810	18.319	31.679	38.651	30.999	41.826
PLACE1010702	18.288	30.872	29.474	49.880	16.196	19.234	12.868	56.417
PLACE1010709	65.293	137.910	34.914	39.908	20.047	33.698	24.664	119.725
PLACE1010713	30.772	37.995	14.083	5.649	14.470	23.106	20.135	20.050
PLACE1010714	8.200	4.190	5.041	3.912	6.929	6.468	3.785	5.298
PLACE1010716	23.008	5.374	11.836	10.138	7.071	12.870	12.608	13.906
PLACE1010717	17.845	18.487	9.358	10.750	8.548	10.849	15.442	15.266
PLACE1010720	66.247	125.637	43.070	49.521	29.493	36.612	36.709	48.414
PLACE1010739	14.550	8.279	5.945	5.951	3.067	4.103	5.256	5.571
PLACE1010743	9.101	4.610	3.589	2.256	1.332	3.158	5.514	4.487
PLACE1010752	68.064	30.437	20.104	10.787	15.198	31.010	28.793	18.098

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Table 150

PLACE1010761	26.459	111.645	25.313	97.785	46.971	35.398	19.393	56.313
PLACE1010771	97.575	46.358	30.540	20.492	21.112	45.643	41.271	23.174
PLACE1010784	34.813	13.196	12.948	6.263	8.395	17.778	16.235	12.720
PLACE1010786	35.506	55.424	19.835	19.203	16.991	22.191	24.116	30.768
PLACE1010789	14.662	9.740	10.856	8.035	6.035	6.662	6.785	6.617
PLACE1010800	12.898	11.478	12.969	11.574	8.280	13.756	9.074	10.785
PLACE1010802	9.976	7.639	11.257	6.385	8.708	6.482	9.517	9.615
PLACE1010811	6.267	10.750	6.130	5.326	2.131	5.807	7.023	5.806
PLACE1010813	107.134	54.846	41.785	19.939	26.019	51.877	79.848	45.993
PLACE1010827	11.543	12.554	6.090	2.687	4.360	10.117	10.344	9.099
PLACE1010833	70.712	36.952	36.612	16.799	28.163	60.904	40.462	31.469
PLACE1010839	56.261	52.196	32.723	40.363	32.757	24.743	30.658	33.056
PLACE1010856	15.444	56.200	14.751	17.041	11.951	20.702	14.170	62.029
PLACE1010857	16.284	24.674	22.222	15.965	8.058	13.468	10.994	20.619
PLACE1010870	11.360	15.311	10.708	17.750	6.704	9.120	10.270	16.911
PLACE1010877	12.253	23.451	12.897	9.474	11.687	13.857	6.866	12.944
PLACE1010882	24.453	43.270	15.698	9.810	8.334	17.859	26.634	77.062
PLACE1010891	12.636	7.098	6.674	7.840	6.799	5.426	7.441	5.870
PLACE1010896	35.110	39.870	19.987	16.507	18.760	17.466	22.357	29.192
PLACE1010900	50.692	63.882	25.595	31.970	25.080	27.551	37.245	35.556
PLACE1010916	17.218	31.574	12.713	10.089	10.861	13.485	21.811	16.868
PLACE1010917	8.779	3.044	3.185	15.098	6.120	5.344	6.106	5.656
PLACE1010924	25.229	20.092	9.911	8.013	6.493	10.958	23.409	11.594
PLACE1010925	49.823	61.948	23.489	34.123	17.969	19.262	17.175	29.154
PLACE1010926	49.767	50.605	22.959	20.111	18.009	24.065	29.924	33.816
PLACE1010942	85.218	46.665	26.680	26.313	22.818	28.713	30.538	39.140
PLACE1010943	316.403	113.988	93.186	72.867	91.388	149.579	188.191	112.743
PLACE1010944	48.129	50.381	15.305	17.574	14.904	18.649	33.779	24.890
PLACE1010947	51.058	49.164	23.114	19.450	16.597	21.983	21.814	17.333
PLACE1010954	73.590	77.560	34.775	41.312	25.097	30.688	27.071	36.359
PLACE1010960	5.163	5.378	16.789	7.998	6.612	8.441	8.411	7.942
PLACE1010965	12.476	21.628	7.886	8.825	4.194	19.265	13.526	8.153
PLACE1010968	34.696	21.848	9.662	5.337	11.298	19.848	21.002	15.864
PLACE1010978	34.271	21.883	15.077	11.695	13.575	20.670	28.798	23.174
PLACE1010982	11.927	20.104	5.539	9.523	4.555	9.333	27.370	20.028
PLACE1010990	23.709	22.125	15.859	11.150	14.185	15.589	24.495	18.421
PLACE1011017	14.795	20.170	18.473	19.079	18.837	31.530	20.694	25.609
PLACE1011019	60.412	29.348	19.532	15.616	21.011	29.657	32.510	15.026
PLACE1011026	6.403	27.542	4.006	7.156	5.587	9.352	6.378	23.067
PLACE1011032	22.416	44.013	12.767	14.147	7.488	10.613	12.024	9.185
PLACE1011041	43.649	29.675	20.339	13.342	17.790	18.671	26.478	21.550
PLACE1011045	48.770	37.661	20.984	15.020	24.758	23.731	42.534	24.019
PLACE1011046	49.343	48.382	29.451	17.863	35.583	26.848	35.241	25.655
PLACE1011054	107.000	92.094	47.988	57.849	58.878	38.779	50.411	53.030
PLACE1011056	226.902	159.857	111.396	119.852	115.390	99.976	141.062	137.522
PLACE1011057	5.333	7.254	4.880	6.072	5.943	6.298	5.741	6.082
PLACE1011059	9.231	13.844	6.945	5.804	7.325	8.493	13.139	9.998
PLACE1011066	24.382	54.196	22.706	25.109	25.646	15.697	16.286	16.716
PLACE1011087	58.783	144.018	41.548	46.968	28.518	50.611	45.100	50.864
PLACE1011090	53.056	143.896	45.260	34.467	50.933	96.133	280.440	58.429
PLACE1011109	75.794	119.843	42.881	49.952	43.765	33.319	35.583	34.429
PLACE1011114	65.656	71.805	22.254	8.641	15.726	26.074	50.404	27.034
PLACE1011116	145.171	37.399	52.539	10.533	21.813	95.906	74.823	26.509
PLACE1011122	18.160	20.063	14.154	12.032	7.536	12.531	122.844	13.983
PLACE1011133	34.682	47.319	20.752	18.004	8.613	20.124	23.747	24.194
PLACE1011134	63.554	58.080	40.465	29.503	29.773	45.368	61.612	42.362
PLACE1011143	25.496	15.071	13.350	11.072	8.424	16.320	18.023	11.713
PLACE1011146	137.473	50.600	49.582	27.853	30.903	82.379	75.016	44.532
PLACE1011160	24.414	27.486	16.449	13.837	0.000	14.398	28.311	19.373
PLACE1011165	34.715	26.526	18.570	10.047	8.910	23.908	18.184	13.882
PLACE1011181	50.804	33.556	25.933	11.931	14.943	31.434	29.663	23.563
PLACE1011185	98.259	72.519	52.464	76.221	29.442	45.963	38.543	28.172
PLACE1011186	40.892	33.762	25.391	13.563	18.650	28.187	25.736	15.462
PLACE1011203	3.303	2.561	4.585	1.724	8.916	1.824	1.948	1.730

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Table 151

PLACE1011214	19.000	30.499	15.354	20.715	13.540	15.163	22.508	23.615
PLACE1011219	50.422	59.474	25.989	22.358	10.192	25.888	34.747	35.987
PLACE1011221	13.282	16.503	9.149	13.164	7.054	10.970	12.103	12.291
PLACE1011229	21.300	24.016	24.142	11.920	8.874	11.425	16.577	18.885
PLACE1011231	57.691	22.558	21.088	13.366	17.790	47.373	24.485	19.912
PLACE1011236	146.860	58.617	57.365	30.780	34.641	68.303	110.808	74.012
PLACE1011247	65.406	45.970	27.363	22.989	18.925	54.590	38.380	66.200
PLACE1011263	18.980	16.439	15.299	13.023	14.184	8.485	11.883	15.956
PLACE1011273	3.117	3.517	3.011	3.406	3.973	1.889	2.488	3.416
PLACE1011278	99.532	58.735	53.312	77.774	36.414	56.820	55.573	49.298
PLACE1011289	65.724	17.465	19.765	15.982	16.860	28.472	40.138	23.783
PLACE1011291	162.344	63.584	63.268	18.526	59.460	122.088	150.314	35.889
PLACE1011296	60.289	35.108	32.914	21.911	20.435	31.931	32.378	27.683
PLACE1011310	12.375	27.199	12.116	10.122	5.617	13.629	12.674	18.490
PLACE1011311	31.445	29.424	19.821	36.262	15.558	31.421	31.132	47.294
PLACE1011321	48.851	39.888	19.447	21.568	15.965	16.409	16.955	23.945
PLACE1011325	25.927	17.098	14.860	7.351	9.021	14.507	18.423	13.442
PLACE1011332	7.973	13.581	8.965	7.176	12.436	8.470	9.437	8.966
PLACE1011340	135.172	94.377	94.222	121.189	70.843	83.242	78.735	123.304
PLACE1011353	20.244	35.898	18.659	17.306	20.697	18.407	11.957	19.750
PLACE1011360	36.650	86.365	30.582	12.233	27.406	21.790	20.034	18.573
PLACE1011364	63.297	27.430	46.019	13.619	40.083	41.537	38.082	14.810
PLACE1011365	14.275	15.778	11.893	10.572	8.300	11.140	12.421	11.796
PLACE1011371	101.501	43.555	36.081	20.272	24.602	47.751	80.751	51.543
PLACE1011375	11.873	15.442	10.915	7.912	7.069	8.106	9.387	8.664
PLACE1011386	207.095	98.628	73.492	39.642	58.242	102.702	134.598	72.968
PLACE1011399	12.717	15.843	7.670	9.849	6.144	8.677	7.308	6.939
PLACE1011406	60.080	56.205	37.483	22.859	14.794	35.277	39.952	36.888
PLACE1011407	20.446	18.260	16.645	16.900	8.560	17.840	8.090	20.149
PLACE1011419	9.047	8.378	6.933	5.544	4.330	7.245	6.219	8.740
PLACE1011433	13.904	35.637	21.499	14.088	12.024	17.492	15.534	27.379
PLACE1011440	57.799	31.667	21.664	18.327	13.093	34.588	30.019	22.159
PLACE1011452	50.007	42.314	37.053	49.949	18.696	31.802	28.114	34.843
PLACE1011465	35.426	19.398	13.047	12.250	12.486	25.628	23.462	18.107
PLACE1011472	62.882	51.139	24.865	13.679	29.181	24.440	22.986	20.138
PLACE1011477	56.690	73.733	72.345	49.100	38.345	43.680	52.566	88.177
PLACE1011478	63.612	53.418	38.381	43.231	28.020	32.283	28.922	47.558
PLACE1011482	106.290	57.337	44.835	33.949	26.366	41.775	46.645	28.355
PLACE1011498	11.479	10.039	1.690	3.014	1.593	3.917	8.921	0.000
PLACE1011501	6.078	13.915	3.925	4.468	3.927	10.819	15.717	55.041
PLACE1011503	1.874	0.762	1.380	0.243	2.449	3.045	3.606	2.018
PLACE1011509	15.310	13.049	7.406	5.231	8.198	9.010	13.173	13.881
PLACE1011514	63.158	72.840	43.610	53.595	30.828	44.567	49.208	51.604
PLACE1011516	26.859	55.632	40.993	27.965	33.580	27.829	35.366	35.955
PLACE1011520	4.008	12.681	4.680	4.882	2.815	4.425	5.052	6.373
PLACE1011538	46.942	112.381	14.535	10.906	7.023	21.261	18.123	15.061
PLACE1011555	64.949	24.945	16.779	8.387	10.043	27.860	31.802	9.584
PLACE1011561	10.363	15.824	6.531	16.410	4.737	8.801	9.321	17.672
PLACE1011563	10.025	6.203	5.528	4.965	4.378	7.900	10.397	8.513
PLACE1011567	42.901	33.701	15.168	22.187	13.471	15.650	16.469	24.618
PLACE1011569	26.547	51.848	39.883	37.100	23.589	23.252	34.227	41.438
PLACE1011576	65.455	90.143	56.009	77.009	47.187	46.612	36.385	75.351
PLACE1011588	46.138	39.212	16.045	20.957	15.477	22.594	28.411	25.540
PLACE1011635	16.794	16.170	6.079	7.918	5.168	11.027	22.021	10.224
PLACE1011641	1.228	0.000	3.690	2.905	1.954	3.104	3.300	2.256
PLACE1011642	17.749	23.124	9.273	20.132	5.674	11.138	15.685	20.899
PLACE1011643	26.441	17.121	11.726	11.897	5.398	10.061	15.157	16.472
PLACE1011646	84.129	76.809	63.483	68.487	61.819	46.212	52.514	53.689
PLACE1011649	148.652	79.404	41.401	24.880	37.816	60.892	98.048	59.957
PLACE1011650	207.033	106.793	62.104	33.902	59.773	85.346	101.285	59.651
PLACE1011661	89.284	69.963	52.044	60.130	41.229	46.476	38.780	47.335
PLACE1011664	19.831	24.910	9.719	12.162	10.285	14.197	16.087	9.849
PLACE1011672	3.166	4.324	0.000	3.511	2.518	4.317	5.108	6.001
PLACE1011675	5.381	4.183	13.639	3.525	18.043	13.639	14.193	4.640

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Table 152

PLACE1011682	46.195	19.920	15.150	18.241	16.697	20.650	33.169	20.683
PLACE1011708	140.868	80.025	46.997	44.349	48.806	85.376	98.779	53.876
PLACE1011719	81.308	62.978	42.651	25.199	32.975	36.215	54.409	40.754
PLACE1011725	51.825	51.140	27.931	38.736	21.984	25.006	26.264	40.599
PLACE1011729	24.560	24.476	13.172	17.322	11.225	10.549	10.437	11.441
PLACE1011741	10.084	12.651	9.857	10.562	8.885	9.463	12.550	13.970
PLACE1011749	65.367	64.514	37.914	40.516	34.378	23.889	21.546	32.149
PLACE1011757	18.814	44.445	37.496	28.407	37.470	13.419	20.349	44.087
PLACE1011762	22.509	23.571	12.319	14.785	13.545	12.246	16.007	14.719
PLACE1011778	18.861	10.736	11.124	6.662	7.815	9.039	11.917	6.723
PLACE1011783	121.850	129.976	50.595	57.237	55.572	43.090	130.253	61.954
PLACE1011795	31.927	47.460	15.112	14.530	14.324	16.899	13.987	13.824
PLACE1011810	11.913	20.873	9.762	5.145	8.850	7.953	21.006	8.397
PLACE1011824	19.075	38.642	12.337	13.272	9.167	11.037	20.832	9.083
PLACE1011825	101.516	76.411	46.000	26.850	59.669	37.495	57.769	32.550
PLACE1011835	41.770	35.699	13.510	12.484	12.451	13.661	25.449	15.527
PLACE1011836	75.164	61.584	46.814	31.866	60.375	30.344	47.168	42.711
PLACE1011847	13.876	13.405	4.281	8.038	4.394	3.642	10.641	8.968
PLACE1011855	23.160	24.900	11.611	9.421	10.774	9.353	18.255	8.246
PLACE1011858	17.703	19.170	8.339	6.242	7.166	9.321	11.444	10.044
PLACE1011874	25.436	29.797	26.222	32.382	13.428	18.138	15.516	21.195
PLACE1011875	3.069	12.743	6.998	4.382	6.338	8.026	8.980	5.065
PLACE1011877	32.981	22.725	17.384	15.505	5.675	26.880	25.751	19.376
PLACE1011891	49.673	22.359	23.890	9.835	15.099	27.985	35.929	22.229
PLACE1011898	4.107	0.000	3.756	3.007	2.732	0.000	6.891	3.826
PLACE1011920	31.343	26.346	21.681	17.707	11.558	18.630	38.456	21.819
PLACE1011922	42.691	40.664	21.936	29.603	0.000	23.870	31.601	34.831
PLACE1011923	32.608	43.041	19.701	8.083	15.625	16.742	22.157	29.615
PLACE1011937	92.606	35.417	26.508	20.596	9.785	43.673	39.451	0.000
PLACE1011939	84.529	52.763	38.555	19.964	7.336	39.880	62.062	31.494
PLACE1011940	59.607	59.623	43.124	27.246	23.603	35.438	69.861	53.973
PLACE1011962	100.298	63.747	55.070	41.766	37.368	61.832	65.091	63.896
PLACE1011964	11.886	16.598	13.946	17.132	12.848	11.456	26.353	18.276
PLACE1011978	18.640	19.836	21.517	38.291	0.000	21.287	15.757	50.491
PLACE1011980	92.462	82.334	53.193	72.449	39.473	41.547	40.407	54.365
PLACE1011981	61.362	58.174	46.817	28.272	28.476	43.347	64.658	50.398
PLACE1011982	15.790	14.181	4.817	8.312	3.604	7.757	7.260	0.000
PLACE1011995	86.516	35.794	56.068	64.038	31.871	35.426	30.449	43.699
PLACE1012023	13.104	15.527	8.953	7.883	5.966	11.716	15.046	14.091
PLACE1012026	7.250	6.837	6.369	2.909	2.441	4.999	8.264	5.743
PLACE1012031	17.346	7.096	7.365	6.293	4.262	7.545	11.516	13.665
PLACE2000003	208.422	130.772	108.228	143.386	92.061	81.725	104.515	91.349
PLACE2000005	71.165	33.762	15.129	19.141	15.235	28.560	47.298	41.315
PLACE2000006	39.195	31.459	22.805	12.253	19.193	16.829	26.310	26.260
PLACE2000007	49.369	22.909	15.022	10.283	10.043	26.310	24.168	17.472
PLACE2000011	71.136	45.914	39.612	33.759	26.056	33.405	30.793	16.938
PLACE2000014	10.718	21.905	13.060	14.701	8.179	11.383	26.861	29.837
PLACE2000015	5.458	4.184	2.923	3.035	2.593	2.078	3.383	5.945
PLACE2000017	46.332	45.480	23.941	25.987	21.386	18.932	16.284	17.911
PLACE2000021	17.344	18.232	12.294	30.435	15.289	14.854	16.815	25.461
PLACE2000022	214.445	144.482	60.979	80.113	67.083	66.864	70.170	73.024
PLACE2000030	187.619	114.314	81.549	40.158	41.897	68.183	115.701	63.549
PLACE2000032	87.441	77.188	34.877	37.149	26.057	33.214	31.270	38.239
PLACE2000033	19.139	24.471	9.846	10.438	5.300	7.546	9.886	11.140
PLACE2000034	42.847	21.194	15.709	12.449	11.089	18.174	25.238	21.354
PLACE2000035	132.992	122.124	78.507	88.183	73.563	60.606	56.917	66.559
PLACE2000043	79.648	15.614	20.878	20.687	15.011	29.880	42.418	25.222
PLACE2000044	108.910	74.788	39.496	27.081	33.429	62.338	73.844	45.861
PLACE2000047	152.880	109.630	85.453	107.221	45.543	77.024	57.124	107.596
PLACE2000050	152.213	120.823	56.724	48.747	39.963	53.086	55.785	48.395
PLACE2000061	29.004	14.906	13.177	8.299	8.224	15.405	20.467	10.248
PLACE2000062	72.911	31.342	35.172	31.037	24.841	32.494	55.822	37.870
PLACE2000072	26.412	23.969	12.046	11.850	8.875	14.949	13.677	17.280
PLACE2000073	30.538	11.955	9.197	2.761	2.738	11.625	16.675	7.995

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Table 153

PLACE2000097	26.855	20.822	13.598	19.129	11.744	36.567	24.316	26.522
PLACE2000100	65.222	58.680	32.787	36.772	34.459	33.979	29.850	45.558
PLACE2000103	87.537	67.579	43.315	48.791	32.811	36.573	42.226	40.018
PLACE2000106	109.631	86.434	50.857	64.247	33.823	50.406	61.798	50.310
PLACE2000111	67.743	54.614	49.948	32.461	25.661	39.498	39.424	45.128
PLACE2000115	39.616	21.252	16.909	7.307	8.764	18.404	25.904	9.246
PLACE2000118	525.051	269.098	228.675	184.616	169.233	347.407	255.751	198.972
PLACE2000124	349.581	275.812	246.822	261.885	198.107	204.514	181.925	196.861
PLACE2000132	219.428	75.779	55.477	27.845	44.528	98.585	135.305	44.096
PLACE2000136	26.471	13.700	10.948	5.229	9.552	12.386	20.372	16.417
PLACE2000137	136.105	55.207	38.965	25.263	38.081	60.138	77.269	40.309
PLACE2000140	61.894	58.228	35.563	26.913	23.042	43.520	44.482	46.587
PLACE2000147	35.744	28.047	17.366	9.287	7.856	15.456	20.704	13.852
PLACE2000153	10.251	5.138	4.944	3.289	1.583	8.639	8.187	4.258
PLACE2000164	28.952	20.099	15.192	12.672	6.324	15.972	21.497	18.781
PLACE2000170	59.457	56.458	26.480	33.136	22.805	27.949	31.835	29.350
PLACE2000172	44.931	19.156	12.587	7.529	12.190	15.161	26.980	16.906
PLACE2000173	61.374	67.180	25.374	32.768	28.635	32.143	41.210	43.509
PLACE2000174	58.350	40.462	27.593	30.601	30.132	26.716	42.849	36.942
PLACE2000176	67.823	54.888	28.038	22.906	22.587	33.838	40.703	24.007
PLACE2000187	58.492	46.505	35.000	29.053	17.412	35.409	39.960	33.655
PLACE2000216	67.045	48.042	34.386	16.556	25.028	35.589	41.068	25.755
PLACE2000219	102.450	53.525	43.919	40.723	27.590	45.597	40.342	27.793
PLACE2000221	172.504	104.236	71.274	95.080	69.068	73.974	75.780	84.353
PLACE2000223	1.924	0.000	0.337	0.072	0.489	0.000	1.615	0.884
PLACE2000231	46.085	20.513	17.117	6.372	14.358	19.848	38.853	25.391
PLACE2000235	124.328	101.132	67.369	86.561	58.141	54.197	68.871	76.828
PLACE2000245	104.336	91.568	43.204	38.961	37.372	49.589	53.726	38.556
PLACE2000264	80.119	58.341	26.725	32.576	29.924	31.634	35.536	46.483
PLACE2000274	178.113	50.862	46.488	15.876	44.169	82.504	117.862	37.316
PLACE2000287	132.856	101.370	60.760	60.336	35.602	65.837	81.297	70.741
PLACE2000296	49.120	36.473	16.163	15.750	18.250	18.313	35.709	33.015
PLACE2000302	57.145	42.035	23.159	27.707	22.845	20.720	30.271	32.036
PLACE2000305	175.494	200.830	97.799	110.854	103.121	82.645	117.383	111.334
PLACE2000317	43.989	47.859	17.789	17.969	19.049	22.044	50.064	40.575
PLACE2000324	0.000	7.097	5.063	2.422	6.266	5.462	10.248	7.127
PLACE2000334	68.183	58.423	27.660	13.890	19.395	41.882	61.667	32.402
PLACE2000335	124.754	148.141	79.507	92.542	69.951	70.762	73.634	60.750
PLACE2000340	26.477	26.590	14.223	11.260	9.640	12.040	23.150	14.154
PLACE2000341	77.833	55.873	31.663	25.403	26.509	38.745	65.207	46.925
PLACE2000342	106.364	52.711	44.616	37.588	44.103	48.901	80.882	45.540
PLACE2000347	135.574	132.050	56.804	42.203	56.182	70.882	92.167	64.861
PLACE2000357	93.053	95.338	40.039	30.886	41.634	43.514	108.320	66.738
PLACE2000358	37.940	54.020	19.892	24.091	19.855	30.828	46.656	38.072
PLACE2000359	44.601	31.382	22.450	28.212	15.793	15.150	23.074	23.575
PLACE2000366	121.162	103.772	44.748	43.347	42.993	37.451	42.382	49.575
PLACE2000371	30.423	16.028	14.211	9.577	16.570	13.288	16.943	9.168
PLACE2000373	103.200	59.241	36.611	28.313	27.244	41.111	69.708	39.196
PLACE2000374	113.892	55.366	30.642	21.105	30.506	39.759	73.431	35.604
PLACE2000379	20.349	15.495	7.621	6.080	7.432	5.799	10.929	11.275
PLACE2000386	2957.979	598.564	744.423	192.993	914.385	1779.750	2073.338	474.610
PLACE2000388	71.861	48.309	26.919	20.159	20.978	36.369	40.361	36.550
PLACE2000392	352.525	278.976	168.585	149.394	126.536	186.631	228.238	160.402
PLACE2000394	53.696	72.722	49.507	50.392	15.244	41.226	40.124	40.112
PLACE2000398	108.135	94.821	58.643	43.978	38.270	58.649	64.162	55.535
PLACE2000399	67.901	42.851	38.688	28.243	32.488	41.332	58.492	32.287
PLACE2000402	63.927	53.000	27.854	20.310	22.733	39.649	49.188	31.169
PLACE2000404	52.116	29.153	35.080	21.348	20.859	36.900	57.711	32.512
PLACE2000411	344.233	265.387	148.539	150.545	127.069	193.357	280.999	166.692
PLACE2000418	98.999	55.110	38.643	40.087	26.858	47.480	51.418	37.707
PLACE2000419	173.685	127.508	108.969	93.659	63.793	86.077	101.959	100.024
PLACE2000425	48.498	43.030	24.787	27.067	15.782	34.775	41.783	22.576
PLACE2000427	68.431	46.153	34.785	21.591	19.224	40.769	48.213	24.735
PLACE2000433	85.693	46.037	39.587	31.830	25.730	41.985	45.179	36.070

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Table 154

PLACE2000435	627.805	144.999	138.039	57.999	150.754	199.419	268.624	106.234
PLACE2000438	56.718	23.072	24.569	11.907	16.555	28.249	47.594	27.160
PLACE2000450	154.687	141.268	71.263	118.445	53.787	64.455	51.630	74.221
PLACE2000455	67.470	36.100	20.827	16.588	21.358	35.782	37.471	28.970
PLACE2000458	104.672	42.860	43.528	21.379	21.800	58.644	70.147	47.611
PLACE2000464	105.901	34.595	41.144	17.313	27.129	60.407	69.472	24.244
PLACE2000465	80.401	104.292	71.810	73.398	40.246	50.872	47.384	76.283
PLACE2000473	420.021	269.633	211.308	162.099	161.932	255.494	273.349	340.926
PLACE2000477	15.988	4.741	4.305	5.801	6.451	4.611	5.267	7.301
PLACE3000004	150.291	87.960	55.053	66.698	49.843	55.946	72.642	62.012
PLACE3000009	2308.534	491.939	579.346	337.661	527.298	1010.865	903.209	416.227
PLACE3000020	129.151	97.914	62.838	38.547	45.276	64.510	77.399	65.319
PLACE3000029	65.003	63.572	28.269	34.591	20.999	29.355	27.242	35.815
PLACE3000038	60.832	39.883	31.082	31.184	18.004	26.851	33.481	34.526
PLACE3000052	80.986	57.505	42.010	29.980	28.396	38.406	44.374	46.348
PLACE3000059	14.309	10.723	7.978	9.607	8.219	10.311	10.168	14.892
PLACE3000067	148.633	122.359	72.812	107.464	67.921	73.383	51.333	59.832
PLACE3000069	94.472	58.891	39.254	38.134	38.532	45.365	50.569	49.095
PLACE3000070	606.923	398.146,	277.096	302.922	122.053	340.430	303.517	264.024
PLACE3000103	37.665	49.384	23.681	21.788	14.319	19.018	24.128	23.022
PLACE3000119	71.233	77.814	32.703	36.829	29.100	33.236	32.954	38.558
PLACE3000121	28.770	15.821	15.686	6.769	11.774	14.597	21.083	15.791
PLACE3000124	136.225	102.926	73.102	88.816	50.098	64.249	70.972	88.890
PLACE3000135	5.325	1.538	1.703	2.303	1.771	1.846	2.243	1.568
PLACE3000136	264.467	146.748	117.350	79.000	94.116	149.983	135.199	82.816
PLACE3000142	84.493	43.724	33.445	21.753	29.470	39.958	59.408	36.420
PLACE3000145	202.991	105.472	78.043	43.347	67.611	96.794	127.254	104.646
PLACE3000147	45.022	53.334	28.294	29.723	15.237	24.991	20.260	28.896
PLACE3000148	50.238	25.306	12.752	14.405	11.331	16.047	21.617	14.375
PLACE3000154	16.588	24.537	5.983	4.462	5.238	17.888	19.855	5.659
PLACE3000155	162.823	103.374	73.169	61.895	55.036	69.498	99.138	67.036
PLACE3000156	293.645	80.486	96.151	36.695	86.574	251.934	180.898	69.146
PLACE3000157	77.274	48.353	30.271	23.067	21.480	31.175	45.472	36.779
PLACE3000158	138.262	117.084	66.013	76.854	56.610	58.354	55.566	83.250
PLACE3000160	12.383	13.802	3.360	3.545	2.772	7.038	7.949	11.165
PLACE3000169	112.273	107.072	60.628	74.727	35.758	41.506	37.316	64.578
PLACE3000181	159.980	52.036	66.098	26.437	39.138	112.925	84.309	50.931
PLACE3000194	59.243	40.406	43.072	30.599	27.793	33.533	39.940	36.285
PLACE3000197	2.773	2.051	1.429	3.753	0.000	3.916	96.254	57.504
PLACE3000199	38.435	22.543	11.795	7.257	11.967	16.257	14.819	12.260
PLACE3000205	98.788	82.371	76.207	41.507	69.168	50.577	62.634	65.731
PLACE3000207	107.828	91.992	61.336	61.872	58.924	42.359	53.327	75.106
PLACE3000208	112.570	54.203	55.951	38.351	49.935	44.990	75.532	53.240
PLACE3000213	26.219	39.836	11.741	11.345	7.948	12.842	24.022	17.439
PLACE3000215	90.876	34.688	28.615	9.043	15.498	40.462	43.681	18.877
PLACE3000218	10.221	2.943	2.894	3.797	1.404	4.853	5.114	3.490
PLACE3000220	61.519	52.284	29.152	23.405	20.917	20.102	32.078	28.959
PLACE3000221	57.492	57.641	28.073	44.309	27.289	41.840	33.858	52.488
PLACE3000226	73.279	54.393	35.962	36.879	33.401	26.367	40.176	43.907
PLACE3000228	73.816	45.891	30.595	22.786	30.642	32.460	45.062	32.422
PLACE3000230	46.786	26.306	16.545	6.639	15.988	18.992	43.959	26.308
PLACE3000231	48.528	32.588	17.433	13.571	12.141	20.113	27.942	18.127
PLACE3000235	85.027	89.322	36.118	40.285	33.985	29.150	33.828	45.276
PLACE3000242	40.499	25.236	19.477	11.857	14.018	22.181	24.892	16.933
PLACE3000244	8.374	6.431	4.114	3.304	1.774	5.910	8.022	3.080
PLACE3000253	15.620	19.797	14.659	8.539	11.579	14.844	17.301	13.779
PLACE3000254	1079.768	504.372	399.997	312.953	401.250	606.426	625.003	328.912
PLACE3000271	142.610	130.398	184.934	108.646	196.939	76.216	94.895	90.942
PLACE3000276	50.360	33.423	20.928	13.869	24.274	23.260	48.090	23.254
PLACE3000304	753.417	459.951	316.676	275.105	248.812	389.978	267.542	311.942
PLACE3000309	105.170	114.674	22.694	38.446	20.838	90.058	54.287	66.550
PLACE3000310	16.942	13.275	5.349	3.549	6.010	7.279	9.574	6.330
PLACE3000320	37.064	33.783	10.590	11.058	12.166	12.647	17.232	15.732
PLACE3000322	59.027	28.943	19.280	27.456	23.010	14.895	25.564	32.475

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Table 155

PLACE3000330	216.369	112.324	67.450	57.211	77.413	103.940	153.059	92.002
PLACE3000331	175.154	109.366	65.174	61.976	64.453	62.935	100.525	76.877
PLACE3000336	72.694	51.382	24.596	19.447	23.969	28.997	69.879	41.462
PLACE3000339	30.681	21.404	10.699	10.293	10.726	16.029	27.155	16.949
PLACE3000341	60.229	47.003	23.728	24.494	19.963	23.504	27.314	25.967
PLACE3000350	29.438	30.806	13.412	18.894	10.478	10.194	11.370	19.246
PLACE3000352	133.033	66.842	27.124	22.155	31.563	39.432	49.060	26.130
PLACE3000353	43.758	27.987	13.231	12.753	11.266	21.242	42.590	23.677
PLACE3000362	67.720	68.906	37.576	54.837	39.546	31.556	42.322	53.834
PLACE3000363	57.403	38.780	25.263	14.578	19.607	23.664	46.846	21.687
PLACE3000365	67.367	70.204	26.265	27.858	28.782	28.393	58.355	39.738
PLACE3000373	13.237	14.898	8.160	10.479	10.212	7.337	11.629	6.545
PLACE3000374	65.194	47.989	28.255	34.215	25.888	25.506	40.045	29.881
PLACE3000387	39.123	14.751	9.548	6.520	10.023	13.134	24.323	11.700
PLACE3000388	38.498	49.657	25.044	30.962	16.063	16.391	26.317	35.550
PLACE3000399	148.163	127.490	65.532	74.992	56.760	50.436	71.879	57.275
PLACE3000400	64.113	49.775	24.696	24.323	28.318	34.732	29.297	29.946
PLACE3000401	643.361	789.055	443.841	553.459	428.754	314.650	347.522	356.250
PLACE3000402	93.152	75.383	36.033	35.535	33.800	26.510	39.162	39.094
PLACE3000405	116.575	74.775	47.203	35.397	23.948	53.017	69.999	41.988
PLACE3000406	46.734	47.216	28.404	38.943	18.564	21.735	18.510	22.439
PLACE3000413	172.089	63.768	60.797	25.154	38.861	86.736	100.967	39.294
PLACE3000416	72.812	94.541	27.443	24.126	23.401	36.001	52.778	31.746
PLACE3000425	75.299	85.243	55.831	51.775	29.832	40.724	54.413	42.424
PLACE3000437	152.596	106.131	91.713	79.520	53.901	88.235	140.605	71.376
PLACE3000455	199.980	144.915	86.941	70.024	46.162	89.704	140.865	87.299
PLACE3000476	344.660	151.608	142.664	51.432	168.147	291.157	322.276	96.413
PLACE3000477	105.902	72.097	35.966	23.877	17.322	48.569	53.837	34.942
PLACE4000003	21.542	6.768	7.756	4.338	6.666	15.322	9.008	10.517
PLACE4000008	81.624	76.594	49.347	29.174	47.030	40.800	60.131	38.137
PLACE4000009	254.207	142.614	81.374	67.480	67.588	123.118	127.853	80.493
PLACE4000014	93.227	49.366	32.322	19.702	25.748	40.531	72.266	36.731
PLACE4000029	21.650	25.863	17.118	20.048	17.456	36.449	43.230	27.051
PLACE4000034	49.161	79.725	28.634	23.533	19.403	43.040	40.269	23.537
PLACE4000049	166.916	134.169	69.807	85.324	50.891	74.119	64.317	64.497
PLACE4000052	54.863	57.074	25.752	30.034	15.812	36.433	50.349	23.477
PLACE4000062	78.176	55.581	32.501	23.565	14.025	47.511	74.636	26.040
PLACE4000063	84.945	48.380	39.855	15.974	28.354	50.659	60.330	32.588
PLACE4000089	19.057	35.752	29.230	17.534	17.492	11.406	15.833	13.554
PLACE4000093	26.060	15.272	12.061	6.706	13.618	11.634	18.344	13.777
PLACE4000100	101.893	42.734	31.255	36.161	14.062	33.159	29.333	44.906
PLACE4000103	124.173	34.660	22.754	19.690	20.649	30.763	70.971	19.503
PLACE4000108	98.597	75.194	36.209	29.412	33.084	61.638	76.538	44.570
PLACE4000128	129.329	131.483	60.440	57.978	41.117	68.736	84.185	95.597
PLACE4000129	132.932	37.431	53.267	53.097	33.745	72.527	81.857	45.648
PLACE4000131	156.165	156.169	86.886	106.633	78.888	107.180	102.299	66.814
PLACE4000147	16.492	9.413	7.966	2.107	5.770	5.146	10.290	4.656
PLACE4000168	69.314	72.955	65.884	87.221	44.343	46.822	36.362	77.048
PLACE4000175	60.994	54.028	16.876	13.509	17.492	17.684	32.845	26.309
PLACE4000190	593.634	220.190	171.592	116.664	189.541	260.140	310.147	138.653
PLACE4000192	301.266	121.069	80.280	70.432	67.302	127.637	134.475	72.627
PLACE4000208	259.054	236.436	119.680	97.518	77.872	86.994	97.682	154.492
PLACE4000211	242.387	150.657	98.746	66.861	74.283	149.275	122.028	95.561
PLACE4000214	67.058	61.229	37.510	23.741	22.459	30.120	39.510	34.868
PLACE4000222	106.945	86.369	43.808	41.733	40.284	26.442	41.963	46.046
PLACE4000223	107.887	42.520	26.804	14.769	19.364	37.870	44.089	22.256
PLACE4000229	50.488	20.289	21.176	10.728	15.908	27.323	36.955	19.875
PLACE4000230	83.847	33.508	24.933	10.032	18.791	28.713	41.794	26.235
PLACE4000233	96.059	59.313	60.661	55.448	36.248	37.359	40.716	47.823
PLACE4000239	124.398	94.107	57.093	48.109	34.394	43.667	35.791	41.364
PLACE4000247	54.958	32.352	28.165	18.524	15.208	25.144	27.546	21.593
PLACE4000250	104.404	85.640	73.997	59.563	48.738	59.288	60.153	65.709
PLACE4000252	33.790	23.180	15.501	12.390	6.684	14.866	16.958	13.472
PLACE4000259	113.573	49.555	27.075	21.856	43.353	38.644	52.944	26.431

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Table 156·

PLACE4000261	254.068	48.744	84.359	22.460	69.697	125.015	113.583	36.809
PLACE4000264	39.731	29.931	13.801	9.433	14.239	13.997	27.405	15.510
PLACE4000269	85.391	69.167	59.645	32.049	32.560	45.023	59.556	44.048
PLACE4000270	37.293	35.516	21.356	20.188	22.145	14.735	20.334	24.680
PLACE4000281	132.006	130.790	59.934	124.956	58.105	75.320	65.805	106.301
PLACE4000300	95.228	64.001	50.704	44.034	42.272	39.616	55.059	49.678
PLACE4000320	101.920	74.756	53.518	50.074	37.273	44.289	54.376	57.927
PLACE4000323	106.246	90.568	59.225	75.643	65.195	71.824	67.236	63.467
PLACE4000326	50.786	39.408	21.110	15.693	16.385	24.171	25.892	24.334
PLACE4000344	47.237	25.071	19.282	9.754	15.816	17.064	28.344	22.605
PLACE4000347	270.519	135.102	97.629	73.164	79.089	145.628	174.326	132.718
PLACE4000354	51.402	69.949	21.125	14.137	10.506	24.887	36.668	32.881
PLACE4000367	38.537	21.917	13.300	12.406	12.328	16.184	16.983	12.631
PLACE4000369	87.562	48.818	27.044	18.841	17.942	39.036	46.668	28.559
PLACE4000379	63.427	46.050	34.549	40.613	28.043	28.363	34.411	32.783
PLACE4000387	51.546	28.804	20.204	18.439	20.155	20.584	27.432	22.848
PLACE4000392	16.062	7.012	6.606	5.828	5.717	7.153	9.447	4.556
PLACE4000399	537.973	347.563	216.840	188.160	226.834	294.013	378.986	282.393
PLACE4000401	18.633	16.086	12.450	8.891	4.760	9.336	9.594	9.016
PLACE4000403	122.680	74.783	64.480	32.311	31.018	61.677	74.741	57.710
PLACE4000411	76.474	69.288	26.062	27.151	18.908	24.969	28.090	28.450
PLACE4000415	117.128	42.809	42.067	13.307	25.782	58.009	67.901	23.594
PLACE4000416	155.173	151.945	41.224	24.312	34.852	60.268	78.927	60.597
PLACE4000424	49.737	20.818	19.113	10.882	15.430	26.353	51.392	21.253
PLACE4000431	94.197	46.298	22.172	18.259	30.613	23.575	63.847	39.828
PLACE4000443	5.628	10.390	1.885	3.662	4.723	4.338	8.728	4.152
PLACE4000445	112.063	123.064	82.212	73.969	75.667	71.847	80.872	98.196
PLACE4000450	236.301	129.164	80.479	58.100	59.886	126.244	134.749	85.784
PLACE4000455	48.423	52.624	22.324	12.728	17.652	29.121	33.876	28.299
PLACE4000465	105.018	96.543	76.272	77.100	59.155	46.270	60.646	57.534
PLACE4000466	291.255	313.894	141.390	142.098	110.817	145.538	179.778	235.989
PLACE4000472	361.477	283.612	184.390	172.988	162.349	205.973	249.573	175.977
PLACE4000487	71.130	60.554	31.674	34.491	38.357	27.786	47.292	39.254
PLACE4000489	95.437	42.543	25.117	24.559	29.344	31.561	68.977	55.815
PLACE4000494	88.573	62.176	35.502	19.031	26.845	35.819	41.938	46.527
PLACE4000502	149.633	181.173	61.673	64.434	54.907	64.869	78.120	106.317
PLACE4000521	204.368	58.842	53.769	22.018	39.396	90.039	90.251	41.190
PLACE4000522	70.773	56.092	27.371	16.069	23.518	31.461	43.466	39.760
PLACE4000537	155.193	45.421	44.392	17.892	44.281	65.488	98.332	46.179
PLACE4000548	47.086	28.598	16.763	16.406	16.740	16.619	38.465	30.778
PLACE4000558	10.369	12.539	7.971	5.855	5.400	4.652	8.570	10.740
PLACE4000581	70.383	51.427	22.039	21.955	29.024	23.682	53.726	32.562
PLACE4000590	24.623	8.914	5.754	7.501	7.952	10.260	10.943	10.189
PLACE4000593	72.087	47.632	23.074	21.723	26.365	31.598	47.539	27.961
PLACE4000612	363.116	155.910	113.800	42.737	124.093	178.284	193.620	70.237
PLACE4000638	77.534	58.517	30.744	28.131	38.112	34.764	51.100	28.946
PLACE4000650	45.331	36.490	20.134	15.928	17.671	20.345	43.714	24.670
PLACE4000661	81.785	55.336	31.545	34.295	31.108	38.514	81.922	45.304
PLACE4000664	6.383	10.852	2.069	2.695	5.385	0.000	8.009	5.077
PLACE4000670	26.614	19.086	6.113	5.853	8.977	8.517	8.611	9.175
PLACE4000685	353.509	195.694	218.442	282.931	172.870	251.552	212.919	154.500
PLACE4000687	6.072	45.334	5.252	2.662	3.323	6.156	15.595	9.677
PLACE5000003	40.413	19.764	16.619	10.777	8.559	21.575	38.678	19.632
PLACE5000005	29.397	16.490	10.583	8.840	8.662	14.637	23.435	12.833
PLACE5000019	23.138	11.436	9.892	8.427	12.232	11.988	17.815	11.445
PLACE5000021	11.535	7.575	5.665	2.261	3.314	5.302	13.774	6.297
PLACE5000022	46.567	29.719	16.482	17.005	14.276	21.478	42.140	22.462
PLACE5000024	41.449	27.083	21.424	11.180	17.296	33.257	43.529	32.884
PLACE5000036	70.785	39.582	20.917	20.141	20.809	27.945	49.655	22.062
PLACE5000059	549.980	916.588	204.531	124.489	88.404	320.138	300.571	165.922
PLACE5000076	14.669	19.597	4.256	0.960	4.723	7.492	10.966	10.788
PLACE5000117	42.649	51.048	28.712	26.369	19.372	24.252	35.991	32.282
PLACE5000143	56.211	38.124	31.388	29.118	16.931	30.201	34.414	32.266
PLACE5000152	7.979	4.543	4.880	1.278	1.829	5.715	9.925	4.547

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PLACE5000154	70.894	26.982	21.228	26.625	17.971	32.836	43.570	45.054
PLACE5000155	443.969	270.563	174.040	139.163	137.024	244.271	195.771	169.360
PLACE5000165	529.207	254.686	202.448	123.963	145.432	257.836	242.614	165.245
SKNMC1000004	20.836	13.305	17.789	33.557	11.594	10.964	6.648	21.308
SKNMC1000011	19.687	9.046	7.372	8.263	7.296	15.689	11.182	14.777
SKNMC1000013	9.401	12.821	9.287	3.794	5.931	6.702	10.997	8.736
SKNMC1000014	49.003	43.832	32.008	24.681	23.480	20.065	21.197	18.671
SKNMC1000018	33.522	17.298	13.017	4.236	8.795	16.555	20.822	15.790
SKNMC1000020	41.784	25.172	10.947	6.067	6.258	17.499	22.243	15.547
SKNMC1000046	21.429	19.675	15.389	7.367	8.974	13.224	14.566	12.097
SKNMC1000050	22.145	26.518	10.065	7.977	7.275	14.859	11.644	8.042
SKNMC1000062	338.427	274.434	175.123	132.052	150.251	235.537	155.269	137.370
SKNMC1000075	20.756	21.072	10.730	10.756	8.063	10.684	15.925	10.454
SKNMC1000082	24.604	10.460	9.435	7.978	7.660	10.818	12.376	12.685
SKNMC1000091	36.258	20.984	12.691	12.987	9.671	18.161	17.028	15.150
SKNMC1000099	27.554	15.672	10.331	8.117	8.086	17.003	23.741	6.484
SKNMC1000104	38.010	34.379	9.892	7.092	9.487	18.879	22.259	6.010
SKNMC1000113	39.920	26.152	14.548	11.762	15.067	12.794	17.603	10.906
SKNMC1000119	68.128	70.122	43.005	35.267	28.955	35.214	34.073	39.116
SKNMC1000142	32.190	14.734	11.314	9.644	8.615	13.750	11.275	11.126
SKNMC1000170	27.877	27.618	13.752	9.407	7.172	15.123	19.813	13.284
SKNMC1000178	70.066	63.234	33.059	29.079	25.498	40.509	40.085	31.660
SKNMC1000194	49.613	30.075	14.523	13.545	13.410	19.965	25.730	19.940
SKNMC1000198	36.190	30.269	18.321	16.365	19.849	22.261	23.973	21.923
SKNMC1000225	20.577	23.995	7.702	12.589	11.016	9.595	24.700	19.639
SKNMC1000249	35.318	7.307	2.999	2.393	1.501	10.815	6.991	7.735
SPLEN1000007	17.285	35.392	16.709	18.674	6.880	10.787	9.808	21.699
SPLEN1000012	79.902	26.456	22.780	18.019	22.231	32.118	34.361	44.355
SPLEN1000014	86.560	12.587	39.565	11.907	15.132	29.061	14.109	26.990
SPLEN1000036	39.586	28.908	15.910	11.331	10.780	20.946	21.977	20.383
SPLEN1000059	0.000	0.000	0.000	0.000	0.000	0.000	0.000	2.428
SPLEN1000068	42.216	61.333	16.982	24.191	14.315	17.337	19.640	62.286
SPLEN1000072	80.933	51.171	18.946	13.264	24.375	35.212	43.609	27.418
SPLEN1000101	56.109	102.035	38.061	51.936	36.704	44.974	32.451	43.746
SPLEN1000108	28.462	16.640	8.555	5.187	16.134	11.421	13.414	8.735
SPLEN1000113	51.510	25.822	25.943	12.637	11.070	26.855	29.899	18.889
SPLEN1000114	35.034	24.235	14.342	6.652	10.171	15.802	22.089	21.376
SPLEN1000132	49.855	38.464	20.708	19.052	11.964	26.849	30.806	43.790
SPLEN1000135	69.620	36.735	26.241	10.036	13.578	35.866	51.104	20.505
SPLEN1000136	63.959	49.187	29.950	19.924	33.180	31.548	43.178	34.511
SPLEN1000141	23.876	26.906	13.071	72.200	12.564	17.177	27.098	35.500
SPLEN1000164	16.339	35.856	18.324	17.346	11.288	11.589	21.271	23.356
SPLEN1000166	24.814	15.925	15.170	8.132	3.719	14.352	21.337	12.600
SPLEN1000175	25.901	21.258	13.665	11.257	7.394	16.665	16.969	14.377
SPLEN1000182	18.056	12.663	11.532	12.004	2.626	8.556	12.618	37.351
SPLEN1000185	26.100	41.959	17.505	17.472	10.054	14.816	18.440	19.857
THYMU1000004	44.412	116.214	81.748	45.350	91.679	71.223	84.954	80.324
THYMU1000009	92.202	35.746	24.767	13.955	26.373	40.874	48.694	33.357
THYMU1000015	119.421	76.777	57.343	70.294	56.242	50.116	65.925	70.762
THYMU1000016	74.630	122.372	55.398	55.977	36.943	34.305	35.686	44.484
THYMU1000023	48.992	17.205	14.380	8.188	8.168	17.212	29.149	11.470
THYMU1000034	23.593	20.349	11.577	29.307	8.770	14.408	18.502	24.353
THYMU1000035	4.371	10.319	4.870	4.657	3.211	3.832	10.406	7.814
THYMU1000037	20.625	19.668	15.919	5.609	7.443	10.224	15.344	11.760
THYMU1000042	26.144	27.737	22.945	14.582	17.170	26.145	15.958	21.660
THYMU1000047	82.365	77.958	47.962	65.513	51.443	41.986	46.858	56.202
THYMU1000080	61.757	49.927	18.225	18.738	26.953	26.454	51.613	35.091
THYMU1000094	19.467	64.725	53.131	40.321	30.569	39.369	33.394	98.550
THYMU1000108	149.316	123.466	67.770	64.336	47.280	83.698	92.747	102.494
THYMU1000127	60.503	74.862	44.683	42.056	26.178	36.687	45.486	39.497
THYMU1000130	30.806	32.066	14.328	15.977	15.568	16.818	17.637	28.159
THYMU1000137	52.374	31.029	16.014	9.647	15.418	24.408	35.666	22.622
THYMU1000146	18.567	26.920	15.236	10.270	16.304	10.679	17.254	15.651
THYMU1000159	70.044	154.598	47.360	46.468	39.892	66.239	54.899	103.307

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Table 158

THYMU1000163	230.058	118.595	78.938	55.414	75.224	98.439	193.301	119.439
THYMU1000167	27.217	30.992	12.427	11.600	12.648	14.819	18.104	21.118
THYMU1000186	98.908	32.919	26.632	32.071	21.873	38.437	40.004	37.219
THYRO1000017	32.706	74.720	34.463	29.641	25.692	21.516	24.204	26.183
THYRO1000026	48.577	63.401	19.205	24.272	14.810	18.297	20.045	25.420
THYRO1000034	58.496	36.741	19.420	21.474	9.545	24.247	35.259	20.763
THYRO1000035	16.297	9.507	7.691	4.410	6.774	24.908	13.356	9.119
THYRO1000038	24.463	30.537	12.036	4.674	19.713	10.204	19.617	16.573
THYRO1000040	35.751	45.426	23.899	33.153	24.644	20.641	51.980	52.710
THYRO1000061	55.574	30.112	25.941	16.711	34.951	38.423	43.556	36.625
THYRO1000067	298.802	183.339	157.234	94.003	137.727	187.647	208.613	150.900
THYRO1000070	129.995	57.987	43.780	28.114	29.001	66.142	64.121	39.508
THYRO1000072	48.939	68.453	35.134	30.429	26.627	21.975	26.766	30.117
THYRO1000084	48.307	42.611	21.990	11.064	20.435	19.417	26.995	22.971
THYRO1000085	303.121	193.955	126.839	102.212	129.747	159.374	206.341	159.771
THYRO1000086	18.728	11.012	7.883	6.698	5.384	7.742	20.711	9.575
THYRO1000087	13.421	10.853	10.795	1.978	6.514	3.429	8.955	5.691
THYRO1000092	59.642	76.269	32.514	45.637	33.042	32.861	31.754	32.557
THYRO1000093	29.394	21.625	13.006	10.368	7.983	20.671	22.009	16.350
THYRO1000099	51.966	54.362	21.025	22.941	16.286	25.517	29.813	20.577
THYRO1000107	29.893	53.294	14.175	20.025	13.567	9.104	21.662	17.898
THYRO1000111	21.644	28.232	19.143	17.545	16.222	11.312	15.745	13.162
THYRO1000121	9.799	13.392	8.363	4.392	6.118	7.651	13.401	6.079
THYRO1000124	30.095	17.896	14.782	10.115	12.585	13.557	25.764	13.867
THYRO1000129	30.388	14.967	9.694	7.939	3.251	9.857	13.209	9.668
THYRO1000130	56.966	72.160	26.934	36.742	15.654	23.842	14.862	25.040
THYRO1000132	83.533	105.422	51.451	54.782	42.323	42.319	52.428	41.417
THYRO1000134	33.349	47.368	20.790	21.807	12.940	21.379	41.470	22.575
THYRO1000144	88.955	17.323	7.936	4.025	4.431	18.779	29.660	7.581
THYRO1000155	11.674	3.549	2.761	3.811	1.697	0.000	7.176	2.825
THYRO1000156	35.082	28.027	15.226	28.722	16.993	22.315	19.772	22.116
THYRO1000163	68.114	50.535	54.325	60.945	50.945	39.516	29.854	36.208
THYRO1000173	43.980	34.453	18.714	18.682	5.054	34.676	33.143	20.988
THYRO1000185	150.529	131.750	70.665	53.342	44.898	98.134	69.084	44.946
THYRO1000187	89.162	62.977	42.088	24.103	13.600	31.751	46.152	26.272
THYRO1000190	34.704	43.709	35.680	47.383	21.817	20.074	24.984	29.176
THYRO1000196	12.960	7.875	6.426	3.533	5.208	5.665	10.168	5.312
THYRO1000197	34.949	40.382	35.820	20.214	23.273	18.953	26.665	25.266
THYRO1000199	19.361	13.983	9.085	8.320	10.004	7.851	11.633	10.622
THYRO1000208	47.609	55.960	31.132	10.479	36.037	22.453	19.963	14.483
THYRO1000221	82.534	81.160	38.961	57.909	20.347	30.565	34.158	38.238
THYRO1000222	15.768	62.309	7.359	7.364	8.966	8.443	11.700	23.186
THYRO1000228	23.238	16.601	14.212	15.062	17.974	19.434	9.775	10.964
THYRO1000241	55.874	49.255	57.277	39.823	31.045	29.731	25.058	24.705
THYRO1000242	13.379	26.177	12.762	19.853	8.446	8.035	12.464	24.333
THYRO1000248	7.985	21.129	6.632	7.437	5.012	11.050	8.809	26.581
THYRO1000263	60.014	38.765	34.683	39.349	28.961	21.254	21.340	26.307
THYRO1000270	3.554	0.000	2.696	1.813	2.708	4.022	4.159	3.250
THYRO1000279	14.227	10.091	5.339	3.542	4.797	8.248	7.649	5.892
THYRO1000285	56.886	54.148	33.944	22.809	15.320	32.641	25.655	26.150
THYRO1000288	12.236	23.331	7.807	4.959	7.189	8.692	6.757	6.433
THYRO1000296	68.849	34.305	24.611	18.781	11.941	46.754	36.440	24.815
THYRO1000320	40.309	30.149	19.537	13.455	14.834	15.964	18.078	23.604
THYRO1000322	24.627	37.164	14.062	13.220	24.263	67.227	13.642	17.831
THYRO1000327	26.339	17.202	19.390	6.909	11.125	14.143	17.357	12.537
THYRO1000343	42.016	17.813	9.604	6.474	9.696	16.820	27.338	14.579
THYRO1000345	34.927	30.431	13.357	14.304	4.038	18.892	23.250	25.428
THYRO1000358	127.335	79.228	36.533	19.149	36.183	60.464	53.854	26.909
THYRO1000368	78.311	58.596	30.918	30.458	16.882	27.090	35.669	29.402
THYRO1000375	44.890	71.506	29.159	43.213	19.374	23.353	20.500	28.158
THYRO1000381	8.353	7.688	6.523	4.841	3.834	5.630	10.498	8.428
THYRO1000387	46.186	48.531	25.979	23.533	23.474	20.675	19.353	27.678
THYRO1000394	80.432	59.053	40.610	41.098	48.706	38.355	26.242	29.817
THYRO1000395	97.955	28.782	36.802	20.433	29.363	45.023	48.651	32.418

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Table 159

THYRO1000400	29.261	30.808	14.649	12.890	12.143	17.419	17.865	20.330
THYRO1000401	48.109	37.938	22.638	16.225	12.893	28.523	30.627	19.454
THYRO1000407	20.235	11.480	8.357	3.709	9.881	7.211	13.275	7.999
THYRO1000420	68.894	43.096	35.789	24.115	20.938	30.086	31.852	26.083
THYRO1000438	33.270	20.145	29.159	31.273	12.085	10.585	9.246	12.932
THYRO1000452	53.893	37.152	27.337	22.464	17.753	26.548	22.201	22.293
THYRO1000455	2.280	0.834	0.000	0.976	0.585	1.280	2.641	1.093
THYRO1000471	47.958	25.563	18.216	14.664	13.684	14.209	21.695	20.773
THYRO1000481	31.917	26.285	16.526	11.506	15.682	19.322	21.433	19.881
THYRO1000484	105.966	101.654	49.570	65.106	44.560	42.375	53.422	61.358
THYRO1000488	10.604	11.718	5.980	2.408	1.075	2.903	5.387	5.572
THYRO1000501	27.472	26.976	14.433	9.731	5.970	14.226	13.623	20.839
THYRO1000502	5.447	3.089	4.285	1.572	3.996	4.353	4.902	2.744
THYRO1000505	4.701	9.342	2.729	1.539	2.859	3.412	6.900	4.379
THYRO1000535	36.284	36.608	15.352	10.179	15.441	15.802	32.978	26.549
THYRO1000556	98.555	26.955	23.471	9.941	21.538	34.089	54.689	21.009
THYRO1000558	40.392	34.267	23.559	20.713	24.798	17.657	28.862	27.336
THYRO1000569	873.069	308.078	372.545	155.422	299.039	483.635	445.882	305.921
THYRO1000570	35.246	19.469	12.612	19.448	7.219	17.186	18.803	17.396
THYRO1000572	39.801	10.089	11.294	4.705	3.846	19.606	13.915	6.846
THYRO1000573	16.251	10.017	7.249	4.045	4.497	4.783	12.198	5.097
THYRO1000577	10.585	9.999	5.259	3.391	2.076	7.540	7.747	5.771
THYRO1000580	39.072	33.754	20.407	32.861	20.138	22.441	26.841	38.662
THYRO1000584	56.308	33.150	19.548	14.340	19.384	30.365	39.545	23.407
THYRO1000585	43.561	24.758	28.265	16.580	20.169	22.132	27.817	24.366
THYRO1000596	2.673	0.776	0.000	0.000	4.716	2.198	2.119	1.933
THYRO1000602	94.197	75.969	43.440	45.120	38.294	42.518	37.044	37.636
THYRO1000605	37.030	19.281	9.512	7.831	12.501	20.183	23.421	15.563
THYRO1000615	15.039	14.895	6.698	8.884	6.498	7.491	8.656	8.551
THYRO1000625	49.869	34.253	18.419	29.529	18.526	18.214	20.134	21.544
THYRO1000636	32.799	20.827	9.591	8.974	11.041	15.919	22.990	18.387
THYRO1000637	35.581	23.050	18.908	14.371	24.139	16.485	41.751	19.963
THYRO1000641	28.962	17.660	13.853	8.774	18.253	16.722	20.366	17.183
THYRO1000657	66.685	48.553	43.153	26.769	20.514	33.412	27.427	59.913
THYRO1000658	101.090	94.403	57.365	65.686	46.570	42.965	35.054	51.149
THYRO1000662	30.501	28.754	7.936	6.202	14.884	24.631	23.740	14.132
THYRO1000666	56.263	27.128	11.520	10.878	12.343	19.483	26.494	16.400
THYRO1000676	46.904	34.507	12.093	23.243	14.596	11.035	13.272	18.504
THYRO1000678	12.599	11.709	10.630	7.426	8.273	5.498	7.825	12.309
THYRO1000684	61.875	24.579	20.434	9.128	13.986	27.123	42.335	20.023
THYRO1000694	94.566	65.001	36.187	11.784	39.648	50.883	109.147	47.741
THYRO1000699	228.022	178.345	154.501	107.031	135.907	157.184	148.138	139.950
THYRO1000712	66.420	120.229	65.349	78.931	61.796	42.847	42.817	59.069
THYRO1000715	52.182	30.514	16.829	12.645	16.476	20.968	33.909	18.460
THYRO1000716	34.776	27.624	13.457	11.085	11.113	8.581	20.893	12.979
THYRO1000717	64.920	84.125	21.513	31.324	22.570	21.072	22.860	29.727
THYRO1000723	6.184	6.744	4.434	3.785	5.307	2.617	6.718	7.719
THYRO1000734	15.193	18.494	9.892	17.212	6.183	7.960	17.862	10.472
THYRO1000748	94.224	47.484	24.348	16.194	34.311	34.308	68.067	29.440
THYRO1000755	24.375	26.453	17.994	18.096	13.613	21.492	17.967	32.148
THYRO1000756	50.530	55.367	19.662	10.236	15.906	24.457	28.624	19.162
THYRO1000776	24.132	29.551	15.488	11.113	9.272	17.530	17.901	15.200
THYRO1000777	18.780	26.388	14.190	9.047	9.368	16.446	29.480	15.416
THYRO1000779	1.795	0.000	0.000	2.494	7.457	0.000	6.362	2.532
THYRO1000782	47.931	38.121	28.062	11.863	22.874	28.629	25.108	23.954
THYRO1000783	25.655	14.286	12.376	5.578	6.270	12.787	17.848	13.045
THYRO1000786	52.665	48.137	29.971	29.960	23.410	37.344	61.708	40.990
THYRO1000787	300.022	78.369	95.279	31.225	58.114	149.896	140.608	55.131
THYRO1000792	56.669	16.981	17.506	14.737	10.487	12.435	26.185	19.757
THYRO1000793	21.782	17.626	12.726	12.269	7.738	18.245	14.576	9.048
THYRO1000795	35.732	43.199	24.656	10.920	12.277	22.001	20.250	17.634
THYRO1000796	23.496	27.404	20.088	17.955	13.259	12.893	15.542	13.569
THYRO1000798	46.024	29.017	22.439	17.032	17.838	27.756	29.891	12.085
THYRO1000800	51.341	77.530	54.957	81.739	91.231	44.745	43.380	63.706

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Table 160

THYR01000805	29.203	24.611	12.889	12.552	8.708	24.185	31.195	17.746
THYR01000815	116.955	165.320	75.096	94.269	59.401	58.491	42.135	74.481
THYR01000829	23.576	12.796	8.360	10.367	5.365	10.395	15.475	8.236
THYR01000835	26.167	23.644	13.936	14.093	11.798	32.901	18.905	17.992
THYR01000843	33.508	44.053	31.047	36.013	19.347	21.091	20.171	23.430
THYR01000846	18.033	12.383	7.953	5.357	8.714	8.050	10.459	6.930
THYR01000852	26.571	15.703	9.149	9.589	4.965	8.428	10.204	11.995
THYR01000855	45.596	37.371	20.596	42.732	32.911	16.694	31.555	30.260
THYR01000865	72.472	80.181	43.954	56.430	21.283	38.134	52.647	49.076
THYR01000866	136.754	43.702	88.564	12.275	34.870	89.966	25.647	39.646
THYR01000881	484.415	303.533	220.883	156.089	149.161	314.435	262.114	229.042
THYR01000894	65.638	28.931	14.132	11.237	15.661	21.378	24.165	10.595
THYR01000895	19.040	17.281	11.079	9.005	6.164	7.972	11.149	13.327
THYR01000916	68.849	51.202	36.286	38.745	35.015	21.936	23.241	21.349
THYR01000917	378.890	211.431	172.873	110.307	168.147	239.935	221.829	171.250
THYR01000926	74.104	25.922	17.751	14.409	20.225	27.710	40.030	15.229
THYR01000934	21.900	17.023	11.309	10.688	4.218	13.887	14.363	11.574
THYR01000951	48.727	35.250	16.046	12.962	18.778	26.338	19.255	15.211
THYR01000952	34.577	22.838	17.193	11.759	7.673	21.372	18.800	19.736
THYR01000956	37.412	15.001	11.959	8.197	4.251	13.753	14.833	20.107
THYR01000960	40.709	23.743	5.462	12.106	8.269	13.882	17.580	15.391
THYR01000961	3.619	4.816	1.934	2.829	5.229	4.913	6.632	5.076
THYR01000964	31.761	18.472	14.773	9.113	13.610	18.567	17.379	12.630
THYR01000971	64.832	44.237	30.605	28.185	28.067	36.041	37.405	44.344
THYR01000974	107.219	62.723	34.195	40.953	32.826	39.260	30.469	42.586
THYR01000975	81.132	53.975	52.682	49.142	35.144	34.988	44.912	43.686
THYR01000983	44.267	23.344	30.088	11.305	15.039	29.019	17.082	16.694
THYR01000984	43.136	31.868	22.917	23.200	16.640	18.941	14.847	19.412
THYR01000988	77.046	58.963	40.192	43.118	60.680	33.078	20.658	30.028
THYR01000991	59.477	49.735	27.299	24.412	23.236	36.791	41.514	30.530
THYR01000999	46.173	27.320	24.436	16.574	12.745	22.240	23.460	20.374
THYR01001003	45.343	40.846	34.059	27.728	30.647	22.768	14.074	29.299
THYR01001015	105.149	53.043	34.722	25.220	29.072	70.219	55.045	37.157
THYR01001016	55.018	27.688	20.817	19.166	16.243	14.052	10.907	20.419
THYR01001022	34.560	25.745	16.566	9.263	10.892	16.822	19.126	15.036
THYR01001031	79.734	70.269	57.437	40.146	30.024	20.905	25.507	25.466
THYR01001033	22.581	21.639	10.233	5.613	5.972	14.479	22.263	14.812
THYR01001062	50.552	36.895	25.102	26.692	22.143	17.789	17.845	24.414
THYR01001063	75.298	52.927	34.731	26.645	26.587	31.088	36.388	28.011
THYR01001071	15.221	6.957	5.949	2.033	6.433	6.642	7.745	6.223
THYR01001080	47.009	39.873	20.480	18.101	20.162	20.086	35.494	27.474
THYR01001093	66.980	65.072	31.618	33.564	16.112	27.365	31.863	34.516
THYR01001108	21.067	15.255	12.169	9.015	5.970	14.570	15.506	13.653
THYR01001102	18.746	18.080	6.257	4.335	1.730	11.510	9.775	8.902
THYR01001104	18.657	25.635	14.755	25.137	12.793	22.720	23.958	26.681
THYR01001109	15.251	15.230	8.676	4.654	5.820	7.397	12.338	9.739
THYR01001113	37.344	45.395	7.359	8.259	16.170	12.948	22.426	17.552
THYR01001120	80.202	35.430	22.559	15.448	18.774	31.803	42.346	22.885
THYR01001121	52.621	42.522	27.046	29.236	28.248	24.648	46.988	38.643
THYR01001128	136.958	100.049	61.329	56.461	53.098	61.086	60.358	56.767
THYR01001133	94.452	101.822	62.367	57.536	40.128	46.930	37.716	49.125
THYR01001134	17.941	17.461	8.019	4.846	6.568	9.163	14.613	12.344
THYR01001142	10.016	5.374	4.501	1.699	2.274	4.180	3.267	3.903
THYR01001173	315.883	215.361	158.303	99.619	143.648	173.339	189.443	126.977
THYR01001175	38.323	13.237	7.198	6.214	10.354	14.774	23.098	12.914
THYR01001177	65.825	73.170	30.535	23.781	36.556	23.552	39.234	27.932
THYR01001188	71.764	109.416	54.067	80.715	51.976	45.521	44.962	108.449
THYR01001194	43.753	58.316	68.460	31.797	22.784	16.960	16.508	31.677
THYR01001204	24.393	20.084	15.874	17.477	14.104	29.010	29.959	20.054
THYR01001205	444.098	372.962	225.154	217.033	189.087	246.605	214.186	193.594
THYR01001213	59.798	77.150	45.729	51.526	31.541	26.773	26.362	35.040
THYR01001224	53.123	51.273	33.830	51.454	44.844	34.214	24.649	47.409
THYR01001237	106.442	74.420	27.897	20.382	32.686	50.109	49.913	35.697
THYR01001242	742.882	336.755	278.663	173.174	332.014	438.140	526.417	308.380

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Table 161

THYRO1001258	115.192	68.322	37.962	28.447	39.496	73.140	89.614	50.152
THYRO1001262	29.592	38.992	24.922	22.829	20.191	14.595	14.682	19.309
THYRO1001266	24.695	23.851	16.014	7.968	11.573	18.488	19.268	13.434
THYRO1001271	37.090	37.276	12.145	11.215	2.868	19.505	17.992	11.460
THYRO1001287	69.292	40.644	17.033	16.333	18.990	24.523	40.591	27.350
THYRO1001290	38.183	9.778	9.132	6.909	7.883	17.550	22.844	10.046
THYRO1001291	27.456	31.200	13.335	8.894	13.643	16.343	24.246	14.305
THYRO1001297	22.802	40.193	15.454	24.356	18.908	13.849	19.636	27.811
THYRO1001302	32.724	25.039	21.076	11.586	19.524	23.410	57.069	22.259
THYRO1001313	54.483	44.710	22.791	17.196	22.860	28.535	38.530	26.619
THYRO1001320	67.151	79.399	38.582	43.377	31.441	31.488	30.487	34.150
THYRO1001321	32.185	46.760	20.156	31.133	26.936	21.803	17.729	26.264
THYRO1001322	56.040	44.139	25.288	32.717	26.245	19.900	28.415	30.093
THYRO1001327	11.598	12.117	3.614	3.130	6.285	5.136	8.978	9.997
THYRO1001336	45.342	100.054	38.339	43.663	34.416	23.794	31.249	61.226
THYRO1001347	8.316	11.569	4.451	4.135	3.827	2.861	6.260	3.931
THYRO1001358	96.749	91.718	27.513	38.148	45.764	39.905	54.447	48.267
THYRO1001363	76.229	50.596	45.707	32.563	22.003	40.930	35.965	23.714
THYRO1001365	63.340	44.755,	24.569	15.278	14.500	31.255	62.023	22.216
THYRO1001374	80.359	54.703	28.941	21.895	26.409	86.809	59.724	67.154
THYRO1001401	138.528	81.793	116.025	115.772	62.059	81.850	81.710	84.369
THYRO1001403	75.077	60.253	47.159	43.576	31.391	38.040	41.579	34.801
THYRO1001405	75.788	63.929	37.018	66.708	25.398	44.268	-169.777	92.288
THYRO1001406	99.789	119.681	106.617	111.553	73.294	82.322	63.741	106.694
THYRO1001411	164.801	155.374	122.876	101.166	90.616	97.554	90.344	81.141
THYRO1001420	467.850	125.400	141.742	95.133	79.850	256.705	243.974	168.095
THYRO1001426	179.694	226.744	136.659	182.920	57.912	158.699	76.886	79.382
THYRO1001430	42.233	36.308	24.265	13.334	24.942	28.220	31.096	31.763
THYRO1001434	109.844	40.429	23.142	7.076	19.838	16.721	46.971	13.694
THYRO1001456	86.810	51.093	28.872	22.686	29.334	38.972	42.073	32.789
THYRO1001457	98.410	46.954	51.922	44.428	26.365	68.702	73.800	71.948
THYRO1001458	142.203	61.648	63.756	91.611	29.372	63.294	57.491	83.860
THYRO1001459	98.569	70.732	48.940	49.572	33.394	53.365	59.458	61.428
THYRO1001471	29.011	30.922	22.501	12.339	12.979	11.855	19.026	15.004
THYRO1001478	88.744	24.933	23.684	23.261	16.773	41.417	28.941	16.857
THYRO1001480	198.549	217.139	159.064	171.095	130.028	161.021	98.977	203.804
THYRO1001481	72.983	76.982	51.877	37.940	41.871	34.156	32.190	31.811
THYRO1001487	156.213	112.142	110.985	77.310	74.839	88.309	62.208	64.884
THYRO1001495	60.311	64.175	75.269	57.588	39.964	22.882	51.168	78.626
THYRO1001498	60.093	50.240	28.962	43.623	28.080	27.349	44.121	57.310
THYRO1001510	78.106	71.131	37.969	22.613	29.598	45.141	25.613	34.714
THYRO1001512	146.930	95.726	82.300	47.386	70.311	138.360	106.274	87.137
THYRO1001519	143.411	115.340	57.861	92.182	36.860	89.655	54.540	72.487
THYRO1001522	86.178	52.213	40.302	33.014	28.267	48.497	38.421	32.647
THYRO1001523	42.807	21.996	19.646	7.023	13.176	31.304	17.358	26.586
THYRO1001526	28.272	36.470	18.141	20.984	18.220	25.059	22.056	22.382
THYRO1001529	56.422	40.050	50.636	49.921	36.172	38.431	43.929	41.984
THYRO1001534	79.983	41.665	36.130	45.070	31.736	27.199	39.647	22.708
THYRO1001537	266.845	336.357	127.186	167.167	121.366	235.919	269.119	105.552
THYRO1001541	184.924	142.434	89.266	94.007	73.101	77.708	42.435	36.282
THYRO1001545	45.721	28.807	17.637	23.355	11.596	33.223	26.025	32.640
THYRO1001559	30.285	28.050	27.503	21.583	24.440	18.855	21.731	20.280
THYRO1001563	81.147	53.590	40.132	34.989	31.762	54.315	46.120	51.808
THYRO1001570	160.698	53.241	43.074	13.542	48.479	91.833	66.191	35.765
THYRO1001573	121.318	40.895	58.993	29.240	41.403	54.710	52.876	28.623
THYRO1001584	69.312	78.135	36.886	44.973	43.785	43.480	40.786	52.141
THYRO1001593	44.626	47.299	8.544	35.805	8.587	5.747	5.738	4.447
THYRO1001595	86.656	81.363	41.727	44.260	36.433	28.946	28.668	31.638
THYRO1001598	68.810	32.126	33.747	19.824	25.437	33.051	41.347	20.355
THYRO1001602	83.486	75.627	45.307	63.834	30.332	45.771	44.872	49.010
THYRO1001605	44.557	32.876	26.697	55.092	18.403	5.627	17.556	16.676
THYRO1001608	155.484	67.359	43.850	31.079	31.843	58.215	58.920	39.494
THYRO1001617	84.352	72.661	68.377	48.198	54.691	37.282	30.097	54.744
THYRO1001634	61.852	39.793	24.126	16.827	22.530	35.972	34.077	28.775

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Table 162

THYR01001637	114.477	126.686	100.621	117.804	62.577	74.963	57.380	70.174
THYR01001641	56.288	37.515	23.987	22.669	22.635	47.096	31.301	36.440
THYR01001656	46.272	34.075	24.272	14.259	16.135	20.671	23.336	16.130
THYR01001658	38.715	35.384	15.215	12.669	11.948	23.345	31.267	21.631
THYR01001661	32.296	22.714	17.431	15.015	9.537	9.794	20.777	17.147
THYR01001671	50.011	59.547	50.424	34.364	50.747	38.082	34.858	41.054
THYR01001672	174.047	48.626	52.990	17.925	41.381	103.416	95.249	37.062
THYR01001673	84.547	78.591	41.886	44.045	40.533	34.065	30.562	33.114
THYR01001677	115.789	184.195	53.250	75.184	37.282	129.575	60.337	112.501
THYR01001683	38.015	42.900	56.368	28.898	58.930	62.855	51.341	29.701
THYR01001700	96.033	45.482	30.258	16.461	15.124	50.006	58.501	25.463
THYR01001702	104.525	90.670	66.901	45.679	27.558	56.203	56.767	54.824
THYR01001703	130.645	112.852	65.413	39.114	40.388	88.732	101.241	68.988
THYR01001706	91.082	82.049	58.522	50.870	37.126	36.387	37.277	63.203
THYR01001721	34.852	21.558	20.543	5.921	22.162	9.493	31.475	17.215
THYR01001726	49.609	39.621	22.513	28.557	23.707	34.262	31.779	30.693
THYR01001730	401.603	145.337	161.719	64.173	142.140	284.093	229.429	104.416
THYR01001738	89.896	75.892	33.629	38.777	22.430	45.582	54.154	54.913
THYR01001743	49.231	21.758	27.130	12.056	9.553	33.154	29.680	20.832
THYR01001745	34.753	17.745	12.052	5.744	9.946	20.567	17.357	15.138
THYR01001746	41.622	37.766	23.996	18.634	16.249	24.636	33.799	27.306
THYR01001770	103.357	62.531	51.786	43.073	39.785	65.980	54.332	47.446
THYR01001772	129.127	129.155	79.515	82.371	76.101	53.649	49.368	77.136
THYR01001778	384.882	146.526	97.702	61.349	90.096	136.302	175.998	86.468
THYR01001793	105.591	94.089	51.614	51.310	47.627	57.471	55.262	69.224
THYR01001796	218.755	90.413	86.089	46.396	63.339	153.810	148.699	63.431
THYR01001800	89.126	64.948	37.534	20.212	33.235	41.405	36.130	25.761
THYR01001803	272.135	195.625	179.931	121.130	156.151	183.032	218.545	154.914
THYR01001809	58.170	31.728	28.593	29.699	25.633	36.954	29.839	25.467
THYR01001817	64.728	50.418	26.089	15.924	19.828	34.567	51.140	43.878
THYR01001819	190.982	76.509	54.579	22.923	63.162	79.239	96.822	48.339
THYR01001828	234.551	180.238	92.244	80.148	104.168	85.912	160.310	122.500
THYR01001854	219.242	211.323	112.250	150.918	95.727	100.808	75.437	109.696
THYR01001895	44.632	35.971	20.836	14.220	19.503	17.351	23.442	22.241
THYR01001907	93.660	85.352	41.680	44.441	40.868	38.888	56.595	43.717
TRACH1000006	33.077	27.517	13.610	11.659	11.195	23.390	21.396	13.682
TRACH1000013	26.029	19.365	8.037	11.958	5.076	14.402	20.496	12.167
TRACH1000074	86.302	70.850	32.892	34.317	28.366	44.087	58.165	52.228
TRACH1000085	48.021	44.110	17.672	16.895	20.410	35.389	47.442	40.607
TRACH1000102	160.667	128.745	55.282	64.147	57.430	67.455	96.519	73.638
TRACH1000108	25.597	37.670	13.402	14.907	16.504	16.136	17.158	22.858
TRACH1000126	77.681	74.516	36.350	26.803	33.821	49.762	65.600	50.277
TRACH1000146	73.548	74.493	25.762	17.947	22.979	32.054	38.447	25.115
TRACH1000160	48.076	58.220	20.043	15.138	20.069	33.175	33.858	10.911
TRACH1000184	91.688	86.638	74.932	279.361	88.220	48.252	53.846	52.975
VESEN1000004	62.054	51.690	18.581	21.984	17.610	26.122	42.606	29.900
VESEN1000007	99.131	44.516	29.577	21.187	27.518	43.145	68.086	49.423
VESEN1000013	171.250	57.002	40.813	26.552	35.545	51.737	104.132	45.994
VESEN1000028	154.863	100.292	99.295	65.820	64.165	105.318	97.599	79.474
VESEN1000059	144.402	97.274	74.579	50.603	39.182	86.619	98.065	63.442
VESEN1000100	189.864	121.300	76.817	72.933	34.794	116.439	77.465	65.031
VESEN1000107	86.037	54.735	41.418	35.034	31.521	66.087	66.041	39.378
VESEN1000117	76.673	47.432	28.526	16.406	24.766	41.803	57.926	29.302
VESEN1000122	58.990	42.673	43.051	39.986	31.414	56.718	73.186	51.792
VESEN1000137	28.827	12.637	7.708	3.164	11.517	19.000	24.465	12.213
VESEN1000185	163.283	63.672	50.465	38.118	37.080	54.088	101.701	58.407
VESEN1000215	9.881	2.089	6.413	1.074	2.285	0.000	7.414	9.842
VESEN1000278	402.741	271.057	182.622	118.097	189.914	225.664	188.843	101.819
VESEN1000363	302.568	148.812	122.811	95.469	86.731	148.698	141.113	78.717
VESEN1000388	162.477	40.549	65.388	30.129	37.997	96.063	69.144	66.497
VESEN1000394	142.530	93.533	77.611	46.922	58.268	86.276	96.211	70.505
VESEN1000410	136.126	38.001	29.774	12.727	26.741	68.866	54.097	73.237
VESEN1000411	95.259	49.542	42.301	40.898	26.132	46.132	57.517	59.117
VESEN1000415	97.225	63.935	46.211	36.640	29.907	51.713	51.249	62.215

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Table 163

VESEN1000440	101.690	47.149	49.195	32.607	27.881	49.154	46.485	40.340
VESEN1000452	188.242	75.844	67.861	21.929	49.688	101.557	105.023	55.625
VESEN1000539	393.622	128.413	233.289	155.268	285.073	217.892	156.970	106.498
VESEN1000554	44.150	40.448	28.459	17.920	17.204	20.338	40.271	30.185
VESEN1000557	108.763	50.564	47.257	21.505	36.349	59.158	68.956	34.611
VESEN1000575	151.228	53.084	39.503	26.612	41.610	59.636	65.502	37.895
VESEN1000585	106.127	43.089	41.516	30.022	40.857	51.129	80.130	52.937
VESEN1000592	3.732	4.371	1.727	2.763	2.784	4.336	0.000	0.000
VESEN1000658	122.632	54.799	53.689	27.783	41.778	66.943	69.146	46.823
VESEN1000669	454.284	184.969	184.094	116.303	152.848	275.995	209.035	150.917
VESEN1000743	93.271	66.577	38.667	37.030	25.203	47.385	47.073	46.048
VESEN1000752	132.397	105.539	71.129	71.113	87.050	96.768	63.315	77.177
VESEN1000761	58.860	37.210	39.232	28.055	41.286	48.665	37.844	25.644
VESEN2000039	1610.708	423.257	575.130	281.845	514.008	1029.335	742.044	261.643
VESEN2000102	157.000	68.371	47.526	31.817	43.466	78.881	87.904	46.756
VESEN2000164	67.615	99.316	47.555	50.732	57.545	101.472	141.913	60.455
VESEN2000175	11.198	3.920	4.227	2.329	1.448	2.820	3.186	3.710
VESEN2000186	302.893	166.977	128.067	101.481	89.845	151.983	136.632	157.737
VESEN2000199	364.016	262.765,	186.502	152.072	152.565	198.826	191.332	195.186
VESEN2000200	61.361	28.617	25.760	13.454	12.471	25.754	39.784	31.121
VESEN2000204	59.937	29.170	19.088	10.312	16.203	30.641	61.987	24.109
VESEN2000218	46.156	34.497	30.351	21.300	16.675	31.656	29.879	27.886
VESEN2000230	87.277	57.160	38.252	30.651	31.117	44.365	42.098	43.558
VESEN2000272	18.326	25.046	19.526	14.701	21.471	15.146	23.503	20.851
VESEN2000299	81.003	29.068	28.969	16.886	22.798	37.073	38.504	23.627
VESEN2000323	102.974	73.231	65.632	62.476	64.170	44.083	52.687	53.681
VESEN2000327	273.358	190.493	102.117	60.523	95.669	114.144	160.249	65.341
VESEN2000328	52.003	27.894	15.775	9.884	11.945	24.112	26.254	20.997
VESEN2000330	109.315	77.876	36.393	27.267	44.428	48.237	51.597	44.132
VESEN2000336	55.020	22.112	15.818	14.036	11.558	21.687	27.119	27.342
VESEN2000354	157.246	74.852	37.950	19.235	42.182	51.559	45.485	29.194
VESEN2000378	66.998	66.140	23.647	15.673	16.217	28.709	41.497	35.393
VESEN2000379	54.007	68.263	27.636	45.302	17.881	35.928	44.060	55.125
VESEN2000397	27.834	20.615	10.624	8.727	4.818	15.386	21.163	18.688
VESEN2000416	32.241	18.712	9.825	8.843	5.474	12.685	17.453	16.485
VESEN2000420	26.334	9.499	7.013	2.363	5.104	8.281	2.634	1.015
VESEN2000430	18.312	20.459	12.183	7.101	4.975	13.810	17.050	19.805
VESEN2000448	39.040	15.163	13.638	4.769	9.693	14.334	26.387	13.923
VESEN2000449	130.475	60.437	47.055	28.198	46.878	64.756	79.761	49.783
VESEN2000456	54.149	49.676	24.294	20.921	18.957	24.771	39.745	38.640
VESEN2000562	96.176	59.785	49.030	22.452	26.435	64.420	70.890	48.405
VESEN2000573	9.605	2.326	1.730	0.480	0.850	3.785	3.113	2.414
VESEN2000604	89.021	25.246	24.495	10.300	14.725	40.448	47.664	24.062
VESEN2000614	309.658	310.143	158.396	121.428	98.306	193.176	285.544	193.901
VESEN2000638	20.825	13.750	9.472	3.518	6.018	8.616	15.565	14.138
VESEN2000641	48.159	26.214	12.211	7.625	12.728	19.489	34.963	19.847
VESEN2000645	59.209	24.195	14.955	7.186	18.507	28.178	34.263	17.733
Y79AA1000013	157.258	82.237	47.630	29.858	46.920	77.296	68.488	40.042
Y79AA1000030	243.192	141.007	108.937	74.649	80.890	166.613	137.379	98.647
Y79AA1000033	49.439	83.718	30.433	22.365	22.376	31.534	35.936	31.220
Y79AA1000037	41.732	23.568	14.154	16.224	15.348	13.136	21.199	16.632
Y79AA1000041	32.341	27.270	14.230	18.610	9.838	21.052	18.336	19.147
Y79AA1000059	153.140	85.760	57.915	58.738	48.608	73.595	69.769	54.893
Y79AA1000065	29.024	32.383	43.083	35.688	53.004	14.961	23.027	24.640
Y79AA1000681	173.505	497.689	138.675	253.938	133.917	128.427	148.052	120.067
Y79AA1000127	103.173	80.281	69.484	68.351	62.524	80.674	36.808	76.356
Y79AA1000130	69.801	86.217	30.612	44.271	38.125	34.801	24.913	36.307
Y79AA1000131	153.662	1161.128	226.879	579.469	215.457	854.176	483.175	1147.374
Y79AA1000134	127.126	50.652	49.040	26.779	39.721	89.186	71.223	41.628
Y79AA1000143	38.064	56.092	35.659	31.888	43.450	26.885	22.084	33.064
Y79AA1000144	20.785	16.047	11.172	9.422	12.441	12.606	10.549	17.382
Y79AA1000150	70.908	50.343	31.433	31.813	43.554	44.314	68.333	45.702
Y79AA1000153	473.493	498.355	203.636	356.247	217.748	319.244	390.823	511.885
Y79AA1000166	75.693	64.809	33.184	43.509	28.975	33.094	32.512	48.232

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Table 164

Y79AA1000179	86.164	94.446	49.366	55.296	56.791	60.147	47.613	52.526
Y79AA1000181	80.781	67.215	32.483	29.549	31.500	35.404	49.327	33.106
Y79AA1000202	306.822	216.805	147.425	103.426	137.718	171.835	204.385	165.929
Y79AA1000207	105.429	123.961	53.587	73.034	70.343	43.214	45.289	43.628
Y79AA1000214	383.142	209.292	152.641	183.832	147.889	192.552	228.518	129.266
Y79AA1000222	22.954	21.555	15.620	61.846	15.816	19.929	16.837	13.933
Y79AA1000226	132.385	77.693	43.017	23.388	43.039	51.041	132.959	53.641
Y79AA1000227	115.766	115.677	67.073	61.011	55.085	60.149	67.002	75.560
Y79AA1000230	45.896	40.474	17.716	13.218	16.881	19.738	28.415	24.012
Y79AA1000231	89.296	107.825	54.778	82.032	51.998	46.803	58.529	93.293
Y79AA1000239	50.494	47.587	29.697	28.552	35.135	32.631	62.953	29.843
Y79AA1000258	45.676	53.770	28.305	21.170	27.158	24.070	38.214	28.393
Y79AA1000268	116.499	61.766	35.684	30.031	40.259	65.427	65.925	48.582
Y79AA1000269	36.988	41.536	21.854	18.345	26.984	89.369	74.183	28.252
Y79AA1000270	70.349	65.424	33.771	24.490	36.913	20.903	38.891	30.089
Y79AA1000280	52.901	53.162	47.984	50.005	29.457	37.014	42.331	53.345
Y79AA1000285	37.272	42.207	25.179	14.304	14.336	34.801	24.865	20.291
Y79AA1000295	10.340	10.594	11.909	7.559	12.902	8.040	7.052	8.641
Y79AA1000307	67.533	64.757,	61.969	64.592	36.178	56.127	56.928	58.020
Y79AA1000313	224.230	107.870	95.224	65.861	65.836	94.564	146.279	83.495
Y79AA1000314	150.954	88.811	114.139	31.101	138.725	106.102	94.884	43.590
Y79AA1000328	25.270	21.003	21.314	15.992	13.358	17.078	25.728	22.062
Y79AA1000334	70.086	48.685	34.036	32.394	26.966	25.485	44.339	35.712
Y79AA1000342	445.189	140.661	207.068	102.538	170.033	280.562	201.342	123.827
Y79AA1000346	44.966	28.105	25.613	13.811	29.974	38.613	18.724	15.227
Y79AA1000347	163.577	87.476	90.030	89.865	36.284	83.081	92.665	49.209
Y79AA1000349	180.947	135.094	102.606	92.069	66.005	137.226	121.401	90.266
Y79AA1000355	81.202	61.139	54.018	52.567	41.342	46.383	35.944	35.848
Y79AA1000368	45.079	38.521	25.612	35.417	24.877	35.299	37.961	39.102
Y79AA1000388	34.856	29.318	53.178	46.283	64.992	15.602	20.395	27.793
Y79AA1000392	274.040	169.752	96.625	109.904	62.391	137.141	143.707	98.881
Y79AA1000405	52.788	38.000	27.665	15.987	21.983	34.628	36.536	24.328
Y79AA1000410	367.438	401.406	216.699	294.500	169.645	216.009	99.999	119.786
Y79AA1000420	19.321	19.430	17.167	18.384	13.307	17.286	11.353	16.663
Y79AA1000423	54.384	64.128	38.233	39.006	35.194	25.311	19.482	25.935
Y79AA1000426	51.920	32.060	27.489	16.208	18.993	28.308	30.801	19.059
Y79AA1000432	31.920	23.564	18.505	7.033	17.684	13.924	19.534	15.486
Y79AA1000453	100.064	106.207	64.195	87.842	32.741	36.705	43.951	75.421
Y79AA1000465	32.600	20.760	8.375	9.114	6.582	11.349	19.307	16.375
Y79AA1000469	97.006	89.211	57.415	39.971	51.138	78.959	69.898	46.327
Y79AA1000480	49.123	43.661	36.763	32.840	25.674	27.684	32.111	29.981
Y79AA1000502	29.200	23.820	30.903	19.340	29.500	19.819	9.990	17.119
Y79AA1000521	165.752	60.574	64.764	35.797	44.981	81.691	94.837	59.780
Y79AA1000534	40.465	37.392	29.025	27.278	27.637	22.639	17.299	34.366
Y79AA1000538	90.033	71.681	68.241	72.663	53.051	55.445	40.270	39.870
Y79AA1000539	97.472	118.331	83.966	95.779	78.679	49.286	67.204	89.085
Y79AA1000540	164.490	95.071	40.165	43.390	40.045	64.022	69.258	38.304
Y79AA1000560	281.384	217.439	285.257	233.113	463.011	163.480	137.130	150.237
Y79AA1000574	52.065	23.181	20.651	12.249	16.138	19.256	27.792	16.219
Y79AA1000584	15.379	9.124	5.767	2.558	1.074	7.940	8.373	2.978
Y79AA1000589	183.820	100.432	70.853	66.366	57.641	89.842	106.272	87.142
Y79AA1000598	56.202	33.205	22.835	19.082	16.494	26.476	39.963	26.495
Y79AA1000600	41.902	41.896	21.689	16.420	16.929	48.490	27.963	19.342
Y79AA1000609	57.576	39.029	30.052	30.165	27.140	36.576	46.377	40.338
Y79AA1000618	125.086	117.263	62.983	91.667	44.430	82.703	59.073	106.707
Y79AA1000627	79.733	52.406	33.263	16.064	26.240	36.354	35.482	26.093
Y79AA1000636	39.025	110.754	63.444	78.431	38.373	40.282	27.825	50.545
Y79AA1000649	40.819	24.415	21.283	16.111	23.390	22.853	24.218	28.136
Y79AA1000656	34.895	43.071	26.370	23.075	19.462	31.058	38.717	36.845
Y79AA1000673	41.347	29.023	17.877	14.456	10.280	27.689	23.125	20.111
Y79AA1000674	262.849	127.516	120.736	76.530	76.511	135.175	156.724	108.424
Y79AA1000678	101.577	71.902	37.125	32.459	39.727	50.727	49.198	41.789
Y79AA1000682	206.911	109.200	74.410	66.092	82.312	114.912	88.981	92.050
Y79AA1000683	48.942	45.045	30.764	23.661	15.359	27.974	25.066	30.575

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Table 165

Y79AA1000697	593.441	140.294	205.250	128.388	180.538	358.317	185.955	157.146
Y79AA1000700	21.077	45.357	16.113	12.299	6.003	17.423	23.401	24.353
Y79AA1000702	62.438	42.446	9.035	13.744	21.360	47.616	22.905	32.458
Y79AA1000704	19.430	7.058	5.353	3.179	5.193	12.141	10.206	6.710
Y79AA1000705	10.998	17.592	10.298	10.719	8.004	6.779	14.333	13.157
Y79AA1000717	81.752	30.031	27.106	19.428	22.464	33.577	31.373	29.033
Y79AA1000722	36.212	18.986	16.192	21.995	16.249	16.693	21.786	16.366
Y79AA1000724	38.197	38.149	22.178	41.307	9.368	15.888	23.618	33.068
Y79AA1000726	145.871	38.218	60.209	20.692	45.339	70.264	60.747	27.206
Y79AA1000734	39.812	31.718	23.656	19.757	17.790	29.383	24.308	23.170
Y79AA1000748	27.090	25.462	9.232	12.141	5.845	15.311	22.833	15.914
Y79AA1000750	117.327	94.348	68.179	74.017	55.324	60.996	55.270	67.659
Y79AA1000752	1.118	1.818	0.920	1.289	0.825	1.965	2.636	3.173
Y79AA1000774	28.946	29.201	13.619	12.927	18.788	15.530	30.498	24.069
Y79AA1000776	62.397	39.548	26.589	27.629	27.128	25.527	51.928	36.475
Y79AA1000777	88.093	76.872	25.449	23.295	19.771	37.889	47.008	33.768
Y79AA1000778	89.017	55.709	39.247	33.579	21.743	40.267	35.715	34.927
Y79AA1000782	67.565	23.947	20.966	11.489	12.105	36.578	36.040	18.916
Y79AA1000784	39.988	33.246	27.325	20.358	20.827	23.886	24.033	27.859
Y79AA1000794	41.650	24.812	15.477	16.092	14.809	22.064	28.950	21.010
Y79AA1000800	41.806	25.329	17.225	7.394	11.113	22.848	25.673	22.742
Y79AA1000802	11.595	15.878	4.838	4.573	8.562	8.929	13.772	8.772
Y79AA1000805	65.610	45.406	23.562	18.162	27.677	27.293	47.887	38.440
Y79AA1000814	63.932	47.479	31.983	34.426	26.716	43.371	35.784	35.139
Y79AA1000823	22.185	48.954	19.279	19.138	20.407	22.530	21.540	22.820
Y79AA1000824	27.742	25.712	19.443	10.124	16.886	17.840	25.211	16.052
Y79AA1000827	25.479	15.274	10.916	8.366	10.528	8.349	18.396	16.070
Y79AA1000831	72.020	40.592	97.281	14.517	90.381	82.278	84.325	35.373
Y79AA1000833	471.030	168.358	184.092	104.334	176.646	249.032	310.721	135.495
Y79AA1000850	68.647	36.187	20.372	16.113	21.247	21.299	56.582	51.148
Y79AA1000856	77.469	45.416	31.674	22.522	37.097	33.815	62.486	52.013
Y79AA1000862	113.504	90.763	34.743	41.876	44.348	44.281	54.080	52.382
Y79AA1000876	9.498	19.259	12.167	8.739	10.542	5.725	6.252	6.011
Y79AA1000888	44.286	18.430	12.128	10.726	16.431	17.727	35.647	22.169
Y79AA1000902	25.675	20.186	13.114	21.076	13.224	15.117	12.128	12.728
Y79AA1000935	349.462	152.766	266.451	85.379	264.556	178.067	253.603	154.565
Y79AA1000959	32.431	15.556	16.803	4.756	23.529	16.748	16.620	10.584
Y79AA1000962	37.877	67.978	25.428	20.228	38.757	20.056	35.087	28.250
Y79AA1000963	77.792	69.690	30.704	66.559	22.376	45.923	60.514	78.400
Y79AA1000966	60.459	53.027	38.303	43.259	53.012	58.436	77.798	55.788
Y79AA1000967	112.210	96.985	52.461	31.773	74.280	67.804	71.776	42.966
Y79AA1000968	67.156	75.011	31.312	31.786	52.133	37.934	58.710	32.052
Y79AA1000969	73.694	47.137	29.787	20.498	30.555	33.354	44.510	23.718
Y79AA1000976	19.416	22.033	12.239	12.727	10.894	13.904	19.193	13.612
Y79AA1000978	50.835	57.439	51.253	31.538	53.350	33.330	50.341	51.246
Y79AA1000985	162.170	116.991	54.747	54.678	61.116	58.535	131.703	97.692
Y79AA1000989	160.869	133.278	169.716	48.057	196.947	67.040	105.199	90.492
Y79AA1000991	172.776	159.227	83.980	68.958	59.956	152.374	108.299	84.387
Y79AA1001013	199.195	153.480	107.292	61.287	92.604	113.848	154.343	119.100
Y79AA1001014	68.728	72.126	41.236	31.089	17.667	51.104	41.121	35.352
Y79AA1001019	66.003	34.676	36.574	22.751	21.527	33.525	40.467	35.925
Y79AA1001020	58.188	33.720	31.511	41.189	21.352	33.976	46.407	37.451
Y79AA1001023	75.610	41.776	31.044	17.988	30.650	42.942	60.331	30.561
Y79AA1001030	103.273	36.017	33.752	31.467	19.917	43.990	63.269	32.983
Y79AA1001035	0.000	0.000	28.444	28.051	16.127	41.569	62.544	47.884
Y79AA1001041	77.214	55.578	30.400	23.683	26.174	46.066	33.311	28.914
Y79AA1001043	62.920	86.930	40.257	39.379	42.525	44.192	65.573	44.307
Y79AA1001048	69.373	57.191	47.559	29.744	25.491	59.541	61.196	33.290
Y79AA1001056	28.105	21.448	25.068	14.638	27.011	27.941	27.218	31.106
Y79AA1001061	77.662	63.993	57.624	52.048	42.369	42.698	30.186	47.071
Y79AA1001062	23.211	15.295	22.974	9.450	20.841	12.268	15.522	19.189
Y79AA1001068	89.610	80.709	62.102	78.040	39.496	47.635	42.292	49.445
Y79AA1001073	167.563	77.800	50.531	46.973	52.260	47.272	72.297	55.883
Y79AA1001077	128.286	91.034	82.531	52.366	71.149	130.932	105.677	65.133

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Table 166

Y79AA1001078	23.435	19.289	16.494	16.707	8.916	16.759	28.013	25.651
Y79AA1001081	80.143	68.142	45.763	36.383	26.159	35.757	38.026	35.885
Y79AA1001088	317.039	242.117	151.726	124.084	134.444	174.586	238.334	149.593
Y79AA1001089	198.139	98.655	80.498	49.545	55.190	98.837	117.534	77.578
Y79AA1001090	80.451	60.910	39.633	42.380	36.692	37.452	32.352	35.391
Y79AA1001105	242.673	66.561	63.208	31.037	76.586	75.243	109.216	60.833
Y79AA1001142	79.091	23.396	18.843	28.396	19.935	55.429	96.508	34.254
Y79AA1001145	227.540	201.081	125.013	108.956	107.663	126.922	147.749	112.199
Y79AA1001162	32.474	21.215	17.402	13.823	7.016	14.608	10.831	11.076
Y79AA1001167	81.840	38.276	27.439	20.713	20.465	39.401	27.977	21.861
Y79AA1001176	37.234	30.174	29.821	28.145	17.772	23.084	23.905	31.875
Y79AA1001177	157.278	72.492	47.515	31.006	45.407	62.162	74.915	44.631
Y79AA1001179	155.289	77.734	66.981	49.326	60.911	108.763	101.419	45.761
Y79AA1001185	42.293	30.499	20.818	18.392	18.203	25.381	22.095	14.576
Y79AA1001201	70.267	62.245	55.927	64.637	42.307	55.945	44.441	55.417
Y79AA1001205	76.691	73.411	29.446	25.089	10.867	25.196	31.540	23.771
Y79AA1001211	69.077	77.295	43.109	54.773	26.171	19.436	23.382	36.508
Y79AA1001212	60.509	40.760	30.464	21.472	22.536	28.939	31.790	27.996
Y79AA1001216	107.414	112.384	51.845	90.341	48.098	86.493	78.661	128.332
Y79AA1001228	191.014	98.191	77.471	55.138	68.036	114.392	95.311	72.216
Y79AA1001233	165.200	46.959	55.748	19.356	50.639	93.326	77.766	29.974
Y79AA1001236	76.419	41.716	32.067	19.238	31.896	34.830	44.490	38.856
Y79AA1001239	348.195	155.335	206.398	93.364	264.580	150.282	141.282	138.685
Y79AA1001240	97.619	55.824	32.015	19.335	24.480	129.654	123.682	27.590
Y79AA1001255	60.196	39.594	29.713	32.087	23.430	42.093	44.389	40.863
Y79AA1001264	23.500	30.229	13.518	13.380	8.385	20.450	18.219	19.822
Y79AA1001272	172.136	148.159	89.874	101.905	67.677	109.162	89.962	89.461
Y79AA1001281	23.625	18.360	9.518	9.700	6.169	17.324	15.120	11.543
Y79AA1001299	257.530	138.510	106.642	92.167	96.141	155.017	156.902	114.884
Y79AA1001312	28.599	18.932	11.140	5.860	16.123	10.337	9.558	9.283
Y79AA1001319	233.396	111.817	90.283	51.100	80.506	137.595	117.523	59.456
Y79AA1001323	46.240	62.299	28.364	20.915	20.142	36.013	31.769	19.583
Y79AA1001328	166.188	85.958	71.107	51.952	47.867	98.151	92.634	63.952
Y79AA1001343	5293.557	1957.671	3529.524	508.017	5447.748	3598.173	4563.395	1662.056
Y79AA1001351	23.608	13.189	12.127	7.610	6.082	11.346	6.319	6.967
Y79AA1001364	23.462	34.748	26.228	44.078	18.806	18.623	17.892	57.833
Y79AA1001367	74.110	39.168	25.534	16.038	21.213	33.215	35.782	29.409
Y79AA1001384	44.135	26.692	19.494	6.267	19.195	15.742	34.303	21.015
Y79AA1001391	88.486	45.427	33.937	20.520	35.938	38.414	60.920	32.481
Y79AA1001394	73.046	48.196	27.660	26.614	16.092	26.264	37.409	30.457
Y79AA1001402	277.943	171.103	185.389	101.994	137.576	164.575	126.561	96.457
Y79AA1001410	37.405	47.535	22.875	21.151	18.753	29.322	20.709	19.883
Y79AA1001414	40.424	18.548	20.585	8.705	9.528	27.024	20.661	18.409
Y79AA1001426	128.039	45.365	44.982	17.958	30.855	79.863	82.932	35.756
Y79AA1001427	102.517	75.088	38.728	26.901	42.573	49.818	79.641	82.907
Y79AA1001430	88.291	44.524	17.775	15.144	26.578	35.825	47.406	24.141
Y79AA1001439	22.600	31.240	12.643	11.993	13.637	8.923	33.792	21.060
Y79AA1001485	12.457	15.083	6.416	6.180	7.239	8.477	11.343	9.667
Y79AA1001493	3.325	3.087	0.808	0.913	0.895	2.370	3.288	1.535
Y79AA1001511	34.387	42.870	31.800	22.668	30.480	30.907	27.949	41.671
Y79AA1001523	131.638	41.082	28.617	24.376	38.748	38.384	55.678	16.232
Y79AA1001530	64.263	17.602	37.936	9.778	39.229	26.821	36.155	15.958
Y79AA1001532	84.756	81.487	57.603	49.296	52.833	44.930	58.976	47.094
Y79AA1001533	71.806	80.795	31.639	34.117	34.465	30.573	56.137	27.551
Y79AA1001541	21.702	23.664	13.568	13.443	17.622	19.043	24.725	17.890
Y79AA1001548	160.662	125.939	91.450	78.443	96.657	102.345	81.132	92.148
Y79AA1001555	154.131	77.112	44.627	26.543	33.269	64.477	72.908	37.245
Y79AA1001562	19.278	39.676	21.323	15.462	21.126	20.650	11.744	27.432
Y79AA1001581	29.260	1.846	4.472	2.139	6.817	9.566	8.517	4.043
Y79AA1001585	10.832	9.273	5.154	4.611	8.363	3.849	8.753	6.599
Y79AA1001592	95.166	61.837	49.013	45.123	38.746	42.497	50.134	62.013
Y79AA1001594	58.652	50.427	16.817	20.106	22.571	18.261	35.915	34.587
Y79AA1001603	161.097	182.934	69.481	89.900	86.153	86.111	124.142	148.708
Y79AA1001613	143.075	94.475	65.178	44.394	70.764	86.215	108.731	75.786

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Y79AA1001630	13.646	12.156	6.553	6.307	8.775	5.570	14.006	7.900
Y79AA1001647	43.380	30.209	38.642	18.607	50.749	13.890	27.635	18.826
Y79AA1001664	50.619	62.037	23.222	35.535	31.203	25.999	33.586	35.257
Y79AA1001665	78.815	50.214	28.199	20.230	28.531	39.239	43.686	24.873
Y79AA1001679	182.502	59.845	49.481	32.964	56.908	102.379	88.857	48.625
Y79AA1001692	48.740	44.701	21.354	18.732	23.271	21.639	35.010	24.377
Y79AA1001696	6.780	14.124	10.007	8.631	14.623	7.512	6.730	10.898
Y79AA1001705	84.869	54.294	35.569	21.435	39.991	44.064	55.777	37.387
Y79AA1001711	62.806	75.073	36.984	31.331	32.851	38.989	52.758	53.508
Y79AA1001717	21.280	34.089	12.028	10.889	15.395	11.748	24.174	10.438
Y79AA1001719	43.417	51.690	17.623	19.362	20.441	20.351	30.934	27.264
Y79AA1001727	73.341	78.139	42.958	28.661	54.868	25.062	43.179	39.080
Y79AA1001750	294.250	240.534	123.295	113.859	147.591	113.999	151.389	151.480
Y79AA1001760	186.817	180.985	65.822	68.036	91.745	92.228	144.742	103.455
Y79AA1001777	125.250	87.579	38.902	31.498	34.787	51.175	61.299	47.365
Y79AA1001781	0.000	0.000	0.000	3.210	1.473	0.000	0.000	0.000
Y79AA1001787	114.565	61.166	49.706	30.708	31.661	57.179	72.608	56.355
Y79AA1001793	186.933	88.770	84.898	59.826	48.463	74.105	167.655	89.090
Y79AA1001795	17.050	21.582	20.234	15.314	13.998	18.815	13.699	16.861
Y79AA1001799	86.419	58.330	51.694	35.379	30.638	47.701	71.948	46.535
Y79AA1001800	511.812	97.958	354.971	49.190	235.401	413.230	490.565	73.961
Y79AA1001801	67.645	45.550	11.683	27.943	20.138	30.425	59.231	35.253
Y79AA1001803	57.387	56.011	59.286	17.563	64.207	39.997	39.216	36.149
Y79AA1001805	146.263	170.531	125.538	76.023	66.375	74.500	58.882	68.354
Y79AA1001807	112.057	63.466	54.660	28.588	34.253	46.384	86.296	39.426
Y79AA1001827	70.024	30.424	44.198	33.684	23.703	26.135	51.859	17.610
Y79AA1001845	25.975	42.461	56.527	62.241	32.960	50.520	20.001	36.949
Y79AA1001848	35.746	22.982	23.160	9.894	16.543	12.462	26.092	21.091
Y79AA1001853	281.071	150.082	159.752	107.770	164.169	199.036	174.168	111.109
Y79AA1001863	190.420	108.799	96.407	63.758	66.145	100.694	163.628	77.595
Y79AA1001866	24.530	46.991	37.466	28.167	24.388	28.450	20.721	74.899
Y79AA1001874	1.221	5.487	0.848	1.231	0.291	0.598	1.506	1.497
Y79AA1001875	63.952	58.462	47.436	36.846	24.598	39.313	45.106	40.636
Y79AA1001907	124.410	250.090	50.333	92.943	49.772	74.402	107.811	194.562
Y79AA1001908	12.574	13.547	9.612	6.931	5.169	7.911	11.534	9.867
Y79AA1001923	33.869	14.234	14.248	5.718	8.352	12.798	25.326	7.829
Y79AA1001927	186.717	76.975	44.024	41.115	46.490	154.336	107.236	39.239
Y79AA1001930	33.259	33.470	18.855	24.382	15.694	32.271	26.423	29.042
Y79AA1001932	27.741	23.277	12.768	9.914	14.699	8.522	10.994	25.644
Y79AA1001933	34.948	36.160	27.478	18.608	18.230	17.284	30.314	30.361
Y79AA1001942	28.803	28.253	22.497	11.034	11.547	51.771	43.263	5.042
Y79AA1001963	68.323	43.878	42.080	36.240	33.736	26.445	62.945	56.785
Y79AA1001968	55.189	120.287	31.107	72.431	32.780	37.209	52.124	87.863
Y79AA1001983	91.447	44.245	40.209	17.481	29.219	49.886	55.561	26.162
Y79AA1002000	78.569	42.344	37.253	28.054	28.700	41.938	31.511	26.090
Y79AA1002004	135.629	61.297	65.308	50.333	46.897	62.884	62.767	36.527
Y79AA1002008	151.334	65.685	44.780	33.954	37.173	46.166	78.471	49.925
Y79AA1002012	140.300	132.533	88.285	105.977	78.145	59.701	57.183	104.179
Y79AA1002017	38.327	28.859	17.564	7.197	8.297	22.866	39.108	18.179
Y79AA1002022	197.012	109.640	111.812	71.115	68.794	122.840	108.973	82.268
Y79AA1002027	7.861	6.807	5.719	3.405	5.503	3.619	4.936	6.690
Y79AA1002050	52.645	57.007	34.182	49.101	29.451	26.571	25.198	32.168
Y79AA1002058	162.814	86.786	63.856	46.043	84.452	92.949	131.501	99.159
Y79AA1002060	74.517	43.157	38.911	33.852	57.622	27.031	33.624	43.906
Y79AA1002062	163.546	122.645	81.975	88.856	64.753	92.465	75.321	73.162
Y79AA1002065	72.537	83.880	24.771	44.298	22.044	30.756	35.287	75.559
Y79AA1002067	18.914	16.681	8.561	6.098	4.972	7.856	26.231	10.844
Y79AA1002069	153.130	40.848	44.030	9.535	26.886	75.515	76.585	29.038
Y79AA1002070	255.333	63.953	64.787	58.175	89.400	172.062	64.355	62.998
Y79AA1002074	168.399	367.145	81.099	265.515	107.873	170.520	153.058	388.635
Y79AA1002076	36.931	26.480	13.779	8.886	11.642	20.354	19.122	14.650
Y79AA1002083	100.267	39.527	25.359	13.076	27.519	42.095	30.686	16.092
Y79AA1002084	31.602	37.320	24.313	14.210	13.535	21.829	27.098	16.412
Y79AA1002086	43.060	38.449	21.971	18.749	10.203	19.023	17.056	19.318

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Table 168

Y79AA1002087	13.030	15.226	11.425	22.378	3.745	12.088	10.009	24.908
Y79AA1002089	40.323	26.458	12.982	15.098	16.218	17.576	3.691	24.665
Y79AA1002093	46.120	27.022	18.769	15.919	7.245	24.041	28.202	24.994
Y79AA1002101	43.837	30.418	18.385	11.894	11.521	24.278	23.182	15.994
Y79AA1002103	43.141	24.675	23.246	31.726	17.340	31.371	32.322	48.954
Y79AA1002115	20.766	22.498	17.048	10.575	15.180	11.669	14.011	12.945
Y79AA1002121	27.091	49.228	19.624	15.594	14.827	12.987	19.044	18.216
Y79AA1002125	48.808	64.875	48.646	23.137	27.474	32.479	34.123	51.389
Y79AA1002129	20.607	25.472	14.117	14.375	7.485	13.555	11.317	12.960
Y79AA1002131	46.336	22.411	18.720	14.115	7.829	20.162	15.429	12.884
Y79AA1002139	17.296	11.713	5.758	6.335	6.389	11.186	2.854	4.539
Y79AA1002144	45.269	47.677	66.378	20.967	59.407	32.426	31.597	21.322
Y79AA1002177	301.285	121.825	100.055	57.536	81.697	176.423	154.681	88.082
Y79AA1002183	78.011	99.397	37.780	10.625	40.969	35.101	65.850	66.184
Y79AA1002202	57.948	69.118	26.355	26.998	31.172	30.882	39.528	28.104
Y79AA1002204	108.226	53.775	45.674	14.730	26.902	42.785	47.433	32.007
Y79AA1002206	23.882	20.653	11.579	11.189	8.007	20.198	14.716	14.423
Y79AA1002208	17.539	19.145	14.805	15.985	9.466	19.745	11.177	17.666
Y79AA1002209	12.404	10.671	11.592	3.770	5.884	7.681	9.212	6.769
Y79AA1002210	36.693	21.704	11.197	4.453	8.279	31.518	24.637	13.120
Y79AA1002211	60.744	40.012	23.317	18.415	22.277	33.188	47.655	53.021
Y79AA1002213	88.865	66.933	24.906	28.654	40.420	32.547	31.240	41.587
Y79AA1002215	57.323	74.421	32.504	25.568	33.392	47.741	30.830	34.812
Y79AA1002220	7.686	27.673	7.325	5.327	8.309	5.571	9.728	9.037
Y79AA1002226	33.811	70.351	53.822	44.642	43.103	43.566	31.798	56.096
Y79AA1002229	133.812	49.906	27.621	14.021	32.478	73.121	60.968	21.211
Y79AA1002234	53.796	27.231	31.097	16.258	22.352	39.228	41.686	31.562
Y79AA1002235	9.109	6.947	3.938	3.201	5.077	8.688	8.099	8.031
Y79AA1002246	46.749	34.031	22.771	19.593	19.245	14.798	40.274	41.271
Y79AA1002258	75.546	58.416	30.618	24.590	30.971	35.864	47.893	50.632
Y79AA1002279	67.007	468.054	23.705	27.332	22.243	72.113	23.817	64.255
Y79AA1002292	107.375	48.724	45.677	27.662	41.581	54.031	48.041	36.807
Y79AA1002298	16.948	16.878	8.834	7.151	8.601	7.054	11.871	9.334
Y79AA1002307	29.343	26.868	16.693	17.533	20.451	13.735	13.467	11.704
Y79AA1002309	38.982	33.605	15.626	14.434	15.282	17.723	25.386	17.397
Y79AA1002311	31.668	30.875	21.323	22.152	19.332	10.916	32.170	15.265
Y79AA1002334	49.431	32.284	18.242	13.025	24.412	19.450	30.870	24.306
Y79AA1002351	41.486	18.773	27.420	13.424	23.100	22.549	45.251	26.383
Y79AA1002355	10.396	23.208	37.472	13.874	42.683	14.865	12.092	15.185
Y79AA1002361	88.085	78.594	36.358	37.149	35.846	41.778	36.660	25.294
Y79AA1002365	17.588	21.447	10.949	7.231	11.431	16.111	15.168	14.782
Y79AA1002373	50.748	39.981	17.086	11.669	21.120	12.396	22.757	15.438
Y79AA1002375	6643.977	1773.590	4553.953	585.102	6666.479	5319.310	5496.197	1220.015
Y79AA1002378	77.584	97.591	29.238	27.161	35.356	35.168	42.325	47.261
Y79AA1002381	141.196	111.531	39.904	43.874	44.814	57.151	75.416	73.250
Y79AA1002388	166.548	86.006	56.942	27.181	60.647	43.749	87.173	61.931
Y79AA1002389	47.127	38.224	20.037	14.800	14.138	25.545	42.014	15.674
Y79AA1002407	14.750	20.995	15.394	14.318	11.321	15.977	15.721	14.711
Y79AA1002413	55.733	94.994	61.674	38.953	26.005	85.902	42.923	62.238
Y79AA1002416	26.021	26.133	18.893	17.489	13.172	17.322	34.129	20.886
Y79AA1002429	29.180	51.475	14.818	24.101	19.762	12.675	14.708	62.243
Y79AA1002431	36.374	37.521	29.072	17.134	16.314	32.188	24.257	19.906
Y79AA1002433	73.392	56.725	40.689	46.773	29.753	44.782	56.569	48.003
Y79AA1002445	206.082	130.492	119.284	81.825	84.172	187.480	65.701	66.873
Y79AA1002461	136.322	87.178	56.327	41.540	30.726	58.954	73.797	51.203
Y79AA1002466	58.460	66.910	32.039	63.994	27.818	62.743	46.169	48.544
Y79AA1002471	22.153	38.198	21.750	19.098	17.619	16.828	33.234	22.949
Y79AA1002472	60.980	65.699	60.101	81.738	43.775	40.296	44.510	52.633
Y79AA1002474	35.222	8.126	16.456	10.777	17.029	18.872	29.379	12.444
Y79AA1002482	72.994	104.184	83.915	153.120	82.291	51.719	43.236	91.558
Y79AA1002487	22.033	18.529	10.754	10.800	9.046	9.098	17.186	12.270
Y79AA1002490	105.735	63.572	40.499	20.017	29.453	73.670	63.467	29.681
Y79AA1002493	72.446	80.901	47.379	55.984	35.093	37.512	30.823	19.166
ZRV6C1006278	37.372	7.298	8.151	3.848	4.644	7.876	6.612	2.417

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Table 169

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Expression of each cDNA in human pulmonary arterial endothelial cells cultured in a medium containing bovine serum albumin, glycosylated bovine serum albumin or advanced glycosylated endproduct of bovine serum albumin (This table also contains clones with no description in Examples).

In the table, EC_G_B/EC_BSA and EC_A_B/EC_BSA represent ratios of EC_glycated_BSA/EC_BSA and EC_AGE_BSA/EC_BSA, respectively.

Clone_name	EC_BSA	EC_glycated_BSA	EC_AGE_BSA	EC_G_B /EC_BSA	EC_A_B /EC_BSA
GAPDH(Cr1)	100.81	134.21	115.16	1.33	1.14
β actin(Cr2)	1101.9	1092.57	997.36	0.99	0.91
ADRGL1000005	26.88	38.27	36.13	1	1
ADRGL1000007	117.89	127.25	133.21	1.08	1.13
ADRGL1000009	29.18	25.65	26.05	1	1
ADRGL1000011	88.9	117.33	142.9	1.32	1.61
ADRGL1000027	33.24	40.53	43.02	1.01	1.08
ADRGL1000058	153.41	208.84	180.05	1.36	1.17
ADRGL1000069	16.8	21.77	29.81	1	1
ADRGL1000077	25.74	24.72	32.86	1	1
ADRGL1000092	84.52	84.15	121.76	1	1.44
ADRGL1000099	76.19	91.53	106.01	1.2	1.39
ADRGL1000136	52.34	44.76	63.06	0.86	1.2
ADRGL1000147	46.08	45.18	52.15	0.98	1.13
ADRGL1000159	31.52	40.24	42.72	1.01	1.07
ADRGL1000160	52.34	60.37	62.29	1.15	1.19
ADRGL1000171	21.46	16.78	25.59	1	1
ADRGL1000181	37.44	45.71	43.65	1.14	1.09
BGGI11000015	52.42	71	65.47	1.35	1.25
BGGI11000016	127.44	122.93	147.57	0.96	1.16
BGGI11000017	25.65	25.74	31.33	1	1
BGGI11000022	32.82	35.19	25.56	1	1
BGGI11000031	44.42	43.8	40.25	0.99	0.91
BGGI11000042	120.38	146.44	165.42	1.22	1.37
BGGI11000046	74.72	58.85	84.95	0.79	1.14
BNGH41000020	4286.0	3584.67	4330.96	0.84	1.01
BNGH41000025	216.67	223.74	257.06	1.03	1.19
BNGH41000026	25.76	28.16	35.52	1	1
BNGH41000027	29.23	23.83	17.86	1	1
BNGH41000035	280.32	238.34	305.66	0.85	1.09
BNGH41000037	59.14	54.86	54.58	0.93	0.92
BNGH41000042	356.1	324.08	411.07	0.91	1.15
BNGH41000048	1201.3	869.03	739.91	0.72	0.62
BNGH41000056	33.94	31.4	40.01	1	1
BNGH41000087	77.58	81.76	91.07	1.05	1.17
BNGH41000091	21.05	21.23	26.82	1	1

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BNGH41000157	81.11	57.28	77.46	0.71	0.95
BNGH41000169	21.1	17.59	22.53	1	1
BNGH41000181	63.54	56.92	70.08	0.9	1.1
BNGH41000198	32.53	26.38	34.37	1	1
BNGH41000219	114.67	161.09	142.46	1.4	1.24
BNGH41000229	130.25	139.85	138.03	1.07	1.06
BNGH41000237	94.54	91.81	114.21	0.97	1.21
BNGH41000238	33.23	62.41	30.4	1.56	1
BNGH41000243	90	78.6	84.17	0.87	0.94
BNGH41000270	22.87	30.92	20.81	1	1
BRAWH1000004	43.72	38.29	36.26	0.91	0.91
BRAWH1000018	28.94	43.05	31.38	1.08	1
BRAWH1000021	33.89	36.68	36.1	1	1
BRAWH1000027	26.95	26.48	21.83	1	1
BRAWH1000029	24.31	26.41	29.83	1	1
BRAWH1000040	49.28	49.78	51.7	1.01	1.05
BRAWH1000050	1118.2	957.41	645.63	0.86	0.58
BRAWH1000051	21.81	14.16	15.84	1	1
BRAWH1000060	902.17	1021.85	719.09	1.13	0.8
BRAWH1000075	40.92	36.18	34.01	0.98	0.98
BRAWH1000081	49.31	40.89	33.79	0.83	0.81
BRAWH1000084	452.29	521.35	444.54	1.15	0.98
BRAWH1000095	28.02	33.29	35.65	1	1
BRAWH1000096	37.75	32.39	37.8	1	1
BRAWH1000097	175.7	181.58	129.9	1.03	0.74
BRAWH1000100	339.32	252.86	326.18	0.75	0.96
BRAWH1000101	189.56	197.54	190.15	1.04	1
BRAWH1000104	45.36	23.5	26.12	0.88	0.88
BRAWH1000107	33.73	27.7	30.64	1	1
BRAWH1000110	202.56	258.75	198.95	1.28	0.98
BRAWH1000111	52.23	52.14	54.17	1	1.04
BRAWH1000135	44.7	32.7	48.5	0.89	1.09
BRAWH1000190	55.01	54.64	53.49	0.99	0.97
HEMBA1000005	106.84	99.81	118.59	0.93	1.11
HEMBA1000006	31.35	30.25	31.42	1	1
HEMBA1000012	934.52	1045.19	733.9	1.12	0.79
HEMBA1000020	1097.3	1001.42	782.76	0.91	0.71
HEMBA1000030	39.47	59.22	55.57	1.48	1.39
HEMBA1000034	41.06	33.37	49.9	0.97	1.22
HEMBA1000042	87.29	119.44	105.36	1.37	1.21
HEMBA1000045	38.05	29.97	32.61	1	1
HEMBA1000046	65.78	48.47	56.5	0.74	0.86
HEMBA1000705	27.41	22.4	26.81	1	1
HEMBA1000713	69.05	62.08	69.75	0.9	1.01
HEMBA1000718	93.98	62.97	81.6	0.67	0.87
HEMBA1000719	26.13	21.62	25.73	1	1

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HEMBA1000722	29.02	25.27	32.96	1	1
HEMBA1000726	117.55	153.37	143.95	1.3	1.22
HEMBA1000727	67.77	72.78	74.89	1.07	1.11
HEMBA1000732	61.56	51.31	53.93	0.83	0.88
HEMBA1000736	38.55	46.78	24.16	1.17	1
HEMBA1000743	32.49	36.94	42.85	1	1.07
HEMBA1000745	57.36	47.79	52.26	0.83	0.91
HEMBA1000747	22.29	18.39	22.12	1	1
HEMBA1000748	36.46	28.26	36.84	1	1
HEMBA1000749	74.95	85.11	86.02	1.14	1.15
HEMBA1000752	39.73	44.73	54.37	1.12	1.36
HEMBA1000753	40.75	48.69	46.01	1.19	1.13
HEMBA1000757	35.64	44.44	40.91	1.11	1.02
HEMBA1000760	69.3	67.6	93.08	0.98	1.34
HEMBA1000769	54.76	52.63	53.06	0.96	0.97
HEMBA1000773	20.96	13.95	22.38	1	1
HEMBA1000774	116.55	94.14	94.73	0.81	0.81
HEMBA1000780	31.69	25.83	27.67	1	1
HEMBA1000783	28.5	36.63	26.55	1	1
HEMBA1000791	99.64	107.65	83.39	1.08	0.84
HEMBA1000793	91.87	96.91	85.78	1.05	0.93
HEMBA1000802	23.17	14.63	15.44	1	1
HEMBA1000813	253.32	254.92	342.09	1.01	1.35
HEMBA1000817	37.46	38.22	41.77	1	1.04
HEMBA1000822	34.66	27.08	34.38	1	1
HEMBA1000827	68.99	39.78	47.79	0.58	0.69
HEMBA1000833	25.58	25.52	30.57	1	1
HEMBA1000835	2111.6	1497.9	1485.01	0.71	0.7
HEMBA1000843	56.27	54.43	55.21	0.97	0.98
HEMBA1000851	31.69	22.56	26.81	1	1
HEMBA1000852	56.96	54.44	50.55	0.96	0.89
HEMBA1000867	48.67	43.93	29.75	0.9	0.82
HEMBA1000869	41.88	38.24	35.91	0.96	0.96
HEMBA1000870	43.48	40.06	36.77	0.92	0.92
HEMBA1000872	104.68	84.86	91.41	0.81	0.87
HEMBA1000875	48.86	58.31	55.26	1.19	1.13
HEMBA1000876	67.93	78.45	71.48	1.15	1.05
HEMBA1000907	70.99	54.09	74.56	0.76	1.05
HEMBA1000908	23.07	15.94	19.03	1	1
HEMBA1000910	32.2	27.08	30.5	1	1
HEMBA1000918	111.32	116.33	81.06	1.05	0.73
HEMBA1000919	22.07	24.98	22.53	1	1
HEMBA1000934	26.39	32.83	28.03	1	1
HEMBA1000935	46.11	38.81	46.64	0.87	1.01
HEMBA1000940	85.36	71.35	78.33	0.84	0.92
HEMBA1000942	70.42	56.83	79.23	0.81	1.13

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HEMBA1000943	12.93	13.15	10.61	1	1
HEMBA1000946	29.7	42.14	32.79	1.05	1
HEMBA1000960	190.41	190.99	180.48	1	0.95
HEMBA1000962	46.12	59.9	54.5	1.3	1.18
HEMBA1000968	33.79	36.55	39.28	1	1
HEMBA1000971	48.24	49.1	51.91	1.02	1.08
HEMBA1000972	38.3	40.09	39.66	1	1
HEMBA1000974	51.97	56.82	49.75	1.09	0.96
HEMBA1000975	46.25	43.7	33.71	0.94	0.86
HEMBA1000979	63.82	70.71	68.55	1.11	1.07
HEMBA1000981	64.65	86.95	94.68	1.34	1.46
HEMBA1000983	51.37	48.15	51.7	0.94	1.01
HEMBA1000985	27.69	27.02	30.11	1	1
HEMBA1000986	53.93	49.72	49.93	0.92	0.93
HEMBA1000991	52.24	42.47	50.43	0.81	0.97
HEMBA1001007	27.01	24.05	28.85	1	1
HEMBA1001008	20.98	17.62	20.17	1	1
HEMBA1001009	20.84	18.86	22.39	1	1
HEMBA1001014	135.14	164.28	150.39	1.22	1.11
HEMBA1001017	34.86	39.24	67.82	1	1.7
HEMBA1001019	37.17	35.97	39.91	1	1
HEMBA1001020	53.82	62.13	66.28	1.15	1.23
HEMBA1001021	26.14	29.34	40.37	1	1.01
HEMBA1001022	41.99	46.11	37.15	1.1	0.95
HEMBA1001024	15.72	18.6	18.46	1	1
HEMBA1001026	17.94	15.49	20.39	1	1
HEMBA1001043	25.75	20.78	29.85	1	1
HEMBA1001051	259.05	315.04	343.57	1.22	1.33
HEMBA1001052	26.16	30.4	30.36	1	1
HEMBA1001059	214.68	230.87	246.86	1.08	1.15
HEMBA1001060	67.75	78.09	75.1	1.15	1.11
HEMBA1001064	25.42	26.4	32.27	1	1
HEMBA1001071	21.34	32.81	30.6	1	1
HEMBA1001077	34.87	36.52	45.31	1	1.13
HEMBA1001078	209.41	158.37	287.22	0.76	1.37
HEMBA1001080	89.83	97.65	106.07	1.09	1.18
HEMBA1001084	62.53	60.01	63.93	0.96	1.02
HEMBA1001085	54.78	46.69	53.3	0.85	0.97
HEMBA1001088	48.42	43.37	46.47	0.9	0.96
HEMBA1001093	49.68	39.8	55.42	0.81	1.12
HEMBA1001094	20.97	21.59	19.98	1	1
HEMBA1001099	21.58	23.52	26.87	1	1
HEMBA1001104	29.79	37.22	32.3	1	1
HEMBA1001109	156.85	194.24	223.99	1.24	1.43
HEMBA1001114	417.97	357.72	505.7	0.86	1.21
HEMBA1001121	34.94	28.76	29.96	1	1

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HEMBA1001122	67.22	71.48	43.07	1.06	0.64
HEMBA1001123	68.59	45.79	49.75	0.67	0.73
HEMBA1001133	26.76	19.02	27.29	1	1
HEMBA1001137	40.48	30.55	37.31	0.99	0.99
HEMBA1001140	47.02	45.97	47.6	0.98	1.01
HEMBA1001144	289.44	310.11	365.12	1.07	1.26
HEMBA1001145	1034.5	1260.22	1691.61	1.22	1.64
HEMBA1001158	66.38	61.98	48.42	0.93	0.73
HEMBA1001172	53.49	53.98	48.67	1.01	0.91
HEMBA1001174	29.2	20.8	21.66	1	1
HEMBA1001175	90.3	84.25	78.88	0.93	0.87
HEMBA1001182	2256.3	1929.4	1478.23	0.86	0.66
HEMBA1001184	24.69	17.33	21.37	1	1
HEMBA1001192	23.55	23.79	26.37	1	1
HEMBA1001196	74.6	73.23	78.22	0.98	1.05
HEMBA1001197	1122.0	1102.8	1110.66	0.98	0.99
HEMBA1001208	31.89	35.83	28.91	1	1
HEMBA1001213	2340.3	1977.61	1520.51	0.85	0.65
HEMBA1001214	32.13	33.1	31.22	1	1
HEMBA1001221	16.36	19.33	16.96	1	1
HEMBA1001225	16.5	18.96	18.59	1	1
HEMBA1001226	184.05	160.45	175.94	0.87	0.96
HEMBA1001228	47.7	51.37	42.2	1.08	0.88
HEMBA1001229	2013.5	2065.33	1644.74	1.03	0.82
HEMBA1001235	127.3	117.6	147.13	0.92	1.16
HEMBA1001238	93.08	83.89	64.54	0.9	0.69
HEMBA1001242	1928.4	1561.31	1343.98	0.81	0.7
HEMBA1001247	84.13	78.26	71.14	0.93	0.85
HEMBA1001253	1657.8	1315.21	940.34	0.79	0.57
HEMBA1001257	40.62	28.56	45.16	0.98	1.11
HEMBA1001261	41.19	36.59	33.36	0.97	0.97
HEMBA1001262	28.33	20.98	26.6	1	1
HEMBA1001265	63.91	58.2	61.44	0.91	0.96
HEMBA1001266	83.23	75.57	83.48	0.91	1
HEMBA1001269	116.72	87.43	124.08	0.75	1.06
HEMBA1001272	29.45	23.23	24.56	1	1
HEMBA1001279	362.45	336.61	230.89	0.93	0.64
HEMBA1001281	380.63	330.72	267.19	0.87	0.7
HEMBA1001286	184.88	156.57	159.52	0.85	0.86
HEMBA1001289	25.32	27.22	27.13	1	1
HEMBA1001291	135.14	121.49	137.23	0.9	1.02
HEMBA1001294	66.23	38.38	63.36	0.6	0.96
HEMBA1001296	66.45	43.63	35.03	0.66	0.6
HEMBA1001297	38.2	62.28	59.53	1.56	1.49
HEMBA1001299	145.18	178.69	152.2	1.23	1.05
HEMBA1001302	91.92	114.12	122.61	1.24	1.33

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HEMBA1001303	50.14	53.38	45.68	1.06	0.91
HEMBA1001306	76.54	82.23	86.06	1.07	1.12
HEMBA1001308	162.05	173.73	151.85	1.07	0.94
HEMBA1001310	35.02	29.23	32.29	1	1
HEMBA1001312	115.41	120.24	124.38	1.04	1.08
HEMBA1001319	31.87	35.57	28.57	1	1
HEMBA1001322	26.44	31.63	29.19	1	1
HEMBA1001323	29.88	29.58	36.66	1	1
HEMBA1001326	74.38	62.6	81.26	0.84	1.09
HEMBA1001327	33.18	52.98	44.45	1.32	1.11
HEMBA1001330	126.71	106.44	132.86	0.84	1.05
HEMBA1001348	38.8	28.5	36.52	1	1
HEMBA1001350	41.43	46.03	43.08	1.11	1.04
HEMBA1001351	111.33	99.5	89.31	0.89	0.8
HEMBA1001352	42.75	54.89	55.25	1.28	1.29
HEMBA1001353	383.71	440.78	378.96	1.15	0.99
HEMBA1001358	143.81	148	158.17	1.03	1.1
HEMBA1001361	29.89	35.45	46.23	1	1.16
HEMBA1001364	30.09	25.6	38.53	1	1
HEMBA1001375	40.61	50.18	55.42	1.24	1.36
HEMBA1001377	123.11	130.48	138.05	1.06	1.12
HEMBA1001383	24.75	21.89	25.34	1	1
HEMBA1001387	133.99	110.07	119.25	0.82	0.89
HEMBA1001388	16.86	15.81	19.96	1	1
HEMBA1001390	162.95	166.12	229.96	1.02	1.41
HEMBA1001391	28.95	25.43	34.84	1	1
HEMBA1001398	71.07	92.62	94.61	1.3	1.33
HEMBA1001405	18.28	22.16	27.71	1	1
HEMBA1001406	47.72	56.62	52.03	1.19	1.09
HEMBA1001407	26.06	28.51	42.35	1	1.06
HEMBA1001411	22.01	23.93	33.22	1	1
HEMBA1001413	26.86	28.89	35.64	1	1
HEMBA1001414	52.92	88.49	97.78	1.67	1.85
HEMBA1001415	43.07	56.61	61.78	1.31	1.43
HEMBA1001416	69.22	70.23	83.44	1.01	1.21
HEMBA1001432	42.98	46.16	57.09	1.07	1.33
HEMBA1001433	79.39	93.43	95.11	1.18	1.2
HEMBA1001435	78.79	81.88	95.67	1.04	1.21
HEMBA1001442	19.58	18.75	24.89	1	1
HEMBA1001446	87.71	99.2	116.86	1.13	1.33
HEMBA1001450	73.99	60.97	62.25	0.82	0.84
HEMBA1001454	86.61	101.22	82.71	1.17	0.95
HEMBA1001455	34.36	33.8	38.01	1	1
HEMBA1001459	36.34	36.67	43.17	1	1.08
HEMBA1001461	32.17	38.47	33.2	1	1
HEMBA1001462	29.08	29.65	31.99	1	1

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HEMBA1001463	59.9	67.79	69.08	1.13	1.15
HEMBA1001469	70.99	49.11	46.76	0.69	0.66
HEMBA1001473	169.16	148.99	167.31	0.88	0.99
HEMBA1001477	24.92	25.29	23.86	1	1
HEMBA1001478	26.37	24.36	30.89	1	1
HEMBA1001480	53.88	56.83	53.79	1.05	1
HEMBA1001483	58.76	52.6	67.18	0.9	1.14
HEMBA1001490	30.29	34.25	39.52	1	1
HEMBA1001495	1054.7	1323.57	1231.86	1.25	1.17
HEMBA1001497	67.32	73.45	74.91	1.09	1.11
HEMBA1001510	164.19	193.22	183.1	1.18	1.12
HEMBA1001515	41.31	50.63	34.96	1.23	0.97
HEMBA1001517	112.81	108.99	110.39	0.97	0.98
HEMBA1001522	29.69	30.46	22.06	1	1
HEMBA1001526	47.88	49.14	54.08	1.03	1.13
HEMBA1001533	76.1	71.35	81.79	0.94	1.07
HEMBA1001547	82.24	84.8	90.33	1.03	1.1
HEMBA1001552	149.34	124.65	127.65	0.83	0.85
HEMBA1001553	464.14	480.55	526.67	1.04	1.13
HEMBA1001557	92.63	94.47	76.06	1.02	0.82
HEMBA1001563	63.54	59.53	45.05	0.94	0.71
HEMBA1001566	82.82	88.26	79.39	1.07	0.96
HEMBA1001569	128.2	118.39	122.68	0.92	0.96
HEMBA1001570	155.44	162.32	161.01	1.04	1.04
HEMBA1001579	56.65	97.72	71.55	1.72	1.26
HEMBA1001581	114.87	159.23	140.29	1.39	1.22
HEMBA1001582	41.6	30.97	50.61	0.96	1.22
HEMBA1001585	47.86	54.87	46.66	1.15	0.97
HEMBA1001589	41.81	47.65	37.92	1.14	0.96
HEMBA1001595	62.62	45.3	48.48	0.72	0.77
HEMBA1001604	28.63	29.02	33.97	1	1
HEMBA1001608	185.33	155.85	151.37	0.84	0.82
HEMBA1001615	751.08	926.26	957.18	1.23	1.27
HEMBA1001620	143.66	147.63	174.25	1.03	1.21
HEMBA1001621	26.51	20.21	24.38	1	1
HEMBA1001635	54.68	45.05	34.75	0.82	0.73
HEMBA1001636	31.94	20.65	28.41	1	1
HEMBA1001640	86.56	74.45	107.35	0.86	1.24
HEMBA1001647	2431.2	2251.04	2043.18	0.93	0.84
HEMBA1001651	96.42	110.51	108.89	1.15	1.13
HEMBA1001655	72.11	77.88	73	1.08	1.01
HEMBA1001658	51.19	33.83	42.59	0.78	0.83
HEMBA1001661	24.48	27.02	32.12	1	1
HEMBA1001665	33.13	33.84	28.98	1	1
HEMBA1001670	84.62	69.39	98.47	0.82	1.16
HEMBA1001672	36.68	36.31	39.34	1	1

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HEMBA1001673	82.64	87.42	58.92	1.06	0.71
HEMBA1001675	33.32	36.24	36.07	1	1
HEMBA1001676	500.75	567.16	633.55	1.13	1.27
HEMBA1001678	291.29	282.33	287.87	0.97	0.99
HEMBA1001680	59	71.89	67.27	1.22	1.14
HEMBA1001681	43.9	53.31	69.16	1.21	1.58
HEMBA1001684	121.85	101.34	128.16	0.83	1.05
HEMBA1001695	27.37	28.18	28.49	1	1
HEMBA1001702	25.6	36.11	34.21	1	1
HEMBA1001709	23.11	23.23	24.21	1	1
HEMBA1001711	41.29	49.57	49.1	1.2	1.19
HEMBA1001712	22.12	21.69	26.49	1	1
HEMBA1001714	138.21	150.33	176.72	1.09	1.28
HEMBA1001717	29.27	28.98	29.74	1	1
HEMBA1001718	108.75	108.53	111.93	1	1.03
HEMBA1001723	86.07	96.41	63.93	1.12	0.74
HEMBA1001731	26.03	27.17	29.94	1	1
HEMBA1001734	60.16	66.91	55.53	1.11	0.92
HEMBA1001736	48.23	61.31	61.56	1.27	1.28
HEMBA1001741	43.58	39.35	44.77	0.92	1.03
HEMBA1001744	23.18	17.43	22.95	1	1
HEMBA1001745	18.96	20.05	34.02	1	1
HEMBA1001746	60.21	60.61	65.09	1.01	1.08
HEMBA1001761	41.31	48.07	52.97	1.16	1.28
HEMBA1001762	87.22	82.14	101.34	0.94	1.16
HEMBA1001781	39.61	36.99	39.24	1	1
HEMBA1001784	46.9	54.9	68.72	1.17	1.47
HEMBA1001791	46.46	66.14	73.08	1.42	1.57
HEMBA1001794	106.21	133.9	156.75	1.26	1.48
HEMBA1001800	1613.9	1898.36	1564.1	1.18	0.97
HEMBA1001803	25.79	35.11	28.19	1	1
HEMBA1001804	142.96	169.79	195.66	1.19	1.37
HEMBA1001808	33.67	33.25	41.14	1	1.03
HEMBA1001809	89.79	79.05	92.5	0.88	1.03
HEMBA1001811	91.99	100.48	102.21	1.09	1.11
HEMBA1001815	44.4	56.35	56.79	1.27	1.28
HEMBA1001816	21.82	19.93	29.04	1	1
HEMBA1001819	73.56	65.42	75.42	0.89	1.03
HEMBA1001820	19.68	22.61	21.88	1	1
HEMBA1001822	36.93	40.45	37.76	1.01	1
HEMBA1001824	169.42	187.12	202.26	1.1	1.19
HEMBA1001835	40.45	29.39	36.01	0.99	0.99
HEMBA1001844	79.83	89.37	81.98	1.12	1.03
HEMBA1001847	33.76	29.06	36.37	1	1
HEMBA1001849	77.65	116.04	94.33	1.49	1.21
HEMBA1001850	142.47	147.28	101.43	1.03	0.71

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HEMBA1001861	26.36	23.37	20.95	1	1
HEMBA1001862	520.25	506.65	561.78	0.97	1.08
HEMBA1001864	33.43	36.34	50.44	1	1.26
HEMBA1001866	88.55	103.03	113.87	1.16	1.29
HEMBA1001869	65.34	67.41	64.56	1.03	0.99
HEMBA1001871	582.28	492.28	509.64	0.85	0.88
HEMBA1001876	157.23	129.25	159.26	0.82	1.01
HEMBA1001878	45.56	47.78	44.75	1.05	0.98
HEMBA1001879	34.37	34.3	29.06	1	1
HEMBA1001884	41.39	38.01	37.87	0.97	0.97
HEMBA1001886	49.65	48.62	51.77	0.98	1.04
HEMBA1001888	110.87	124.27	117.94	1.12	1.06
HEMBA1001890	42.99	43.36	39.58	1.01	0.93
HEMBA1001896	27.32	28.53	28.11	1	1
HEMBA1001899	448.8	458.41	380.57	1.02	0.85
HEMBA1001904	2489.0	2362	2247.7	0.95	0.9
HEMBA1001910	32.16	21.39	18.7	1	1
HEMBA1001911	102.05	84.21	89.81	0.83	0.88
HEMBA1001912	753.72	615.96	496.77	0.82	0.66
HEMBA1001913	56.58	69.81	74.33	1.23	1.31
HEMBA1001915	26.54	25.2	30.07	1	1
HEMBA1001918	66.46	78.62	61.54	1.18	0.93
HEMBA1001921	37.68	40.38	33.39	1.01	1
HEMBA1001931	17.26	20.51	14.88	1	1
HEMBA1001939	34.9	29.42	29.03	1	1
HEMBA1001940	67.23	55.22	56.02	0.82	0.83
HEMBA1001942	28.65	19.95	24.59	1	1
HEMBA1001944	850.15	917.16	769.79	1.08	0.91
HEMBA1001945	29.67	29.26	33.14	1	1
HEMBA1001950	33.98	37.1	38.34	1	1
HEMBA1001951	168.24	149.14	144.1	0.89	0.86
HEMBA1001958	30.76	28.04	28.27	1	1
HEMBA1001960	117.72	104	125.36	0.88	1.06
HEMBA1001962	21.33	21.92	20.74	1	1
HEMBA1001964	41.27	36.48	40.09	0.97	0.97
HEMBA1001967	56.3	61.72	58.17	1.1	1.03
HEMBA1001979	37.7	31.5	32.33	1	1
HEMBA1001987	157.73	155.43	158.33	0.99	1
HEMBA1001991	115.83	119.27	118.39	1.03	1.02
HEMBA1002003	145.52	124.44	174.33	0.86	1.2
HEMBA1002005	95.84	82.27	75.78	0.86	0.79
HEMBA1002008	93.11	93.59	67.04	1.01	0.72
HEMBA1002018	30.7	31.56	29.3	1	1
HEMBA1002022	29.42	33.11	28.77	1	1
HEMBA1002029	1143.0	788.12	855.8	0.69	0.75
HEMBA1002030	37.21	35.38	36.56	1	1

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HEMBA1002035	32.58	39.5	34.54	1	1
HEMBA1002037	35.32	25.71	34.06	1	1
HEMBA1002038	80.78	95.24	87.43	1.18	1.08
HEMBA1002039	29.27	41.94	45.05	1.05	1.13
HEMBA1002042	69.56	82.26	75.06	1.18	1.08
HEMBA1002043	94.56	132.79	125.69	1.4	1.33
HEMBA1002048	27.06	23.59	27.16	1	1
HEMBA1002049	98.28	115.71	107.64	1.18	1.1
HEMBA1002053	109.41	96.4	115.83	0.88	1.06
HEMBA1002055	94.18	84.55	102.03	0.9	1.08
HEMBA1002056	36.57	41.32	37.72	1.03	1
HEMBA1002061	30.02	37.92	40.57	1	1.01
HEMBA1002080	217.45	341.32	408.08	1.57	1.88
HEMBA1002084	25.19	26.67	28.24	1	1
HEMBA1002085	39.74	35.38	59.04	1	1.48
HEMBA1002092	25.03	22.15	28	1	1
HEMBA1002098	29.75	28.25	35.17	1	1
HEMBA1002100	290.2	250.1	284.9	0.86	0.98
HEMBA1002101	141.62	117.14	110	0.83	0.78
HEMBA1002102	63.92	79.33	78.63	1.24	1.23
HEMBA1002105	104.76	105.75	87.22	1.01	0.83
HEMBA1002107	651.41	734.58	1023.32	1.13	1.57
HEMBA1002113	209.87	180.63	238.46	0.86	1.14
HEMBA1002119	783.32	765.1	693.78	0.98	0.89
HEMBA1002125	81.76	58.98	98.89	0.72	1.21
HEMBA1002131	61.47	44.91	63	0.73	1.02
HEMBA1002133	41.34	51.09	47.54	1.24	1.15
HEMBA1002139	22.23	20.8	27.64	1	1
HEMBA1002141	30.33	26.59	38.58	1	1
HEMBA1002144	62.71	82.97	95.04	1.32	1.52
HEMBA1002147	55.36	91.25	90.72	1.65	1.64
HEMBA1002150	14.67	23.86	28.41	1	1
HEMBA1002151	99.61	91.89	115.21	0.92	1.16
HEMBA1002153	58.68	76.71	67.7	1.31	1.15
HEMBA1002156	14.27	16.44	17.5	1	1
HEMBA1002160	54.01	78.26	90.28	1.45	1.67
HEMBA1002161	170.98	192.46	221.4	1.13	1.29
HEMBA1002162	52.85	75.43	72.69	1.43	1.38
HEMBA1002163	110.56	123.56	148.01	1.12	1.34
HEMBA1002164	765.65	871.05	766.76	1.14	1
HEMBA1002166	549.48	498.57	670.97	0.91	1.22
HEMBA1002167	38.8	26.87	36.06	1	1
HEMBA1002173	49.98	53.97	49.35	1.08	0.99
HEMBA1002177	28.1	26.26	30.98	1	1
HEMBA1002178	44.04	38.21	56.1	0.91	1.27
HEMBA1002179	242.19	300.94	273.96	1.24	1.13

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HEMBA1002185	170.25	180.38	169.67	1.06	1
HEMBA1002188	49.99	55.72	64.06	1.11	1.28
HEMBA1002189	93.99	109.04	134.1	1.16	1.43
HEMBA1002191	72.79	83.6	75.92	1.15	1.04
HEMBA1002192	42	46.84	42.55	1.12	1.01
HEMBA1002195	54.39	56.23	65.6	1.03	1.21
HEMBA1002196	44.2	43.54	63.36	0.99	1.43
HEMBA1002199	37.95	40.26	40.09	1.01	1
HEMBA1002204	23.94	31.87	26.05	1	1
HEMBA1002208	441.74	403.49	389.44	0.91	0.88
HEMBA1002212	39.66	25.82	32.44	1	1
HEMBA1002215	42.63	39.95	40.56	0.94	0.95
HEMBA1002217	1267.6	1497.14	1240.47	1.18	0.98
HEMBA1002220	22.33	21.45	25.27	1	1
HEMBA1002226	228.01	236.81	242	1.04	1.06
HEMBA1002227	325.68	357.19	334.86	1.1	1.03
HEMBA1002229	107.66	103.52	123.73	0.96	1.15
HEMBA1002237	78.82	82.87	75.28	1.05	0.96
HEMBA1002239	2304.8	2194.9	1725.53	0.95	0.75
HEMBA1002241	851.36	754.66	596.7	0.89	0.7
HEMBA1002253	47.66	33.51	38.9	0.84	0.84
HEMBA1002257	23.46	24.24	20.65	1	1
HEMBA1002259	28	17.9	26.65	1	1
HEMBA1002262	170.24	202.87	176.45	1.19	1.04
HEMBA1002265	31.93	31.84	33.14	1	1
HEMBA1002267	60.05	70.88	58.1	1.18	0.97
HEMBA1002270	80.52	78.06	58.36	0.97	0.72
HEMBA1002286	20.22	21.23	21.47	1	1
HEMBA1002290	39.01	40.25	44.87	1.01	1.12
HEMBA1002302	171.26	184.71	149.25	1.08	0.87
HEMBA1002304	79.98	57.92	62.29	0.72	0.78
HEMBA1002307	343.22	402.44	441.62	1.17	1.29
HEMBA1002316	43.33	44.78	43.11	1.03	0.99
HEMBA1002319	79.54	70.87	88.85	0.89	1.12
HEMBA1002320	31.21	22.68	27.16	1	1
HEMBA1002321	33.5	29.95	24.57	1	1
HEMBA1002328	31.99	44.02	42.84	1.1	1.07
HEMBA1002333	27.85	26.55	26.56	1	1
HEMBA1002337	92.69	96.97	92.69	1.05	1
HEMBA1002339	3068.2	3357.21	2424.94	1.09	0.79
HEMBA1002341	29.27	25.97	35.7	1	1
HEMBA1002348	45.72	50.98	51.42	1.12	1.12
HEMBA1002349	23.97	27.43	26.69	1	1
HEMBA1002353	47.91	43.17	43.08	0.9	0.9
HEMBA1002356	137.17	151.54	132.62	1.1	0.97
HEMBA1002357	2695.9	3477.73	2585.96	1.29	0.96

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HEMBA1002360	119.97	102.96	109.34	0.86	0.91
HEMBA1002363	39.83	33.85	40.98	1	1.02
HEMBA1002365	42.88	34.97	39.04	0.93	0.93
HEMBA1002370	24.04	18.89	25.62	1	1
HEMBA1002374	69.9	49.95	80.12	0.71	1.15
HEMBA1002376	2716.4	2235.67	2311.2	0.82	0.85
HEMBA1002377	131.79	168.08	175.4	1.28	1.33
HEMBA1002380	105.4	120.28	112.72	1.14	1.07
HEMBA1002381	90.89	94.67	100.47	1.04	1.11
HEMBA1002384	25.99	33.81	24.8	1	1
HEMBA1002389	65.37	61.03	39.69	0.93	0.61
HEMBA1002396	92.1	92.86	105.59	1.01	1.15
HEMBA1002402	34.85	27.12	36.05	1	1
HEMBA1002417	28.14	23.18	39.92	1	1
HEMBA1002419	23.6	33.07	24.23	1	1
HEMBA1002420	104.82	108.83	115.26	1.04	1.1
HEMBA1002421	25.47	33.19	32.71	1	1
HEMBA1002423	30.15	32.72	35.32	1	1
HEMBA1002424	48.32	50.34	58.57	1.04	1.21
HEMBA1002426	95.14	82.18	130.83	0.86	1.38
HEMBA1002430	31.11	22.86	48.75	1	1.22
HEMBA1002439	45.81	39.45	35.77	0.87	0.87
HEMBA1002441	190.36	151.58	198.51	0.8	1.04
HEMBA1002454	18.11	16.69	21.15	1	1
HEMBA1002458	89.76	106.49	140.61	1.19	1.57
HEMBA1002460	48.27	40.03	48.58	0.83	1.01
HEMBA1002462	62.66	51.68	93.06	0.82	1.49
HEMBA1002465	24.06	23.59	34.77	1	1
HEMBA1002469	1141.3	1105.08	878	0.97	0.77
HEMBA1002475	50.7	45.86	52.13	0.9	1.03
HEMBA1002477	72.48	89.51	88.81	1.23	1.23
HEMBA1002480	66.92	53.09	65.74	0.79	0.98
HEMBA1002481	88.24	115.58	122.29	1.31	1.39
HEMBA1002486	65.78	70.33	89.87	1.07	1.37
HEMBA1002490	62.02	55.01	60.14	0.89	0.97
HEMBA1002495	28.09	28.23	37.46	1	1
HEMBA1002498	31.63	39.98	50.12	1	1.25
HEMBA1002501	200.17	232.86	229.22	1.16	1.15
HEMBA1002503	60.15	65.1	76.49	1.08	1.27
HEMBA1002504	71.66	92.18	96.39	1.29	1.35
HEMBA1002508	96.31	97.62	141.37	1.01	1.47
HEMBA1002513	25.15	20.42	33.54	1	1
HEMBA1002515	28.62	28.92	24.09	1	1
HEMBA1002524	17.75	29.99	28.95	1	1
HEMBA1002538	23.56	33.86	28.82	1	1
HEMBA1002542	100.57	85.68	127.33	0.85	1.27

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HEMBA1002544	36.36	43.78	37.89	1.09	1
HEMBA1002546	233.93	235.61	280.15	1.01	1.2
HEMBA1002547	104.87	101.89	134.44	0.97	1.28
HEMBA1002550	77.5	74.04	63.14	0.96	0.81
HEMBA1002551	32.81	34.15	38.69	1	1
HEMBA1002552	68.67	77.66	73.63	1.13	1.07
HEMBA1002555	18.78	18.95	18.73	1	1
HEMBA1002558	89.84	96.83	105.37	1.08	1.17
HEMBA1002561	66.15	70.22	75.71	1.06	1.14
HEMBA1002562	18.32	22.04	22.77	1	1
HEMBA1002568	37.87	37.42	38.86	1	1
HEMBA1002569	42.87	36.63	53.23	0.93	1.24
HEMBA1002570	77.85	65.44	95.45	0.84	1.23
HEMBA1002574	24.93	18.6	20.86	1	1
HEMBA1002583	53.05	51.72	50.08	0.97	0.94
HEMBA1002587	156.82	157.42	134.58	1	0.86
HEMBA1002590	128.54	122.14	121.34	0.95	0.94
HEMBA1002592	77.18	75.31	82.11	0.98	1.06
HEMBA1002595	31.08	27.57	36.21	1	1
HEMBA1002609	700.66	946.91	778.73	1.35	1.11
HEMBA1002617	108.51	91.58	109.76	0.84	1.01
HEMBA1002619	53.7	51.89	47.88	0.97	0.89
HEMBA1002621	25.77	20.09	21.51	1	1
HEMBA1002624	122.93	107.08	101.57	0.87	0.83
HEMBA1002628	46.21	31.91	41.12	0.87	0.89
HEMBA1002629	52.6	81.02	53.39	1.54	1.02
HEMBA1002632	113.01	97.63	105.71	0.86	0.94
HEMBA1002645	91.47	117.47	109.31	1.28	1.2
HEMBA1002651	44.04	49.34	47.34	1.12	1.07
HEMBA1002652	57.48	51.49	60.52	0.9	1.05
HEMBA1002659	71.71	69.66	66.98	0.97	0.93
HEMBA1002661	45.57	46.97	41.7	1.03	0.92
HEMBA1002666	31.14	34.85	20.48	1	1
HEMBA1002667	22.1	24.84	22.87	1	1
HEMBA1002673	159.38	123.39	164.21	0.77	1.03
HEMBA1002678	72.5	72.15	68.16	1	0.94
HEMBA1002679	28.83	30.33	32.02	1	1
HEMBA1002688	83.9	60.71	83.94	0.72	1
HEMBA1002696	40.11	28.05	35.95	1	1
HEMBA1002703	88.57	94.66	125.63	1.07	1.42
HEMBA1002706	37.7	53.4	47.13	1.34	1.18
HEMBA1002712	135.74	141.19	141.71	1.04	1.04
HEMBA1002715	1896.2	1480.77	1150.31	0.78	0.61
HEMBA1002716	34.19	33.83	36.74	1	1
HEMBA1002718	160.42	97.63	151.44	0.61	0.94
HEMBA1002728	95.36	105.61	106.33	1.11	1.12

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HEMBA1002730	100.98	92.09	106.69	0.91	1.06
HEMBA1002734	63.61	55.32	63.59	0.87	1
HEMBA1002742	34.13	33.17	32.33	1	1
HEMBA1002746	36.99	31.17	37.84	1	1
HEMBA1002748	44.71	48.28	41.23	1.08	0.92
HEMBA1002750	66.35	77.01	77	1.16	1.16
HEMBA1002755	96.93	94.45	103.73	0.97	1.07
HEMBA1002759	39.04	40.64	57.32	1.02	1.43
HEMBA1002763	1698.8	1337.96	1262.67	0.79	0.74
HEMBA1002767	56.12	43.14	69.82	0.77	1.24
HEMBA1002768	34.99	42.89	38.86	1.07	1
HEMBA1002769	31.5	32.49	43.28	1	1.08
HEMBA1002770	78.52	93	93.35	1.18	1.19
HEMBA1002777	32.18	32.84	36.1	1	1
HEMBA1002779	80.28	88.2	99.28	1.1	1.24
HEMBA1002780	89.11	91.7	97.2	1.03	1.09
HEMBA1002790	77.91	77.32	81.02	0.99	1.04
HEMBA1002794	28.57	30.2	40.09	1	1
HEMBA1002798	45.03	43.12	47.67	0.96	1.06
HEMBA1002801	29.52	30.11	32.1	1	1
HEMBA1002810	48.87	55.01	71.45	1.13	1.46
HEMBA1002816	29.61	34.48	41.11	1	1.03
HEMBA1002818	1627.1	1785.51	1207.17	1.1	0.74
HEMBA1002820	103.36	106.18	120.59	1.03	1.17
HEMBA1002826	46.54	37.96	64.29	0.86	1.38
HEMBA1002833	107.41	125.28	100.54	1.17	0.94
HEMBA1002850	24.01	25.95	26.09	1	1
HEMBA1002862	240.02	315.35	291.51	1.31	1.21
HEMBA1002863	44.25	38.73	38.24	0.9	0.9
HEMBA1002867	33.51	29.59	29.49	1	1
HEMBA1002876	55.95	60.55	78.99	1.08	1.41
HEMBA1002886	23.5	21.75	42.15	1	1.05
HEMBA1002896	52.27	44.86	64.45	0.86	1.23
HEMBA1002913	43.88	51.85	67.01	1.18	1.53
HEMBA1002921	19.64	28.3	24.8	1	1
HEMBA1002924	39.54	32.67	39.68	1	1
HEMBA1002934	218	245.83	293	1.13	1.34
HEMBA1002935	64.16	64.74	108.58	1.01	1.69
HEMBA1002937	31.03	35.04	62.25	1	1.56
HEMBA1002939	27.09	34.91	34.91	1	1
HEMBA1002944	33.42	57.33	79.04	1.43	1.98
HEMBA1002951	25.27	32.36	31.84	1	1
HEMBA1002954	35.46	39.4	35.12	1	1
HEMBA1002962	106.17	111.59	142.58	1.05	1.34
HEMBA1002968	41.69	58.91	59.23	1.41	1.42
HEMBA1002970	149.32	307.3	233.48	2.06	1.56

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HEMBA1002971	28.82	44.02	38.42	1.1	1
HEMBA1002973	110.85	145.12	152.71	1.31	1.38
HEMBA1002978	16.45	23.54	27.46	1	1
HEMBA1002981	24.06	22.9	29.89	1	1
HEMBA1002985	31.59	36.67	46.14	1	1.15
HEMBA1002986	57.56	55.19	65.26	0.96	1.13
HEMBA1002988	31.87	39.37	50.95	1	1.27
HEMBA1002992	278.6	350.09	353.67	1.26	1.27
HEMBA1002995	63.13	64.31	70.57	1.02	1.12
HEMBA1002997	27.92	31.58	41.04	1	1.03
HEMBA1002999	16.45	18.81	22.48	1	1
HEMBA1003004	14.72	14.99	19.67	1	1
HEMBA1003006	42.56	39.38	47.56	0.94	1.12
HEMBA1003008	37.59	33.5	43.5	1	1.09
HEMBA1003021	140.64	160.55	158.62	1.14	1.13
HEMBA1003027	54.32	59.67	62.18	1.1	1.14
HEMBA1003029	350.87	306.67	345.82	0.87	0.99
HEMBA1003031	99.91	89.75	89.48	0.9	0.9
HEMBA1003032	54.33	54.76	58.64	1.01	1.08
HEMBA1003033	115.33	147.1	133.35	1.28	1.16
HEMBA1003034	137.5	178.84	195.02	1.3	1.42
HEMBA1003035	19.36	18.2	25.53	1	1
HEMBA1003037	52.07	37.83	48.71	0.77	0.94
HEMBA1003041	142.44	158.26	165.95	1.11	1.17
HEMBA1003046	191.35	197.3	201.43	1.03	1.05
HEMBA1003047	63.52	70.12	63.88	1.1	1.01
HEMBA1003048	33.24	27.22	36.82	1	1
HEMBA1003064	91.27	75.36	69.57	0.83	0.76
HEMBA1003067	52.1	51.43	56.27	0.99	1.08
HEMBA1003071	39.64	57.64	58.19	1.44	1.45
HEMBA1003072	33.87	32.7	35.83	1	1
HEMBA1003076	262.68	221.2	263.78	0.84	1
HEMBA1003077	21.44	19.93	32.74	1	1
HEMBA1003078	41.19	40.76	37.58	0.99	0.97
HEMBA1003079	97.77	101.97	97.73	1.04	1
HEMBA1003083	113.8	121.46	124.26	1.07	1.09
HEMBA1003086	52.19	50.66	57.16	0.97	1.1
HEMBA1003090	106.49	84.22	107.55	0.79	1.01
HEMBA1003094	22.18	25.87	27.93	1	1
HEMBA1003096	28.21	31.54	41.6	1	1.04
HEMBA1003098	79.4	81.64	100.06	1.03	1.26
HEMBA1003101	48.08	38.19	54.34	0.83	1.13
HEMBA1003109	24.92	25.81	24.36	1	1
HEMBA1003114	51.66	56.64	61.7	1.1	1.19
HEMBA1003117	33.2	28.07	35.72	1	1
HEMBA1003120	66.51	67.4	55.48	1.01	0.83

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HEMBA1003129	171.02	190.86	212.79	1.12	1.24
HEMBA1003133	64.48	64.84	68.91	1.01	1.07
HEMBA1003136	28.75	29.95	35.68	1	1
HEMBA1003142	85.8	71.23	84.93	0.83	0.99
HEMBA1003148	21.58	18.05	30.73	1	1
HEMBA1003151	44.39	33.7	45.39	0.9	1.02
HEMBA1003152	73.95	101.12	37.82	1.37	0.54
HEMBA1003157	23.61	44.7	43.82	1.12	1.1
HEMBA1003166	396.48	495.89	465.55	1.25	1.17
HEMBA1003171	24.29	24.02	38.03	1	1
HEMBA1003175	91.24	109.33	99.96	1.2	1.1
HEMBA1003179	511.42	505.09	456.99	0.99	0.89
HEMBA1003186	130.84	115.22	160.21	0.88	1.22
HEMBA1003196	60.73	69.31	68.65	1.14	1.13
HEMBA1003197	23.09	32.24	20.62	1	1
HEMBA1003199	30.15	33.48	35.67	1	1
HEMBA1003202	160.12	213.03	163.11	1.33	1.02
HEMBA1003204	82.45	94.23	93.26	1.14	1.13
HEMBA1003210	172.76	185.07	241.07	1.07	1.4
HEMBA1003212	116.79	142.68	125.64	1.22	1.08
HEMBA1003218	24.25	41.53	25.18	1.04	1
HEMBA1003220	773.18	750.15	891.78	0.97	1.15
HEMBA1003222	28.08	37.8	35.63	1	1
HEMBA1003225	12.05	15.97	15.46	1	1
HEMBA1003229	19.34	28.79	31.73	1	1
HEMBA1003230	29.02	27.3	35.38	1	1
HEMBA1003235	83.94	111.1	89.7	1.32	1.07
HEMBA1003236	116.94	93.69	123	0.8	1.05
HEMBA1003250	19.27	17.29	26.24	1	1
HEMBA1003252	223.8	213.62	219.85	0.95	0.98
HEMBA1003257	92.06	123.27	119.67	1.34	1.3
HEMBA1003268	28.28	31.5	39.23	1	1
HEMBA1003273	47.51	54.61	57.42	1.15	1.21
HEMBA1003276	46.48	44.59	55.78	0.96	1.2
HEMBA1003277	10.01	11.06	17.36	1	1
HEMBA1003278	28.31	26.64	38.31	1	1
HEMBA1003280	44.23	40.4	53.2	0.91	1.2
HEMBA1003281	21.59	28.71	27.7	1	1
HEMBA1003284	24.93	27.01	26.49	1	1
HEMBA1003286	717.88	933.33	607.04	1.3	0.85
HEMBA1003291	38.98	45.07	55.08	1.13	1.38
HEMBA1003294	54.23	62.34	71.14	1.15	1.31
HEMBA1003296	1300.6	1413.66	1115.39	1.09	0.86
HEMBA1003304	22.85	28.8	27.12	1	1
HEMBA1003306	49.18	55.93	68.74	1.14	1.4
HEMBA1003309	25.09	28.4	32.7	1	1

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HEMBA1003314	37.17	44.82	59.15	1.12	1.48
HEMBA1003315	124.59	124.67	175.23	1	1.41
HEMBA1003322	56.36	76.18	78.78	1.35	1.4
HEMBA1003326	30.66	36.54	33.24	1	1
HEMBA1003327	36.18	42.14	47.09	1.05	1.18
HEMBA1003328	38.64	49.8	59.69	1.25	1.49
HEMBA1003330	83.32	95.56	101.26	1.15	1.22
HEMBA1003348	228.39	290.07	281.18	1.27	1.23
HEMBA1003369	35.08	34.25	41.3	1	1.03
HEMBA1003370	113.05	127.15	160.35	1.12	1.42
HEMBA1003373	30.18	41.81	33.29	1.05	1
HEMBA1003376	151.06	175.71	168.37	1.16	1.11
HEMBA1003380	23.37	31.1	35.25	1	1
HEMBA1003384	23.97	29.28	28.6	1	1
HEMBA1003387	14.31	18.54	15.1	1	1
HEMBA1003392	26.1	18.97	37.16	1	1
HEMBA1003395	35.41	46.06	38.3	1.15	1
HEMBA1003399	22.92	23.91	34.6	1	1
HEMBA1003400	49.2	47.83	55.33	0.97	1.12
HEMBA1003402	19.93	22.88	27.46	1	1
HEMBA1003403	916.83	1093.91	744.48	1.19	0.81
HEMBA1003408	31.78	32.87	29.66	1	1
HEMBA1003412	104.21	93.23	112.18	0.89	1.08
HEMBA1003417	38.97	45.45	46.16	1.14	1.15
HEMBA1003418	134.53	157.73	180.06	1.17	1.34
HEMBA1003420	184	159.93	205.39	0.87	1.12
HEMBA1003425	23.51	25.24	25.02	1	1
HEMBA1003433	19.55	20.01	22.1	1	1
HEMBA1003440	18.36	16.3	18.41	1	1
HEMBA1003442	118.4	96.59	106.66	0.82	0.9
HEMBA1003447	1244.4	1339.73	857.98	1.08	0.69
HEMBA1003453	95.87	93.02	110.27	0.97	1.15
HEMBA1003461	26.09	23.67	34.23	1	1
HEMBA1003463	32.85	40.67	36.19	1.02	1
HEMBA1003465	32.65	35.86	39.45	1	1
HEMBA1003480	150.99	182.03	160.32	1.21	1.06
HEMBA1003485	60.29	58.81	46.93	0.98	0.78
HEMBA1003487	41.67	32.72	45.62	0.96	1.09
HEMBA1003492	50.94	51.03	58.23	1	1.14
HEMBA1003494	81.07	64.25	63.81	0.79	0.79
HEMBA1003497	20.15	20.93	23.08	1	1
HEMBA1003503	21.56	27.38	27.4	1	1
HEMBA1003511	24.64	26.19	33.32	1	1
HEMBA1003528	30.56	30.02	32.98	1	1
HEMBA1003530	21.5	15.27	27.5	1	1
HEMBA1003531	78.01	75.06	79.44	0.96	1.02

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HEMBA1003532	97.65	102.85	110.25	1.05	1.13
HEMBA1003538	103.67	110.46	109.77	1.07	1.06
HEMBA1003545	40.23	24.96	21.54	0.99	0.99
HEMBA1003546	26.04	26.92	35.27	1	1
HEMBA1003548	108.9	123.89	109.3	1.14	1
HEMBA1003553	46.21	39.71	61.93	0.87	1.34
HEMBA1003555	26.42	35.77	39.61	1	1
HEMBA1003556	54.88	44.61	59.09	0.81	1.08
HEMBA1003560	166.71	191.62	174.51	1.15	1.05
HEMBA1003565	201.56	195.27	284.97	0.97	1.41
HEMBA1003568	24.9	29.68	22.4	1	1
HEMBA1003569	39.46	50.94	62.36	1.27	1.56
HEMBA1003571	75.65	79.3	86.06	1.05	1.14
HEMBA1003579	25.07	31.44	38.45	1	1
HEMBA1003580	26.85	27.07	30.17	1	1
HEMBA1003581	23.83	19.2	21.85	1	1
HEMBA1003591	119.29	100.77	115.09	0.84	0.96
HEMBA1003595	24.19	41.42	25.76	1.04	1
HEMBA1003597	65.92	77.48	80.25	1.18	1.22
HEMBA1003598	20.14	18.68	21.51	1	1
HEMBA1003600	100.74	116.78	113.04	1.16	1.12
HEMBA1003602	89.14	96.53	109.44	1.08	1.23
HEMBA1003604	27.67	30.92	37.17	1	1
HEMBA1003610	28.27	27.79	34.55	1	1
HEMBA1003615	58.86	61.03	56.92	1.04	0.97
HEMBA1003617	26.21	41.84	38.91	1.05	1
HEMBA1003620	65.82	61.48	83.33	0.93	1.27
HEMBA1003621	85.87	101.22	103.55	1.18	1.21
HEMBA1003622	28.46	22.42	26.9	1	1
HEMBA1003630	21.72	20.46	24.57	1	1
HEMBA1003637	43.95	46.03	63.5	1.05	1.44
HEMBA1003640	102.34	99.09	109.82	0.97	1.07
HEMBA1003645	22.81	24.65	19.83	1	1
HEMBA1003646	23.59	29.71	31.99	1	1
HEMBA1003647	15.69	19.27	20.76	1	1
HEMBA1003656	96.49	161.88	151.69	1.68	1.57
HEMBA1003662	30.59	27.04	45.76	1	1.14
HEMBA1003666	10.75	13.44	15.76	1	1
HEMBA1003667	73.07	59.07	108.02	0.81	1.48
HEMBA1003670	19.08	13.39	19.91	1	1
HEMBA1003674	288.8	295.13	431.7	1.02	1.49
HEMBA1003677	55.17	79.59	79.49	1.44	1.44
HEMBA1003679	62.99	65.84	77.2	1.05	1.23
HEMBA1003680	93.24	87.1	126.5	0.93	1.36
HEMBA1003684	24.94	28.67	31.31	1	1
HEMBA1003690	92.14	94.42	111.37	1.02	1.21

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HEMBA1003692	58.18	64.91	87.68	1.12	1.51
HEMBA1003702	29.67	40.2	41.34	1.01	1.03
HEMBA1003711	32.3	33.55	41.53	1	1.04
HEMBA1003714	11.66	12.85	14.26	1	1
HEMBA1003715	127.28	128.58	176.49	1.01	1.39
HEMBA1003717	36.23	47.11	56.82	1.18	1.42
HEMBA1003720	72.7	104.3	95.71	1.43	1.32
HEMBA1003725	30.21	29.52	45.16	1	1.13
HEMBA1003728	19.89	22.33	35.98	1	1
HEMBA1003729	34.19	28.4	38.87	1	1
HEMBA1003732	24.57	23.52	26.8	1	1
HEMBA1003733	32.05	38.41	35.69	1	1
HEMBA1003742	91.11	74.8	121.1	0.82	1.33
HEMBA1003743	20.87	27.7	36.19	1	1
HEMBA1003758	155.66	212.5	192.43	1.37	1.24
HEMBA1003760	19.4	24.15	21.44	1	1
HEMBA1003764	50.94	59.98	66.6	1.18	1.31
HEMBA1003769	243.2	236.31	294.05	0.97	1.21
HEMBA1003773	23.79	30.65	30.94	1	1
HEMBA1003783	46.84	51.35	61.57	1.1	1.31
HEMBA1003784	23.33	24.87	32.65	1	1
HEMBA1003794	98.42	151.82	160.49	1.54	1.63
HEMBA1003799	24	20.43	26.88	1	1
HEMBA1003803	92.09	92.45	94.87	1	1.03
HEMBA1003804	11.79	13.4	13.71	1	1
HEMBA1003805	62.9	47.84	57.71	0.76	0.92
HEMBA1003807	35	33.04	37.16	1	1
HEMBA1003810	49.79	42.58	48.65	0.86	0.98
HEMBA1003827	214.33	220.34	247.88	1.03	1.16
HEMBA1003836	105.3	131.09	152.63	1.24	1.45
HEMBA1003838	201.86	193.21	218.25	0.96	1.08
HEMBA1003843	95.01	80.4	81.33	0.85	0.86
HEMBA1003846	584.93	521.93	524.6	0.89	0.9
HEMBA1003856	37.85	19.35	24.84	1	1
HEMBA1003857	84.45	85.97	93	1.02	1.1
HEMBA1003864	45.81	48.61	52.54	1.06	1.15
HEMBA1003866	22.19	14.38	26.76	1	1
HEMBA1003868	127.43	154.52	171.8	1.21	1.35
HEMBA1003879	60.94	75.5	61.32	1.24	1.01
HEMBA1003880	63.83	74.3	59.16	1.16	0.93
HEMBA1003884	295.83	265.18	244.1	0.9	0.83
HEMBA1003885	77.57	77.54	85.49	1	1.1
HEMBA1003887	43.2	44.46	51.02	1.03	1.18
HEMBA1003890	34.02	30.68	46.62	1	1.17
HEMBA1003893	89.77	90.01	86.46	1	0.96
HEMBA1003896	70.89	108.77	130.61	1.53	1.84

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HEMBA1003902	72.1	82.48	88.57	1.14	1.23
HEMBA1003904	26.68	30.31	35.19	1	1
HEMBA1003908	20.58	24.77	17.24	1	1
HEMBA1003926	817.82	708.16	810.39	0.87	0.99
HEMBA1003937	74.16	92.69	106.26	1.25	1.43
HEMBA1003939	189.88	194.21	169.09	1.02	0.89
HEMBA1003940	27.59	32.67	41.23	1	1.03
HEMBA1003941	39.11	38.63	32.44	1	1
HEMBA1003942	29.31	36.49	35.17	1	1
HEMBA1003945	101.81	111.03	153.5	1.09	1.51
HEMBA1003949	26.89	23.59	31.98	1	1
HEMBA1003950	108.43	101.22	111.88	0.93	1.03
HEMBA1003953	33.64	26.45	19.18	1	1
HEMBA1003958	172.27	318.81	393.92	1.85	2.29
HEMBA1003959	37.17	45.76	40.45	1.14	1.01
HEMBA1003960	41.6	37.03	46.77	0.96	1.12
HEMBA1003966	50.41	56.91	67.77	1.13	1.34
HEMBA1003967	35.26	32.76	36.11	1	1
HEMBA1003968	17.83	15.7	30.29	1	1
HEMBA1003974	5265.0	4839.83	4912.1	0.92	0.93
HEMBA1003976	20.51	33.59	27.16	1	1
HEMBA1003977	23.04	26.84	23.25	1	1
HEMBA1003978	37.27	32.98	40.15	1	1
HEMBA1003981	108	97.04	117.19	0.9	1.09
HEMBA1003982	1665.9	1749.33	1773.93	1.05	1.06
HEMBA1003985	26.77	25.32	36.45	1	1
HEMBA1003987	33.45	37.68	41.63	1	1.04
HEMBA1003989	63.17	62.72	76.11	0.99	1.2
HEMBA1004000	58.48	80.61	79.89	1.38	1.37
HEMBA1004006	88.99	136.49	109.66	1.53	1.23
HEMBA1004007	98.97	105.35	103.51	1.06	1.05
HEMBA1004010	777.44	800.96	1113.06	1.03	1.43
HEMBA1004011	23.51	25.26	29.93	1	1
HEMBA1004012	55.61	56.63	63.69	1.02	1.15
HEMBA1004015	67.35	53.48	69.58	0.79	1.03
HEMBA1004024	98.84	120.03	126.27	1.21	1.28
HEMBA1004029	23.09	21.98	27.27	1	1
HEMBA1004038	23.15	29.19	29.88	1	1
HEMBA1004042	20.59	28.59	29.34	1	1
HEMBA1004045	30	25.74	41.36	1	1.03
HEMBA1004048	87.48	104.2	129.71	1.19	1.48
HEMBA1004049	46.55	56.7	79.44	1.22	1.71
HEMBA1004051	24.85	23.39	30.94	1	1
HEMBA1004053	83.24	94.23	123.5	1.13	1.48
HEMBA1004055	21.51	22.83	28.17	1	1
HEMBA1004056	118.22	132.94	128.78	1.12	1.09

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HEMBA1004060	21.47	25.47	26.19	1	1
HEMBA1004061	45.85	35.4	57.87	0.87	1.26
HEMBA1004067	2265.5	2569.69	1924.71	1.13	0.85
HEMBA1004071	77.09	62.79	82.9	0.81	1.08
HEMBA1004074	40.68	72.63	70.18	1.79	1.73
HEMBA1004078	40.24	47.53	55.41	1.18	1.38
HEMBA1004085	18.3	21.25	28.75	1	1
HEMBA1004086	35.29	42.02	43.85	1.05	1.1
HEMBA1004097	40.37	31.39	52.78	0.99	1.31
HEMBA1004100	34.17	46.53	60.42	1.16	1.51
HEMBA1004103	68.55	98.24	83.29	1.43	1.22
HEMBA1004110	23.71	32.68	36.86	1	1
HEMBA1004111	284.54	302.67	319.82	1.06	1.12
HEMBA1004124	1302.5	1284.27	1199.49	0.99	0.92
HEMBA1004130	58.56	63.88	69.1	1.09	1.18
HEMBA1004131	35.69	32.82	47.96	1	1.2
HEMBA1004132	55.08	55.48	67.89	1.01	1.23
HEMBA1004133	38.6	44.72	38.69	1.12	1
HEMBA1004138	23.71	27.92	36.47	1	1
HEMBA1004143	101.54	113.63	105.34	1.12	1.04
HEMBA1004146	43.85	45.09	46.96	1.03	1.07
HEMBA1004148	23.02	28.45	29.41	1	1
HEMBA1004149	20.96	23.07	27.74	1	1
HEMBA1004150	14.64	17.63	22.2	1	1
HEMBA1004154	46.52	40.02	43.15	0.86	0.93
HEMBA1004164	86.6	102.3	136.34	1.18	1.57
HEMBA1004168	37.96	42.06	56.91	1.05	1.42
HEMBA1004199	18.47	19.61	21.64	1	1
HEMBA1004200	38.51	51.72	53.71	1.29	1.34
HEMBA1004201	287.85	308.67	253.09	1.07	0.88
HEMBA1004202	36.61	30	36.83	1	1
HEMBA1004203	27.32	31.45	39.33	1	1
HEMBA1004207	23.04	26.05	27.12	1	1
HEMBA1004210	22.18	19.54	24.88	1	1
HEMBA1004225	61.67	92.92	90.65	1.51	1.47
HEMBA1004227	77.96	98.34	88.73	1.26	1.14
HEMBA1004235	37.75	53.13	57.82	1.33	1.45
HEMBA1004237	30.26	30.64	36.42	1	1
HEMBA1004238	71.6	81.63	69.55	1.14	0.97
HEMBA1004241	19.88	16.68	17.35	1	1
HEMBA1004242	176.71	159.48	236.75	0.9	1.34
HEMBA1004243	35.34	46.8	43.58	1.17	1.09
HEMBA1004246	93.29	98.73	111.32	1.06	1.19
HEMBA1004247	27.47	26.7	24.25	1	1
HEMBA1004248	38.46	46.23	37.87	1.16	1
HEMBA1004250	17.87	16	20.26	1	1

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HEMBA1004252	30.3	36.55	38.17	1	1
HEMBA1004260	47.34	30.07	51.36	0.84	1.08
HEMBA1004264	19.37	22.18	22.53	1	1
HEMBA1004267	181.44	213.87	223.86	1.18	1.23
HEMBA1004272	17.52	21.46	26.5	1	1
HEMBA1004274	1989.4	2038.01	1978.3	1.02	0.99
HEMBA1004275	33.93	16.43	18.95	1	1
HEMBA1004276	25.68	23.43	34.9	1	1
HEMBA1004279	29.84	43.35	34.99	1.08	1
HEMBA1004284	62.7	66.83	78.49	1.07	1.25
HEMBA1004286	24.85	23.45	26.11	1	1
HEMBA1004289	81.09	94.81	91.9	1.17	1.13
HEMBA1004293	351.58	311.41	478.13	0.89	1.36
HEMBA1004295	25.46	34.45	34.22	1	1
HEMBA1004302	21.24	18.51	23.69	1	1
HEMBA1004306	73	62.96	88.15	0.86	1.21
HEMBA1004312	45.15	58.45	45.47	1.29	1.01
HEMBA1004314	33.26	38.47	39.65	1	1
HEMBA1004321	68.15	70.09	57.87	1.03	0.85
HEMBA1004323	74.23	99.88	95.43	1.35	1.29
HEMBA1004327	23.63	33.37	30.8	1	1
HEMBA1004329	113.01	94.45	117.35	0.84	1.04
HEMBA1004330	39.91	33.13	43.35	1	1.08
HEMBA1004334	55.45	36.72	62.06	0.72	1.12
HEMBA1004335	67.79	97.37	82.86	1.44	1.22
HEMBA1004341	10.43	15.12	14.1	1	1
HEMBA1004344	239.01	301.14	269	1.26	1.13
HEMBA1004347	34.96	28.93	43.64	1	1.09
HEMBA1004349	72.96	85.1	92.18	1.17	1.26
HEMBA1004352	77.96	87.43	92.18	1.12	1.18
HEMBA1004353	193.95	170.09	196.91	0.88	1.02
HEMBA1004354	81.49	96.77	106.65	1.19	1.31
HEMBA1004356	65.79	77.83	79.61	1.18	1.21
HEMBA1004360	23.12	23.99	27.25	1	1
HEMBA1004366	28.22	43.02	37.58	1.08	1
HEMBA1004372	9.15	15.66	15.18	1	1
HEMBA1004377	79.63	75.92	82.84	0.95	1.04
HEMBA1004389	46.56	45.08	58.79	0.97	1.26
HEMBA1004391	17.83	18.26	20.23	1	1
HEMBA1004393	387.04	382.7	478.71	0.99	1.24
HEMBA1004394	14.25	16.28	19.75	1	1
HEMBA1004396	31.93	37.55	33.79	1	1
HEMBA1004401	63.61	56.1	64.07	0.88	1.01
HEMBA1004405	60.61	75.08	64.19	1.24	1.06
HEMBA1004408	61.03	61.54	75.75	1.01	1.24
HEMBA1004414	73.58	85.01	90.29	1.16	1.23

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HEMBA1004429	57.83	50.69	77.84	0.88	1.35
HEMBA1004433	51.59	56.5	69.01	1.1	1.34
HEMBA1004440	42.17	44.03	61.04	1.04	1.45
HEMBA1004444	58.82	67.68	71.11	1.15	1.21
HEMBA1004446	21.24	27.74	26.9	1	1
HEMBA1004451	202.16	185.25	309.86	0.92	1.53
HEMBA1004452	37.69	35.29	51.92	1	1.3
HEMBA1004454	36.68	41.61	60.58	1.04	1.51
HEMBA1004460	51.62	74.71	90.25	1.45	1.75
HEMBA1004461	15.58	19.08	18.45	1	1
HEMBA1004468	97.94	110.46	134.63	1.13	1.37
HEMBA1004479	54.01	60.48	65.38	1.12	1.21
HEMBA1004482	24.3	22.13	36.54	1	1
HEMBA1004491	25.87	27.15	37.91	1	1
HEMBA1004499	1360.1	1727.41	1510.19	1.27	1.11
HEMBA1004502	23.53	36.65	37.04	1	1
HEMBA1004505	25.58	32.28	39.37	1	1
HEMBA1004506	29.27	32.76	32.25	1	1
HEMBA1004507	761.04	756.3	944.55	0.99	1.24
HEMBA1004509	30.03	33.56	38.25	1	1
HEMBA1004523	19.89	27.93	39.2	1	1
HEMBA1004528	1640.0	1746.66	1685.13	1.07	1.03
HEMBA1004534	129.91	154.42	179.78	1.19	1.38
HEMBA1004536	28.89	48.11	31.06	1.2	1
HEMBA1004538	82.07	62.79	83.14	0.77	1.01
HEMBA1004542	186.75	193.13	171.45	1.03	0.92
HEMBA1004552	18.5	23.69	33.11	1	1
HEMBA1004554	17.02	20.01	22.23	1	1
HEMBA1004558	206.56	234.05	278.21	1.13	1.35
HEMBA1004560	24.49	30.95	31.65	1	1
HEMBA1004564	105.15	118.21	94.09	1.12	0.89
HEMBA1004566	308.77	338.48	296.3	1.1	0.96
HEMBA1004573	23.31	14.9	26.08	1	1
HEMBA1004576	125.61	120.34	138.15	0.96	1.1
HEMBA1004577	46.19	59.63	51.44	1.29	1.11
HEMBA1004586	78.7	67.86	74.8	0.86	0.95
HEMBA1004596	544.79	585.43	619.1	1.07	1.14
HEMBA1004604	683.5	780.45	593.75	1.14	0.87
HEMBA1004607	33	37.86	37.58	1	1
HEMBA1004610	30.83	29.88	29.51	1	1
HEMBA1004617	31.85	36.77	34.63	1	1
HEMBA1004622	61.18	64.79	65.54	1.06	1.07
HEMBA1004626	30.36	31.68	36.7	1	1
HEMBA1004629	54.48	51.45	55.65	0.94	1.02
HEMBA1004631	34.23	33.96	35.95	1	1
HEMBA1004632	24.4	17.93	26.26	1	1

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HEMBA1004633	56.35	62.95	61.62	1.12	1.09
HEMBA1004636	18.09	17.86	15.51	1	1
HEMBA1004637	41.52	45.54	42.59	1.1	1.03
HEMBA1004638	13.24	11.19	11.18	1	1
HEMBA1004645	62.08	62.36	59.64	1	0.96
HEMBA1004656	35.26	33.9	35.28	1	1
HEMBA1004657	175.89	240.84	247.24	1.37	1.41
HEMBA1004666	18.42	26.24	24.05	1	1
HEMBA1004669	60.89	63.21	62.26	1.04	1.02
HEMBA1004670	31.16	44.91	39.7	1.12	1
HEMBA1004672	50.37	48.32	44.51	0.96	0.88
HEMBA1004689	612.96	746.44	665.62	1.22	1.09
HEMBA1004690	237.25	229.52	180.85	0.97	0.76
HEMBA1004693	96.88	85.44	79.45	0.88	0.82
HEMBA1004697	34.51	37.98	31.43	1	1
HEMBA1004702	107.99	91.25	129.2	0.84	1.2
HEMBA1004704	46.93	56.01	58.17	1.19	1.24
HEMBA1004705	24.38	25.69	26.15	1	1
HEMBA1004706	27.49	21.87	23.6	1	1
HEMBA1004709	123.5	132.22	135.32	1.07	1.1
HEMBA1004711	32.7	17.62	26.81	1	1
HEMBA1004723	146.46	95.76	140.47	0.65	0.96
HEMBA1004725	66.54	67.24	63.13	1.01	0.95
HEMBA1004730	41.03	28.45	38	0.97	0.97
HEMBA1004733	13.34	14.69	13.37	1	1
HEMBA1004734	33.38	28.45	32.83	1	1
HEMBA1004736	62.63	55.95	71.48	0.89	1.14
HEMBA1004748	33.98	34.08	31.99	1	1
HEMBA1004749	159.81	193.55	206.24	1.21	1.29
HEMBA1004751	67	87.32	78.24	1.3	1.17
HEMBA1004752	40.19	50.19	43.88	1.25	1.09
HEMBA1004753	1005.7	865.26	931.03	0.86	0.93
HEMBA1004755	89.86	115.77	119.47	1.29	1.33
HEMBA1004756	39.38	24.19	23.93	1	1
HEMBA1004758	37.57	36.02	43.25	1	1.08
HEMBA1004763	65.79	75.15	63.16	1.14	0.96
HEMBA1004768	18.03	27.83	26.53	1	1
HEMBA1004770	18.4	20.53	18.48	1	1
HEMBA1004771	35.9	45.95	39.86	1.15	1
HEMBA1004775	29.97	34.82	37.03	1	1
HEMBA1004776	39.58	37.62	29.97	1	1
HEMBA1004778	62.86	64.6	53.56	1.03	0.85
HEMBA1004784	59.8	62.34	60.65	1.04	1.01
HEMBA1004785	47.08	48.99	46.13	1.04	0.98
HEMBA1004789	22.43	35.09	34.19	1	1
HEMBA1004795	23.46	23.62	28.22	1	1

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HEMBA1004797	69.02	75.8	68.09	1.1	0.99
HEMBA1004803	139.28	172.03	148.1	1.24	1.06
HEMBA1004806	20.24	18.76	19.51	1	1
HEMBA1004807	25.93	24.81	28.08	1	1
HEMBA1004816	66.84	72.32	80.51	1.08	1.2
HEMBA1004820	20.72	27.49	22.78	1	1
HEMBA1004833	58.77	77.82	68.76	1.32	1.17
HEMBA1004847	55.11	54.09	68.09	0.98	1.24
HEMBA1004850	41.24	94.77	74.52	2.3	1.81
HEMBA1004863	17.09	30.6	32.89	1	1
HEMBA1004864	47.54	48.72	67.61	1.02	1.42
HEMBA1004865	37.45	42.36	43.32	1.06	1.08
HEMBA1004880	67.85	83.27	79.43	1.23	1.17
HEMBA1004882	55.71	59.71	71.5	1.07	1.28
HEMBA1004885	5.26	5.42	10.69	1	1
HEMBA1004889	39.97	53.79	59.53	1.34	1.49
HEMBA1004900	24.64	37.16	35.42	1	1
HEMBA1004909	37.38	55.77	52.81	1.39	1.32
HEMBA1004918	52.56	69.3	75.53	1.32	1.44
HEMBA1004923	66.42	56.65	57.91	0.85	0.87
HEMBA1004929	14.53	20.24	16.08	1	1
HEMBA1004930	64.2	73.28	84.98	1.14	1.32
HEMBA1004933	25.53	28.37	38.67	1	1
HEMBA1004934	34.74	34.56	31.42	1	1
HEMBA1004937	30.99	32.44	39.53	1	1
HEMBA1004943	26.88	32.39	33.5	1	1
HEMBA1004944	47.48	54.15	57.28	1.14	1.21
HEMBA1004946	110.22	99.09	106.8	0.9	0.97
HEMBA1004952	18.65	22.44	23.74	1	1
HEMBA1004954	51.59	56.66	59.07	1.1	1.14
HEMBA1004956	24.4	30.29	25.59	1	1
HEMBA1004960	50.95	69.7	77.84	1.37	1.53
HEMBA1004971	147.9	185.55	169.84	1.25	1.15
HEMBA1004972	25.23	21.63	24.54	1	1
HEMBA1004973	29.7	24.12	26.9	1	1
HEMBA1004977	68.37	56.37	65.48	0.82	0.96
HEMBA1004978	87.36	98.52	102.09	1.13	1.17
HEMBA1004980	64.46	65.18	58.56	1.01	0.91
HEMBA1004982	19.91	18.27	24.85	1	1
HEMBA1004983	48.65	57.05	55.03	1.17	1.13
HEMBA1004995	54.11	50.11	50.53	0.93	0.93
HEMBA1005004	35.78	37.22	37.94	1	1
HEMBA1005008	56.93	57.2	46.58	1	0.82
HEMBA1005009	60.37	59.99	53.66	0.99	0.89
HEMBA1005019	52.03	55.66	59.82	1.07	1.15
HEMBA1005021	75.62	83.62	95.86	1.11	1.27

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HEMBA1005029	36.58	36.57	46.56	1	1.16
HEMBA1005035	133.62	207.34	190.82	1.55	1.43
HEMBA1005036	135.49	137.85	151.71	1.02	1.12
HEMBA1005039	39.73	46.17	37.99	1.15	1
HEMBA1005047	43.76	40.29	30.12	0.92	0.91
HEMBA1005050	39.18	50.59	44.99	1.26	1.12
HEMBA1005062	28.28	45.6	26.45	1.14	1
HEMBA1005066	33.83	32.74	34.07	1	1
HEMBA1005067	64.14	45.18	73.75	0.7	1.15
HEMBA1005070	54.68	77.81	71.9	1.42	1.31
HEMBA1005075	37.34	61.27	56.48	1.53	1.41
HEMBA1005078	113.49	116.87	127.98	1.03	1.13
HEMBA1005079	160.59	122.85	152.75	0.76	0.95
HEMBA1005083	18.35	16.81	17.58	1	1
HEMBA1005084	46.51	54.54	42.84	1.17	0.92
HEMBA1005088	43.64	60.51	45.16	1.39	1.03
HEMBA1005089	61.74	51.52	61.56	0.83	1
HEMBA1005090	105.63	138.47	121.67	1.31	1.15
HEMBA1005096	42.07	33.65	49.45	0.95	1.18
HEMBA1005101	26.09	26.59	25.34	1	1
HEMBA1005107	21.42	19.81	20.4	1	1
HEMBA1005113	18.23	16.65	19.32	1	1
HEMBA1005123	113.26	124.65	121.19	1.1	1.07
HEMBA1005133	52.66	72.24	58.53	1.37	1.11
HEMBA1005135	20.53	27.86	28.87	1	1
HEMBA1005145	129.53	185.54	139.75	1.43	1.08
HEMBA1005149	105.14	107.37	128.13	1.02	1.22
HEMBA1005152	40.94	51.64	44.14	1.26	1.08
HEMBA1005159	19.64	30.68	23.8	1	1
HEMBA1005172	549.33	423.49	522.02	0.77	0.95
HEMBA1005185	27.83	32.13	29	1	1
HEMBA1005186	31.44	40.67	40.41	1.02	1.01
HEMBA1005195	30.45	27	25.61	1	1
HEMBA1005201	49.29	58.3	63.02	1.18	1.28
HEMBA1005202	70.57	63.53	80.67	0.9	1.14
HEMBA1005204	1441.0	1471.8	1504.01	1.02	1.04
HEMBA1005206	1267.1	1396.64	1098.21	1.1	0.87
HEMBA1005219	92.71	99.01	97.94	1.07	1.06
HEMBA1005223	35.53	49.33	39.97	1.23	1
HEMBA1005229	17.39	21.61	24.91	1	1
HEMBA1005230	44.26	41.7	42.03	0.94	0.95
HEMBA1005232	18.52	24.8	21.23	1	1
HEMBA1005238	98.46	92.2	118.11	0.94	1.2
HEMBA1005241	95.82	77.58	102.25	0.81	1.07
HEMBA1005244	25.28	24.01	39.17	1	1
HEMBA1005246	40.93	31.04	30.37	0.98	0.98

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HEMBA1005251	58.46	66.35	54.93	1.13	0.94
HEMBA1005252	31.06	40.09	35.67	1	1
HEMBA1005267	64.34	68.6	48.93	1.07	0.76
HEMBA1005274	41.67	51.95	41.77	1.25	1
HEMBA1005275	48.94	74.69	58.63	1.53	1.2
HEMBA1005288	80.5	85.35	109.87	1.06	1.36
HEMBA1005293	17.13	15.88	21.11	1	1
HEMBA1005296	5061.4	5395.06	4099.51	1.07	0.81
HEMBA1005301	580.58	663.26	578.44	1.14	1
HEMBA1005304	98.73	113.81	117.71	1.15	1.19
HEMBA1005305	26.2	26.45	41.46	1	1.04
HEMBA1005311	14.17	16.88	20.79	1	1
HEMBA1005313	27.1	29.72	29.8	1	1
HEMBA1005314	10.04	9.99	14.27	1	1
HEMBA1005315	45.17	74.09	65.59	1.64	1.45
HEMBA1005317	13.57	17.99	16.44	1	1
HEMBA1005318	22.82	21.56	32	1	1
HEMBA1005324	631.71	819.78	667.23	1.3	1.06
HEMBA1005331	480.23	422.6	497.23	0.88	1.04
HEMBA1005337	1129.3	1330.67	1427.51	1.18	1.26
HEMBA1005338	124.75	122.63	151.85	0.98	1.22
HEMBA1005344	23.29	22.5	29.97	1	1
HEMBA1005353	49.48	59.24	74.7	1.2	1.51
HEMBA1005359	76.32	73.69	94.58	0.97	1.24
HEMBA1005362	22.69	31.43	24.58	1	1
HEMBA1005364	18.21	24.09	27.02	1	1
HEMBA1005367	22.29	23.56	32.01	1	1
HEMBA1005372	22.19	25.81	27.76	1	1
HEMBA1005374	65.46	85.61	74.4	1.31	1.14
HEMBA1005379	40.77	51.93	44.43	1.27	1.09
HEMBA1005382	1299.7	1582.71	1305.08	1.22	1
HEMBA1005384	18.14	23.2	21.84	1	1
HEMBA1005386	32.14	39.69	40.42	1	1.01
HEMBA1005389	34.53	35.33	40.31	1	1.01
HEMBA1005394	30.2	31.77	46.12	1	1.15
HEMBA1005403	58.22	63.4	76.15	1.09	1.31
HEMBA1005408	79.24	90.19	71.04	1.14	0.9
HEMBA1005410	26.31	17.63	18.45	1	1
HEMBA1005411	58.66	70.13	58.65	1.2	1
HEMBA1005423	27.68	24.75	27.73	1	1
HEMBA1005426	15.55	22.35	21.3	1	1
HEMBA1005427	100.39	97.02	129.7	0.97	1.29
HEMBA1005430	19.95	20.5	28.54	1	1
HEMBA1005438	21.96	28.57	34.1	1	1
HEMBA1005443	184.65	173.07	217.21	0.94	1.18
HEMBA1005447	36.34	38.78	32.32	1	1

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HEMBA1005449	27.11	20.9	18.06	1	1
HEMBA1005452	1749.5	1574.26	1381.13	0.9	0.79
HEMBA1005454	57.35	50.65	61.79	0.88	1.08
HEMBA1005468	39.84	38.73	30.62	1	1
HEMBA1005469	52.33	50.78	61.14	0.97	1.17
HEMBA1005472	67.91	67.09	69.48	0.99	1.02
HEMBA1005474	76.28	97.92	79.64	1.28	1.04
HEMBA1005475	82.29	87.13	80.97	1.06	0.98
HEMBA1005489	21.1	15.18	17.8	1	1
HEMBA1005497	14.01	12.95	12.69	1	1
HEMBA1005500	108.69	118.44	77.44	1.09	0.71
HEMBA1005506	16.1	14.16	14.79	1	1
HEMBA1005508	77.23	92.99	88.01	1.2	1.14
HEMBA1005511	44.44	61.96	53.02	1.39	1.19
HEMBA1005513	320.36	340.16	308.95	1.06	0.96
HEMBA1005517	50.25	44.24	53.12	0.88	1.06
HEMBA1005518	37.38	32.96	29.46	1	1
HEMBA1005520	128.78	152.2	129.21	1.18	1
HEMBA1005522	13.55	19.21	22.51	1	1
HEMBA1005526	66.47	79.4	72.29	1.19	1.09
HEMBA1005528	121.39	128.02	143.91	1.05	1.19
HEMBA1005530	48.31	43.23	40.68	0.89	0.84
HEMBA1005538	51.11	32.89	51	0.78	1
HEMBA1005539	61.9	52.75	50.74	0.85	0.82
HEMBA1005545	21.26	20.05	30.78	1	1
HEMBA1005548	73.2	41.84	75.19	0.57	1.03
HEMBA1005552	155.17	162.03	157.1	1.04	1.01
HEMBA1005558	36.74	50.67	34.64	1.27	1
HEMBA1005568	68.03	74.69	67.19	1.1	0.99
HEMBA1005570	29.68	44.23	43.18	1.11	1.08
HEMBA1005576	87.86	63.16	75.62	0.72	0.86
HEMBA1005577	14.59	21.1	17.23	1	1
HEMBA1005581	43.92	35.09	40.32	0.91	0.92
HEMBA1005582	30.93	27.9	28.13	1	1
HEMBA1005583	25.05	39.07	31.31	1	1
HEMBA1005588	75.46	101.03	81.56	1.34	1.08
HEMBA1005593	48.89	47.53	50.91	0.97	1.04
HEMBA1005595	37.81	36.31	34.6	1	1
HEMBA1005597	56.7	53.58	57.71	0.94	1.02
HEMBA1005606	96.79	118.58	123.28	1.23	1.27
HEMBA1005609	50.11	59.31	53.45	1.18	1.07
HEMBA1005616	57.75	43.48	49.07	0.75	0.85
HEMBA1005621	22.52	26.54	23.96	1	1
HEMBA1005627	128.53	153.5	141.71	1.19	1.1
HEMBA1005628	91.12	137.09	152.28	1.5	1.67
HEMBA1005631	70.72	83.63	90.58	1.18	1.28

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HEMBA1005632	56.14	89.14	77.66	1.59	1.38
HEMBA1005634	94.99	99.26	99.89	1.04	1.05
HEMBA1005662	15.74	15.42	24.33	1	1
HEMBA1005666	68.78	45.9	55.04	0.67	0.8
HEMBA1005670	54.67	63.96	54.71	1.17	1
HEMBA1005671	60.32	69.36	68.2	1.15	1.13
HEMBA1005679	75.85	72.36	91.25	0.95	1.2
HEMBA1005680	78.6	93.34	88.38	1.19	1.12
HEMBA1005685	31.53	25	34.88	1	1
HEMBA1005698	81.18	62.44	96.83	0.77	1.19
HEMBA1005699	43.73	29.98	43.73	0.91	1
HEMBA1005703	22.98	30.65	28.69	1	1
HEMBA1005705	80.17	81.2	98.18	1.01	1.22
HEMBA1005712	27.91	25.24	25	1	1
HEMBA1005717	26.32	22.89	31.51	1	1
HEMBA1005718	75.65	102.94	120.34	1.36	1.59
HEMBA1005721	143.77	170.19	201.45	1.18	1.4
HEMBA1005722	175.35	147.53	219.57	0.84	1.25
HEMBA1005724	22.96	24.34	31.28	1	1
HEMBA1005732	39.59	42.76	47.26	1.07	1.18
HEMBA1005737	13.7	18.75	18.51	1	1
HEMBA1005742	21.96	18.5	27.58	1	1
HEMBA1005746	30.47	25.8	32.38	1	1
HEMBA1005747	26.08	36.08	34.76	1	1
HEMBA1005749	75.71	83.98	91.4	1.11	1.21
HEMBA1005755	32.37	44.22	40.84	1.11	1.02
HEMBA1005760	55.92	58.01	59.67	1.04	1.07
HEMBA1005765	76.25	82.82	91.9	1.09	1.21
HEMBA1005766	1721.6	2117.83	1755.83	1.23	1.02
HEMBA1005780	51.15	47.75	61.92	0.93	1.21
HEMBA1005795	42.92	32.14	60.55	0.93	1.41
HEMBA1005809	112.7	114.55	128.25	1.02	1.14
HEMBA1005813	118.27	153.59	152.74	1.3	1.29
HEMBA1005815	25.93	31.46	27.65	1	1
HEMBA1005822	113.82	108.65	123.61	0.95	1.09
HEMBA1005829	54.92	49.17	65.71	0.9	1.2
HEMBA1005833	24.77	24.28	30.22	1	1
HEMBA1005834	67.28	78.69	79.45	1.17	1.18
HEMBA1005844	448.34	484.29	677.66	1.08	1.51
HEMBA1005852	64.77	55.85	79.64	0.86	1.23
HEMBA1005853	223.97	241.44	258.64	1.08	1.15
HEMBA1005878	107.8	114.1	115.09	1.06	1.07
HEMBA1005883	27.06	27.03	28.08	1	1
HEMBA1005884	33.02	39.71	28.59	1	1
HEMBA1005891	32.65	31.8	34.38	1	1
HEMBA1005894	177.83	189.9	180.04	1.07	1.01

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HEMBA1005898	76.61	56.72	72.07	0.74	0.94
HEMBA1005902	36.94	44.99	48.38	1.12	1.21
HEMBA1005907	33.89	35.42	39.01	1	1
HEMBA1005909	20	16.58	16.88	1	1
HEMBA1005911	70.18	71.57	70.9	1.02	1.01
HEMBA1005912	94.37	67.24	90.84	0.71	0.96
HEMBA1005913	26.53	26.21	24.78	1	1
HEMBA1005921	78.13	94.23	86.56	1.21	1.11
HEMBA1005922	38.98	26.59	44.41	1	1.11
HEMBA1005929	73.32	85.81	78.29	1.17	1.07
HEMBA1005931	73.87	75.36	71.89	1.02	0.97
HEMBA1005934	119.14	148.81	133.21	1.25	1.12
HEMBA1005945	45.96	49.87	33.79	1.09	0.87
HEMBA1005962	23.78	24.27	23.11	1	1
HEMBA1005963	20.69	19.85	22.33	1	1
HEMBA1005990	371.29	452.57	488.7	1.22	1.32
HEMBA1005991	76.4	71.65	72.05	0.94	0.94
HEMBA1005999	163.46	193.71	185.28	1.19	1.13
HEMBA1006002	51.91	49.46	53.43	0.95	1.03
HEMBA1006005	27.64	20.71	18.42	1	1
HEMBA1006011	201.51	134.93	163.98	0.67	0.81
HEMBA1006013	57.33	37.23	46.54	0.7	0.81
HEMBA1006016	32.96	43.07	31.14	1.08	1
HEMBA1006019	45.94	43.72	44.48	0.95	0.97
HEMBA1006021	45.05	35.48	38.09	0.89	0.89
HEMBA1006022	40.63	59.84	40.89	1.47	1.01
HEMBA1006031	25.51	30.4	22.42	1	1
HEMBA1006035	35.53	33.9	38.41	1	1
HEMBA1006036	73.66	64.8	77.95	0.88	1.06
HEMBA1006042	61.05	60.03	62.6	0.98	1.03
HEMBA1006044	20.84	19.57	18.21	1	1
HEMBA1006045	88.75	106.88	103.44	1.2	1.17
HEMBA1006048	34.99	44.21	45.99	1.11	1.15
HEMBA1006053	31.59	39.99	36.94	1	1
HEMBA1006055	33.06	32.62	34.27	1	1
HEMBA1006058	72.6	84.59	88.08	1.17	1.21
HEMBA1006063	121.72	103.02	118.87	0.85	0.98
HEMBA1006067	47.95	39.33	44.18	0.83	0.92
HEMBA1006081	19.04	26.31	17.66	1	1
HEMBA1006089	43.74	46.87	54.23	1.07	1.24
HEMBA1006090	24.5	20.39	27.83	1	1
HEMBA1006091	65.09	63.07	67.29	0.97	1.03
HEMBA1006093	25.42	35.02	31.19	1	1
HEMBA1006099	122.69	108.51	130	0.88	1.06
HEMBA1006100	177.95	191.4	199.76	1.08	1.12
HEMBA1006108	33.04	37.85	37.87	1	1

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HEMBA1006114	165.38	214.54	183.07	1.3	1.11
HEMBA1006121	28.68	36.78	29.75	1	1
HEMBA1006124	28.34	40.19	32.6	1	1
HEMBA1006125	151.17	145.16	199.95	0.96	1.32
HEMBA1006130	49.13	50.89	49.42	1.04	1.01
HEMBA1006138	164.35	155.97	188.72	0.95	1.15
HEMBA1006142	108.94	109.15	127.38	1	1.17
HEMBA1006150	161.32	199.53	172.3	1.24	1.07
HEMBA1006151	24.32	35.14	23.12	1	1
HEMBA1006155	19.86	19.43	21.29	1	1
HEMBA1006158	56.05	50.79	48.34	0.91	0.86
HEMBA1006164	77.61	101.9	103.33	1.31	1.33
HEMBA1006171	232.47	258.36	296.25	1.11	1.27
HEMBA1006173	769.5	879.52	703.94	1.14	0.91
HEMBA1006176	2196.9	1519.73	2623.29	0.69	1.19
HEMBA1006182	82.97	76.02	99.68	0.92	1.2
HEMBA1006197	57.65	73.65	66.57	1.28	1.15
HEMBA1006198	141.44	129.98	180.04	0.92	1.27
HEMBA1006213	27.45	30.62	35.14	1	1
HEMBA1006217	239.11	254.86	390.29	1.07	1.63
HEMBA1006226	194.44	274.68	387.17	1.41	1.99
HEMBA1006235	25.56	27.62	36.66	1	1
HEMBA1006248	32.99	49.78	64.95	1.24	1.62
HEMBA1006251	51.67	51.01	50.16	0.99	0.97
HEMBA1006252	41.55	37.43	58.37	0.96	1.4
HEMBA1006253	58.42	36.18	63.49	0.68	1.09
HEMBA1006259	46.71	59.59	66.45	1.28	1.42
HEMBA1006261	202.64	250.41	314.65	1.24	1.55
HEMBA1006268	47.6	76.51	48.48	1.61	1.02
HEMBA1006271	124.82	153.29	187.21	1.23	1.5
HEMBA1006272	35.83	28.27	48.23	1	1.21
HEMBA1006273	25.54	21.15	32.03	1	1
HEMBA1006276	39.52	30.49	62.37	1	1.56
HEMBA1006278	54.8	47.3	56.27	0.86	1.03
HEMBA1006283	59.01	53.07	66.08	0.9	1.12
HEMBA1006284	45.22	71.21	60.42	1.57	1.34
HEMBA1006291	21.82	22.91	28.59	1	1
HEMBA1006292	108.84	123.22	111.42	1.13	1.02
HEMBA1006293	18.72	17.29	23.98	1	1
HEMBA1006299	68.22	77.05	71.76	1.13	1.05
HEMBA1006309	48.02	55.3	55.94	1.15	1.16
HEMBA1006310	36.57	39.01	45.25	1	1.13
HEMBA1006311	45.43	36.61	42.9	0.88	0.94
HEMBA1006313	38.11	36.61	33.79	1	1
HEMBA1006316	42.07	50.95	43.14	1.21	1.03
HEMBA1006328	215.04	266.07	216.01	1.24	1

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HEMBA1006334	23.97	20.16	23.11	1	1
HEMBA1006335	231.03	212.95	229.29	0.92	0.99
HEMBA1006344	126.42	147.5	102.66	1.17	0.81
HEMBA1006347	31.39	29.8	39.13	1	1
HEMBA1006349	55.67	48.81	56.87	0.88	1.02
HEMBA1006352	36.85	37.05	36.62	1	1
HEMBA1006357	114.26	119.16	119.11	1.04	1.04
HEMBA1006358	62.64	58.47	47.39	0.93	0.76
HEMBA1006359	64.09	54.69	62.96	0.85	0.98
HEMBA1006360	30.97	21.85	25.81	1	1
HEMBA1006364	42.86	42.92	38.82	1	0.93
HEMBA1006377	127.2	113.19	117.55	0.89	0.92
HEMBA1006380	86.73	104.08	102.67	1.2	1.18
HEMBA1006381	96.01	83.46	72.37	0.87	0.75
HEMBA1006385	122.36	148.43	124.74	1.21	1.02
HEMBA1006390	162.49	159.79	141.6	0.98	0.87
HEMBA1006391	45.71	36.54	40.84	0.88	0.89
HEMBA1006398	40.34	35.01	26.12	0.99	0.99
HEMBA1006405	99.45	95.46	107.31	0.96	1.08
HEMBA1006410	66.36	38.84	64.23	0.6	0.97
HEMBA1006416	65.22	81.33	69.04	1.25	1.06
HEMBA1006418	95.02	125.03	122.14	1.32	1.29
HEMBA1006419	146.03	164.04	167.75	1.12	1.15
HEMBA1006421	42.14	42.91	39.72	1.02	0.95
HEMBA1006424	29.97	26.24	20.79	1	1
HEMBA1006426	84.9	95.57	85.37	1.13	1.01
HEMBA1006430	88.74	93.74	81.66	1.06	0.92
HEMBA1006438	58.04	60.13	58.13	1.04	1
HEMBA1006445	52.68	37.55	35.41	0.76	0.76
HEMBA1006446	28.35	26.35	32.68	1	1
HEMBA1006456	249.97	219.38	229.78	0.88	0.92
HEMBA1006461	87.29	85	88.5	0.97	1.01
HEMBA1006467	30.4	28.63	31.38	1	1
HEMBA1006470	347.33	351.67	353.51	1.01	1.02
HEMBA1006471	137.42	87.18	88.67	0.63	0.65
HEMBA1006474	1789.8	1430.88	1232.25	0.8	0.69
HEMBA1006476	2257.2	2770.26	2078.83	1.23	0.92
HEMBA1006482	2300.5	1981.59	2335.39	0.86	1.02
HEMBA1006483	57.11	64.18	55.52	1.12	0.97
HEMBA1006485	112.67	77.55	77.34	0.69	0.69
HEMBA1006486	137.38	90.05	136.42	0.66	0.99
HEMBA1006489	28.55	29.64	25.22	1	1
HEMBA1006492	74.33	84.86	79.89	1.14	1.07
HEMBA1006494	35.87	31.77	38.16	1	1
HEMBA1006497	28.48	33.13	35.42	1	1
HEMBA1006501	1322.8	1464.09	1151.57	1.11	0.87

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HEMBA1006502	203.78	205.79	199.07	1.01	0.98
HEMBA1006507	1257.6	1335.71	929.85	1.06	0.74
HEMBA1006517	47.07	56.05	44.11	1.19	0.94
HEMBA1006521	38.97	34.28	35.58	1	1
HEMBA1006529	53.22	88.78	67.94	1.67	1.28
HEMBA1006530	23.56	23.29	21.79	1	1
HEMBA1006535	21.7	30.27	31.61	1	1
HEMBA1006536	38.77	46.24	51.22	1.16	1.28
HEMBA1006540	35.87	35.11	34.6	1	1
HEMBA1006544	46.98	41.48	40.14	0.88	0.85
HEMBA1006546	82.24	58.56	71.79	0.71	0.87
HEMBA1006549	31.4	28.54	26.48	1	1
HEMBA1006559	26.52	29.33	28.36	1	1
HEMBA1006562	53.07	57.38	54	1.08	1.02
HEMBA1006566	16.88	19.7	20.05	1	1
HEMBA1006569	44.85	41.2	45.4	0.92	1.01
HEMBA1006572	24.35	16.83	24.86	1	1
HEMBA1006579	333.02	301.87	401.53	0.91	1.21
HEMBA1006583	106.57	90.73	118.88	0.85	1.12
HEMBA1006595	58.49	65.44	72.77	1.12	1.24
HEMBA1006597	74.88	99.8	90.56	1.33	1.21
HEMBA1006606	58.51	50.93	64.23	0.87	1.1
HEMBA1006612	53.34	56.72	71.12	1.06	1.33
HEMBA1006617	51.61	69.96	67.99	1.36	1.32
HEMBA1006624	190.29	188.59	254.65	0.99	1.34
HEMBA1006631	125.49	105.71	113.21	0.84	0.9
HEMBA1006635	35.22	49.25	41.72	1.23	1.04
HEMBA1006639	34.73	39.02	61.08	1	1.53
HEMBA1006643	20.9	15.82	39.18	1	1
HEMBA1006648	58.04	95.64	112.81	1.65	1.94
HEMBA1006652	84.3	114.62	98.96	1.36	1.17
HEMBA1006653	23.23	26.41	39.21	1	1
HEMBA1006658	84.91	105.27	118.94	1.24	1.4
HEMBA1006659	941.83	1067.73	1010.69	1.13	1.07
HEMBA1006665	30.47	32.49	29.34	1	1
HEMBA1006666	28.07	28.01	32.6	1	1
HEMBA1006671	74.34	97.94	97.83	1.32	1.32
HEMBA1006674	79.53	108.22	92.41	1.36	1.16
HEMBA1006676	58.58	44.49	61.1	0.76	1.04
HEMBA1006682	40.43	23.36	41.75	0.99	1.03
HEMBA1006688	59.27	57.63	50.54	0.97	0.85
HEMBA1006695	179.01	229.55	180.8	1.28	1.01
HEMBA1006696	38.89	45.83	40.59	1.15	1.01
HEMBA1006702	35.75	41.1	41.39	1.03	1.03
HEMBA1006707	50.69	49.87	48.91	0.98	0.96
HEMBA1006708	39	38.05	42.03	1	1.05

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HEMBA1006709	70.68	83.04	78.31	1.17	1.11
HEMBA1006717	38.12	36.77	49.45	1	1.24
HEMBA1006724	71.57	63.58	53.66	0.89	0.75
HEMBA1006731	47.63	40.89	39.82	0.86	0.84
HEMBA1006737	37.34	28.54	25.67	1	1
HEMBA1006742	46.8	59.11	50.27	1.26	1.07
HEMBA1006743	79.64	78.41	96.22	0.98	1.21
HEMBA1006744	97.31	123.15	112.9	1.27	1.16
HEMBA1006749	37.6	26.96	34.75	1	1
HEMBA1006752	262.94	259.84	207.32	0.99	0.79
HEMBA1006754	50.01	56.58	38.66	1.13	0.8
HEMBA1006758	31.72	39.79	30.71	1	1
HEMBA1006767	32.59	28.24	27.59	1	1
HEMBA1006770	45.76	36.32	39.83	0.87	0.87
HEMBA1006779	110.56	97.17	106.18	0.88	0.96
HEMBA1006780	103.83	138.11	127.08	1.33	1.22
HEMBA1006789	31.72	31.4	43.61	1	1.09
HEMBA1006795	74.38	86.15	67.66	1.16	0.91
HEMBA1006796	33.73	30.14	26.67	1	1
HEMBA1006805	49.79	62.87	59.15	1.26	1.19
HEMBA1006807	548.33	590.98	647.3	1.08	1.18
HEMBA1006813	8.39	11.05	8.41	1	1
HEMBA1006819	48.81	41.74	53.15	0.86	1.09
HEMBA1006821	67.17	58.94	65.94	0.88	0.98
HEMBA1006824	134.05	123.87	134.81	0.92	1.01
HEMBA1006832	879.78	794.16	837.41	0.9	0.95
HEMBA1006834	214.89	195.31	233.74	0.91	1.09
HEMBA1006835	76.09	66.54	70.44	0.87	0.93
HEMBA1006843	178.51	145.01	204.76	0.81	1.15
HEMBA1006849	97.85	90.86	92.39	0.93	0.94
HEMBA1006850	70.16	62.71	77.59	0.89	1.11
HEMBA1006861	194.04	239.06	193.48	1.23	1
HEMBA1006865	386.56	391.92	347.27	1.01	0.9
HEMBA1006867	79.38	60.98	80.49	0.77	1.01
HEMBA1006873	52.52	56.67	65.26	1.08	1.24
HEMBA1006877	27.89	25.52	34.04	1	1
HEMBA1006878	49.79	52.97	52.03	1.06	1.04
HEMBA1006879	81.48	83.18	87	1.02	1.07
HEMBA1006884	75.59	78.05	49.54	1.03	0.66
HEMBA1006885	108.4	116.23	124.06	1.07	1.14
HEMBA1006886	214.12	109.45	199.57	0.51	0.93
HEMBA1006889	34.16	36.64	43.52	1	1.09
HEMBA1006896	220.54	199.25	269.98	0.9	1.22
HEMBA1006900	107.14	70.06	100.64	0.65	0.94
HEMBA1006902	36.24	30.36	46.46	1	1.16
HEMBA1006912	131.15	168.96	176.75	1.29	1.35

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HEMBA1006914	146.34	169.19	176.67	1.16	1.21
HEMBA1006916	52.95	56.07	60.34	1.06	1.14
HEMBA1006921	36.5	34.51	36.7	1	1
HEMBA1006926	77.03	69.9	74.35	0.91	0.97
HEMBA1006927	44.25	40.49	39.14	0.92	0.9
HEMBA1006929	69.53	57.01	84.15	0.82	1.21
HEMBA1006936	55.75	51.71	50.1	0.93	0.9
HEMBA1006938	23.46	22.99	33.94	1	1
HEMBA1006941	120.09	148.4	171.2	1.24	1.43
HEMBA1006942	51.55	51.02	67.47	0.99	1.31
HEMBA1006945	147.67	133.57	162.14	0.9	1.1
HEMBA1006949	36.98	32	38.51	1	1
HEMBA1006952	26.21	16.38	20.43	1	1
HEMBA1006960	119.55	91.16	103.2	0.76	0.86
HEMBA1006973	46.84	41.23	42.76	0.88	0.91
HEMBA1006974	55.98	56.29	60.32	1.01	1.08
HEMBA1006976	19.82	21.32	28.22	1	1
HEMBA1006989	26.84	25.58	16.05	1	1
HEMBA1006993	182.72	200.99	251.9	1.1	1.38
HEMBA1006996	60.21	48.29	59.31	0.8	0.99
HEMBA1007001	85.98	92.33	107.02	1.07	1.24
HEMBA1007002	582.79	497.36	417.94	0.85	0.72
HEMBA1007013	36.06	36.09	53.33	1	1.33
HEMBA1007016	56.83	57.85	70.62	1.02	1.24
HEMBA1007017	16.8	14.66	24.57	1	1
HEMBA1007018	46.23	55.58	72.9	1.2	1.58
HEMBA1007044	15.5	24.82	26.92	1	1
HEMBA1007045	23.66	29.58	33.2	1	1
HEMBA1007051	49.75	61.27	61.22	1.23	1.23
HEMBA1007052	18.89	26.23	22.47	1	1
HEMBA1007053	16.28	18.78	25.93	1	1
HEMBA1007057	45.54	28.27	40.73	0.88	0.89
HEMBA1007062	28.01	29.68	46.11	1	1.15
HEMBA1007063	82.38	79.09	95.04	0.96	1.15
HEMBA1007066	31.73	30.67	38.83	1	1
HEMBA1007069	40.65	46.44	46.9	1.14	1.15
HEMBA1007073	47.03	42.88	39.88	0.91	0.85
HEMBA1007076	76.46	49.12	59.8	0.64	0.78
HEMBA1007078	199.02	221.44	236.05	1.11	1.19
HEMBA1007080	277.65	213.4	348.49	0.77	1.26
HEMBA1007084	62.45	60.83	76.19	0.97	1.22
HEMBA1007085	86.67	79.35	79.11	0.92	0.91
HEMBA1007087	57.7	48.94	58.87	0.85	1.02
HEMBA1007089	33.79	40.64	39.67	1.02	1
HEMBA1007095	716.73	458.74	659.39	0.64	0.92
HEMBA1007101	90.79	94.46	112.55	1.04	1.24

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HEMBA1007104	64.05	65.12	81.29	1.02	1.27
HEMBA1007106	83.77	71.95	100.73	0.86	1.2
HEMBA1007112	20.95	18.05	31.4	1	1
HEMBA1007113	78.2	88.7	92.61	1.13	1.18
HEMBA1007121	1670.9	2028.2	1526.93	1.21	0.91
HEMBA1007129	58.9	40.87	36.31	0.69	0.68
HEMBA1007147	75.4	83.08	80.12	1.1	1.06
HEMBA1007149	51.73	56.45	48.17	1.09	0.93
HEMBA1007151	36.86	35.04	42.02	1	1.05
HEMBA1007172	43.02	39.48	48.49	0.93	1.13
HEMBA1007174	31.78	28.19	39.4	1	1
HEMBA1007176	55.69	81.88	73.91	1.47	1.33
HEMBA1007178	59.85	45.52	70.37	0.76	1.18
HEMBA1007185	46.86	36.84	46.32	0.85	0.99
HEMBA1007186	62.4	50.3	58.62	0.81	0.94
HEMBA1007194	92.89	79.86	89.13	0.86	0.96
HEMBA1007200	61.75	37.17	67.35	0.65	1.09
HEMBA1007203	40.29	49.91	49.85	1.24	1.24
HEMBA1007206	116.15	103.23	122.05	0.89	1.05
HEMBA1007224	81.68	74.36	86.93	0.91	1.06
HEMBA1007226	739.66	812.15	601.79	1.1	0.81
HEMBA1007240	30.85	27.04	31.61	1	1
HEMBA1007241	25.15	19.41	19.22	1	1
HEMBA1007242	20.95	17.87	15.33	1	1
HEMBA1007243	1590.7	1699.25	1066.29	1.07	0.67
HEMBA1007251	23.4	22.06	27.03	1	1
HEMBA1007256	61.3	61.26	58.74	1	0.96
HEMBA1007267	83.81	92.15	112.23	1.1	1.34
HEMBA1007273	40.69	32.55	43.29	0.98	1.06
HEMBA1007279	67.04	66.24	62.74	0.99	0.94
HEMBA1007281	25.38	26.74	33.04	1	1
HEMBA1007283	51.41	38.12	56.01	0.78	1.09
HEMBA1007288	51.91	66.01	62.48	1.27	1.2
HEMBA1007291	38.95	29.21	29.93	1	1
HEMBA1007299	111.39	103.48	87.67	0.93	0.79
HEMBA1007300	92.24	50.39	49.42	0.55	0.54
HEMBA1007301	37.69	29.64	39.91	1	1
HEMBA1007319	41.53	37.23	37.78	0.96	0.96
HEMBA1007320	35.6	27.02	32.58	1	1
HEMBA1007322	530.56	428.04	604.38	0.81	1.14
HEMBA1007323	22.91	19.84	20.93	1	1
HEMBA1007326	157.13	256.76	242.08	1.63	1.54
HEMBA1007327	92.05	97.41	93.64	1.06	1.02
HEMBA1007332	63.18	56.21	66.34	0.89	1.05
HEMBA1007341	92.22	98.29	109.84	1.07	1.19
HEMBA1007342	19.93	23.16	29.38	1	1

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HEMBA1007347	81.68	60.66	72.94	0.74	0.89
HEMBA1007353	51.19	59.84	26.91	1.17	0.78
HEMBB1000005	57.19	66.16	57.45	1.16	1
HEMBB1000008	109.3	118.18	114.8	1.08	1.05
HEMBB1000018	167.05	137.19	171	0.82	1.02
HEMBB1000024	94.57	116.07	104.2	1.23	1.1
HEMBB1000025	37.67	30.41	43.75	1	1.09
HEMBB1000030	137.19	145.34	148.55	1.06	1.08
HEMBB1000036	68.1	46.9	71.59	0.69	1.05
HEMBB1000037	59.06	51.17	62.08	0.87	1.05
HEMBB1000039	51.06	58.76	53.76	1.15	1.05
HEMBB1000044	60.18	71.4	78.13	1.19	1.3
HEMBB1000048	42.59	46.3	51.73	1.09	1.21
HEMBB1000050	52.62	59.79	62.1	1.14	1.18
HEMBB1000054	83.36	101.52	82.18	1.22	0.99
HEMBB1000055	1317.1	1091.88	1374	0.83	1.04
HEMBB1000059	298.73	247.82	268.67	0.83	0.9
HEMBB1000072	1530	1479.03	1077.07	0.97	0.7
HEMBB1000081	76.48	76.79	72.27	1	0.94
HEMBB1000083	72.67	77.6	92.07	1.07	1.27
HEMBB1000089	77.88	93.51	103.34	1.2	1.33
HEMBB1000094	82.82	68.77	56.25	0.83	0.68
HEMBB1000097	42.72	43.11	39.53	1.01	0.94
HEMBB1000099	80.78	85.34	92.59	1.06	1.15
HEMBB1000103	240.15	222.89	227.09	0.93	0.95
HEMBB1000106	48.93	51.65	72.9	1.06	1.49
HEMBB1000113	33.03	33.87	43.48	1	1.09
HEMBB1000119	32.11	27.8	32.66	1	1
HEMBB1000133	276.3	245.83	374.07	0.89	1.35
HEMBB1000134	53.67	55.05	73.65	1.03	1.37
HEMBB1000136	95.97	118.8	115.71	1.24	1.21
HEMBB1000141	72.88	93.59	90.74	1.28	1.25
HEMBB1000144	36.76	52.21	52.43	1.31	1.31
HEMBB1000147	36.54	37.97	31.18	1	1
HEMBB1000152	17.09	24.92	34.4	1	1
HEMBB1000154	26.44	37.27	43.72	1	1.09
HEMBB1000155	76.37	77.11	83.34	1.01	1.09
HEMBB1000173	137.61	179.24	208.33	1.3	1.51
HEMBB1000175	49.86	51.17	61.2	1.03	1.23
HEMBB1000176	79.1	95.72	117.8	1.21	1.49
HEMBB1000198	22.26	20.15	26.86	1	1
HEMBB1000208	20.07	19.09	21.21	1	1
HEMBB1000209	31.14	31.8	36.87	1	1
HEMBB1000212	28.5	30.95	34.95	1	1
HEMBB1000215	64.1	69.03	70.81	1.08	1.1
HEMBB1000217	126.09	127.07	128.51	1.01	1.02

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HEMBB1000218	153.77	188.87	195.38	1.23	1.27
HEMBB1000226	71.68	76.69	73.04	1.07	1.02
HEMBB1000230	18.37	18.26	19.92	1	1
HEMBB1000240	22.74	28.44	20.91	1	1
HEMBB1000244	55.24	53.55	47.17	0.97	0.85
HEMBB1000250	8.93	11.82	11.43	1	1
HEMBB1000258	75.75	71.02	75.53	0.94	1
HEMBB1000264	91.56	119.36	138.69	1.3	1.51
HEMBB1000266	55.49	64.06	67.32	1.15	1.21
HEMBB1000272	98.32	91.75	76.63	0.93	0.78
HEMBB1000274	53.15	58.91	64.19	1.11	1.21
HEMBB1000276	26.14	21.51	25.75	1	1
HEMBB1000284	32.01	29.92	33.16	1	1
HEMBB1000307	46.61	44.56	51.49	0.96	1.1
HEMBB1000309	46.44	41.39	48.48	0.89	1.04
HEMBB1000312	76.78	69.08	85.39	0.9	1.11
HEMBB1000317	37.03	23.95	35.88	1	1
HEMBB1000318	61.31	70.38	46.57	1.15	0.76
HEMBB1000332	32.8	30.69	25.75	1	1
HEMBB1000335	47.43	46.59	54.83	0.98	1.16
HEMBB1000336	27.38	34.93	21.79	1	1
HEMBB1000337	79.48	81.43	80.87	1.02	1.02
HEMBB1000338	140.18	106.88	137.74	0.76	0.98
HEMBB1000339	103.9	152.22	126.74	1.47	1.22
HEMBB1000341	36.79	43.04	42.91	1.08	1.07
HEMBB1000343	130	160.36	121.55	1.23	0.94
HEMBB1000354	203.84	225	204.66	1.1	1
HEMBB1000358	19.65	18.45	17.79	1	1
HEMBB1000369	34.71	38.3	37.92	1	1
HEMBB1000373	32.63	25.25	42.46	1	1.06
HEMBB1000374	190.18	222.71	190.88	1.17	1
HEMBB1000376	95.05	116.77	117.74	1.23	1.24
HEMBB1000383	32.16	31.74	35.34	1	1
HEMBB1000391	108.55	84.34	90.98	0.78	0.84
HEMBB1000399	35.8	25.8	28.35	1	1
HEMBB1000402	61.34	35.9	38.85	0.65	0.65
HEMBB1000404	19.22	19.32	23.67	1	1
HEMBB1000407	53.68	45.64	42.74	0.85	0.8
HEMBB1000420	89.38	82.19	78.12	0.92	0.87
HEMBB1000430	321.41	266.82	280.69	0.83	0.87
HEMBB1000434	136.61	152	155.43	1.11	1.14
HEMBB1000438	21.68	29.13	29.65	1	1
HEMBB1000441	121.63	122.62	145.02	1.01	1.19
HEMBB1000447	232.61	183.92	234.47	0.79	1.01
HEMBB1000449	32.55	23.71	35.9	1	1
HEMBB1000453	116.82	93.5	121.29	0.8	1.04

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HEMBB1000455	119.59	104.77	79.92	0.88	0.67
HEMBB1000472	57.39	60.37	66.17	1.05	1.15
HEMBB1000480	71.36	80.49	88.4	1.13	1.24
HEMBB1000486	134.75	137.81	154.53	1.02	1.15
HEMBB1000487	40.78	42.41	42.74	1.04	1.05
HEMBB1000490	232.23	188.11	395.85	0.81	1.7
HEMBB1000491	77.18	109.79	92.42	1.42	1.2
HEMBB1000492	51.12	52.24	47.41	1.02	0.93
HEMBB1000493	43.28	58.21	61.51	1.34	1.42
HEMBB1000510	102.58	139.75	126	1.36	1.23
HEMBB1000516	32.96	43.33	44.13	1.08	1.1
HEMBB1000518	27.52	27.41	22.29	1	1
HEMBB1000523	91.19	84.79	101.27	0.93	1.11
HEMBB1000530	47.75	38.91	45.32	0.84	0.95
HEMBB1000542	64.84	47.56	63.01	0.73	0.97
HEMBB1000550	29.41	33.42	39.1	1	1
HEMBB1000554	197.92	218.42	242.94	1.1	1.23
HEMBB1000556	35.02	38.6	53.74	1	1.34
HEMBB1000564	79.26	72.47	58.63	0.91	0.74
HEMBB1000567	49.89	48.25	53.66	0.97	1.08
HEMBB1000569	712.18	479.07	738.28	0.67	1.04
HEMBB1000573	141.98	154.34	162.6	1.09	1.15
HEMBB1000575	120.37	123.61	125.81	1.03	1.05
HEMBB1000579	32.88	29.62	29.89	1	1
HEMBB1000585	57	50.39	59.8	0.88	1.05
HEMBB1000586	77.21	82.02	93.03	1.06	1.2
HEMBB1000589	56.79	59.99	75.39	1.06	1.33
HEMBB1000591	66.42	70.78	95.55	1.07	1.44
HEMBB1000592	19.28	13.47	21.28	1	1
HEMBB1000593	1619.6	1589.1	1454.16	0.98	0.9
HEMBB1000595	116.22	132.44	159.52	1.14	1.37
HEMBB1000598	73.47	85.73	105.19	1.17	1.43
HEMBB1000611	22.29	21.4	32.86	1	1
HEMBB1000617	90.29	126.5	148.98	1.4	1.65
HEMBB1000623	32.43	38.42	43.04	1	1.08
HEMBB1000630	14.71	17.73	27.53	1	1
HEMBB1000631	121.97	135.17	204.11	1.11	1.67
HEMBB1000632	106.57	132.95	161.15	1.25	1.51
HEMBB1000636	116.26	106.1	145.04	0.91	1.25
HEMBB1000637	438.57	531.3	620.72	1.21	1.42
HEMBB1000638	43.41	56.02	61.01	1.29	1.41
HEMBB1000642	121.04	167.85	221.23	1.39	1.83
HEMBB1000643	29.65	41.11	39.29	1.03	1
HEMBB1000649	84.51	118.77	119.83	1.41	1.42
HEMBB1000652	72.62	83.65	92.93	1.15	1.28
HEMBB1000655	12.02	17.77	18.7	1	1

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HEMBB1000665	15.09	23.39	20.82	1	1
HEMBB1000668	26.65	29.56	33.82	1	1
HEMBB1000671	79.24	139.27	156.56	1.76	1.98
HEMBB1000673	30.79	25.59	30.22	1	1
HEMBB1000679	22.54	26.71	27.35	1	1
HEMBB1000684	74.05	109.82	105.18	1.48	1.42
HEMBB1000692	14.74	10.72	16.85	1	1
HEMBB1000693	10.21	19.99	16.8	1	1
HEMBB1000705	72.16	105.33	74.07	1.46	1.03
HEMBB1000706	17.56	23.12	26.47	1	1
HEMBB1000709	78.92	121.25	118.45	1.54	1.5
HEMBB1000714	42.83	40.87	60.17	0.95	1.4
HEMBB1000725	43.89	36.35	31.19	0.91	0.91
HEMBB1000726	71.51	96.8	91.47	1.35	1.28
HEMBB1000729	44.04	39.88	43.72	0.91	0.99
HEMBB1000738	57.44	58.35	38.91	1.02	0.7
HEMBB1000749	118.34	150.21	175.52	1.27	1.48
HEMBB1000763	26.3	35.92	36.14	1	1
HEMBB1000770	111.79	158.96	143.21	1.42	1.28
HEMBB1000774	37.07	38.75	36.44	1	1
HEMBB1000777	66.33	81.52	69.84	1.23	1.05
HEMBB1000781	54.3	53.17	55.99	0.98	1.03
HEMBB1000788	25.28	22.69	19.82	1	1
HEMBB1000789	17.24	17.71	15.66	1	1
HEMBB1000790	64.58	78.2	73.56	1.21	1.14
HEMBB1000794	33.53	32.2	41.69	1	1.04
HEMBB1000807	30.13	30.58	33	1	1
HEMBB1000809	807.04	898	744.53	1.11	0.92
HEMBB1000810	46.1	58.09	42.39	1.26	0.92
HEMBB1000821	19.14	23.68	19.53	1	1
HEMBB1000822	26.86	24.81	19.65	1	1
HEMBB1000826	185.63	196.71	180.62	1.06	0.97
HEMBB1000827	51.36	54.88	46.53	1.07	0.91
HEMBB1000831	34.51	29.87	40.16	1	1
HEMBB1000835	144.12	231.94	176.43	1.61	1.22
HEMBB1000840	62.45	63.82	81.34	1.02	1.3
HEMBB1000848	99.68	123.69	111.08	1.24	1.11
HEMBB1000852	11.24	13.83	11.5	1	1
HEMBB1000857	54.24	46.38	51.26	0.86	0.95
HEMBB1000858	50	36.71	33.69	0.8	0.8
HEMBB1000867	68.5	85.51	71.5	1.25	1.04
HEMBB1000870	72.76	81.83	67.8	1.12	0.93
HEMBB1000876	43.35	49.98	46.2	1.15	1.07
HEMBB1000881	39.02	48.73	55.93	1.22	1.4
HEMBB1000883	27.77	27.83	32.89	1	1
HEMBB1000887	266.89	206.91	273.83	0.78	1.03

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HEMBB1000888	17.01	15.62	22.89	1	1
HEMBB1000890	137.74	161.89	115.78	1.18	0.84
HEMBB1000893	74.94	56.68	80.9	0.76	1.08
HEMBB1000900	20.11	30.62	30.2	1	1
HEMBB1000905	102.51	124.91	83.08	1.22	0.81
HEMBB1000908	78.02	96.72	70.96	1.24	0.91
HEMBB1000910	49.48	58.33	49.88	1.18	1.01
HEMBB1000913	46.72	50.63	52.5	1.08	1.12
HEMBB1000915	1235.1	1265.8	1596.28	1.02	1.29
HEMBB1000917	69.87	84.21	77.72	1.21	1.11
HEMBB1000927	15.28	21.63	16.34	1	1
HEMBB1000932	45.3	54.47	57.04	1.2	1.26
HEMBB1000933	136.08	158.95	162.12	1.17	1.19
HEMBB1000936	64.3	53.14	77.64	0.83	1.21
HEMBB1000939	68.9	76.02	84.43	1.1	1.23
HEMBB1000941	33.76	28.93	53.13	1	1.33
HEMBB1000947	35.6	29.13	35.69	1	1
HEMBB1000954	28.25	29.37	27.54	1	1
HEMBB1000959	63.24	88.65	77.46	1.4	1.22
HEMBB1000973	25.02	27.91	25.38	1	1
HEMBB1000975	16.17	19.83	18.15	1	1
HEMBB1000981	20.67	24.33	27.87	1	1
HEMBB1000985	42.97	44	49.41	1.02	1.15
HEMBB1000991	20.6	19.71	27.25	1	1
HEMBB1000996	100.51	115.97	153.69	1.15	1.53
HEMBB1001000	33.13	32.47	31.91	1	1
HEMBB1001004	14.02	13.99	23.74	1	1
HEMBB1001008	29.03	29.07	27.37	1	1
HEMBB1001011	28.26	27.11	28.64	1	1
HEMBB1001014	35.72	32.4	51.5	1	1.29
HEMBB1001020	53.84	59.19	61.08	1.1	1.13
HEMBB1001024	103.64	109.34	125.21	1.05	1.21
HEMBB1001026	119.18	76.31	81.91	0.64	0.69
HEMBB1001037	57.7	74.41	69.67	1.29	1.21
HEMBB1001042	14.13	15.47	21.5	1	1
HEMBB1001046	14.85	32.01	16.89	1	1
HEMBB1001047	39.94	47.76	56.41	1.19	1.41
HEMBB1001048	65.35	74.67	76.93	1.14	1.18
HEMBB1001051	28.42	37.58	37.86	1	1
HEMBB1001056	34.89	38.36	38.94	1	1
HEMBB1001058	39.94	48.58	50.58	1.21	1.26
HEMBB1001060	22.94	36.58	33.65	1	1
HEMBB1001063	27.68	28.29	27.17	1	1
HEMBB1001068	29.13	24.56	27.82	1	1
HEMBB1001082	54.37	76.72	82.56	1.41	1.52
HEMBB1001095	64.85	66.69	68.18	1.03	1.05

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HEMBB1001096	35.36	34.3	47.52	1	1.19
HEMBB1001101	70.64	76.12	108.45	1.08	1.54
HEMBB1001102	55.02	67.57	69.72	1.23	1.27
HEMBB1001104	31.97	34.94	53.24	1	1.33
HEMBB1001105	39.59	45.27	43.09	1.13	1.08
HEMBB1001112	1937.9	2340.04	1919.36	1.21	0.99
HEMBB1001113	119.22	209.57	183.19	1.76	1.54
HEMBB1001114	66.75	84.71	86.32	1.27	1.29
HEMBB1001115	125.29	189.44	185.24	1.51	1.48
HEMBB1001117	17.26	18.96	19.58	1	1
HEMBB1001119	21.66	26.01	29.87	1	1
HEMBB1001126	19.77	28.11	24.45	1	1
HEMBB1001133	49.05	49.8	45.99	1.02	0.94
HEMBB1001137	31.19	34.96	38.92	1	1
HEMBB1001142	154.22	227.21	222.73	1.47	1.44
HEMBB1001145	109.76	160.03	153.65	1.46	1.4
HEMBB1001151	86.89	104.79	83.56	1.21	0.96
HEMBB1001153	58.18	70.9	76.77	1.22	1.32
HEMBB1001158	90.29	81.21	81.82	0.9	0.91
HEMBB1001169	60.62	58.13	45.38	0.96	0.75
HEMBB1001170	14.32	18.12	14.61	1	1
HEMBB1001175	38.59	38.42	37.59	1	1
HEMBB1001177	77.78	88.34	87.47	1.14	1.12
HEMBB1001182	32.82	42.62	24.94	1.07	1
HEMBB1001192	80.28	76.99	77.01	0.96	0.96
HEMBB1001199	17.28	18.75	21.24	1	1
HEMBB1001200	26.94	35.48	20.73	1	1
HEMBB1001208	44.06	56.77	48.01	1.29	1.09
HEMBB1001209	63.56	67.06	62.58	1.06	0.98
HEMBB1001210	71.99	103.26	94.81	1.43	1.32
HEMBB1001215	73.3	58.01	87.59	0.79	1.19
HEMBB1001217	27.5	24.28	23.56	1	1
HEMBB1001218	73.09	74.04	61.15	1.01	0.84
HEMBB1001221	15.99	14.74	11.54	1	1
HEMBB1001224	67.43	59.78	51.21	0.89	0.76
HEMBB1001230	15.17	18.56	16.93	1	1
HEMBB1001234	174.88	139.37	127.94	0.8	0.73
HEMBB1001235	89.51	128.87	114.32	1.44	1.28
HEMBB1001237	111.1	109.23	147.82	0.98	1.33
HEMBB1001242	33.34	27.71	36.97	1	1
HEMBB1001244	13.8	13.89	25.16	1	1
HEMBB1001249	37.6	39.46	46.29	1	1.16
HEMBB1001253	38.5	21.7	24.93	1	1
HEMBB1001254	28.55	27.23	28.37	1	1
HEMBB1001266	16.64	22.02	23.99	1	1
HEMBB1001267	149.8	192.98	138.61	1.29	0.93

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HEMBB1001271	88.15	79.26	86.96	0.9	0.99
HEMBB1001282	32.03	31.05	30.41	1	1
HEMBB1001287	419.44	318.76	528.38	0.76	1.26
HEMBB1001288	38.98	33.86	42.84	1	1.07
HEMBB1001289	70.66	73.29	75.6	1.04	1.07
HEMBB1001290	31.62	26.06	34.42	1	1
HEMBB1001294	91.96	98.71	69.25	1.07	0.75
HEMBB1001299	96.72	92.49	107.77	0.96	1.11
HEMBB1001302	29.26	31.92	32.51	1	1
HEMBB1001304	14.82	18.15	15.52	1	1
HEMBB1001314	15.41	18.59	23.2	1	1
HEMBB1001315	14.94	10.56	13.85	1	1
HEMBB1001317	58.3	58.02	73.81	1	1.27
HEMBB1001326	16.42	24.59	29.89	1	1
HEMBB1001331	45.9	52.43	52.18	1.14	1.14
HEMBB1001335	25.08	25.49	26.94	1	1
HEMBB1001337	66.68	73.29	86.76	1.1	1.3
HEMBB1001339	34.17	39.93	38.51	1	1
HEMBB1001344	16.27	18.45	19.11	1	1
HEMBB1001346	85.3	73.62	90.05	0.86	1.06
HEMBB1001348	36.51	41.63	44.53	1.04	1.11
HEMBB1001350	15.34	23.05	24.69	1	1
HEMBB1001356	22.63	23.4	28.24	1	1
HEMBB1001364	20.61	23.66	24.07	1	1
HEMBB1001366	50.22	53.62	56.58	1.07	1.13
HEMBB1001367	69.9	76.44	83.78	1.09	1.2
HEMBB1001369	26.44	22.55	27.62	1	1
HEMBB1001380	171.26	143.01	162.1	0.84	0.95
HEMBB1001381	73.48	74.31	73.18	1.01	1
HEMBB1001384	44.03	64.21	59.91	1.46	1.36
HEMBB1001387	20.53	24.62	28.6	1	1
HEMBB1001394	42.51	51.55	39.96	1.21	0.94
HEMBB1001407	15.57	7.66	12.38	1	1
HEMBB1001410	14.03	15.55	15.55	1	1
HEMBB1001413	47.83	55.28	67.45	1.16	1.41
HEMBB1001419	64.89	77.57	88.76	1.2	1.37
HEMBB1001421	66.7	50.13	88.74	0.75	1.33
HEMBB1001424	10.11	11.01	13.13	1	1
HEMBB1001426	54.99	65.14	98.53	1.18	1.79
HEMBB1001429	62.79	72.71	103.33	1.16	1.65
HEMBB1001436	45.79	72.64	65.4	1.59	1.43
HEMBB1001443	76.47	69.58	89.55	0.91	1.17
HEMBB1001449	56.36	79.77	85.76	1.42	1.52
HEMBB1001454	31.29	46.07	43.57	1.15	1.09
HEMBB1001458	33.09	34.75	41.94	1	1.05
HEMBB1001461	29.16	27.23	33.16	1	1

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HEMBB1001463	72.24	90.46	104.02	1.25	1.44
HEMBB1001464	23.46	21.78	37.99	1	1
HEMBB1001466	16.1	19.74	19.07	1	1
HEMBB1001482	17.83	20.35	28.05	1	1
HEMBB1001500	15.7	22.21	24.09	1	1
HEMBB1001505	94.04	100.71	142.94	1.07	1.52
HEMBB1001521	103.43	145.17	124.1	1.4	1.2
HEMBB1001527	131.08	140.61	151.25	1.07	1.15
HEMBB1001530	36.09	36.05	49.12	1	1.23
HEMBB1001531	33.37	48.83	53.23	1.22	1.33
HEMBB1001532	28.14	26.34	28.19	1	1
HEMBB1001535	57.33	59.45	67.05	1.04	1.17
HEMBB1001536	70.64	87.3	85.56	1.24	1.21
HEMBB1001537	74.37	83.2	97.94	1.12	1.32
HEMBB1001542	40.51	31.55	41.06	0.99	1.01
HEMBB1001543	43.2	62.46	50.41	1.45	1.17
HEMBB1001547	18.22	16.49	23.58	1	1
HEMBB1001548	88.24	78.53	93.21	0.89	1.06
HEMBB1001551	36.53	30.82	31.09	1	1
HEMBB1001555	94.63	117.35	103.49	1.24	1.09
HEMBB1001562	42.29	46.25	50.21	1.09	1.19
HEMBB1001564	2416.1	2403.39	2489.42	0.99	1.03
HEMBB1001565	47.78	61.12	56.85	1.28	1.19
HEMBB1001569	40.38	38.64	43.67	0.99	1.08
HEMBB1001573	91.13	87.69	118.66	0.96	1.3
HEMBB1001585	58.7	70.42	71.28	1.2	1.21
HEMBB1001586	34.52	35.37	47.59	1	1.19
HEMBB1001588	130.12	154.25	147.73	1.19	1.14
HEMBB1001595	39.93	38.52	30.87	1	1
HEMBB1001596	21.79	17.7	27.27	1	1
HEMBB1001599	20.62	12.88	23.14	1	1
HEMBB1001603	28.41	32.46	35.47	1	1
HEMBB1001606	19.58	23.2	23.14	1	1
HEMBB1001612	104.65	107.67	111.6	1.03	1.07
HEMBB1001618	53.27	69.19	57.77	1.3	1.08
HEMBB1001619	185.35	220.52	184.44	1.19	1
HEMBB1001623	26.47	34.01	20.65	1	1
HEMBB1001625	22.27	24.39	26.92	1	1
HEMBB1001630	29.24	29.43	26.37	1	1
HEMBB1001635	27.09	32.68	26.69	1	1
HEMBB1001637	54.41	61.98	51.91	1.14	0.95
HEMBB1001641	19.29	25.96	30.67	1	1
HEMBB1001653	73.78	65.14	76.15	0.88	1.03
HEMBB1001665	16.57	18.46	22.14	1	1
HEMBB1001666	31.84	32.58	24.43	1	1
HEMBB1001667	38.86	23.96	25.41	1	1

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HEMBB1001668	21.49	29.6	22.85	1	1
HEMBB1001669	28.36	21.28	22.1	1	1
HEMBB1001670	51.71	46.68	59.09	0.9	1.14
HEMBB1001673	37.71	41.67	47.94	1.04	1.2
HEMBB1001675	28.06	22.86	29.91	1	1
HEMBB1001679	24.36	22.13	26.54	1	1
HEMBB1001684	34.74	24.6	35.34	1	1
HEMBB1001685	50.59	43.26	73.56	0.86	1.45
HEMBB1001695	13.35	12.25	11.06	1	1
HEMBB1001703	60.44	91.94	70.43	1.52	1.17
HEMBB1001704	82.46	97.18	95.24	1.18	1.15
HEMBB1001706	83.37	117.2	106.73	1.41	1.28
HEMBB1001707	61.04	73.44	81.82	1.2	1.34
HEMBB1001717	39.68	52.71	51.1	1.32	1.28
HEMBB1001731	227.77	174.99	294.71	0.77	1.29
HEMBB1001734	85.8	69.09	61.64	0.81	0.72
HEMBB1001735	35.46	40.72	32.35	1.02	1
HEMBB1001736	111.13	114.46	99.96	1.03	0.9
HEMBB1001747	28.25	30.44	34.85	1	1
HEMBB1001749	108.55	128.31	133.78	1.18	1.23
HEMBB1001753	174.76	181.17	163.68	1.04	0.94
HEMBB1001756	53.47	55.22	43.62	1.03	0.82
HEMBB1001757	33.26	33.55	33.65	1	1
HEMBB1001760	29.47	27.29	21.28	1	1
HEMBB1001762	24.71	24.07	23.26	1	1
HEMBB1001780	101.85	121.84	104.01	1.2	1.02
HEMBB1001785	19.76	25.8	20.32	1	1
HEMBB1001788	71.19	76.95	91.78	1.08	1.29
HEMBB1001793	107.24	130.17	151.56	1.21	1.41
HEMBB1001797	31.63	35.13	38.46	1	1
HEMBB1001802	582.82	495.71	564.82	0.85	0.97
HEMBB1001812	130.02	154.31	156.09	1.19	1.2
HEMBB1001815	329.05	251.94	348.74	0.77	1.06
HEMBB1001816	87.87	108.75	117.81	1.24	1.34
HEMBB1001831	24.56	22.28	25.02	1	1
HEMBB1001834	4642.6	3710.98	3077.01	0.8	0.66
HEMBB1001836	155.09	188.11	192.34	1.21	1.24
HEMBB1001839	13.4	10.71	14.97	1	1
HEMBB1001841	128.1	101.32	161.52	0.79	1.26
HEMBB1001844	64.7	67.28	95.48	1.04	1.48
HEMBB1001847	100.34	97.67	105.69	0.97	1.05
HEMBB1001848	159.62	172.01	173.93	1.08	1.09
HEMBB1001850	48.27	54.22	57.24	1.12	1.19
HEMBB1001859	92.79	111.95	122.61	1.21	1.32
HEMBB1001863	107.69	137.37	149.04	1.28	1.38
HEMBB1001867	23.27	19.58	31.26	1	1

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HEMBB1001868	19.92	15.65	17.69	1	1
HEMBB1001869	53.45	74.68	65.05	1.4	1.22
HEMBB1001872	15.58	14.62	18.91	1	1
HEMBB1001874	12.68	14.64	32.88	1	1
HEMBB1001875	19.14	16.27	28.06	1	1
HEMBB1001880	64.42	64.66	86.26	1	1.34
HEMBB1001899	23.8	25	27.85	1	1
HEMBB1001903	35.02	65.12	66.61	1.63	1.67
HEMBB1001905	38.95	47.46	42.15	1.19	1.05
HEMBB1001906	24.03	21.97	25.04	1	1
HEMBB1001908	38.72	32.45	50.8	1	1.27
HEMBB1001910	53.91	57.53	56.52	1.07	1.05
HEMBB1001911	58.61	65.63	76.92	1.12	1.31
HEMBB1001915	27.02	33.13	25.95	1	1
HEMBB1001921	83.08	130.77	96.88	1.57	1.17
HEMBB1001922	46.48	57.84	57.09	1.24	1.23
HEMBB1001925	63	71.85	57.59	1.14	0.91
HEMBB1001930	10.72	15.27	14.73	1	1
HEMBB1001944	99.93	110.88	118.51	1.11	1.19
HEMBB1001945	18.8	20.04	21.84	1	1
HEMBB1001947	22.24	25.63	30.26	1	1
HEMBB1001950	41.78	59.71	67.72	1.43	1.62
HEMBB1001952	41.88	46.24	56.15	1.1	1.34
HEMBB1001953	74.15	84.35	68.08	1.14	0.92
HEMBB1001957	36.9	41.13	47.59	1.03	1.19
HEMBB1001959	30.03	29.41	28.99	1	1
HEMBB1001962	42.35	42.73	45.14	1.01	1.07
HEMBB1001967	83.92	92.43	100.36	1.1	1.2
HEMBB1001973	152.67	174.78	199.04	1.14	1.3
HEMBB1001978	45.74	65.26	65.19	1.43	1.43
HEMBB1001983	258.71	323.73	294.81	1.25	1.14
HEMBB1001987	31.95	46.82	41.53	1.17	1.04
HEMBB1001988	20.41	35.61	26.45	1	1
HEMBB1001990	64.25	52.7	66.13	0.82	1.03
HEMBB1001996	16.43	14.96	15.12	1	1
HEMBB1001997	76.92	97.16	85.13	1.26	1.11
HEMBB1001999	180.01	173.11	234.29	0.96	1.3
HEMBB1002002	31.88	40.79	40.58	1.02	1.01
HEMBB1002005	99.52	121.19	111.38	1.22	1.12
HEMBB1002009	22.42	22.96	24.92	1	1
HEMBB1002013	22.19	20.11	12.6	1	1
HEMBB1002015	38.57	32.14	52.41	1	1.31
HEMBB1002024	243.3	254.6	284.25	1.05	1.17
HEMBB1002035	37.52	44.6	40.17	1.12	1
HEMBB1002039	47.67	58.57	48.53	1.23	1.02
HEMBB1002041	127.13	143.91	152.63	1.13	1.2

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HEMBB1002042	154.54	163.56	178.51	1.06	1.16
HEMBB1002043	72.46	75.82	97	1.05	1.34
HEMBB1002044	17.24	15.51	18.1	1	1
HEMBB1002045	98.34	87.64	102.2	0.89	1.04
HEMBB1002049	32.4	37.78	33.9	1	1
HEMBB1002050	54.46	75.81	73.59	1.39	1.35
HEMBB1002051	33.04	38.18	42.06	1	1.05
HEMBB1002068	15.75	31.23	28.8	1	1
HEMBB1002069	131.41	166.12	180.05	1.26	1.37
HEMBB1002075	46.06	43.3	54.43	0.94	1.18
HEMBB1002079	15.66	14.19	21.42	1	1
HEMBB1002080	52.15	37.47	68.67	0.77	1.32
HEMBB1002082	31.89	25.21	29.19	1	1
HEMBB1002084	62.5	72.46	56.82	1.16	0.91
HEMBB1002088	197.89	188.34	224.69	0.95	1.14
HEMBB1002092	66.56	87.6	82.43	1.32	1.24
HEMBB1002094	91.56	127.86	111.14	1.4	1.21
HEMBB1002103	61.83	54.9	60.97	0.89	0.99
HEMBB1002109	48.27	43.16	49.47	0.89	1.02
HEMBB1002115	857.39	822.35	823.07	0.96	0.96
HEMBB1002120	22.84	31.18	14.06	1	1
HEMBB1002121	14.42	28.53	17.26	1	1
HEMBB1002134	3160.4	2063.94	1503.86	0.65	0.48
HEMBB1002136	32.71	34.06	29.63	1	1
HEMBB1002138	104.95	97.39	111.19	0.93	1.06
HEMBB1002139	60.25	63.72	74.93	1.06	1.24
HEMBB1002141	65.38	51.79	81.86	0.79	1.25
HEMBB1002142	62.23	77.64	79.89	1.25	1.28
HEMBB1002145	16.46	17.63	21.94	1	1
HEMBB1002152	54.41	64.9	49.38	1.19	0.91
HEMBB1002162	61.42	78.05	69.51	1.27	1.13
HEMBB1002173	68.41	64.52	53.57	0.94	0.78
HEMBB1002189	136.72	167.57	164.55	1.23	1.2
HEMBB1002190	139.28	145.12	157.03	1.04	1.13
HEMBB1002193	24.18	31.41	40.95	1	1.02
HEMBB1002217	56.58	64.06	69.33	1.13	1.23
HEMBB1002218	94.72	110.13	105.73	1.16	1.12
HEMBB1002228	47.66	54.29	54.62	1.14	1.15
HEMBB1002232	48.01	43.11	53.29	0.9	1.11
HEMBB1002245	11.99	15.52	21.46	1	1
HEMBB1002247	16.26	18.68	16.94	1	1
HEMBB1002249	100.78	117.71	157.81	1.17	1.57
HEMBB1002254	61.71	51.83	73.55	0.84	1.19
HEMBB1002255	43.98	23.05	26.61	0.91	0.91
HEMBB1002266	9.14	12.33	12.6	1	1
HEMBB1002271	508.25	501.52	568.22	0.99	1.12

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HEMBB1002280	24.18	33.34	31.01	1	1
HEMBB1002296	86.16	100.21	127.77	1.16	1.48
HEMBB1002300	17.71	19.09	24.93	1	1
HEMBB1002302	30.05	23.46	33.42	1	1
HEMBB1002306	40.13	58	60.38	1.45	1.5
HEMBB1002316	16.69	17.28	23.77	1	1
HEMBB1002326	81.83	99.4	119.99	1.21	1.47
HEMBB1002327	35.54	38.54	48.52	1	1.21
HEMBB1002329	30.07	31.66	36.11	1	1
HEMBB1002340	24.11	29.9	35.58	1	1
HEMBB1002342	129.57	130.41	177.97	1.01	1.37
HEMBB1002358	61.43	80.15	95.03	1.3	1.55
HEMBB1002359	58.57	64.77	77.76	1.11	1.33
HEMBB1002364	54.51	51.22	59.19	0.94	1.09
HEMBB1002366	214	214.42	298.38	1	1.39
HEMBB1002371	14.46	16.02	21.36	1	1
HEMBB1002381	52.02	57.2	76.43	1.1	1.47
HEMBB1002383	49.37	62.28	51.75	1.26	1.05
HEMBB1002387	23.32	20.99	27.12	1	1
HEMBB1002409	506.66	605.69	558.23	1.2	1.1
HEMBB1002413	149.03	166.79	171.59	1.12	1.15
HEMBB1002415	35.44	43.47	41.67	1.09	1.04
HEMBB1002424	22.24	21.25	24.67	1	1
HEMBB1002425	135.36	149.68	142.03	1.11	1.05
HEMBB1002427	46.13	49.89	59.65	1.08	1.29
HEMBB1002442	99.28	114.08	117.75	1.15	1.19
HEMBB1002447	77.99	93.46	83.09	1.2	1.07
HEMBB1002453	82.49	90.51	96.94	1.1	1.18
HEMBB1002457	73.38	81.14	82.29	1.11	1.12
HEMBB1002458	19.51	25.3	26.65	1	1
HEMBB1002463	116.77	98.82	130.07	0.85	1.11
HEMBB1002465	33.87	23.1	30.42	1	1
HEMBB1002477	27.07	36.38	35.32	1	1
HEMBB1002479	2900.8	2377.52	3071.06	0.82	1.06
HEMBB1002489	35.79	25.02	32.47	1	1
HEMBB1002492	22.69	23.51	21.81	1	1
HEMBB1002495	74.11	53.94	51.34	0.73	0.69
HEMBB1002502	35.08	33.32	27.37	1	1
HEMBB1002509	19.41	17.15	21.35	1	1
HEMBB1002510	14.26	10.08	9.56	1	1
HEMBB1002520	101.31	137.34	151.37	1.36	1.49
HEMBB1002522	36.29	34.97	34.07	1	1
HEMBB1002527	77.04	76.11	70.59	0.99	0.92
HEMBB1002530	26.36	27.7	24.52	1	1
HEMBB1002531	11.96	12.25	14.9	1	1
HEMBB1002534	83.5	67.59	84.95	0.81	1.02

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HEMBB1002536	464.77	496.27	321.57	1.07	0.69
HEMBB1002544	58.71	57.24	77	0.97	1.31
HEMBB1002545	54.36	85.62	71.58	1.58	1.32
HEMBB1002550	21.32	24.29	26.21	1	1
HEMBB1002556	170.5	165.4	179.56	0.97	1.05
HEMBB1002571	150.91	139.67	146.79	0.93	0.97
HEMBB1002579	61.93	68.98	62.63	1.11	1.01
HEMBB1002582	76.28	87.18	70.47	1.14	0.92
HEMBB1002584	27.06	24.61	29.19	1	1
HEMBB1002587	126.78	104.89	111.57	0.83	0.88
HEMBB1002590	77.71	96.19	88.97	1.24	1.14
HEMBB1002596	79.69	93.93	93.8	1.18	1.18
HEMBB1002600	48.29	48.15	59.2	1	1.23
HEMBB1002601	76.17	78.03	72.28	1.02	0.95
HEMBB1002603	63.58	58.02	64.41	0.91	1.01
HEMBB1002607	50.88	53.82	46.96	1.06	0.92
HEMBB1002610	40.81	24.85	39.15	0.98	0.98
HEMBB1002613	84.13	73.88	79.6	0.88	0.95
HEMBB1002614	55.77	65.17	56.78	1.17	1.02
HEMBB1002615	32.1	41.61	32.84	1.04	1
HEMBB1002617	43.98	56.91	54.95	1.29	1.25
HEMBB1002623	61.69	51.24	65.34	0.83	1.06
HEMBB1002624	114.08	103.2	134.52	0.9	1.18
HEMBB1002631	26.27	25.91	24.77	1	1
HEMBB1002635	59.87	85.52	66.59	1.43	1.11
HEMBB1002644	139.11	158.91	142.7	1.14	1.03
HEMBB1002654	52.89	70.6	61.87	1.33	1.17
HEMBB1002661	70.84	52.78	50.31	0.75	0.71
HEMBB1002663	81.54	98.17	92.68	1.2	1.14
HEMBB1002664	100.14	100.11	92.32	1	0.92
HEMBB1002677	21.57	13.57	24.4	1	1
HEMBB1002683	108.83	136.61	116.97	1.26	1.07
HEMBB1002684	39.36	55.34	44.35	1.38	1.11
HEMBB1002686	24.6	22.07	27.4	1	1
HEMBB1002692	35.51	37.14	46.88	1	1.17
HEMBB1002693	174.54	185.71	206.77	1.06	1.18
HEMBB1002697	34.66	43.25	36.12	1.08	1
HEMBB1002699	90.85	98.78	97.19	1.09	1.07
HEMBB1002702	35.47	35.8	38.5	1	1
HEMBB1002705	82.62	60.19	70.82	0.73	0.86
HEMBB1002712	34.6	35.18	32.31	1	1
IMR321000028	26.43	23.98	31.41	1	1
IMR321000031	38.71	53.74	50.35	1.34	1.26
IMR321000034	229.65	237.36	269.41	1.03	1.17
IMR321000039	137.21	86.65	176.38	0.63	1.29
IMR321000044	5.53	5.51	9.28	1	1

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IMR321000063	449.64	312.4	473.91	0.69	1.05
IMR321000085	228.02	247.44	291.45	1.09	1.28
IMR321000089	26.07	22.18	35.91	1	1
IMR321000091	82.21	68.33	89.36	0.83	1.09
LIVER1000004	789.21	977.7	936.93	1.24	1.19
LIVER1000008	11.78	16.57	20.04	1	1
LIVER1000011	193.38	153.19	255.98	0.79	1.32
LIVER1000022	78.18	73.59	116.09	0.94	1.48
LIVER1000025	91.35	117.4	141.4	1.29	1.55
LIVER1000030	20.21	20.08	20.87	1	1
LIVER1000045	19.25	18.24	28.01	1	1
LIVER1000046	16.05	22.11	31.24	1	1
LIVER1000072	66.61	60.53	67.94	0.91	1.02
LIVER1000077	30.05	33.76	50.02	1	1.25
LIVER1000080	25.97	34.88	44.41	1	1.11
LIVER1000086	1565.3	1521.72	1599.4	0.97	1.02
LIVER1000092	38.68	48.54	49.31	1.21	1.23
LIVER1000095	14.08	10.56	25.15	1	1
LIVER1000097	51.26	31.34	52.84	0.78	1.03
LIVER1000098	24.13	24.78	31.17	1	1
LIVER1000100	42.58	45.39	52.33	1.07	1.23
LIVER1000101	18.77	13.86	19.76	1	1
LIVER1000106	9.93	7.64	11.86	1	1
LIVER1000108	81.22	77.63	106.3	0.96	1.31
LIVER1000115	63.17	81.27	65.78	1.29	1.04
LIVER1000120	24.34	20.44	29.34	1	1
LIVER1000138	22.43	16.05	23.85	1	1
LIVER1000146	75.52	89.3	103.41	1.18	1.37
LIVER1000148	15.97	20.61	22.81	1	1
LIVER1000157	292.6	254.48	264.66	0.87	0.9
LIVER1000161	18.02	17.63	18.27	1	1
LIVER1000167	136.18	116.28	107.84	0.85	0.79
LIVER1000174	17.38	20.25	15.52	1	1
LIVER1000185	25.51	26.27	35.78	1	1
LIVER1000187	32.1	20.92	31.14	1	1
LIVER1000190	22.76	21.48	25.48	1	1
LIVER1000192	24.43	19.22	24.96	1	1
MAMMA1000009	69.7	85.49	89.43	1.23	1.28
MAMMA1000015	60.76	69.14	62.3	1.14	1.03
MAMMA1000019	48.99	44.67	46.39	0.91	0.95
MAMMA1000020	96.56	91.16	88.5	0.94	0.92
MAMMA1000024	25.06	26.11	27.75	1	1
MAMMA1000025	99.11	110.53	110.71	1.12	1.12
MAMMA1000043	121.02	170.89	142.18	1.41	1.17
MAMMA1000045	28.59	32.78	35.67	1	1
MAMMA1000046	44.13	42.12	42.99	0.95	0.97

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MAMMA1000055	40.22	41.24	36.01	1.03	0.99
MAMMA1000057	161.73	194.84	175.78	1.2	1.09
MAMMA1000060	291.4	210.32	271.7	0.72	0.93
MAMMA1000069	35.81	33.15	36.22	1	1
MAMMA1000084	114.03	106.93	111.12	0.94	0.97
MAMMA1000085	43.33	58.01	75.93	1.34	1.75
MAMMA1000092	57.19	75.89	64.44	1.33	1.13
MAMMA1000096	42.82	40.28	49.85	0.94	1.16
MAMMA1000097	42.53	33.83	38.68	0.94	0.94
MAMMA1000102	81.65	99.16	83.23	1.21	1.02
MAMMA1000103	42.11	37.74	47.16	0.95	1.12
MAMMA1000106	62.58	61.22	63.47	0.98	1.01
MAMMA1000117	66.99	39.66	34.24	0.6	0.6
MAMMA1000118	25.07	29.4	30.08	1	1
MAMMA1000129	38.75	39.15	52.64	1	1.32
MAMMA1000133	32.65	39.44	37.83	1	1
MAMMA1000134	63.77	64.83	88.01	1.02	1.38
MAMMA1000139	44.14	39.4	40.55	0.91	0.92
MAMMA1000141	43.18	34.69	38.35	0.93	0.93
MAMMA1000143	41.08	31.74	52.28	0.97	1.27
MAMMA1000150	38.43	39.44	37.59	1	1
MAMMA1000155	108.1	136.51	115.14	1.26	1.07
MAMMA1000163	52.95	43.36	48.01	0.82	0.91
MAMMA1000171	85.1	94.99	106.68	1.12	1.25
MAMMA1000173	83.44	81.65	108.07	0.98	1.3
MAMMA1000175	47.92	24.82	29.47	0.83	0.83
MAMMA1000183	70.5	79.77	55.11	1.13	0.78
MAMMA1000191	182.99	198.74	232.45	1.09	1.27
MAMMA1000192	84.79	90.13	71.73	1.06	0.85
MAMMA1000193	14.45	14.31	18.14	1	1
MAMMA1000198	91.45	124.27	126.6	1.36	1.38
MAMMA1000204	113.18	114.52	133	1.01	1.18
MAMMA1000207	40.29	27.8	25.73	0.99	0.99
MAMMA1000214	69.38	52.25	88.97	0.75	1.28
MAMMA1000220	149.2	142.85	157.09	0.96	1.05
MAMMA1000221	25.6	29.23	25.67	1	1
MAMMA1000226	17.74	17.54	16.59	1	1
MAMMA1000227	80.09	88.2	92.52	1.1	1.16
MAMMA1000230	56.5	49.07	55.35	0.87	0.98
MAMMA1000241	144.42	164.35	199.06	1.14	1.38
MAMMA1000245	2016.8	1292.45	1737.36	0.64	0.86
MAMMA1000248	211.46	211.41	221.96	1	1.05
MAMMA1000251	71.02	75.25	69.37	1.06	0.98
MAMMA1000254	43.16	44.31	43.38	1.03	1.01
MAMMA1000257	348.53	336.17	304.96	0.96	0.87
MAMMA1000262	149.97	155.35	172.25	1.04	1.15

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MAMMA1000264	50.09	69.7	77.41	1.39	1.55
MAMMA1000266	42.19	53.01	62.54	1.26	1.48
MAMMA1000270	110.29	123.04	119.59	1.12	1.08
MAMMA1000271	65.91	71.69	92.57	1.09	1.4
MAMMA1000277	31.88	41.41	51.95	1.04	1.3
MAMMA1000278	27.39	28.41	31.86	1	1
MAMMA1000279	76.59	72.3	86.05	0.94	1.12
MAMMA1000283	12.23	18.73	26.04	1	1
MAMMA1000284	61.7	80.62	89.85	1.31	1.46
MAMMA1000287	117.81	159.92	176.65	1.36	1.5
MAMMA1000294	51.27	62.36	84.78	1.22	1.65
MAMMA1000298	19.88	31.82	29	1	1
MAMMA1000302	43.09	48.77	59.12	1.13	1.37
MAMMA1000303	22.93	25.44	35.42	1	1
MAMMA1000305	56.48	48.44	66.38	0.86	1.18
MAMMA1000307	122.05	123.68	154.96	1.01	1.27
MAMMA1000309	26.05	29.95	34.22	1	1
MAMMA1000312	20.73	19.63	24.38	1	1
MAMMA1000313	21.37	27.58	41.71	1	1.04
MAMMA1000331	38.08	36.14	40.81	1	1.02
MAMMA1000335	53.67	64.05	83.91	1.19	1.56
MAMMA1000339	10.22	10.27	17.3	1	1
MAMMA1000340	43.7	42.93	51.78	0.98	1.18
MAMMA1000348	61.54	66.76	90.8	1.08	1.48
MAMMA1000356	130.69	145.54	158.44	1.11	1.21
MAMMA1000358	51.48	56.3	60.81	1.09	1.18
MAMMA1000360	54.55	61.19	64.51	1.12	1.18
MAMMA1000361	117.23	145.09	161.91	1.24	1.38
MAMMA1000363	28.7	40.47	42.91	1.01	1.07
MAMMA1000370	23.94	21.88	25.41	1	1
MAMMA1000371	69.05	56.2	78.4	0.81	1.14
MAMMA1000372	159.51	211.06	195.86	1.32	1.23
MAMMA1000385	102.13	124.35	133.16	1.22	1.3
MAMMA1000388	75.01	86.34	84.4	1.15	1.13
MAMMA1000395	22.37	19.56	19.84	1	1
MAMMA1000402	72.36	76.1	78.86	1.05	1.09
MAMMA1000403	72.37	70.33	78.58	0.97	1.09
MAMMA1000410	33.58	33.5	34.11	1	1
MAMMA1000413	57.45	51.95	64.59	0.9	1.12
MAMMA1000414	20.57	22.19	40.1	1	1
MAMMA1000416	158.25	149.38	193.05	0.94	1.22
MAMMA1000421	188.05	211.01	182.22	1.12	0.97
MAMMA1000422	73.61	67.23	76.18	0.91	1.03
MAMMA1000423	94.51	71.44	79.7	0.76	0.84
MAMMA1000424	15.4	17.71	20.58	1	1
MAMMA1000429	83.68	91.15	103.56	1.09	1.24

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MAMMA1000431	98.85	87.11	96.03	0.88	0.97
MAMMA1000432	24.16	28.51	31.19	1	1
MAMMA1000437	124.16	164.26	174.14	1.32	1.4
MAMMA1000444	136.7	182.7	147.18	1.34	1.08
MAMMA1000446	19.46	14.8	13.08	1	1
MAMMA1000449	71.54	67.04	67.59	0.94	0.94
MAMMA1000457	35.29	33.26	37.36	1	1
MAMMA1000458	29.28	23	26.05	1	1
MAMMA1000468	12.04	8.94	8.92	1	1
MAMMA1000472	56.4	74.66	80.11	1.32	1.42
MAMMA1000473	42.04	44.75	42.13	1.06	1
MAMMA1000477	209.43	261.33	217.02	1.25	1.04
MAMMA1000478	171.46	137.3	142.48	0.8	0.83
MAMMA1000483	173.33	130.85	175.19	0.75	1.01
MAMMA1000490	27.98	34.31	36.95	1	1
MAMMA1000496	21.15	23.28	19.05	1	1
MAMMA1000500	30.34	24.81	24.96	1	1
MAMMA1000501	200.89	257.95	251.06	1.28	1.25
MAMMA1000503	20.19	19.29	25.03	1	1
MAMMA1000506	249.78	268.35	237.02	1.07	0.95
MAMMA1000510	89.34	85.46	95.59	0.96	1.07
MAMMA1000515	99.62	98.07	114.14	0.98	1.15
MAMMA1000516	58.39	53.74	62.5	0.92	1.07
MAMMA1000522	40.02	48.31	39.29	1.21	1
MAMMA1000524	82.61	76.55	71.62	0.93	0.87
MAMMA1000528	41.23	50.62	46.62	1.23	1.13
MAMMA1000534	21.88	22.24	31.94	1	1
MAMMA1000541	98.56	97.52	145.81	0.99	1.48
MAMMA1000550	28.38	24.01	30.73	1	1
MAMMA1000556	29.7	33.84	22.71	1	1
MAMMA1000559	65.27	58.52	51.21	0.9	0.78
MAMMA1000565	43.64	52.38	50.91	1.2	1.17
MAMMA1000567	59.61	51.2	53.35	0.86	0.89
MAMMA1000576	252.37	347.25	302.1	1.38	1.2
MAMMA1000582	34.27	45.25	37.74	1.13	1
MAMMA1000583	38.51	42.54	53.91	1.06	1.35
MAMMA1000585	70.54	69.89	89.76	0.99	1.27
MAMMA1000587	31.89	29.28	30.16	1	1
MAMMA1000591	31.83	38.96	36.66	1	1
MAMMA1000594	95.96	108.1	103.51	1.13	1.08
MAMMA1000597	112.71	119.49	115.95	1.06	1.03
MAMMA1000605	227.96	309.33	345.3	1.36	1.51
MAMMA1000612	50.29	57.92	62.96	1.15	1.25
MAMMA1000614	105.01	111.54	146.23	1.06	1.39
MAMMA1000616	28.23	16.94	25.27	1	1
MAMMA1000621	48.19	38.93	40.79	0.83	0.85

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MAMMA1000623	16.15	20.37	14.71	1	1
MAMMA1000625	476.24	434.14	591.82	0.91	1.24
MAMMA1000635	22.75	16.99	27.2	1	1
MAMMA1000643	61.07	69.63	70.89	1.14	1.16
MAMMA1000646	103.03	97.67	111.43	0.95	1.08
MAMMA1000652	80.37	88.11	98.22	1.1	1.22
MAMMA1000657	67.99	54.13	63.05	0.8	0.93
MAMMA1000664	69.53	91.36	91.87	1.31	1.32
MAMMA1000667	44.02	42.24	43.86	0.96	1
MAMMA1000668	25.86	31.44	31.04	1	1
MAMMA1000669	32.4	23.75	38.33	1	1
MAMMA1000670	42.16	45.95	68.34	1.09	1.62
MAMMA1000672	46.46	51.31	62.93	1.1	1.35
MAMMA1000681	16.87	17.54	34.21	1	1
MAMMA1000684	305.51	315.27	468.25	1.03	1.53
MAMMA1000696	81.12	110.66	105.52	1.36	1.3
MAMMA1000702	33.08	38.47	56.72	1	1.42
MAMMA1000706	16.07	17.64	26.71	1	1
MAMMA1000707	15.71	9.39	11.75	1	1
MAMMA1000713	47.84	58.17	69.33	1.22	1.45
MAMMA1000714	44.22	51.16	63.18	1.16	1.43
MAMMA1000718	77.39	105.19	113	1.36	1.46
MAMMA1000720	106.05	102.56	143.39	0.97	1.35
MAMMA1000723	80.22	89.12	106.97	1.11	1.33
MAMMA1000731	37.93	41.02	42.13	1.03	1.05
MAMMA1000732	76.66	75.96	89.16	0.99	1.16
MAMMA1000733	24.26	21.73	27.58	1	1
MAMMA1000734	76.35	77.56	87.95	1.02	1.15
MAMMA1000736	93.07	91.84	103.02	0.99	1.11
MAMMA1000738	22.99	26.49	33.75	1	1
MAMMA1000744	61.59	73.7	72.42	1.2	1.18
MAMMA1000746	34.62	35.33	39.65	1	1
MAMMA1000748	94.62	85.38	106.73	0.9	1.13
MAMMA1000751	334.01	360.17	399.46	1.08	1.2
MAMMA1000752	172.02	164.07	214.33	0.95	1.25
MAMMA1000757	127.85	148.73	157.88	1.16	1.23
MAMMA1000760	124.78	124.43	142.19	1	1.14
MAMMA1000761	86.33	79.3	87.55	0.92	1.01
MAMMA1000775	54.85	44.33	57.63	0.81	1.05
MAMMA1000776	173.91	164.83	163.92	0.95	0.94
MAMMA1000778	91.05	95.45	94.19	1.05	1.03
MAMMA1000781	63.26	51.61	53.06	0.82	0.84
MAMMA1000782	39.83	31.75	40.39	1	1.01
MAMMA1000784	28.48	29.6	29.08	1	1
MAMMA1000788	31.29	37.38	42.21	1	1.06
MAMMA1000798	42.43	39.93	36.22	0.94	0.94

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MAMMA1000802	204.67	220.69	236.34	1.08	1.15
MAMMA1000810	181.51	178.05	161.35	0.98	0.89
MAMMA1000813	69.7	53.3	75.76	0.76	1.09
MAMMA1000814	161.77	141.29	176.21	0.87	1.09
MAMMA1000824	426.4	265.37	303.66	0.62	0.71
MAMMA1000827	33.46	41.83	43.11	1.05	1.08
MAMMA1000831	25.86	20.61	24.91	1	1
MAMMA1000838	76.35	66.41	79.25	0.87	1.04
MAMMA1000839	216.78	217.48	209.61	1	0.97
MAMMA1000841	34.24	33.58	34.14	1	1
MAMMA1000842	43.49	37.62	46.94	0.92	1.08
MAMMA1000843	18.06	15.02	20.55	1	1
MAMMA1000845	30.07	23.03	21.66	1	1
MAMMA1000851	68.26	91.68	101.42	1.34	1.49
MAMMA1000854	50.96	37.12	52.14	0.78	1.02
MAMMA1000855	21.13	26.08	16.44	1	1
MAMMA1000856	29.86	26.37	27.71	1	1
MAMMA1000859	210.87	235.81	245.69	1.12	1.17
MAMMA1000862	25.4	18.52	20.07	1	1
MAMMA1000863	133.72	117.26	123.5	0.88	0.92
MAMMA1000865	8.05	7.46	11.88	1	1
MAMMA1000867	40.13	53.74	45.08	1.34	1.12
MAMMA1000875	80.24	74.31	83.92	0.93	1.05
MAMMA1000876	39.02	30.27	35.95	1	1
MAMMA1000877	235.29	224.62	274.3	0.95	1.17
MAMMA1000878	125.27	150.03	140.88	1.2	1.12
MAMMA1000880	58.45	71.34	62.54	1.22	1.07
MAMMA1000881	59.96	63.04	60.23	1.05	1
MAMMA1000883	26.98	21.14	23.42	1	1
MAMMA1000897	14.38	18.53	10.3	1	1
MAMMA1000898	39.29	43.51	45.49	1.09	1.14
MAMMA1000905	148.77	169.61	174.87	1.14	1.18
MAMMA1000906	34.31	39.55	42.69	1	1.07
MAMMA1000908	44.43	36.38	41.1	0.9	0.93
MAMMA1000911	16.94	19.46	21.06	1	1
MAMMA1000914	20.53	38.29	25.07	1	1
MAMMA1000920	56.31	40.07	48.77	0.71	0.87
MAMMA1000921	109.2	135.38	126.4	1.24	1.16
MAMMA1000931	103.32	107	98.57	1.04	0.95
MAMMA1000940	127.64	155.71	158.21	1.22	1.24
MAMMA1000941	271.5	295.28	308.87	1.09	1.14
MAMMA1000942	152.89	177.91	161.87	1.16	1.06
MAMMA1000943	127.01	163.61	158.89	1.29	1.25
MAMMA1000952	94.17	106.13	98.04	1.13	1.04
MAMMA1000956	31.86	41.02	39.77	1.03	1
MAMMA1000957	72.13	98.94	103.59	1.37	1.44

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MAMMA1000962	252.41	298.31	262.27	1.18	1.04
MAMMA1000966	156.85	159.16	190.9	1.01	1.22
MAMMA1000968	93.54	91.83	103.73	0.98	1.11
MAMMA1000972	45.33	70.56	49.25	1.56	1.09
MAMMA1000973	26.23	35.54	23.12	1	1
MAMMA1000975	36.47	39.39	34.34	1	1
MAMMA1000976	120	131.07	135.45	1.09	1.13
MAMMA1000979	81.81	103.45	99.17	1.26	1.21
MAMMA1000986	158.57	159.05	191.42	1	1.21
MAMMA1000987	57.4	84.16	91.08	1.47	1.59
MAMMA1000988	75.15	72.65	96.1	0.97	1.28
MAMMA1000994	27.63	33.67	40.47	1	1.01
MAMMA1000998	78.87	118.19	114.8	1.5	1.46
MAMMA1001003	66.74	106.44	94.32	1.59	1.41
MAMMA1001007	6.88	9.58	9.34	1	1
MAMMA1001008	206.14	273.89	337.36	1.33	1.64
MAMMA1001013	97.67	194.03	226	1.99	2.31
MAMMA1001014	35.56	37.02	32	1	1
MAMMA1001021	61.57	79.85	97.7	1.3	1.59
MAMMA1001024	30.2	42.99	48.29	1.07	1.21
MAMMA1001025	35.75	26.02	24.22	1	1
MAMMA1001028	22.44	22.28	40.5	1	1.01
MAMMA1001030	18.75	19.35	24.92	1	1
MAMMA1001035	167.06	225.8	216.5	1.35	1.3
MAMMA1001036	86.15	103.57	125.98	1.2	1.46
MAMMA1001037	65.76	93.97	91.94	1.43	1.4
MAMMA1001038	46.07	37.73	38.15	0.87	0.87
MAMMA1001041	38.7	46.04	45.48	1.15	1.14
MAMMA1001043	19.96	33.97	47.97	1	1.2
MAMMA1001050	80.2	93.8	132.58	1.17	1.65
MAMMA1001054	118.17	161.33	181.89	1.37	1.54
MAMMA1001059	79.17	99.84	79.26	1.26	1
MAMMA1001066	248.86	317.69	298.37	1.28	1.2
MAMMA1001067	70.02	87.32	85.22	1.25	1.22
MAMMA1001072	69.05	45.91	61.77	0.66	0.89
MAMMA1001073	22.24	36.36	20.85	1	1
MAMMA1001074	86.26	84.64	87.84	0.98	1.02
MAMMA1001075	45.62	73.96	64.89	1.62	1.42
MAMMA1001078	157.83	227.17	200.75	1.44	1.27
MAMMA1001080	81.82	76.62	93.78	0.94	1.15
MAMMA1001082	35.46	34.7	31.33	1	1
MAMMA1001091	15.15	9.23	12.07	1	1
MAMMA1001092	30.47	38.5	39.31	1	1
MAMMA1001094	42.81	42.79	50.52	1	1.18
MAMMA1001105	96.06	108.12	124.68	1.13	1.3
MAMMA1001110	19.1	17.52	12.03	1	1

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MAMMA1001126	230.15	262.47	272.86	1.14	1.19
MAMMA1001133	166.47	210.85	181.25	1.27	1.09
MAMMA1001139	419.48	374.33	290.68	0.89	0.69
MAMMA1001141	41.76	36.72	42.73	0.96	1.02
MAMMA1001143	108.13	110.64	110.27	1.02	1.02
MAMMA1001145	58.31	54.02	55.09	0.93	0.94
MAMMA1001150	43.43	37.73	38.82	0.92	0.92
MAMMA1001154	95.57	99.29	114.69	1.04	1.2
MAMMA1001159	16.67	27.46	19.51	1	1
MAMMA1001161	315.39	360.28	346.44	1.14	1.1
MAMMA1001162	33.69	40.74	20.09	1.02	1
MAMMA1001181	110.12	116.3	92.41	1.06	0.84
MAMMA1001186	97.3	99.68	92.18	1.02	0.95
MAMMA1001189	48.61	53.3	60.63	1.1	1.25
MAMMA1001191	29.52	28.11	24.6	1	1
MAMMA1001198	5705	4545.38	5099.12	0.8	0.89
MAMMA1001202	312.18	444.44	429.76	1.42	1.38
MAMMA1001203	92.89	145.14	135.57	1.56	1.46
MAMMA1001206	113.98	105.28	98.69	0.92	0.87
MAMMA1001208	24.53	23.15	31.64	1	1
MAMMA1001215	103.37	114.09	113.25	1.1	1.1
MAMMA1001220	106.22	118.22	108.8	1.11	1.02
MAMMA1001222	33.99	25.05	23.51	1	1
MAMMA1001223	45.33	39.79	49.61	0.88	1.09
MAMMA1001232	79.57	99.97	78.25	1.26	0.98
MAMMA1001234	97.07	109.17	157.27	1.12	1.62
MAMMA1001237	81.14	74.52	96.58	0.92	1.19
MAMMA1001243	24.26	27.23	23.89	1	1
MAMMA1001244	26.99	20.39	28.43	1	1
MAMMA1001249	63.22	48.62	47.34	0.77	0.75
MAMMA1001256	102.65	763.83	491.67	7.44	4.79
MAMMA1001259	52.74	90.18	78.32	1.71	1.49
MAMMA1001260	70.58	57.59	52.62	0.82	0.75
MAMMA1001262	85.62	56.57	59.95	0.66	0.7
MAMMA1001268	61.25	80.01	74.88	1.31	1.22
MAMMA1001271	243.97	206.58	324.35	0.85	1.33
MAMMA1001274	198.42	192.2	258.23	0.97	1.3
MAMMA1001280	25.14	26.54	39.97	1	1
MAMMA1001283	72.62	92.88	94.17	1.28	1.3
MAMMA1001284	86.99	94.13	102.44	1.08	1.18
MAMMA1001286	65.18	57.61	69.97	0.88	1.07
MAMMA1001289	244.96	233.14	255.3	0.95	1.04
MAMMA1001292	60.39	76.64	79.13	1.27	1.31
MAMMA1001296	264.24	279.38	330.94	1.06	1.25
MAMMA1001298	59.57	56.62	63.72	0.95	1.07
MAMMA1001305	59.13	69.24	60.9	1.17	1.03

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MAMMA1001309	22.23	27.7	29.89	1	1
MAMMA1001310	57.87	56.54	51.58	0.98	0.89
MAMMA1001322	29	37.01	38.15	1	1
MAMMA1001324	59.4	71.72	58	1.21	0.98
MAMMA1001330	133.84	127.64	102.1	0.95	0.76
MAMMA1001333	206.6	224.44	220.16	1.09	1.07
MAMMA1001334	51.34	55.82	76.01	1.09	1.48
MAMMA1001337	58	54.86	53.03	0.95	0.91
MAMMA1001341	62.18	84.2	73.36	1.35	1.18
MAMMA1001343	159.94	269.05	131.35	1.68	0.82
MAMMA1001344	69.02	79.37	85.82	1.15	1.24
MAMMA1001346	31.69	36.45	35.49	1	1
MAMMA1001383	154.67	143.39	192.73	0.93	1.25
MAMMA1001388	63.38	80.21	82.17	1.27	1.3
MAMMA1001396	223.03	210.97	276.79	0.95	1.24
MAMMA1001397	138.22	191.56	182.09	1.39	1.32
MAMMA1001401	208.09	215.5	266.72	1.04	1.28
MAMMA1001408	14.68	26.28	16.11	1	1
MAMMA1001411	39.71	42.94	38.71	1.07	1
MAMMA1001414	66.27	60.65	62.01	0.92	0.94
MAMMA1001415	56.78	56.22	70.37	0.99	1.24
MAMMA1001418	52.12	47.17	52.35	0.91	1
MAMMA1001419	60.74	62.4	66.89	1.03	1.1
MAMMA1001420	53.75	51.8	48.15	0.96	0.9
MAMMA1001426	169.21	169.93	272.45	1	1.61
MAMMA1001428	68.95	86.43	107.74	1.25	1.56
MAMMA1001432	97.82	94.28	103.58	0.96	1.06
MAMMA1001435	54.35	65.6	74.82	1.21	1.38
MAMMA1001442	130.74	148.57	183.27	1.14	1.4
MAMMA1001446	87.98	139.3	98.34	1.58	1.12
MAMMA1001450	45.81	54.83	60.63	1.2	1.32
MAMMA1001452	111.82	117.99	155.55	1.06	1.39
MAMMA1001465	226	256.84	286.61	1.14	1.27
MAMMA1001476	45.56	30.18	39.95	0.88	0.88
MAMMA1001478	82.89	84.38	76.22	1.02	0.92
MAMMA1001479	73.98	71.93	65.74	0.97	0.89
MAMMA1001487	51.61	40.68	48.06	0.79	0.93
MAMMA1001498	97.5	123.08	133.32	1.26	1.37
MAMMA1001501	35.04	30.91	37.31	1	1
MAMMA1001502	120.15	147.17	130.6	1.22	1.09
MAMMA1001510	21.02	14.68	17.56	1	1
MAMMA1001522	53.04	83.68	73.55	1.58	1.39
MAMMA1001529	50.7	64.29	57.98	1.27	1.14
MAMMA1001532	59.82	62.64	55.25	1.05	0.92
MAMMA1001533	19.25	21.28	16.38	1	1
MAMMA1001534	23.37	16.71	19.41	1	1

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MAMMA1001535	24.43	25.67	26.22	1	1
MAMMA1001547	135.02	139.89	124.87	1.04	0.92
MAMMA1001551	53.38	41.49	46.12	0.78	0.86
MAMMA1001569	20.53	23.86	25.02	1	1
MAMMA1001575	37.03	25.5	26.38	1	1
MAMMA1001576	74.96	60.39	55.22	0.81	0.74
MAMMA1001584	40.8	54.88	37.5	1.35	0.98
MAMMA1001586	20.62	22.63	18.22	1	1
MAMMA1001590	97.37	85.63	86.26	0.88	0.89
MAMMA1001599	89.53	89.35	104.96	1	1.17
MAMMA1001600	57.34	52.02	53.71	0.91	0.94
MAMMA1001604	20.76	32.48	26.25	1	1
MAMMA1001606	52.99	60.37	56.17	1.14	1.06
MAMMA1001609	73.89	66.47	54.23	0.9	0.73
MAMMA1001614	45.9	53.39	35.31	1.16	0.87
MAMMA1001615	77.63	52.12	60.37	0.67	0.78
MAMMA1001619	38.3	32.53	36.46	1	1
MAMMA1001620	93.43	94.98	90.13	1.02	0.96
MAMMA1001623	53.6	41.59	52.4	0.78	0.98
MAMMA1001626	29.04	39.82	34.58	1	1
MAMMA1001627	23.85	21.09	23.17	1	1
MAMMA1001630	97.14	57.64	75.01	0.59	0.77
MAMMA1001633	184.79	213.84	171.67	1.16	0.93
MAMMA1001634	117.18	129.13	131.66	1.1	1.12
MAMMA1001635	119.91	165.38	146.11	1.38	1.22
MAMMA1001649	43.18	45.18	37.46	1.05	0.93
MAMMA1001654	387.96	356.49	290.7	0.92	0.75
MAMMA1001660	249.04	242.66	201.14	0.97	0.81
MAMMA1001663	117.23	144.12	158.29	1.23	1.35
MAMMA1001670	43.24	47.08	48.59	1.09	1.12
MAMMA1001671	21.05	20.04	23.84	1	1
MAMMA1001679	82.17	50.83	74.26	0.62	0.9
MAMMA1001683	99.95	115.5	132.76	1.16	1.33
MAMMA1001686	45.15	43.61	54.4	0.97	1.2
MAMMA1001688	817.95	1182.97	807.37	1.45	0.99
MAMMA1001689	50.45	66.35	33.92	1.32	0.79
MAMMA1001692	74.89	83.11	93.15	1.11	1.24
MAMMA1001711	89.73	95.5	100.43	1.06	1.12
MAMMA1001715	64.1	64.36	78.55	1	1.23
MAMMA1001730	29.11	20.27	24.59	1	1
MAMMA1001735	320.11	302.75	434.86	0.95	1.36
MAMMA1001740	37.92	56.4	45.76	1.41	1.14
MAMMA1001743	326.51	295.63	345.77	0.91	1.06
MAMMA1001744	8.24	9.47	10.89	1	1
MAMMA1001745	83.91	100.2	95.22	1.19	1.13
MAMMA1001751	61.01	66.28	70.21	1.09	1.15

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MAMMA1001752	60.8	68.51	67.12	1.13	1.1
MAMMA1001754	83.25	77.68	87.09	0.93	1.05
MAMMA1001757	24.52	28.93	30.43	1	1
MAMMA1001760	175.1	336.22	275.64	1.92	1.57
MAMMA1001764	119.04	123.82	120.12	1.04	1.01
MAMMA1001767	42.13	45.98	55.25	1.09	1.31
MAMMA1001768	70.77	68.81	96.18	0.97	1.36
MAMMA1001769	226.94	251.56	288.88	1.11	1.27
MAMMA1001771	49.16	26.77	87.14	0.81	1.77
MAMMA1001773	30.28	47.69	46.79	1.19	1.17
MAMMA1001778	51.63	47.87	47.78	0.93	0.93
MAMMA1001783	290.62	18.35	11.15	0.14	0.14
MAMMA1001785	84.27	83.87	90.95	1	1.08
MAMMA1001788	15.25	18.1	14.18	1	1
MAMMA1001790	67.38	72.53	94.45	1.08	1.4
MAMMA1001800	11.7	12.42	19.29	1	1
MAMMA1001804	13.19	17.8	29.98	1	1
MAMMA1001806	116.78	94.49	108.56	0.81	0.93
MAMMA1001812	49.43	67.86	70.89	1.37	1.43
MAMMA1001815	41.4	2.21	3.74	0.97	0.97
MAMMA1001817	60.98	48.66	77.43	0.8	1.27
MAMMA1001818	37.52	69.75	54.44	1.74	1.36
MAMMA1001819	100.49	163.6	131.37	1.63	1.31
MAMMA1001820	58.39	77.5	79.24	1.33	1.36
MAMMA1001824	133.13	184.64	189.86	1.39	1.43
MAMMA1001832	23.04	30.35	29.04	1	1
MAMMA1001836	47.28	72.32	68.41	1.53	1.45
MAMMA1001837	72.99	100.42	119.29	1.38	1.63
MAMMA1001848	142.87	120.22	154.65	0.84	1.08
MAMMA1001850	141.05	199.83	211.75	1.42	1.5
MAMMA1001851	55.74	64.8	82.75	1.16	1.48
MAMMA1001852	117.56	142.11	161.67	1.21	1.38
MAMMA1001854	198.63	258.12	249.48	1.3	1.26
MAMMA1001858	73.6	66.11	62.8	0.9	0.85
MAMMA1001864	39.82	42.28	53	1.06	1.33
MAMMA1001868	23.21	18.07	30.54	1	1
MAMMA1001874	20.19	15.52	18.77	1	1
MAMMA1001878	129.7	164.48	141.72	1.27	1.09
MAMMA1001880	130.34	172.34	159.8	1.32	1.23
MAMMA1001885	56.12	66.87	62.57	1.19	1.11
MAMMA1001890	292.68	392.69	309.08	1.34	1.06
MAMMA1001893	57.97	54.08	50.64	0.93	0.87
MAMMA1001901	146.41	179.65	186.48	1.23	1.27
MAMMA1001907	112.54	89.72	83.39	0.8	0.74
MAMMA1001908	42.16	47.26	59.99	1.12	1.42
MAMMA1001919	21.76	12.18	15.45	1	1

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MAMMA1001931	41.78	43.18	32.4	1.03	0.96
MAMMA1001937	48.4	38.88	45.73	0.83	0.94
MAMMA1001951	87.37	79.86	90.46	0.91	1.04
MAMMA1001956	234.73	359.13	220.55	1.53	0.94
MAMMA1001957	79.25	63.52	76.54	0.8	0.97
MAMMA1001960	79.1	81.05	79.07	1.02	1
MAMMA1001963	40.15	26.12	27.02	1	1
MAMMA1001969	144.31	160.63	181.1	1.11	1.25
MAMMA1001970	113.97	120.16	133.72	1.05	1.17
MAMMA1001978	15.01	24.76	10.72	1	1
MAMMA1001992	113.3	96.25	115.89	0.85	1.02
MAMMA1001994	183.27	182.89	161.61	1	0.88
MAMMA1002008	113.21	84.2	118.3	0.74	1.04
MAMMA1002009	99.04	94.33	113.6	0.95	1.15
MAMMA1002011	32.32	38.8	47.36	1	1.18
MAMMA1002022	115.36	130.9	120.26	1.13	1.04
MAMMA1002024	240.6	268.72	213.78	1.12	0.89
MAMMA1002032	135.35	127.09	143.87	0.94	1.06
MAMMA1002033	129.51	166.84	118.92	1.29	0.92
MAMMA1002041	49.82	40.41	32.72	0.81	0.8
MAMMA1002042	60.07	63.35	52.78	1.05	0.88
MAMMA1002045	57.46	74.01	51.68	1.29	0.9
MAMMA1002047	226.73	176.73	161.74	0.78	0.71
MAMMA1002056	165.9	236.12	219.21	1.42	1.32
MAMMA1002058	152.14	178.5	178.27	1.17	1.17
MAMMA1002060	28.48	25.19	35.5	1	1
MAMMA1002065	94.78	114.46	137.47	1.21	1.45
MAMMA1002068	94.55	126.92	106.44	1.34	1.13
MAMMA1002070	22.8	24.18	32.43	1	1
MAMMA1002078	45.63	54.13	41.72	1.19	0.91
MAMMA1002080	42.41	35.89	50.88	0.94	1.2
MAMMA1002082	208.8	248.09	242.83	1.19	1.16
MAMMA1002084	79.76	70.29	79.22	0.88	0.99
MAMMA1002087	81.38	70.67	55.21	0.87	0.68
MAMMA1002091	69.24	33.81	40.25	0.58	0.58
MAMMA1002093	49.3	47.88	40.92	0.97	0.83
MAMMA1002095	62.92	48.63	62.62	0.77	1
MAMMA1002108	34.11	43.72	31.18	1.09	1
MAMMA1002112	49.85	43.66	60.6	0.88	1.22
MAMMA1002118	18.66	25.04	22.99	1	1
MAMMA1002119	35.7	50.09	51.64	1.25	1.29
MAMMA1002125	85.62	83.71	104.13	0.98	1.22
MAMMA1002126	212.53	243.59	247.23	1.15	1.16
MAMMA1002128	28.9	36.64	28.73	1	1
MAMMA1002132	178.8	385.83	208.5	2.16	1.17
MAMMA1002140	84.02	97.49	94.54	1.16	1.13

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MAMMA1002142	27	29.18	28.39	1	1
MAMMA1002143	32.27	38.19	37.15	1	1
MAMMA1002145	46.7	57.57	62.96	1.23	1.35
MAMMA1002147	51.61	54.42	63.56	1.05	1.23
MAMMA1002153	108.87	95.6	117.84	0.88	1.08
MAMMA1002155	84.91	98.51	118.29	1.16	1.39
MAMMA1002156	23.01	22.57	9.17	1	1
MAMMA1002158	71.65	101.16	89.49	1.41	1.25
MAMMA1002164	69.22	76.31	80.84	1.1	1.17
MAMMA1002165	117.57	158.1	167.22	1.34	1.42
MAMMA1002170	32.5	26.67	26.41	1	1
MAMMA1002174	149.93	124.04	176.18	0.83	1.18
MAMMA1002175	69.03	58.42	73.54	0.85	1.07
MAMMA1002180	670.07	569.26	712.11	0.85	1.06
MAMMA1002198	105.57	108.05	103.95	1.02	0.98
MAMMA1002205	96.55	110.73	136.26	1.15	1.41
MAMMA1002206	128.5	137.17	178.42	1.07	1.39
MAMMA1002209	103.35	116.61	118.58	1.13	1.15
MAMMA1002215	144.58	111.86	170.75	0.77	1.18
MAMMA1002219	51.95	58.88	61.62	1.13	1.19
MAMMA1002224	141.44	128.04	164.13	0.91	1.16
MAMMA1002229	57.2	64.86	98.71	1.13	1.73
MAMMA1002230	107.86	142.95	143.44	1.33	1.33
MAMMA1002233	31.62	39.28	39.22	1	1
MAMMA1002234	61.75	74.01	84.89	1.2	1.37
MAMMA1002236	83.84	77.03	109.79	0.92	1.31
MAMMA1002243	39.55	55.1	29.19	1.38	1
MAMMA1002250	60.55	90.82	107.03	1.5	1.77
MAMMA1002253	61.36	64.18	73.13	1.05	1.19
MAMMA1002267	297.47	346.34	370.39	1.16	1.25
MAMMA1002268	68.44	60.27	84.72	0.88	1.24
MAMMA1002269	17.25	14.88	22.36	1	1
MAMMA1002282	224.02	176.79	233.34	0.79	1.04
MAMMA1002292	58.17	61.14	63.4	1.05	1.09
MAMMA1002293	159.47	189.9	210.71	1.19	1.32
MAMMA1002294	36.74	55.1	60	1.38	1.5
MAMMA1002297	110.35	104.91	144.32	0.95	1.31
MAMMA1002298	36.02	30.43	36.83	1	1
MAMMA1002299	27.82	33.28	23.98	1	1
MAMMA1002308	49.56	49.95	69.74	1.01	1.41
MAMMA1002310	165.04	197.01	216.29	1.19	1.31
MAMMA1002311	115.42	135.43	128.21	1.17	1.11
MAMMA1002312	60.66	71.64	65.83	1.18	1.09
MAMMA1002317	64.84	89.05	52.81	1.37	0.81
MAMMA1002319	98.83	108.07	99.44	1.09	1.01
MAMMA1002322	193.48	224.61	208.37	1.16	1.08

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MAMMA1002329	22.09	22.7	21.43	1	1
MAMMA1002332	55.75	55.43	64.61	0.99	1.16
MAMMA1002333	55.8	53.89	60.8	0.97	1.09
MAMMA1002335	92.26	115.52	118.6	1.25	1.29
MAMMA1002339	122.3	151.03	173.19	1.23	1.42
MAMMA1002347	103.1	118.34	109.15	1.15	1.06
MAMMA1002351	41.39	39.3	32.76	0.97	0.97
MAMMA1002352	31.88	22.83	24.58	1	1
MAMMA1002353	118.15	80.12	80.69	0.68	0.68
MAMMA1002355	107.29	115.42	118.02	1.08	1.1
MAMMA1002356	85.91	72.76	83.92	0.85	0.98
MAMMA1002359	239.56	269.72	274.12	1.13	1.14
MAMMA1002360	33.78	35.13	31.24	1	1
MAMMA1002361	81.32	123.26	81.09	1.52	1
MAMMA1002362	57.3	52.34	45.66	0.91	0.8
MAMMA1002367	102.09	72.12	73.06	0.71	0.72
MAMMA1002371	128.34	135.45	139.68	1.06	1.09
MAMMA1002380	86.26	89.59	86.64	1.04	1
MAMMA1002384	112.66	123.01	111.84	1.09	0.99
MAMMA1002385	23.7	31.42	42.89	1	1.07
MAMMA1002390	46.77	69.8	58.4	1.49	1.25
MAMMA1002392	52.39	66.03	59.77	1.26	1.14
MAMMA1002396	173.41	188.4	142.24	1.09	0.82
MAMMA1002399	53.98	59.94	54.76	1.11	1.01
MAMMA1002400	23.65	27.25	25.48	1	1
MAMMA1002409	31.67	36.62	33.7	1	1
MAMMA1002411	61.64	46.48	42.21	0.75	0.68
MAMMA1002413	107.43	137.66	143.97	1.28	1.34
MAMMA1002417	40.62	42.91	42.44	1.06	1.04
MAMMA1002427	91.27	105.75	119.89	1.16	1.31
MAMMA1002428	81.13	66.91	84.44	0.82	1.04
MAMMA1002433	59.34	68.93	50.36	1.16	0.85
MAMMA1002434	97.91	119.36	102.53	1.22	1.05
MAMMA1002446	96.19	132.94	77.56	1.38	0.81
MAMMA1002447	100.75	102.66	107.55	1.02	1.07
MAMMA1002454	212.27	262.76	262.03	1.24	1.23
MAMMA1002461	100.78	102.16	96.85	1.01	0.96
MAMMA1002463	67.54	69.41	86.78	1.03	1.28
MAMMA1002464	89.3	65.63	100.63	0.73	1.13
MAMMA1002466	162.04	139.58	172.44	0.86	1.06
MAMMA1002470	62.6	81.06	60.9	1.29	0.97
MAMMA1002475	89.98	80.67	84.2	0.9	0.94
MAMMA1002480	73.43	61.66	55.66	0.84	0.76
MAMMA1002485	151.28	174.3	205.8	1.15	1.36
MAMMA1002494	60.94	55.77	82.07	0.92	1.35
MAMMA1002498	30.46	44.86	40.61	1.12	1.02

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MAMMA1002524	84.66	60.71	94.15	0.72	1.11
MAMMA1002530	72.63	72.29	66.75	1	0.92
MAMMA1002538	26.16	44	28.65	1.1	1
MAMMA1002545	104.11	118.05	134.17	1.13	1.29
MAMMA1002554	81.76	70.43	72.28	0.86	0.88
MAMMA1002556	82.56	101.86	117.7	1.23	1.43
MAMMA1002561	183.06	253.89	286.77	1.39	1.57
MAMMA1002565	43.42	37.17	44.96	0.92	1.04
MAMMA1002566	45.37	41.05	31.94	0.9	0.88
MAMMA1002571	28.16	48.41	27.79	1.21	1
MAMMA1002573	53.09	63.02	56.55	1.19	1.07
MAMMA1002576	52.96	65.22	46.79	1.23	0.88
MAMMA1002584	219.19	312.08	298.56	1.42	1.36
MAMMA1002585	34.42	59.49	43.82	1.49	1.1
MAMMA1002586	53.28	40.73	49.68	0.76	0.93
MAMMA1002589	32.01	31.81	33.91	1	1
MAMMA1002590	68.81	98.26	85.79	1.43	1.25
MAMMA1002593	67.9	77.39	76.83	1.14	1.13
MAMMA1002597	138.42	178.56	134.01	1.29	0.97
MAMMA1002598	303.39	326.15	327.16	1.08	1.08
MAMMA1002603	102.25	115.74	118.22	1.13	1.16
MAMMA1002612	117.11	147.25	132.48	1.26	1.13
MAMMA1002617	149.67	125.06	197.58	0.84	1.32
MAMMA1002618	46.88	51.87	66.42	1.11	1.42
MAMMA1002619	53.85	36.68	46.59	0.74	0.87
MAMMA1002622	133.96	141.24	174.33	1.05	1.3
MAMMA1002623	124.5	178	167.47	1.43	1.35
MAMMA1002625	60.29	84.82	98.35	1.41	1.63
MAMMA1002627	6.72	5.74	10.26	1	1
MAMMA1002629	101.23	128.7	162.62	1.27	1.61
MAMMA1002631	13.84	20.24	20.19	1	1
MAMMA1002633	164.41	153.16	191.71	0.93	1.17
MAMMA1002636	87.77	117.27	121.16	1.34	1.38
MAMMA1002637	24.69	35.88	35.76	1	1
MAMMA1002646	21.71	28.07	24.38	1	1
MAMMA1002648	187.58	193.11	255.22	1.03	1.36
MAMMA1002650	8.55	11.51	15.55	1	1
MAMMA1002652	95.38	110.96	177.7	1.16	1.86
MAMMA1002655	36.37	37.11	47.9	1	1.2
MAMMA1002662	41.35	39.65	56.93	0.97	1.38
MAMMA1002665	208.39	264.65	273.08	1.27	1.31
MAMMA1002671	114.62	115.25	130.03	1.01	1.13
MAMMA1002673	69.9	76.31	88.39	1.09	1.26
MAMMA1002684	43.5	41.23	58.19	0.95	1.34
MAMMA1002685	25.34	34.2	33.31	1	1
MAMMA1002692	29.83	34.21	34.19	1	1

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MAMMA1002693	37.14	46.25	44.27	1.16	1.11
MAMMA1002698	36.47	32.49	58.15	1	1.45
MAMMA1002699	24.9	17.42	29.87	1	1
MAMMA1002701	154.17	198.34	189.21	1.29	1.23
MAMMA1002708	122.76	166.01	167.09	1.35	1.36
MAMMA1002711	130.86	139.5	141.81	1.07	1.08
MAMMA1002712	55.07	80.77	70.41	1.47	1.28
MAMMA1002716	38.79	38.47	36.46	1	1
MAMMA1002721	78.03	108.73	89.74	1.39	1.15
MAMMA1002723	64.36	70.73	72.82	1.1	1.13
MAMMA1002727	44.46	47.53	47.61	1.07	1.07
MAMMA1002728	589.74	738.66	622.38	1.25	1.06
MAMMA1002742	45.86	61.22	85.3	1.33	1.86
MAMMA1002743	73.39	77.51	101.73	1.06	1.39
MAMMA1002744	218.06	292.52	320.81	1.34	1.47
MAMMA1002746	20.19	17.71	23.08	1	1
MAMMA1002748	50.4	62.83	63.29	1.25	1.26
MAMMA1002754	107.78	118.98	93.8	1.1	0.87
MAMMA1002758	17.97	12.63	15.18	1	1
MAMMA1002762	356.17	346.77	337.32	0.97	0.95
MAMMA1002764	64.2	72.1	81.24	1.12	1.27
MAMMA1002765	53.77	52.17	60.39	0.97	1.12
MAMMA1002769	54.34	65.21	59.79	1.2	1.1
MAMMA1002771	23.11	42.88	24.17	1.07	1
MAMMA1002775	116.24	172.07	135.7	1.48	1.17
MAMMA1002780	36.93	29	42.08	1	1.05
MAMMA1002782	45.66	38.88	46.78	0.88	1.02
MAMMA1002795	33.01	30.07	32.5	1	1
MAMMA1002796	28.58	28.06	23.6	1	1
MAMMA1002805	41.44	41.79	48.88	1.01	1.18
MAMMA1002806	26.11	21.5	30.88	1	1
MAMMA1002807	126.48	146.99	171.08	1.16	1.35
MAMMA1002814	133.26	170.5	140.5	1.28	1.05
MAMMA1002817	17.38	13.06	18.01	1	1
MAMMA1002820	37.7	25.95	34.49	1	1
MAMMA1002830	704.18	831.94	1027.04	1.18	1.46
MAMMA1002833	160.45	203.1	169.54	1.27	1.06
MAMMA1002835	18.52	14.74	19.2	1	1
MAMMA1002838	82.37	117.11	94.07	1.42	1.14
MAMMA1002842	81.52	91.8	95.14	1.13	1.17
MAMMA1002843	47.69	50.79	54.64	1.07	1.15
MAMMA1002844	59.98	70	69.55	1.17	1.16
MAMMA1002845	21.74	21.48	25.65	1	1
MAMMA1002857	2073.5	2250.92	1940.63	1.09	0.94
MAMMA1002858	4743.6	5047.57	4726.53	1.06	1
MAMMA1002863	53.49	36.79	38.55	0.75	0.75

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MAMMA1002868	271.62	385.57	313.21	1.42	1.15
MAMMA1002869	104.89	129.38	124.78	1.23	1.19
MAMMA1002871	18.06	19.51	22.1	1	1
MAMMA1002875	33.95	29.2	39.35	1	1
MAMMA1002879	291.97	244.07	282.97	0.84	0.97
MAMMA1002880	24.11	36.32	20.66	1	1
MAMMA1002881	46.89	53.96	43.29	1.15	0.92
MAMMA1002885	39.98	39.44	33.43	1	1
MAMMA1002886	96.27	136.15	117.6	1.41	1.22
MAMMA1002887	29.72	36.91	37.05	1	1
MAMMA1002890	43.77	44.43	54.74	1.02	1.25
MAMMA1002892	70.01	89.57	93.8	1.28	1.34
MAMMA1002893	58.74	43.84	59.95	0.75	1.02
MAMMA1002895	33.14	41.53	34.62	1.04	1
MAMMA1002898	28.57	28.64	36.16	1	1
MAMMA1002905	26.4	36.44	39.34	1	1
MAMMA1002906	21.56	30.96	28.68	1	1
MAMMA1002908	58.31	62.78	91.77	1.08	1.57
MAMMA1002909	139.24	195.36	202.09	1.4	1.45
MAMMA1002918	52.04	37.96	55.61	0.77	1.07
MAMMA1002925	1360.7	1505.64	1768.51	1.11	1.3
MAMMA1002926	109.58	117.84	113.15	1.08	1.03
MAMMA1002930	92.19	140.43	130.25	1.52	1.41
MAMMA1002937	909.37	759.77	586.96	0.84	0.65
MAMMA1002938	23.08	23.6	28.88	1	1
MAMMA1002941	41.07	38.39	52.17	0.97	1.27
MAMMA1002947	81.25	74.86	99.6	0.92	1.23
MAMMA1002964	75.93	92.13	106.58	1.21	1.4
MAMMA1002967	45.71	36.3	58.83	0.88	1.29
MAMMA1002970	102.84	120.76	163.7	1.17	1.59
MAMMA1002971	20.08	24.51	31.39	1	1
MAMMA1002972	26.41	22.54	29.15	1	1
MAMMA1002973	96.97	109.41	141.67	1.13	1.46
MAMMA1002979	476.61	431.08	630.64	0.9	1.32
MAMMA1002982	10.28	16.98	16.93	1	1
MAMMA1002987	62.74	86.38	92.57	1.38	1.48
MAMMA1003003	53.6	62.48	71.76	1.17	1.34
MAMMA1003004	82.56	112.51	120.88	1.36	1.46
MAMMA1003007	33.3	29.96	23.91	1	1
MAMMA1003011	24.89	36.15	38.22	1	1
MAMMA1003013	615.04	787.17	714.01	1.28	1.16
MAMMA1003015	33.96	40.39	36.19	1.01	1
MAMMA1003019	28.14	19.56	33.91	1	1
MAMMA1003020	61.07	58.12	91.91	0.95	1.5
MAMMA1003026	16.71	14.22	14.62	1	1
MAMMA1003031	99.88	120.56	140.28	1.21	1.4

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MAMMA1003033	52. 72	43. 53	49. 36	0. 83	0. 94
MAMMA1003035	51. 64	68. 24	58. 51	1. 32	1. 13
MAMMA1003039	52. 03	84. 31	79. 88	1. 62	1. 54
MAMMA1003040	77. 25	100. 92	87. 34	1. 31	1. 13
MAMMA1003044	84. 15	107. 35	98. 74	1. 28	1. 17
MAMMA1003047	71. 14	71. 54	94. 66	1. 01	1. 33
MAMMA1003049	11. 46	12. 1	14. 97	1	1
MAMMA1003055	63. 84	63. 7	59. 5	1	0. 93
MAMMA1003056	16. 39	11. 84	14. 09	1	1
MAMMA1003057	40. 62	50. 42	71. 14	1. 24	1. 75
MAMMA1003066	70. 31	84. 83	86. 92	1. 21	1. 24
MAMMA1003075	22. 54	35. 75	29. 64	1	1
MAMMA1003089	257. 88	298. 45	265. 71	1. 16	1. 03
MAMMA1003092	16. 55	17. 76	24. 62	1	1
MAMMA1003095	17. 63	25. 9	22. 6	1	1
MAMMA1003099	59. 71	66. 74	79. 96	1. 12	1. 34
MAMMA1003102	22. 88	21. 62	18. 31	1	1
MAMMA1003104	17. 91	27. 52	27. 95	1	1
MAMMA1003113	50. 03	52. 88	58. 66	1. 06	1. 17
MAMMA1003126	68. 4	110. 37	87. 04	1. 61	1. 27
MAMMA1003127	56. 89	52. 43	68. 02	0. 92	1. 2
MAMMA1003131	52. 16	51. 75	47. 28	0. 99	0. 91
MAMMA1003135	28. 03	25. 75	24. 29	1	1
MAMMA1003140	23. 44	27. 51	24. 34	1	1
MAMMA1003146	31. 97	33. 68	34. 09	1	1
MAMMA1003150	33. 45	29. 72	33. 2	1	1
MAMMA1003154	24. 68	26. 55	30. 14	1	1
MAMMA1003155	184. 33	236. 53	257. 32	1. 28	1. 4
MAMMA1003157	47. 86	49. 47	50. 68	1. 03	1. 06
MAMMA1003163	23. 97	21. 86	27. 75	1	1
MAMMA1003164	25. 9	25. 18	27. 66	1	1
MAMMA1003166	25. 05	20. 49	30. 25	1	1
NB9N31000010	45. 03	32. 89	39. 27	0. 89	0. 89
NB9N31000016	37. 34	41. 35	50. 09	1. 03	1. 25
NB9N31000043	69. 72	74. 74	98. 75	1. 07	1. 42
NB9N31000045	647. 52	565. 03	653. 87	0. 87	1. 01
NB9N31000054	175. 09	145. 32	162. 93	0. 83	0. 93
NB9N31000076	47. 51	43. 9	50. 65	0. 92	1. 07
NB9N31000086	36. 65	25. 69	25. 73	1	1
NT2RM1000001	30. 35	38. 18	45. 75	1	1. 14
NT2RM1000018	42. 94	49. 48	47. 71	1. 15	1. 11
NT2RM1000032	29. 94	34. 47	32. 41	1	1
NT2RM1000035	38. 26	48. 66	51. 36	1. 22	1. 28
NT2RM1000037	46. 8	41. 24	30. 56	0. 88	0. 85
NT2RM1000039	73. 85	56. 5	62. 97	0. 77	0. 85
NT2RM1000042	931. 69	637. 4	988. 7	0. 68	1. 06

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NT2RM1000055	15.45	19.54	17.22	1	1
NT2RM1000059	50.56	55.16	69.67	1.09	1.38
NT2RM1000062	28.3	29.82	26.26	1	1
NT2RM1000065	422.69	413.14	412.01	0.98	0.97
NT2RM1000066	61.12	52.51	55.55	0.86	0.91
NT2RM1000071	597.25	687.62	752.45	1.15	1.26
NT2RM1000080	40.28	46.41	33.94	1.15	0.99
NT2RM1000086	56.08	45.2	44.41	0.81	0.79
NT2RM1000092	170.39	229.28	181.67	1.35	1.07
NT2RM1000118	6.76	6.45	7.27	1	1
NT2RM1000119	24.26	24	20.67	1	1
NT2RM1000121	19.18	20.12	27.1	1	1
NT2RM1000122	49.55	51.04	78.68	1.03	1.59
NT2RM1000127	17.81	22.59	23.93	1	1
NT2RM1000131	9.35	12.83	12.1	1	1
NT2RM1000132	52.93	59.29	63.2	1.12	1.19
NT2RM1000153	33.12	26.12	36.76	1	1
NT2RM1000184	737.64	846.85	696.89	1.15	0.94
NT2RM1000186	22.98	23.85	18.75	1	1
NT2RM1000187	50.65	44.43	61.01	0.88	1.2
NT2RM1000199	16.32	23.42	24.06	1	1
NT2RM1000213	29.02	29.13	40.51	1	1.01
NT2RM1000215	180.78	149.82	208.12	0.83	1.15
NT2RM1000218	137.01	110.42	124.71	0.81	0.91
NT2RM1000224	143.2	151.71	154.12	1.06	1.08
NT2RM1000236	335.5	368.59	376.44	1.1	1.12
NT2RM1000242	2.7	4.73	2.92	1	1
NT2RM1000244	18.45	18.3	16.85	1	1
NT2RM1000252	47.92	51.57	75.16	1.08	1.57
NT2RM1000256	38.74	44.77	67.74	1.12	1.69
NT2RM1000257	48.98	35.53	65.82	0.82	1.34
NT2RM1000260	229.59	178.36	283.77	0.78	1.24
NT2RM1000269	34.14	29.14	47.8	1	1.2
NT2RM1000271	14.08	7.17	15.71	1	1
NT2RM1000272	904.26	996.51	1381.29	1.1	1.53
NT2RM1000273	142.53	185.62	248.53	1.3	1.74
NT2RM1000274	470.15	693.46	873.52	1.47	1.86
NT2RM1000280	38.3	50.17	57.55	1.25	1.44
NT2RM1000295	5.96	7.76	13.69	1	1
NT2RM1000300	21.47	39.28	30.22	1	1
NT2RM1000304	1409.7	1296.34	2091.21	0.92	1.48
NT2RM1000314	47.95	58.66	57.18	1.22	1.19
NT2RM1000318	530.64	382.21	728.98	0.72	1.37
NT2RM1000335	54.51	54.04	69.39	0.99	1.27
NT2RM1000341	9.49	9.42	18.58	1	1
NT2RM1000350	78.63	76.19	81.31	0.97	1.03

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NT2RM1000354	11.59	13.65	13.44	1	1
NT2RM1000355	295.96	306.13	356.48	1.03	1.2
NT2RM1000361	20.2	18.71	24.25	1	1
NT2RM1000365	7.44	6.34	16.74	1	1
NT2RM1000372	273.86	199.66	315.14	0.73	1.15
NT2RM1000377	68.51	64.66	68.73	0.94	1
NT2RM1000388	20.87	27.84	26.34	1	1
NT2RM1000394	10.48	8.92	13.44	1	1
NT2RM1000399	26.45	18.72	31.61	1	1
NT2RM1000407	25.21	24.57	34.38	1	1
NT2RM1000421	7.96	5.9	5.56	1	1
NT2RM1000422	678.77	596.46	808.74	0.88	1.19
NT2RM1000430	25.05	22.13	31.78	1	1
NT2RM1000462	83.02	120.5	108.41	1.45	1.31
NT2RM1000499	45.97	54.03	56.81	1.18	1.24
NT2RM1000512	189.86	192.34	205.11	1.01	1.08
NT2RM1000519	384.12	375.59	411.71	0.98	1.07
NT2RM1000527	760.37	671.53	650.7	0.88	0.86
NT2RM1000539	88.72	87.36	87.5	0.98	0.99
NT2RM1000542	20.49	18.93	21.72	1	1
NT2RM1000553	669.45	501.93	597.88	0.75	0.89
NT2RM1000555	169.88	154.66	164.12	0.91	0.97
NT2RM1000558	68.82	91.81	106.89	1.33	1.55
NT2RM1000563	64.93	65.54	70.44	1.01	1.08
NT2RM1000566	49.22	39.52	49.43	0.81	1
NT2RM1000570	622.11	491.14	631.52	0.79	1.02
NT2RM1000571	169.52	152.17	177.3	0.9	1.05
NT2RM1000574	71.06	105.39	142.76	1.48	2.01
NT2RM1000580	42.99	39.35	54.02	0.93	1.26
NT2RM1000620	80.91	72.21	81.54	0.89	1.01
NT2RM1000623	15.13	5.78	5.07	1	1
NT2RM1000630	22.04	19.4	19.92	1	1
NT2RM1000633	297.44	227.28	286.39	0.76	0.96
NT2RM1000634	31.48	26.17	31.2	1	1
NT2RM1000642	96.27	296.36	209.26	3.08	2.17
NT2RM1000647	408.84	239.71	480.33	0.59	1.17
NT2RM1000648	76.59	65.92	58.67	0.86	0.77
NT2RM1000650	59.69	74.28	85.87	1.24	1.44
NT2RM1000661	94.98	86.95	84.38	0.92	0.89
NT2RM1000666	9.8	9.05	12.53	1	1
NT2RM1000669	27.96	21.57	31.61	1	1
NT2RM1000672	94.01	100.66	97.51	1.07	1.04
NT2RM1000681	340.2	325.38	502.93	0.96	1.48
NT2RM1000691	31.12	33.13	37.23	1	1
NT2RM1000698	160.32	104.14	152.85	0.65	0.95
NT2RM1000699	29.28	40.61	46.71	1.02	1.17

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NT2RM1000702	68.88	68.39	79.17	0.99	1.15
NT2RM1000703	187.35	168.81	235.46	0.9	1.26
NT2RM1000704	330.88	171.18	314.74	0.52	0.95
NT2RM1000725	568.88	353.38	602.8	0.62	1.06
NT2RM1000726	42.21	41.97	38.33	0.99	0.95
NT2RM1000731	58	90.22	85.36	1.56	1.47
NT2RM1000741	30.63	29.93	36.08	1	1
NT2RM1000742	140.95	128.62	165.54	0.91	1.17
NT2RM1000744	71.14	57.53	74.65	0.81	1.05
NT2RM1000746	38.9	43.44	44.92	1.09	1.12
NT2RM1000747	401.56	293.92	412.42	0.73	1.03
NT2RM1000752	52.82	41.21	37.74	0.78	0.76
NT2RM1000767	375.81	459.95	361.68	1.22	0.96
NT2RM1000770	50.4	51.03	54.09	1.01	1.07
NT2RM1000772	7.34	7.75	7.47	1	1
NT2RM1000779	239.32	298.01	289.19	1.25	1.21
NT2RM1000780	35.5	29.18	37.11	1	1
NT2RM1000781	32.29	37.98	39.88	1	1
NT2RM1000789	744.47	945.63	820.28	1.27	1.1
NT2RM1000800	53.22	67.68	57.28	1.27	1.08
NT2RM1000802	234.95	284.25	274.37	1.21	1.17
NT2RM1000811	29.87	21.46	29.19	1	1
NT2RM1000826	73.25	88.22	112.17	1.2	1.53
NT2RM1000829	71.56	73.99	82.84	1.03	1.16
NT2RM1000831	3369.2	3434.64	3154.36	1.02	0.94
NT2RM1000833	310.68	313.19	377.53	1.01	1.22
NT2RM1000834	100.1	103.18	105.83	1.03	1.06
NT2RM1000841	222.44	158.99	212.83	0.71	0.96
NT2RM1000848	58.02	48.22	63.19	0.83	1.09
NT2RM1000850	72.68	65.74	91.52	0.9	1.26
NT2RM1000852	60.7	81.71	93.62	1.35	1.54
NT2RM1000853	35.29	41.08	46.81	1.03	1.17
NT2RM1000855	220.34	208.12	226.99	0.94	1.03
NT2RM1000857	136.66	172.01	209.85	1.26	1.54
NT2RM1000858	114.93	105.62	133.67	0.92	1.16
NT2RM1000867	153.05	186.09	242.59	1.22	1.59
NT2RM1000874	112.58	150.04	162.03	1.33	1.44
NT2RM1000882	36.89	51.4	54.14	1.29	1.35
NT2RM1000883	149.54	169.14	238.11	1.13	1.59
NT2RM1000885	68.22	69.88	83.22	1.02	1.22
NT2RM1000893	196.95	306.68	360.48	1.56	1.83
NT2RM1000894	83.04	73.42	111.3	0.88	1.34
NT2RM1000898	48.3	63.84	99.15	1.32	2.05
NT2RM1000899	39.53	47.77	39.35	1.19	1
NT2RM1000905	692.08	986.97	1383.31	1.43	2
NT2RM1000910	114.21	83.53	124.57	0.73	1.09

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NT2RM1000914	167.66	213.79	244.64	1.28	1.46
NT2RM1000919	92.88	111.21	118.4	1.2	1.27
NT2RM1000921	25.87	27.11	32.93	1	1
NT2RM1000922	71.07	68.28	84.76	0.96	1.19
NT2RM1000924	27.43	28.42	34.35	1	1
NT2RM1000927	40.19	39.93	40.39	1	1
NT2RM1000951	111.55	131.39	134.34	1.18	1.2
NT2RM1000956	120.01	100.12	132.78	0.83	1.11
NT2RM1000960	341.25	294.92	351.79	0.86	1.03
NT2RM1000961	100.89	121.89	131.35	1.21	1.3
NT2RM1000962	60.37	67.91	79.19	1.12	1.31
NT2RM1000973	224.41	240.99	282.75	1.07	1.26
NT2RM1000978	7.97	8.68	8.31	1	1
NT2RM1000982	77.39	62.06	76.81	0.8	0.99
NT2RM1000991	32.68	28.11	41.1	1	1.03
NT2RM1000994	149.25	143.43	196.82	0.96	1.32
NT2RM1001002	135.28	118.9	162.51	0.88	1.2
NT2RM1001003	75.66	85.12	105.02	1.13	1.39
NT2RM1001008	31.5	29.87	36.32	1	1
NT2RM1001011	89.55	138.92	134.07	1.55	1.5
NT2RM1001013	33.1	43.02	37.21	1.08	1
NT2RM1001017	20.65	15.24	15.98	1	1
NT2RM1001018	822.67	853.12	1001.49	1.04	1.22
NT2RM1001026	44.68	40.96	55.15	0.92	1.23
NT2RM1001028	45.25	36.32	40.25	0.88	0.89
NT2RM1001043	54.68	64.09	61.67	1.17	1.13
NT2RM1001044	49.22	65.59	61.37	1.33	1.25
NT2RM1001059	37.42	44.69	50.77	1.12	1.27
NT2RM1001063	31.53	30.07	33.41	1	1
NT2RM1001066	26.76	24.91	28.09	1	1
NT2RM1001072	11.02	9.39	12.65	1	1
NT2RM1001074	40.55	30.89	47.07	0.99	1.16
NT2RM1001076	34.66	35.71	44.5	1	1.11
NT2RM1001082	89.68	96.46	90.11	1.08	1
NT2RM1001085	11.8	9.18	8.15	1	1
NT2RM1001092	157.45	135.71	134	0.86	0.85
NT2RM1001102	21.77	16.75	21.28	1	1
NT2RM1001103	54.97	45.35	59.22	0.82	1.08
NT2RM1001105	6.69	10.38	19.57	1	1
NT2RM1001112	31.76	23.24	33.19	1	1
NT2RM1001115	75.76	69.74	81.09	0.92	1.07
NT2RM1001122	63.45	45.93	73.53	0.72	1.16
NT2RM1001136	16.27	16.84	16.53	1	1
NT2RM1001139	80.08	83.57	71.22	1.04	0.89
NT2RM2000003	26.2	25.73	27.78	1	1
NT2RM2000006	93.09	88.54	92.22	0.95	0.99

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NT2RM2000010	112.67	106.5	119.94	0.95	1.06
NT2RM2000013	882.41	888.03	725.41	1.01	0.82
NT2RM2000030	209.67	163.23	165.14	0.78	0.79
NT2RM2000032	71.72	86.39	82.13	1.2	1.15
NT2RM2000039	43.29	37.16	60.28	0.92	1.39
NT2RM2000042	76.21	70.14	70.85	0.92	0.93
NT2RM2000092	20.53	19.15	27.51	1	1
NT2RM2000093	106.58	95.15	109.02	0.89	1.02
NT2RM2000101	1000.0	922.42	907.38	0.92	0.91
NT2RM2000104	237.47	271.01	241.15	1.14	1.02
NT2RM2000124	34.25	25.82	31.82	1	1
NT2RM2000155	59.66	44.43	65.9	0.74	1.1
NT2RM2000191	114.23	156.75	130.09	1.37	1.14
NT2RM2000192	27.75	29.05	35.26	1	1
NT2RM2000239	50.61	43.38	45.7	0.86	0.9
NT2RM2000240	595.44	507.8	582.48	0.85	0.98
NT2RM2000241	69	111.38	114.26	1.61	1.66
NT2RM2000250	50.12	48.31	55.4	0.96	1.11
NT2RM2000259	41.58	60	50.09	1.44	1.2
NT2RM2000260	59.39	66.81	56.51	1.12	0.95
NT2RM2000265	10.8	11.43	20.69	1	1
NT2RM2000287	165.28	155.05	206.66	0.94	1.25
NT2RM2000306	137.57	133.65	148.84	0.97	1.08
NT2RM2000312	112.75	127.29	115.44	1.13	1.02
NT2RM2000322	19.42	23.32	29.66	1	1
NT2RM2000343	273.35	276.77	270.61	1.01	0.99
NT2RM2000359	48.38	45.37	76.75	0.94	1.59
NT2RM2000362	633.68	567.62	528.29	0.9	0.83
NT2RM2000363	29.75	33.63	40.91	1	1.02
NT2RM2000368	155.03	136.37	184.84	0.88	1.19
NT2RM2000371	1164.3	1096.97	1448.66	0.94	1.24
NT2RM2000374	78.53	97.18	92.65	1.24	1.18
NT2RM2000387	107.71	123.51	126.32	1.15	1.17
NT2RM2000393	39.26	41.43	49.68	1.04	1.24
NT2RM2000395	22.33	13.96	26.91	1	1
NT2RM2000402	124.66	148.47	146.41	1.19	1.17
NT2RM2000405	24.8	23.2	32.03	1	1
NT2RM2000407	69.92	72.3	102.54	1.03	1.47
NT2RM2000410	353.58	316.96	524.54	0.9	1.48
NT2RM2000420	38.62	37.9	66.12	1	1.65
NT2RM2000422	54.77	57.05	66.72	1.04	1.22
NT2RM2000423	84.64	123.57	137.59	1.46	1.63
NT2RM2000452	31.07	27.94	42.47	1	1.06
NT2RM2000469	20.79	21.85	18.93	1	1
NT2RM2000490	31.24	58.29	39.28	1.46	1
NT2RM2000497	28.84	31.92	24.53	1	1

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NT2RM2000502	57.07	59.73	58.56	1.05	1.03
NT2RM2000504	48.43	83.86	47.93	1.73	0.99
NT2RM2000514	13.84	26.76	21.93	1	1
NT2RM2000522	6.05	7.14	8.16	1	1
NT2RM2000540	48.83	81.33	66.53	1.67	1.36
NT2RM2000556	9.71	10.82	12.13	1	1
NT2RM2000565	37.14	54.23	38.47	1.36	1
NT2RM2000566	98.01	90.47	82.77	0.92	0.84
NT2RM2000567	29.72	25.04	26.37	1	1
NT2RM2000569	62.65	62.91	59.91	1	0.96
NT2RM2000577	72.31	74.41	91.55	1.03	1.27
NT2RM2000581	40.57	41.35	43.8	1.02	1.08
NT2RM2000582	149.36	151.72	121	1.02	0.81
NT2RM2000588	488.52	620.92	435.36	1.27	0.89
NT2RM2000589	85.88	92.01	73.68	1.07	0.86
NT2RM2000594	21.29	23.82	19.24	1	1
NT2RM2000599	97.98	141.01	124.7	1.44	1.27
NT2RM2000609	49.6	62.4	53.7	1.26	1.08
NT2RM2000612	52.83	49.57	47.87	0.94	0.91
NT2RM2000622	305.81	375.38	330.87	1.23	1.08
NT2RM2000623	63.37	75.68	55.42	1.19	0.87
NT2RM2000624	113.24	216.21	165.59	1.91	1.46
NT2RM2000632	38.68	42.1	43.68	1.05	1.09
NT2RM2000635	47.15	52.8	40.14	1.12	0.85
NT2RM2000636	68.84	65.67	51.54	0.95	0.75
NT2RM2000639	45.38	35.69	42.59	0.88	0.94
NT2RM2000649	68.44	68.93	70.35	1.01	1.03
NT2RM2000658	75.72	114.04	120.15	1.51	1.59
NT2RM2000660	135.8	174.73	132.16	1.29	0.97
NT2RM2000669	69.53	77.97	62.95	1.12	0.91
NT2RM2000689	288.03	495.52	315.38	1.72	1.09
NT2RM2000691	39.01	46.34	37.46	1.16	1
NT2RM2000714	64.18	56.41	48.15	0.88	0.75
NT2RM2000718	35.5	35.88	35.5	1	1
NT2RM2000732	91.02	109.27	85.72	1.2	0.94
NT2RM2000735	37.95	74.72	61.59	1.87	1.54
NT2RM2000740	59.49	72.51	62.93	1.22	1.06
NT2RM2000743	37.31	42.53	51.48	1.06	1.29
NT2RM2000772	71.69	113.52	86.58	1.58	1.21
NT2RM2000773	96.92	136.9	106.05	1.41	1.09
NT2RM2000776	113.97	161.61	113.81	1.42	1
NT2RM2000784	48.29	82.83	70.2	1.72	1.45
NT2RM2000795	75.8	108.46	101.32	1.43	1.34
NT2RM2000796	12.15	14.44	21.22	1	1
NT2RM2000798	3656.8	4567.8	2703.07	1.25	0.74
NT2RM2000801	2581.8	2980.63	2435.01	1.15	0.94

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NT2RM2000821	60.79	57.56	58.61	0.95	0.96
NT2RM2000829	113.59	134.23	144.98	1.18	1.28
NT2RM2000837	31.59	45.21	45.96	1.13	1.15
NT2RM2000924	117.07	137.86	133.22	1.18	1.14
NT2RM2000930	126.11	169.96	164.45	1.35	1.3
NT2RM2000937	30.72	50.75	52.96	1.27	1.32
NT2RM2000939	27.36	34.56	30.46	1	1
NT2RM2000942	1256.0	1512.27	923.28	1.2	0.74
NT2RM2000951	28.28	23.17	22.72	1	1
NT2RM2000952	56.92	49.04	56.19	0.86	0.99
NT2RM2000966	2658.2	2039.19	1871.45	0.77	0.7
NT2RM2000973	123.66	342.92	338.45	2.77	2.74
NT2RM2000983	99.79	180.78	148.99	1.81	1.49
NT2RM2000984	42	65.32	47.77	1.56	1.14
NT2RM2000994	114.16	88.68	81.68	0.78	0.72
NT2RM2001004	242.68	275.63	252.42	1.14	1.04
NT2RM2001022	1730.4	2249.51	2213.86	1.3	1.28
NT2RM2001035	139.99	225.12	176.18	1.61	1.26
NT2RM2001038	91.13	106.12	117.24	1.16	1.29
NT2RM2001043	44.12	81.75	86.82	1.85	1.97
NT2RM2001050	29.87	34.66	37.92	1	1
NT2RM2001055	23.49	30.34	33.25	1	1
NT2RM2001065	62.4	73.23	66.9	1.17	1.07
NT2RM2001075	1350.5	1350.28	1215.36	1	0.9
NT2RM2001083	52.05	38.85	44.52	0.77	0.86
NT2RM2001100	1743.0	1583.8	1492.51	0.91	0.86
NT2RM2001105	50.52	70.21	68.29	1.39	1.35
NT2RM2001109	42.95	85.38	92.75	1.99	2.16
NT2RM2001110	115.95	98.15	124.56	0.85	1.07
NT2RM2001126	39.79	63.82	43.63	1.6	1.09
NT2RM2001131	175.04	160.54	172.03	0.92	0.98
NT2RM2001141	70.88	76.66	72.04	1.08	1.02
NT2RM2001152	37.6	40.73	29.73	1.02	1
NT2RM2001177	44.29	51.24	43.11	1.16	0.97
NT2RM2001194	56.4	70.13	62.83	1.24	1.11
NT2RM2001195	57.4	95.17	84.28	1.66	1.47
NT2RM2001196	31.25	44.94	37.86	1.12	1
NT2RM2001201	243.06	286.14	242	1.18	1
NT2RM2001221	24.56	28.87	31.42	1	1
NT2RM2001238	28.69	23.85	29.04	1	1
NT2RM2001243	67.91	92.26	67.57	1.36	0.99
NT2RM2001244	95.64	151.29	119.32	1.58	1.25
NT2RM2001247	3320.8	3016.61	2845.07	0.91	0.86
NT2RM2001256	31.93	38.8	35.66	1	1
NT2RM2001269	38.59	52.49	51.87	1.31	1.3
NT2RM2001278	54.6	59.71	49.01	1.09	0.9

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NT2RM2001291	31.01	32.62	37.43	1	1
NT2RM2001294	111.61	152.6	125.32	1.37	1.12
NT2RM2001295	20.87	23.3	22.82	1	1
NT2RM2001302	45.07	42.65	37.73	0.95	0.89
NT2RM2001306	28.43	30.16	33	1	1
NT2RM2001312	23.88	30.8	37.9	1	1
NT2RM2001319	35.78	33.67	42.95	1	1.07
NT2RM2001324	109.82	110.38	110.4	1.01	1.01
NT2RM2001345	57.37	78.54	51.97	1.37	0.91
NT2RM2001360	53.08	64.78	45.26	1.22	0.85
NT2RM2001370	44.51	55.87	48.6	1.26	1.09
NT2RM2001391	32.86	44.41	32.93	1.11	1
NT2RM2001393	54.84	54.16	58.29	0.99	1.06
NT2RM2001420	37.83	35.94	34.2	1	1
NT2RM2001423	56.58	55.56	53.84	0.98	0.95
NT2RM2001424	77.16	90.01	61.97	1.17	0.8
NT2RM2001482	98.58	141.22	77.96	1.43	0.79
NT2RM2001499	37.23	47.68	38.61	1.19	1
NT2RM2001504	45.64	49.32	33	1.08	0.88
NT2RM2001524	39.38	32.8	45.75	1	1.14
NT2RM2001530	25.37	18.11	18.68	1	1
NT2RM2001533	100	110.47	98.43	1.1	0.98
NT2RM2001540	82.26	75.41	90.07	0.92	1.09
NT2RM2001544	30.57	35.64	26.42	1	1
NT2RM2001547	113.82	170.69	88.48	1.5	0.78
NT2RM2001558	27.04	29.91	27.88	1	1
NT2RM2001575	38.07	32.74	35.81	1	1
NT2RM2001582	63.32	65.97	60.23	1.04	0.95
NT2RM2001588	45.43	52.78	51.44	1.16	1.13
NT2RM2001592	25.83	34.96	29.52	1	1
NT2RM2001603	41.11	50.81	63.01	1.24	1.53
NT2RM2001605	15.1	18.15	15.41	1	1
NT2RM2001611	45.41	56.27	37.62	1.24	0.88
NT2RM2001613	84.79	134.35	109.36	1.58	1.29
NT2RM2001626	27.1	33.98	27.05	1	1
NT2RM2001632	57.31	58.65	55.45	1.02	0.97
NT2RM2001633	35.59	38.69	38.84	1	1
NT2RM2001635	42.07	61.16	53.47	1.45	1.27
NT2RM2001636	43.4	50.37	62.67	1.16	1.44
NT2RM2001637	49.8	45.86	39.37	0.92	0.8
NT2RM2001639	46.64	57.26	41.93	1.23	0.9
NT2RM2001641	34.29	37.35	34.63	1	1
NT2RM2001643	36.23	38.44	36.77	1	1
NT2RM2001648	69.86	111.45	98.14	1.6	1.4
NT2RM2001652	30.65	37.93	36.61	1	1
NT2RM2001659	29.52	40.61	41.27	1.02	1.03

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NT2RM2001660	24.6	26.68	27.01	1	1
NT2RM2001664	28.91	41.7	28.7	1.04	1
NT2RM2001668	38.35	46.94	36.46	1.17	1
NT2RM2001670	38.83	42.43	34.18	1.06	1
NT2RM2001671	36.58	43.04	39.89	1.08	1
NT2RM2001675	18.5	17.86	19.87	1	1
NT2RM2001681	18.39	37.29	26.11	1	1
NT2RM2001685	15.64	21.66	24.73	1	1
NT2RM2001688	23.01	41.87	44.27	1.05	1.11
NT2RM2001695	98.33	126.9	96.61	1.29	0.98
NT2RM2001696	49.02	89.68	59.78	1.83	1.22
NT2RM2001698	30.08	26.73	26.29	1	1
NT2RM2001699	78.93	86.63	95.27	1.1	1.21
NT2RM2001700	33.38	16.05	20.94	1	1
NT2RM2001704	17.97	38.56	30.22	1	1
NT2RM2001706	50.39	76.82	81.6	1.52	1.62
NT2RM2001714	30.22	38.4	43.36	1	1.08
NT2RM2001716	21.62	19.2	19.6	1	1
NT2RM2001718	26.75	30.2	27.67	1	1
NT2RM2001723	49.63	47.71	45.35	0.96	0.91
NT2RM2001727	54.03	85.56	76.25	1.58	1.41
NT2RM2001730	49.7	51.68	45.32	1.04	0.91
NT2RM2001738	37.73	62.96	64.04	1.57	1.6
NT2RM2001743	32.37	29.73	33.48	1	1
NT2RM2001753	79.31	92.28	97.29	1.16	1.23
NT2RM2001755	23.7	21.4	19.26	1	1
NT2RM2001760	122.09	158.19	131.06	1.3	1.07
NT2RM2001765	23.31	22.7	20.41	1	1
NT2RM2001767	2713.8	2499.05	1813.58	0.92	0.67
NT2RM2001768	41.28	39.78	29.58	0.97	0.97
NT2RM2001771	33.47	71.23	58.4	1.78	1.46
NT2RM2001778	19.9	17.02	18.14	1	1
NT2RM2001782	29.1	32.91	29.65	1	1
NT2RM2001784	19.63	18.32	17.2	1	1
NT2RM2001785	103.23	122.74	120.69	1.19	1.17
NT2RM2001792	34.48	51.05	32.22	1.28	1
NT2RM2001795	18.89	21.04	20.19	1	1
NT2RM2001797	56.08	46.01	43.68	0.82	0.78
NT2RM2001800	27.31	36.49	40.72	1	1.02
NT2RM2001803	27.63	33.93	34.79	1	1
NT2RM2001805	19.29	23.48	22.45	1	1
NT2RM2001806	56.8	44.6	57.05	0.79	1
NT2RM2001813	22.18	20.51	27.32	1	1
NT2RM2001814	15.92	16.08	13.67	1	1
NT2RM2001818	12.25	9.17	6.42	1	1
NT2RM2001823	12.03	12	13.53	1	1

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NT2RM2001825	76.73	90.21	66.21	1.18	0.86
NT2RM2001832	34.07	31.74	31.71	1	1
NT2RM2001839	162.77	158.21	120.87	0.97	0.74
NT2RM2001840	46.43	92.96	35.82	2	0.86
NT2RM2001851	56.46	98.84	57.03	1.75	1.01
NT2RM2001855	34.65	54.11	46.81	1.35	1.17
NT2RM2001867	22.22	30.28	27.81	1	1
NT2RM2001869	447.45	643.55	446.24	1.44	1
NT2RM2001879	17.71	23.87	21.56	1	1
NT2RM2001883	13.11	15.38	22.62	1	1
NT2RM2001886	17.93	24.26	25.9	1	1
NT2RM2001887	42.52	57.65	53.13	1.36	1.25
NT2RM2001896	4419.7	5310.5	5033.88	1.2	1.14
NT2RM2001902	11.41	18.33	15.33	1	1
NT2RM2001903	123.86	148.86	143.22	1.2	1.16
NT2RM2001930	86.13	79.38	80.88	0.92	0.94
NT2RM2001935	25.35	21.03	25.89	1	1
NT2RM2001936	66.92	45.01	62.78	0.67	0.94
NT2RM2001939	23.38	22.8	22.06	1	1
NT2RM2001941	35.01	38.97	37.96	1	1
NT2RM2001950	50.73	76.42	44.15	1.51	0.87
NT2RM2001952	29.77	39.16	27.84	1	1
NT2RM2001976	121.91	188.78	129	1.55	1.06
NT2RM2001982	31.22	28.95	27.53	1	1
NT2RM2001983	42.27	48.47	44.09	1.15	1.04
NT2RM2001984	49.97	43.52	48.82	0.87	0.98
NT2RM2001989	28.31	21.87	20.58	1	1
NT2RM2001996	81.51	110.55	74.43	1.36	0.91
NT2RM2001997	59.77	108.59	91.08	1.82	1.52
NT2RM2001998	44.53	55.01	36.52	1.24	0.9
NT2RM2001999	45.7	43.85	38.36	0.96	0.88
NT2RM2002003	85.31	93.73	87.67	1.1	1.03
NT2RM2002004	24.04	18.65	22.6	1	1
NT2RM2002009	51.6	60.27	47.47	1.17	0.92
NT2RM2002014	27.62	38.89	29.9	1	1
NT2RM2002019	167.06	233.63	137.59	1.4	0.82
NT2RM2002029	65.52	80.57	67.67	1.23	1.03
NT2RM2002030	23.58	22	21.82	1	1
NT2RM2002034	163.22	180.28	154.43	1.1	0.95
NT2RM2002049	38.61	40.38	38.66	1.01	1
NT2RM2002055	32.73	36.75	31.4	1	1
NT2RM2002072	70.41	95.01	77.04	1.35	1.09
NT2RM2002088	112.28	167.17	146.91	1.49	1.31
NT2RM2002091	46.88	64.47	38.65	1.38	0.85
NT2RM2002100	47.76	59.77	49.45	1.25	1.04
NT2RM2002109	25.65	17.4	21.1	1	1

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NT2RM2002126	114.58	153.08	117.89	1.34	1.03
NT2RM2002128	17.42	17.67	22	1	1
NT2RM2002129	52.79	58.86	70.9	1.11	1.34
NT2RM2002142	29.54	51.36	36.39	1.28	1
NT2RM2002144	13.15	19.95	16.09	1	1
NT2RM2002145	47.66	74.03	56.03	1.55	1.18
NT2RM2002153	39.07	44.81	35.1	1.12	1
NT2RM2002163	29.19	25.14	33.1	1	1
NT2RM2002170	31.15	34.65	35.86	1	1
NT2RM2002178	22.89	27.95	24.54	1	1
NT2RM2002179	24.7	31.59	40.28	1	1.01
NT2RM2002270	18.55	21.94	28.6	1	1
NT2RM2002326	26.57	30.5	31.25	1	1
NT2RM2002337	39.81	52.54	49.46	1.31	1.24
NT2RM2002339	26.15	30.92	28.63	1	1
NT2RM2002345	31.22	26.01	33.32	1	1
NT2RM2002368	68.16	123.77	85.06	1.82	1.25
NT2RM2002381	17.23	29.03	21.95	1	1
NT2RM2002424	30.7	51.74	46	1.29	1.15
NT2RM2002450	17.63	18.06	22.55	1	1
NT2RM2002482	17.94	23.88	18.95	1	1
NT2RM2002492	294.08	358.61	254.88	1.22	0.87
NT2RM2002575	61.21	78.65	69.09	1.28	1.13
NT2RM2002580	41.88	46.34	57.05	1.11	1.36
NT2RM2002592	87.11	110.86	101.17	1.27	1.16
NT2RM2002608	518.64	853.07	1012.69	1.64	1.95
NT2RM2002615	28.47	47.78	49.24	1.19	1.23
NT2RM2002622	61.25	96.44	85.88	1.57	1.4
NT2RM2002630	73.68	105.07	65.38	1.43	0.89
NT2RM2002634	49.43	65.77	39.39	1.33	0.81
NT2RM2002645	1900.0	2628.17	2533.79	1.38	1.33
NT2RM2002646	140.18	181.81	171.65	1.3	1.22
NT2RM2002647	171.23	185.67	190.54	1.08	1.11
NT2RM2002652	26.99	49.71	47.19	1.24	1.18
NT2RM2002692	56.76	65.85	77.78	1.16	1.37
NT2RM2002721	209.8	325.22	326.81	1.55	1.56
NT2RM2002748	456.49	569.84	473.45	1.25	1.04
NT2RM2002764	32.77	36.19	26.01	1	1
NT2RM2002772	86	101.51	91.94	1.18	1.07
NT2RM2002811	63.6	91.71	63.24	1.44	0.99
NT2RM2002818	61.95	83.22	71.32	1.34	1.15
NT2RM2002879	55.94	81.51	59.34	1.46	1.06
NT2RM2002979	149	177.61	167.96	1.19	1.13
NT2RM2002981	15.33	24.11	20.58	1	1
NT2RM2002995	23.74	22.97	21.67	1	1
NT2RM2003031	31.13	31	32.86	1	1

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NT2RM2003042	52.77	47.81	47.37	0.91	0.9
NT2RM2003044	21.88	28.24	23.68	1	1
NT2RM2003090	37.06	44.44	47.57	1.11	1.19
NT2RM2003095	39.67	38.29	35.58	1	1
NT2RM2003116	75.97	90.02	97.49	1.18	1.28
NT2RM2003222	24.92	29.13	28.49	1	1
NT2RM2003224	76.09	91.02	85.48	1.2	1.12
NT2RM2003250	1448.2	1629.07	1307.85	1.12	0.9
NT2RM2003258	37.67	54.29	51.5	1.36	1.29
NT2RM2003262	28.29	41.7	34.99	1.04	1
NT2RM4000023	58.12	54.39	70.19	0.94	1.21
NT2RM4000024	30.45	31.42	38.17	1	1
NT2RM4000027	22.17	23.92	23.87	1	1
NT2RM4000030	29.3	33.27	45.07	1	1.13
NT2RM4000033	46.39	38.82	43.27	0.86	0.93
NT2RM4000034	36.05	36.61	43.23	1	1.08
NT2RM4000046	31.66	30.69	31.78	1	1
NT2RM4000052	26.61	25.11	24.31	1	1
NT2RM4000054	87.42	110.33	85.18	1.26	0.97
NT2RM4000061	20.42	23.5	26.75	1	1
NT2RM4000074	313.23	336.15	321.27	1.07	1.03
NT2RM4000085	79.52	71.43	74.49	0.9	0.94
NT2RM4000086	38.11	34.34	34.82	1	1
NT2RM4000100	82.69	133.64	102.71	1.62	1.24
NT2RM4000101	49.6	72.37	51.94	1.46	1.05
NT2RM4000102	296.47	320.39	244.39	1.08	0.82
NT2RM4000104	30.24	29.49	27.42	1	1
NT2RM4000115	40.54	29.89	25.05	0.99	0.99
NT2RM4000129	16.18	18.72	13.9	1	1
NT2RM4000139	37.23	30.85	34.98	1	1
NT2RM4000149	28.75	23.8	27.19	1	1
NT2RM4000155	67.13	66.15	40.36	0.99	0.6
NT2RM4000156	77.61	122.83	120.41	1.58	1.55
NT2RM4000167	17.03	15.76	18.3	1	1
NT2RM4000169	173.93	182.7	173.15	1.05	1
NT2RM4000191	28.35	29.47	28.47	1	1
NT2RM4000197	25.63	34.42	23.43	1	1
NT2RM4000198	49.85	61.16	61.58	1.23	1.24
NT2RM4000199	31.97	35.93	37.39	1	1
NT2RM4000200	20.72	24.18	17.08	1	1
NT2RM4000202	27.14	38.84	27.43	1	1
NT2RM4000210	19.36	18.43	15.27	1	1
NT2RM4000215	24.6	28.07	23.03	1	1
NT2RM4000220	41.55	49.24	44.58	1.19	1.07
NT2RM4000229	21.54	23.38	26.1	1	1
NT2RM4000231	60.97	77.3	115.23	1.27	1.89

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NT2RM4000233	240.26	261.62	202.28	1.09	0.84
NT2RM4000244	18.19	25.51	23.24	1	1
NT2RM4000251	49.99	59.79	61.37	1.2	1.23
NT2RM4000255	22.72	29.75	24.7	1	1
NT2RM4000265	75.96	79.41	84.53	1.05	1.11
NT2RM4000283	358.39	644.7	428.65	1.8	1.2
NT2RM4000284	171	239.9	237.18	1.4	1.39
NT2RM4000290	39.25	39.42	53.37	1	1.33
NT2RM4000295	15.4	18.28	17.97	1	1
NT2RM4000306	117.05	178.24	124.29	1.52	1.06
NT2RM4000307	23.32	34.3	29.47	1	1
NT2RM4000309	17.33	19.41	27.3	1	1
NT2RM4000313	31.75	39.61	36.79	1	1
NT2RM4000318	48.22	44.18	49.48	0.92	1.03
NT2RM4000324	18.71	22.77	25.35	1	1
NT2RM4000326	24.35	26.77	33.97	1	1
NT2RM4000327	37.76	53.78	45.07	1.34	1.13
NT2RM4000344	104.19	157.97	123.91	1.52	1.19
NT2RM4000349	128.63	167.79	143.99	1.3	1.12
NT2RM4000354	23.1	31.29	29.61	1	1
NT2RM4000356	16.53	19.2	21.47	1	1
NT2RM4000366	300.72	464.08	427.64	1.54	1.42
NT2RM4000368	35.92	50.17	46.4	1.25	1.16
NT2RM4000373	58.47	82.55	88.16	1.41	1.51
NT2RM4000386	22.34	22.08	21.23	1	1
NT2RM4000395	73.43	115.71	73.2	1.58	1
NT2RM4000414	26.98	31.47	23.2	1	1
NT2RM4000417	33.77	38.59	37.6	1	1
NT2RM4000421	22.06	26.97	26.45	1	1
NT2RM4000425	203.58	252.97	282.57	1.24	1.39
NT2RM4000433	20.3	18.86	24.84	1	1
NT2RM4000436	44.17	47.94	53.05	1.09	1.2
NT2RM4000444	44.54	62.42	47.09	1.4	1.06
NT2RM4000457	83.64	88.64	62.96	1.06	0.75
NT2RM4000471	47.29	48.74	45.3	1.03	0.96
NT2RM4000472	87.96	113.61	69.04	1.29	0.78
NT2RM4000486	58.45	86.44	79.78	1.48	1.36
NT2RM4000490	44.5	60.67	65.59	1.36	1.47
NT2RM4000496	18.34	17.04	19.81	1	1
NT2RM4000505	304.12	389.73	380.13	1.28	1.25
NT2RM4000511	279.37	374.65	312.32	1.34	1.12
NT2RM4000514	98.69	98.31	78.56	1	0.8
NT2RM4000515	45.21	52.73	43.23	1.17	0.96
NT2RM4000517	562.77	844.94	663.78	1.5	1.18
NT2RM4000520	18.17	17.16	20.49	1	1
NT2RM4000531	40.98	43.93	41.58	1.07	1.01

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NT2RM4000532	26.61	28.47	36.68	1	1
NT2RM4000533	22.04	24.1	25.28	1	1
NT2RM4000534	21.25	21.81	21.99	1	1
NT2RM4000563	61.12	69.77	61.28	1.14	1
NT2RM4000566	34.47	33.15	28.88	1	1
NT2RM4000568	85	99.21	80.71	1.17	0.95
NT2RM4000585	19.2	21.36	19.99	1	1
NT2RM4000587	54.21	49.03	49.32	0.9	0.91
NT2RM4000590	21.22	20.51	18.97	1	1
NT2RM4000593	43.35	54.74	42.19	1.26	0.97
NT2RM4000595	22.5	21.31	15.11	1	1
NT2RM4000603	47.46	52.36	30.94	1.1	0.84
NT2RM4000611	112.75	149.85	98.72	1.33	0.88
NT2RM4000616	24.89	32.7	28.1	1	1
NT2RM4000621	586.97	596.18	566.72	1.02	0.97
NT2RM4000648	16.44	24.32	21.21	1	1
NT2RM4000649	31.45	45.34	49.92	1.13	1.25
NT2RM4000658	38.27	39.09	44.92	1	1.12
NT2RM4000661	344.07	426.94	456.15	1.24	1.33
NT2RM4000673	48.13	49.2	38.85	1.02	0.83
NT2RM4000674	36.05	34.21	29.68	1	1
NT2RM4000689	45.85	54.66	53.97	1.19	1.18
NT2RM4000698	168.33	215.6	154.89	1.28	0.92
NT2RM4000700	23.61	26.01	19.96	1	1
NT2RM4000701	560.54	767.88	596.32	1.37	1.06
NT2RM4000712	63.58	62.9	53.16	0.99	0.84
NT2RM4000717	76.78	76.45	65.9	1	0.86
NT2RM4000733	88.99	108.19	68.25	1.22	0.77
NT2RM4000734	48.34	49.53	40.71	1.02	0.84
NT2RM4000741	37.41	36.38	35.7	1	1
NT2RM4000744	50.1	56.11	43.02	1.12	0.86
NT2RM4000749	151.91	171	171.02	1.13	1.13
NT2RM4000751	74.43	90.92	65.74	1.22	0.88
NT2RM4000752	48.77	59.44	39.02	1.22	0.82
NT2RM4000760	48.06	52.56	43.03	1.09	0.9
NT2RM4000761	5512.3	5636.72	6090.26	1.02	1.1
NT2RM4000764	1096.1	1461.51	1326.8	1.33	1.21
NT2RM4000768	91.31	103.86	68.77	1.14	0.75
NT2RM4000778	38.3	45.36	38.05	1.13	1
NT2RM4000779	71.59	89.76	60.48	1.25	0.84
NT2RM4000787	69.06	72.72	79.08	1.05	1.15
NT2RM4000790	69.92	79.59	86.27	1.14	1.23
NT2RM4000795	25.12	31.01	28.77	1	1
NT2RM4000796	51.85	66.18	46.64	1.28	0.9
NT2RM4000798	31.23	41.47	30.68	1.04	1
NT2RM4000800	193.24	196.15	170.31	1.02	0.88

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NT2RM4000813	72.25	67.46	70.62	0.93	0.98
NT2RM4000820	57.88	65.59	61.2	1.13	1.06
NT2RM4000827	150.9	184.01	182.14	1.22	1.21
NT2RM4000830	34.32	58.31	48.34	1.46	1.21
NT2RM4000833	35.06	39.65	30.68	1	1
NT2RM4000841	144.75	152.53	123.89	1.05	0.86
NT2RM4000846	71.01	67.53	68.33	0.95	0.96
NT2RM4000848	54.02	46.42	53.49	0.86	0.99
NT2RM4000852	64.65	64.24	80.81	0.99	1.25
NT2RM4000855	52.1	86.57	82.73	1.66	1.59
NT2RM4000859	189.28	266.27	200.94	1.41	1.06
NT2RM4000868	37.81	51.68	52.14	1.29	1.3
NT2RM4000870	69.64	71.73	62.8	1.03	0.9
NT2RM4000879	29.32	38.04	47.94	1	1.2
NT2RM4000882	114.2	126.87	135.99	1.11	1.19
NT2RM4000887	32.04	40.23	39.81	1.01	1
NT2RM4000895	43.41	53.66	46.64	1.24	1.07
NT2RM4000897	27.69	35.03	36.98	1	1
NT2RM4000901	27.66	45.28	48.97	1.13	1.22
NT2RM4000950	20.59	37.66	34.91	1	1
NT2RM4000965	45.68	53.17	51.76	1.16	1.13
NT2RM4000971	64.84	80.18	67.9	1.24	1.05
NT2RM4000979	142.52	148.94	119.27	1.05	0.84
NT2RM4000987	31.43	37.32	44.18	1	1.1
NT2RM4000989	28.59	43.4	37.05	1.09	1
NT2RM4000991	29.44	45.26	31.41	1.13	1
NT2RM4000992	44.11	68.26	69.06	1.55	1.57
NT2RM4000996	103.78	134.79	109.57	1.3	1.06
NT2RM4000997	131.96	140.8	92.09	1.07	0.7
NT2RM4001001	387.75	597.27	512.2	1.54	1.32
NT2RM4001002	95.34	112.64	83.9	1.18	0.88
NT2RM4001016	46.48	65.81	53.55	1.42	1.15
NT2RM4001025	1120.1	2182.44	1538.36	1.95	1.37
NT2RM4001027	11.41	21.59	21.88	1	1
NT2RM4001032	54.95	76.57	79.24	1.39	1.44
NT2RM4001047	20.31	26.47	21.93	1	1
NT2RM4001049	41.67	40.94	40.95	0.98	0.98
NT2RM4001051	86.69	126.5	98.09	1.46	1.13
NT2RM4001052	374.43	359.9	370.56	0.96	0.99
NT2RM4001053	243.59	314.69	242.83	1.29	1
NT2RM4001054	27.68	45.1	35.2	1.13	1
NT2RM4001059	35.15	56.85	57.54	1.42	1.44
NT2RM4001071	39.62	51.93	56.26	1.3	1.41
NT2RM4001084	30.93	43	25.89	1.08	1
NT2RM4001092	2340.6	2106.53	2296.21	0.9	0.98
NT2RM4001100	125.1	153.1	154.34	1.22	1.23

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NT2RM4001116	26.66	32.54	21.98	1	1
NT2RM4001119	37.3	46.22	42.48	1.16	1.06
NT2RM4001140	98.86	108.14	103.73	1.09	1.05
NT2RM4001148	241.24	313.97	326.06	1.3	1.35
NT2RM4001151	37.8	58.59	57.49	1.46	1.44
NT2RM4001155	25.49	32.8	22.32	1	1
NT2RM4001157	21.15	25.2	22.25	1	1
NT2RM4001160	29.37	29.18	25.97	1	1
NT2RM4001163	188.84	218.95	223.49	1.16	1.18
NT2RM4001187	33.63	31.17	31.33	1	1
NT2RM4001191	93.85	93.19	89.05	0.99	0.95
NT2RM4001200	58.01	77.21	62.21	1.33	1.07
NT2RM4001203	97.25	136.78	120.84	1.41	1.24
NT2RM4001204	16.42	21.03	14.62	1	1
NT2RM4001217	52.31	56.77	56.78	1.09	1.09
NT2RM4001245	117.18	210.42	145.55	1.8	1.24
NT2RM4001247	47.47	61.42	62.83	1.29	1.32
NT2RM4001256	23.06	28.92	33.6	1	1
NT2RM4001258	91.96	113.16	130.83	1.23	1.42
NT2RM4001267	37.34	41.64	56.31	1.04	1.41
NT2RM4001273	45.19	54.62	56.43	1.21	1.25
NT2RM4001281	38.05	40.25	42.48	1.01	1.06
NT2RM4001286	2695.2	4490.27	2125.09	1.67	0.79
NT2RM4001290	171.42	206.7	191.39	1.21	1.12
NT2RM4001309	39.15	37.18	45.31	1	1.13
NT2RM4001313	70.83	70.3	67.6	0.99	0.95
NT2RM4001316	80.4	94.19	72.75	1.17	0.9
NT2RM4001320	50.01	54.89	54.42	1.1	1.09
NT2RM4001321	49.09	48.14	47.99	0.98	0.98
NT2RM4001325	40.9	39.81	41.61	0.98	1.02
NT2RM4001333	94.89	131.88	83.44	1.39	0.88
NT2RM4001340	102.71	124.42	115.76	1.21	1.13
NT2RM4001344	41.58	38.12	24.95	0.96	0.96
NT2RM4001347	41.49	37.09	45.9	0.96	1.11
NT2RM4001357	46.95	42.22	51.68	0.9	1.1
NT2RM4001360	38.4	43	35.59	1.08	1
NT2RM4001371	50.67	46.7	57.44	0.92	1.13
NT2RM4001377	100.94	115.7	92.79	1.15	0.92
NT2RM4001382	517.54	545.22	413.05	1.05	0.8
NT2RM4001384	43.78	53.97	37.59	1.23	0.91
NT2RM4001400	39.16	27.1	29.78	1	1
NT2RM4001409	41.09	44.07	37.04	1.07	0.97
NT2RM4001410	192.37	214.02	205.45	1.11	1.07
NT2RM4001411	33.91	33.4	38.9	1	1
NT2RM4001412	24.63	35.91	34.18	1	1
NT2RM4001414	36.77	36.77	41.05	1	1.03

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NT2RM4001436	128.77	134.34	131.03	1.04	1.02
NT2RM4001437	101.14	115.23	107.5	1.14	1.06
NT2RM4001444	105.54	118.22	124.45	1.12	1.18
NT2RM4001454	48.96	49.52	53.38	1.01	1.09
NT2RM4001455	81.56	82.19	88.12	1.01	1.08
NT2RM4001483	78.45	99.23	104.79	1.26	1.34
NT2RM4001489	47.1	51.74	60.66	1.1	1.29
NT2RM4001495	29.03	30.9	30.94	1	1
NT2RM4001499	44.22	41.31	47.55	0.93	1.08
NT2RM4001515	42.83	46.77	40.83	1.09	0.95
NT2RM4001519	24.23	25.17	30.37	1	1
NT2RM4001522	76.58	90.42	88.46	1.18	1.16
NT2RM4001523	32.34	32.57	40.73	1	1.02
NT2RM4001550	75.85	134.84	100.89	1.78	1.33
NT2RM4001553	85.31	127.57	122.67	1.5	1.44
NT2RM4001554	18.43	21.73	21.9	1	1
NT2RM4001557	58.79	70.12	60.85	1.19	1.04
NT2RM4001565	45.35	52.67	45.34	1.16	1
NT2RM4001566	61.94	75.08	70.99	1.21	1.15
NT2RM4001569	38.74	50.71	51.25	1.27	1.28
NT2RM4001579	103.13	134.66	158.5	1.31	1.54
NT2RM4001582	21.76	31.48	31.89	1	1
NT2RM4001589	131.35	221.23	207.98	1.68	1.58
NT2RM4001592	23.88	28.13	24.11	1	1
NT2RM4001594	53.36	86.81	73.21	1.63	1.37
NT2RM4001597	86.59	101.21	105.48	1.17	1.22
NT2RM4001605	38.87	46.76	45.33	1.17	1.13
NT2RM4001609	470.35	772.76	612.86	1.64	1.3
NT2RM4001610	74.61	214.37	211.62	2.87	2.84
NT2RM4001611	17.67	22.94	23.7	1	1
NT2RM4001618	73.31	92.96	99.03	1.27	1.35
NT2RM4001622	129.72	196.57	165.1	1.52	1.27
NT2RM4001624	29.01	38.04	28.5	1	1
NT2RM4001625	378.34	355.51	322.46	0.94	0.85
NT2RM4001629	67.9	70.33	82.81	1.04	1.22
NT2RM4001632	144	273.9	177.01	1.9	1.23
NT2RM4001642	17.13	23.27	32.21	1	1
NT2RM4001647	73.98	94.17	83.91	1.27	1.13
NT2RM4001650	26.38	38.17	30.22	1	1
NT2RM4001662	52.72	65.79	42.61	1.25	0.81
NT2RM4001666	81.46	97.83	86	1.2	1.06
NT2RM4001670	93.23	85.3	81.42	0.91	0.87
NT2RM4001682	131.21	154.85	129.54	1.18	0.99
NT2RM4001710	1564.6	1258.34	1595.53	0.8	1.02
NT2RM4001712	47.21	56.06	67.91	1.19	1.44
NT2RM4001714	108.2	130.13	130.93	1.2	1.21

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NT2RM4001715	48.21	64.51	45.2	1.34	0.94
NT2RM4001727	33.93	42.19	40.7	1.05	1.02
NT2RM4001731	64.1	84.77	68.29	1.32	1.07
NT2RM4001735	130.25	240.87	194.73	1.85	1.5
NT2RM4001739	46.6	73.41	52.35	1.58	1.12
NT2RM4001741	150.84	167.77	171.21	1.11	1.14
NT2RM4001746	52.99	69.49	59.02	1.31	1.11
NT2RM4001754	32.3	38.91	29.66	1	1
NT2RM4001757	30.03	35.17	27.03	1	1
NT2RM4001758	13.36	11.49	14.67	1	1
NT2RM4001768	96.48	105.15	97.81	1.09	1.01
NT2RM4001775	22.11	29.57	30.89	1	1
NT2RM4001776	27.94	32.75	25.04	1	1
NT2RM4001783	31.33	23.78	18.49	1	1
NT2RM4001793	104.3	118.71	90.15	1.14	0.86
NT2RM4001810	19.21	22.67	20.86	1	1
NT2RM4001813	25.45	38.87	31.61	1	1
NT2RM4001818	49.27	73.6	58.32	1.49	1.18
NT2RM4001819	28.39	45.99	35.45	1.15	1
NT2RM4001823	19.4	26.64	20.38	1	1
NT2RM4001828	46.53	63.27	52.81	1.36	1.13
NT2RM4001835	72.73	76.67	66.98	1.05	0.92
NT2RM4001836	36.86	45.13	45.38	1.13	1.13
NT2RM4001841	45.96	59.76	64.05	1.3	1.39
NT2RM4001842	36.71	55.55	50.22	1.39	1.26
NT2RM4001843	87.81	100.09	81.6	1.14	0.93
NT2RM4001856	101.66	119.4	91.73	1.17	0.9
NT2RM4001858	75.04	83.03	78.7	1.11	1.05
NT2RM4001861	47.89	56.65	53.77	1.18	1.12
NT2RM4001863	82.59	88.16	94.21	1.07	1.14
NT2RM4001865	44.38	46.73	44.55	1.05	1
NT2RM4001869	71.91	72.02	66.99	1	0.93
NT2RM4001873	76.83	89.92	86.62	1.17	1.13
NT2RM4001876	65.14	84.75	73.54	1.3	1.13
NT2RM4001880	70.4	91.64	56.11	1.3	0.8
NT2RM4001885	89.67	106.02	82	1.18	0.91
NT2RM4001889	125.4	151.99	114.93	1.21	0.92
NT2RM4001894	34.91	45.46	35.99	1.14	1
NT2RM4001897	204.89	250.5	226.21	1.22	1.1
NT2RM4001899	49.07	47.42	44.74	0.97	0.91
NT2RM4001905	51.67	62.26	52.17	1.2	1.01
NT2RM4001922	72.78	89.67	75.58	1.23	1.04
NT2RM4001930	62.44	81.25	84.09	1.3	1.35
NT2RM4001938	50.58	51.81	41.75	1.02	0.83
NT2RM4001940	33.09	32.33	28.61	1	1
NT2RM4001942	231.6	297.21	275.86	1.28	1.19

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NT2RM4001953	90.74	103.72	94.35	1.14	1.04
NT2RM4001965	61	62.15	58.39	1.02	0.96
NT2RM4001966	50.99	72.66	73.93	1.42	1.45
NT2RM4001969	60.18	87.8	55.07	1.46	0.92
NT2RM4001974	33.56	32.93	31.15	1	1
NT2RM4001979	64.41	88.18	57.12	1.37	0.89
NT2RM4001980	74.49	76.02	83.45	1.02	1.12
NT2RM4001984	27.39	25.41	23.52	1	1
NT2RM4001987	50.28	50.66	53.71	1.01	1.07
NT2RM4002013	76.6	122.64	108.44	1.6	1.42
NT2RM4002018	29.09	40.83	36.67	1.02	1
NT2RM4002033	63.99	86.98	65.4	1.36	1.02
NT2RM4002034	70.16	84.88	75.16	1.21	1.07
NT2RM4002044	185.8	186.97	170.3	1.01	0.92
NT2RM4002047	35.32	26.91	30.73	1	1
NT2RM4002054	27.83	27.58	40.24	1	1.01
NT2RM4002055	735.97	697.35	680.21	0.95	0.92
NT2RM4002059	107.36	187.77	151.56	1.75	1.41
NT2RM4002061	28.08	36.56	28.2	1	1
NT2RM4002062	52.85	63.2	68.42	1.2	1.29
NT2RM4002063	139.09	194.1	144.59	1.4	1.04
NT2RM4002066	58.76	47.19	38.74	0.8	0.68
NT2RM4002067	71.01	84.76	83.09	1.19	1.17
NT2RM4002073	49.87	62.39	67.69	1.25	1.36
NT2RM4002074	21.07	29.86	30.61	1	1
NT2RM4002075	24.92	31.67	33.6	1	1
NT2RM4002076	20.99	35.64	27.04	1	1
NT2RM4002078	140.95	156.5	164.11	1.11	1.16
NT2RM4002081	154.92	222.7	196.89	1.44	1.27
NT2RM4002082	39.22	39.05	38.19	1	1
NT2RM4002093	24.97	49.83	51.24	1.25	1.28
NT2RM4002109	55.04	88.88	81.99	1.61	1.49
NT2RM4002115	20.02	26.21	31.13	1	1
NT2RM4002118	32.38	41.04	40.68	1.03	1.02
NT2RM4002128	17.53	57.8	26.93	1.45	1
NT2RM4002137	69.79	86.66	89.45	1.24	1.28
NT2RM4002139	78.9	93.29	80.11	1.18	1.02
NT2RM4002140	61.2	81.46	80.66	1.33	1.32
NT2RM4002145	125.43	159.63	189.03	1.27	1.51
NT2RM4002146	42.26	93.75	74.56	2.22	1.76
NT2RM4002161	22.27	26.36	32.51	1	1
NT2RM4002174	56.11	78.09	64.94	1.39	1.16
NT2RM4002178	84.11	112.94	98.26	1.34	1.17
NT2RM4002180	126.18	175.67	127.46	1.39	1.01
NT2RM4002185	227.51	283.91	209.65	1.25	0.92
NT2RM4002189	35.87	54.27	40.06	1.36	1

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NT2RM4002194	234.93	303.59	311.99	1.29	1.33
NT2RM4002198	60.18	103.92	105.8	1.73	1.76
NT2RM4002205	63.59	81.56	95.39	1.28	1.5
NT2RM4002213	68.29	70.3	57.36	1.03	0.84
NT2RM4002216	120.44	159.77	134.22	1.33	1.11
NT2RM4002226	65.73	68.23	61.3	1.04	0.93
NT2RM4002237	60.58	77.04	71.59	1.27	1.18
NT2RM4002240	32.5	32.18	22.63	1	1
NT2RM4002251	32.19	55.68	39.66	1.39	1
NT2RM4002256	131.2	154.84	140.76	1.18	1.07
NT2RM4002262	34.41	53.21	40.28	1.33	1.01
NT2RM4002266	21.1	25.53	23.16	1	1
NT2RM4002276	73.79	106.16	89.43	1.44	1.21
NT2RM4002278	60.49	64.39	52.32	1.06	0.86
NT2RM4002281	258.84	344.35	312.86	1.33	1.21
NT2RM4002287	47.54	55.56	40.05	1.17	0.84
NT2RM4002294	29.47	46.4	45	1.16	1.13
NT2RM4002298	302.27	344.18	321.18	1.14	1.06
NT2RM4002301	31.89	35.33	38.21	1	1
NT2RM4002306	26.05	40.11	34.8	1	1
NT2RM4002323	28.21	27.23	28.89	1	1
NT2RM4002334	580.89	1027.34	1103.66	1.77	1.9
NT2RM4002339	14.17	18.79	16.96	1	1
NT2RM4002344	26.3	31.72	26.25	1	1
NT2RM4002345	29.42	25.59	40.41	1	1.01
NT2RM4002352	23.35	29.18	28.7	1	1
NT2RM4002362	48.61	61.66	54.63	1.27	1.12
NT2RM4002373	30.54	34.73	33.37	1	1
NT2RM4002374	34.69	40.67	37.19	1.02	1
NT2RM4002376	41.81	48.59	42.6	1.16	1.02
NT2RM4002383	135.71	164.55	129.75	1.21	0.96
NT2RM4002390	34.77	39.51	31.28	1	1
NT2RM4002398	468.57	536.7	330.57	1.15	0.71
NT2RM4002409	34.25	33.68	33.12	1	1
NT2RM4002414	39.64	34.37	32.35	1	1
NT2RM4002438	43.02	46.06	42.19	1.07	0.98
NT2RM4002440	60.59	83.4	56.84	1.38	0.94
NT2RM4002446	51.81	47.54	53.11	0.92	1.03
NT2RM4002450	101.02	150.54	99.31	1.49	0.98
NT2RM4002452	29.15	37.09	34.26	1	1
NT2RM4002457	63.86	70.64	54.41	1.11	0.85
NT2RM4002458	35.89	37.71	41.79	1	1.04
NT2RM4002460	18.75	16.58	13.77	1	1
NT2RM4002464	93.31	89.95	91.27	0.96	0.98
NT2RM4002479	46.93	62.64	65.31	1.33	1.39
NT2RM4002482	220.94	263.38	188.95	1.19	0.86

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NT2RM4002489	130.41	160.4	124.11	1.23	0.95
NT2RM4002493	26.7	23.86	26.1	1	1
NT2RM4002499	723.07	714.76	577.95	0.99	0.8
NT2RM4002504	82.32	98.69	90.29	1.2	1.1
NT2RM4002506	42.74	55.77	49.68	1.3	1.16
NT2RM4002510	17.83	17.89	26.59	1	1
NT2RM4002527	16.36	27.03	27.7	1	1
NT2RM4002532	77.69	101.78	68.2	1.31	0.88
NT2RM4002534	30.41	25.95	24.78	1	1
NT2RM4002535	103.87	108.49	101.17	1.04	0.97
NT2RM4002554	25.04	22.11	30.21	1	1
NT2RM4002558	187.08	176.68	159.85	0.94	0.85
NT2RM4002565	50.69	59.63	51.48	1.18	1.02
NT2RM4002567	23.13	28.86	28.57	1	1
NT2RM4002571	52.84	62.95	49.94	1.19	0.95
NT2RM4002572	49.74	57.06	60.16	1.15	1.21
NT2RM4002577	44.63	41.54	51.32	0.93	1.15
NT2RM4002583	27.56	25.22	26.78	1	1
NT2RM4002584	38.86	57.26	34.08	1.43	1
NT2RM4002593	18.84	38.67	29.43	1	1
NT2RM4002594	354.93	379.73	374.74	1.07	1.06
NT2RM4002604	26.08	39.7	31.32	1	1
NT2RM4002614	31.33	45.73	41.53	1.14	1.04
NT2RM4002616	29.74	33.63	31.98	1	1
NT2RM4002623	33.8	44.76	43.98	1.12	1.1
NT2RM4002634	28.34	30.06	29.65	1	1
NT2RM4002636	28.98	42.07	35.72	1.05	1
NT2RP1000002	783.56	989.83	762.7	1.26	0.97
NT2RP1000006	19.15	36.13	28.97	1	1
NT2RP1000015	13.29	15.95	23	1	1
NT2RP1000018	18.26	41.62	31.24	1.04	1
NT2RP1000034	364.83	512.17	477	1.4	1.31
NT2RP1000035	29.11	44.37	46.07	1.11	1.15
NT2RP1000040	23.69	27.1	25.25	1	1
NT2RP1000042	6.4	10.06	13.92	1	1
NT2RP1000048	36.49	42.88	58.49	1.07	1.46
NT2RP1000050	21.19	24.55	22.35	1	1
NT2RP1000056	11.56	17.63	19.99	1	1
NT2RP1000058	13.29	17.52	14.1	1	1
NT2RP1000063	25.2	27.15	22.59	1	1
NT2RP1000068	23.48	32.44	29.33	1	1
NT2RP1000072	410.19	494.58	455.88	1.21	1.11
NT2RP1000073	13.77	16.92	23.11	1	1
NT2RP1000078	12.42	19.14	17.5	1	1
NT2RP1000079	88.57	146.42	140.53	1.65	1.59
NT2RP1000080	84.31	128.13	122.29	1.52	1.45

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NT2RP1000086	14.64	20.28	16.73	1	1
NT2RP1000087	38.81	34.88	33.82	1	1
NT2RP1000089	83.36	91.96	101.65	1.1	1.22
NT2RP1000090	658.23	773.56	742.13	1.18	1.13
NT2RP1000100	26.81	35.69	33.94	1	1
NT2RP1000101	29.01	52.82	42.04	1.32	1.05
NT2RP1000111	28.66	35.46	26.31	1	1
NT2RP1000112	18	18.11	16.98	1	1
NT2RP1000124	41.64	52.58	33.79	1.26	0.96
NT2RP1000125	132.34	127.41	167.85	0.96	1.27
NT2RP1000129	49.17	56.4	51.37	1.15	1.04
NT2RP1000130	39.86	55.33	54.56	1.38	1.36
NT2RP1000154	36.13	70.31	61.72	1.76	1.54
NT2RP1000163	20.3	24.34	22.01	1	1
NT2RP1000170	27.8	33.5	35.68	1	1
NT2RP1000174	9.66	12.07	11.39	1	1
NT2RP1000181	56.18	73.68	44.71	1.31	0.8
NT2RP1000191	30.42	27.7	32.42	1	1
NT2RP1000202	16.39	36.7	21.43	1	1
NT2RP1000239	15.42	18.36	16.94	1	1
NT2RP1000243	9.8	13.91	10.59	1	1
NT2RP1000255	10.44	15.35	15.97	1	1
NT2RP1000259	25.33	24.87	25.12	1	1
NT2RP1000261	16.28	26.77	21.7	1	1
NT2RP1000269	70.97	75.54	44.54	1.06	0.63
NT2RP1000271	265.86	322.88	238.83	1.21	0.9
NT2RP1000272	107.61	115.56	103.3	1.07	0.96
NT2RP1000279	30.15	35.07	28.86	1	1
NT2RP1000290	119.73	118.06	107.31	0.99	0.9
NT2RP1000293	50.14	62.09	53.34	1.24	1.06
NT2RP1000300	104.9	133.59	133.34	1.27	1.27
NT2RP1000324	43.55	50.12	54.58	1.15	1.25
NT2RP1000325	553.32	721.95	728.53	1.3	1.32
NT2RP1000326	94.79	121.32	78.46	1.28	0.83
NT2RP1000331	192.2	265.13	178.81	1.38	0.93
NT2RP1000333	60.04	53.75	48.29	0.9	0.8
NT2RP1000336	37.44	46	33.17	1.15	1
NT2RP1000347	37.49	29.56	37.34	1	1
NT2RP1000348	20.27	26.29	31.08	1	1
NT2RP1000349	22.82	24.76	33.06	1	1
NT2RP1000353	601.73	926.82	584.38	1.54	0.97
NT2RP1000356	1019.1	1168.51	580.55	1.15	0.57
NT2RP1000357	216.2	246.38	162.17	1.14	0.75
NT2RP1000358	65.53	58.82	53.03	0.9	0.81
NT2RP1000360	226.31	295.84	223.91	1.31	0.99
NT2RP1000363	195.18	231.63	193	1.19	0.99

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NT2RP1000376	32.51	35.46	36.21	1	1
NT2RP1000386	1016.5	1321.61	867.33	1.3	0.85
NT2RP1000407	5.32	7.59	7.57	1	1
NT2RP1000409	59.78	56.82	65.46	0.95	1.1
NT2RP1000413	69.79	90.57	67.29	1.3	0.96
NT2RP1000416	15.86	15.64	19.44	1	1
NT2RP1000418	21.75	42.24	39.79	1.06	1
NT2RP1000420	7.52	8.26	7.99	1	1
NT2RP1000434	16.09	22.34	23.5	1	1
NT2RP1000439	50.13	63.29	56.81	1.26	1.13
NT2RP1000443	16.84	27.95	21.68	1	1
NT2RP1000447	28.73	28	31.84	1	1
NT2RP1000448	15.3	21.28	21.33	1	1
NT2RP1000451	40.15	41.54	44.05	1.03	1.1
NT2RP1000458	269.22	327.11	237.22	1.22	0.88
NT2RP1000460	84.79	115.17	89.13	1.36	1.05
NT2RP1000465	234.03	289.93	240.48	1.24	1.03
NT2RP1000468	29.6	45.39	39.04	1.13	1
NT2RP1000470	63.42	55.78	47.48	0.88	0.75
NT2RP1000477	10.67	11.81	16.87	1	1
NT2RP1000478	77.73	68.35	70.15	0.88	0.9
NT2RP1000481	18.06	21.34	26.36	1	1
NT2RP1000493	9.94	13.74	13.87	1	1
NT2RP1000513	78.14	123.56	96.07	1.58	1.23
NT2RP1000522	105.66	144.02	128.95	1.36	1.22
NT2RP1000533	25.12	30.6	33.21	1	1
NT2RP1000544	14.99	21.19	18.76	1	1
NT2RP1000547	7.89	8.41	17.28	1	1
NT2RP1000551	23.73	21.25	35.01	1	1
NT2RP1000567	23.89	31.17	31.14	1	1
NT2RP1000574	16.56	17.25	21.41	1	1
NT2RP1000577	14.71	28.07	27.4	1	1
NT2RP1000579	24.14	36.54	33.55	1	1
NT2RP1000581	16.95	25.65	26.78	1	1
NT2RP1000593	47.34	64.88	47.77	1.37	1.01
NT2RP1000604	61.56	64.82	69.77	1.05	1.13
NT2RP1000609	27.53	20.7	28.27	1	1
NT2RP1000613	9.98	15.45	16.45	1	1
NT2RP1000622	100.7	132.83	133.07	1.32	1.32
NT2RP1000627	80.14	142.3	142.74	1.78	1.78
NT2RP1000629	17.5	20.44	32.13	1	1
NT2RP1000630	41.06	61.66	58.37	1.5	1.42
NT2RP1000639	11.12	15.75	23.46	1	1
NT2RP1000640	967.4	1351.99	969.32	1.4	1
NT2RP1000646	162.45	212.03	182.01	1.31	1.12
NT2RP1000659	134.99	155.78	136	1.15	1.01

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NT2RP1000674	131.94	163.57	174.72	1.24	1.32
NT2RP1000677	73.07	87.05	108.07	1.19	1.48
NT2RP1000679	17.51	26.33	34.64	1	1
NT2RP1000688	25.02	40.14	33.36	1	1
NT2RP1000689	19.07	18.37	21.44	1	1
NT2RP1000695	23.53	23.83	26.74	1	1
NT2RP1000701	13.89	12.36	19.61	1	1
NT2RP1000702	27.4	27.02	27.46	1	1
NT2RP1000713	16.38	17.12	24.49	1	1
NT2RP1000721	41.04	61.53	48.82	1.5	1.19
NT2RP1000730	32.13	35.43	41.3	1	1.03
NT2RP1000733	35.76	52.65	41.11	1.32	1.03
NT2RP1000738	101.02	100.56	128.79	1	1.27
NT2RP1000739	41.47	33.07	43	0.96	1.04
NT2RP1000740	54.41	70.28	43.26	1.29	0.8
NT2RP1000746	32.64	39.28	32.89	1	1
NT2RP1000750	63.2	79.05	71	1.25	1.12
NT2RP1000751	535.84	863.19	692.65	1.61	1.29
NT2RP1000767	10.25	14.45	17.72	1	1
NT2RP1000769	17.06	16.48	14.59	1	1
NT2RP1000780	13.07	9.71	14.07	1	1
NT2RP1000782	86.4	119.97	113.33	1.39	1.31
NT2RP1000796	31.48	28.33	31.78	1	1
NT2RP1000797	19.38	17.89	18.29	1	1
NT2RP1000800	16.74	20.53	23.85	1	1
NT2RP1000825	30.04	40.32	39.98	1.01	1
NT2RP1000833	18.84	22.21	22.77	1	1
NT2RP1000834	225.41	184.16	210.09	0.82	0.93
NT2RP1000836	22.5	22.56	26.12	1	1
NT2RP1000837	49.43	46.34	48.88	0.94	0.99
NT2RP1000846	25.82	27.16	26	1	1
NT2RP1000847	21.34	16.39	20.48	1	1
NT2RP1000851	77.39	76.53	68.29	0.99	0.88
NT2RP1000856	129.86	150.05	143.29	1.16	1.1
NT2RP1000860	47.31	51.35	55.9	1.09	1.18
NT2RP1000902	55.42	61.58	58.95	1.11	1.06
NT2RP1000903	60.13	64.94	57.03	1.08	0.95
NT2RP1000905	54.91	56.45	46.92	1.03	0.85
NT2RP1000915	79.81	85.87	80.31	1.08	1.01
NT2RP1000916	25.83	26.55	26.81	1	1
NT2RP1000921	41.86	53.78	44.26	1.28	1.06
NT2RP1000943	32.85	33.94	35.25	1	1
NT2RP1000944	23.79	28.21	31.66	1	1
NT2RP1000947	89.44	118.73	90.86	1.33	1.02
NT2RP1000954	40.49	55.68	45.57	1.38	1.13
NT2RP1000958	108.25	155.02	121.43	1.43	1.12

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NT2RP1000959	1209.4	1309.09	1127.18	1.08	0.93
NT2RP1000966	194.22	235.85	198.64	1.21	1.02
NT2RP1000974	49.45	40.67	46.56	0.82	0.94
NT2RP1000980	39	48.71	45.93	1.22	1.15
NT2RP1000981	46.88	49.93	57.96	1.07	1.24
NT2RP1000988	49.92	47.71	59.89	0.96	1.2
NT2RP1001002	62.32	64.56	62.48	1.04	1
NT2RP1001004	35.37	45.41	36.39	1.14	1
NT2RP1001007	16.05	12.94	16.09	1	1
NT2RP1001011	42.47	47.86	45.65	1.13	1.07
NT2RP1001013	73.55	107.81	84.27	1.47	1.15
NT2RP1001014	30.74	31.52	34.97	1	1
NT2RP1001020	17.72	19.43	21.66	1	1
NT2RP1001023	2154.0	3334.33	3377.32	1.55	1.57
NT2RP1001027	710.37	814.03	630.79	1.15	0.89
NT2RP1001031	25.79	33.46	28.46	1	1
NT2RP1001033	85.29	106.9	97.68	1.25	1.15
NT2RP1001042	14.85	14.91	21.49	1	1
NT2RP1001045	123.99	172.72	177.9	1.39	1.43
NT2RP1001073	45.13	66.72	76.35	1.48	1.69
NT2RP1001079	39.62	68.89	55.25	1.72	1.38
NT2RP1001080	48.37	69.83	46.73	1.44	0.97
NT2RP1001113	20.66	25.04	24.03	1	1
NT2RP1001159	358.23	321.83	347.05	0.9	0.97
NT2RP1001173	17.28	20.8	25.27	1	1
NT2RP1001176	57.6	87.95	80.33	1.53	1.39
NT2RP1001177	17.96	22.42	30.61	1	1
NT2RP1001185	49.8	67.24	67.81	1.35	1.36
NT2RP1001199	28.05	42.41	52.87	1.06	1.32
NT2RP1001205	142.97	175.9	245.23	1.23	1.72
NT2RP1001215	63.62	70.45	67.2	1.11	1.06
NT2RP1001225	27.07	26.56	30.39	1	1
NT2RP1001245	89.07	125.19	131.45	1.41	1.48
NT2RP1001247	27.49	21.69	26.17	1	1
NT2RP1001248	39.12	71.27	72.36	1.78	1.81
NT2RP1001253	26.83	48.21	45.22	1.21	1.13
NT2RP1001286	47.7	60.65	48.33	1.27	1.01
NT2RP1001294	45.27	69.84	61.91	1.54	1.37
NT2RP1001302	68.44	81.73	70.65	1.19	1.03
NT2RP1001310	98.75	210.95	190.83	2.14	1.93
NT2RP1001311	36.48	30.74	35.87	1	1
NT2RP1001313	55.76	93.63	80.65	1.68	1.45
NT2RP1001324	22.93	36.02	49.17	1	1.23
NT2RP1001349	19.67	34.12	32.23	1	1
NT2RP1001361	124.06	211.05	218.27	1.7	1.76
NT2RP1001379	130.75	156.75	172.56	1.2	1.32

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NT2RP1001385	105.81	138.98	123.83	1.31	1.17
NT2RP1001395	61.03	67.69	72.59	1.11	1.19
NT2RP1001410	160.48	176.66	151.41	1.1	0.94
NT2RP1001424	27.51	35.82	40.24	1	1.01
NT2RP1001432	20.76	34.32	35.47	1	1
NT2RP1001449	35.8	47.61	56.89	1.19	1.42
NT2RP1001457	33.64	48.03	46.99	1.2	1.17
NT2RP1001459	2151.0	2075.54	2104.32	0.96	0.98
NT2RP1001466	112.19	134.67	133.87	1.2	1.19
NT2RP1001475	105.26	128.43	103.27	1.22	0.98
NT2RP1001482	42.59	50.7	47.75	1.19	1.12
NT2RP1001494	51.57	46.05	57.21	0.89	1.11
NT2RP1001500	31.91	58.91	73.75	1.47	1.84
NT2RP1001517	38.05	49.95	54.05	1.25	1.35
NT2RP1001540	52.4	59.26	60.27	1.13	1.15
NT2RP1001543	30.01	34.04	40.7	1	1.02
NT2RP1001546	315.04	335.19	332.76	1.06	1.06
NT2RP1001550	51.55	73.41	60.4	1.42	1.17
NT2RP1001553	28.4	33.91	41.68	1	1.04
NT2RP1001555	339.75	385.1	361	1.13	1.06
NT2RP1001563	29.6	31.22	30.83	1	1
NT2RP1001569	58.73	61.4	56.81	1.05	0.97
NT2RP1001584	111.88	148.14	91.13	1.32	0.81
NT2RP1001599	29.51	27.74	29.16	1	1
NT2RP1001616	65.29	69.86	65.57	1.07	1
NT2RP1001654	95.23	108.9	147.63	1.14	1.55
NT2RP1001665	32.82	35.01	29.4	1	1
NT2RP1001679	2027.1	1858.93	1958.58	0.92	0.97
NT2RP1001681	143.76	120.46	147.72	0.84	1.03
NT2RP1001694	2.56	3.59	40.76	1	1.02
NT2RP2000001	43.33	67.77	35.1	1.56	0.92
NT2RP2000006	44.7	51.87	47.41	1.16	1.06
NT2RP2000007	28.54	28.94	31.16	1	1
NT2RP2000008	39.14	55.21	45.47	1.38	1.14
NT2RP2000010	20.43	21.17	28.83	1	1
NT2RP2000011	130.78	167.97	142.09	1.28	1.09
NT2RP2000027	89.74	130.06	103.43	1.45	1.15
NT2RP2000028	308.45	314.51	478.39	1.02	1.55
NT2RP2000032	23.43	15.84	33.64	1	1
NT2RP2000040	157.96	204.95	168.12	1.3	1.06
NT2RP2000042	99.57	117.18	93.3	1.18	0.94
NT2RP2000045	64.77	72.84	68.28	1.12	1.05
NT2RP2000051	46.96	38.98	38.24	0.85	0.85
NT2RP2000054	46.98	50.21	55.53	1.07	1.18
NT2RP2000056	58.66	54.98	61.96	0.94	1.06
NT2RP2000057	3873.5	3648.58	3956.35	0.94	1.02

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NT2RP2000067	40.41	34.38	30.76	0.99	0.99
NT2RP2000070	64.21	68.17	77.58	1.06	1.21
NT2RP2000076	53.34	63.08	42.82	1.18	0.8
NT2RP2000077	41.3	67.11	45.1	1.62	1.09
NT2RP2000079	78.91	82.96	75.52	1.05	0.96
NT2RP2000088	52.17	45.33	37.25	0.87	0.77
NT2RP2000091	71.46	68.4	58.67	0.96	0.82
NT2RP2000092	134.3	130.12	115.72	0.97	0.86
NT2RP2000097	37.72	49.78	45.83	1.24	1.15
NT2RP2000098	53.5	45.71	53.85	0.85	1.01
NT2RP2000108	128.47	156.67	127.69	1.22	0.99
NT2RP2000114	51.62	41.71	48.24	0.81	0.93
NT2RP2000116	71.27	76.32	71.22	1.07	1
NT2RP2000119	65.35	82.43	67.6	1.26	1.03
NT2RP2000120	51.65	55.51	36.3	1.07	0.77
NT2RP2000126	37.29	39.59	42.6	1	1.07
NT2RP2000133	52.47	59.36	61.64	1.13	1.17
NT2RP2000147	161.46	194.19	148.51	1.2	0.92
NT2RP2000153	145.55	165.48	119.52	1.14	0.82
NT2RP2000156	100.4	144.37	121.8	1.44	1.21
NT2RP2000157	35.22	32.39	36.53	1	1
NT2RP2000161	65.25	68.95	57.51	1.06	0.88
NT2RP2000168	50.39	61.54	59.69	1.22	1.18
NT2RP2000173	2567.9	2567.69	1995.13	1	0.78
NT2RP2000175	21.59	31.61	31.5	1	1
NT2RP2000178	39.4	47.53	43.4	1.19	1.09
NT2RP2000183	126.42	114.91	99.04	0.91	0.78
NT2RP2000195	88.54	85.02	92.28	0.96	1.04
NT2RP2000204	495.67	567.92	463.51	1.15	0.94
NT2RP2000205	33.63	33.34	48.3	1	1.21
NT2RP2000208	57.87	85.28	97.7	1.47	1.69
NT2RP2000224	212.33	268.66	263.12	1.27	1.24
NT2RP2000230	19.59	21.73	25.98	1	1
NT2RP2000231	50.2	63.52	62.3	1.27	1.24
NT2RP2000232	30.2	29.52	38.61	1	1
NT2RP2000233	532.7	537.66	568.3	1.01	1.07
NT2RP2000239	29.23	23.75	38.02	1	1
NT2RP2000240	48.86	52.38	60.8	1.07	1.24
NT2RP2000248	25.68	38.15	32.51	1	1
NT2RP2000256	37.58	60.81	53.52	1.52	1.34
NT2RP2000257	47.21	74.44	58.84	1.58	1.25
NT2RP2000258	53.5	61.82	55.57	1.16	1.04
NT2RP2000261	45.07	58.09	71.4	1.29	1.58
NT2RP2000270	85.48	107.8	90.21	1.26	1.06
NT2RP2000274	27.32	32.17	38.73	1	1
NT2RP2000277	21.36	34.78	29.56	1	1

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NT2RP2000279	26.35	33.28	33.01	1	1
NT2RP2000283	318.76	348.34	367.59	1.09	1.15
NT2RP2000288	37.09	54.85	45.1	1.37	1.13
NT2RP2000289	37.31	48.41	36.96	1.21	1
NT2RP2000297	106.86	195.45	115.76	1.83	1.08
NT2RP2000298	56.85	85.99	71.93	1.51	1.27
NT2RP2000310	22.69	25.14	34.85	1	1
NT2RP2000327	21.36	37.24	39.34	1	1
NT2RP2000328	37.63	75.14	62.02	1.88	1.55
NT2RP2000329	68.46	125.19	115.82	1.83	1.69
NT2RP2000333	34.25	66.09	42.39	1.65	1.06
NT2RP2000337	54.47	58.81	50.01	1.08	0.92
NT2RP2000346	52.42	62.77	53.97	1.2	1.03
NT2RP2000357	78.03	87.75	67.72	1.12	0.87
NT2RP2000358	43.4	35.65	43.97	0.92	1.01
NT2RP2000366	25.87	37.89	38.77	1	1
NT2RP2000369	72.16	113.76	128.11	1.58	1.78
NT2RP2000376	2110.0	2175	2042.6	1.03	0.97
NT2RP2000394	39.98	72.19	67.39	1.8	1.68
NT2RP2000396	150.68	143.23	132.6	0.95	0.88
NT2RP2000412	184.7	185.7	161.5	1.01	0.87
NT2RP2000414	142.17	199.89	151.05	1.41	1.06
NT2RP2000420	24.15	30.61	30.2	1	1
NT2RP2000422	119.59	136.93	125.01	1.14	1.05
NT2RP2000426	986.77	1036.18	1203.44	1.05	1.22
NT2RP2000428	108.12	180.96	150.57	1.67	1.39
NT2RP2000438	45.51	53.56	47.54	1.18	1.04
NT2RP2000447	39.68	32.68	43.83	1	1.1
NT2RP2000448	49.23	46.48	57.06	0.94	1.16
NT2RP2000459	36.77	59.63	39.09	1.49	1
NT2RP2000479	47.21	48.29	48.05	1.02	1.02
NT2RP2000498	103.18	128	103.73	1.24	1.01
NT2RP2000503	29.86	27.28	33.75	1	1
NT2RP2000510	38.67	46.93	35.97	1.17	1
NT2RP2000514	14.99	11.18	16.02	1	1
NT2RP2000516	36.75	51.7	53.43	1.29	1.34
NT2RP2000523	16.51	28.19	21.17	1	1
NT2RP2000533	113.38	150.92	135.46	1.33	1.19
NT2RP2000540	22.38	15.02	18.98	1	1
NT2RP2000547	35.06	40.35	36.33	1.01	1
NT2RP2000557	49.6	52.27	51.73	1.05	1.04
NT2RP2000558	74.22	89.37	70.8	1.2	0.95
NT2RP2000564	49.85	50.78	65.15	1.02	1.31
NT2RP2000565	54.39	78.58	59.75	1.44	1.1
NT2RP2000583	370.72	470.92	369.56	1.27	1
NT2RP2000591	24.01	23.17	19.94	1	1

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NT2RP2000599	12.8	14.55	16.31	1	1
NT2RP2000601	19.39	15.95	21.41	1	1
NT2RP2000603	27.77	21.06	25.88	1	1
NT2RP2000610	69.57	56.72	64.93	0.82	0.93
NT2RP2000614	855.76	949.27	932.88	1.11	1.09
NT2RP2000616	53.74	63.37	53.32	1.18	0.99
NT2RP2000617	74.18	122.29	94.31	1.65	1.27
NT2RP2000623	45.81	53.16	42.68	1.16	0.93
NT2RP2000634	36.25	28.14	30.65	1	1
NT2RP2000636	51.93	54.42	54.52	1.05	1.05
NT2RP2000638	29.95	32.27	25.08	1	1
NT2RP2000644	49.9	42.61	53.89	0.85	1.08
NT2RP2000649	55.42	71.95	82.86	1.3	1.5
NT2RP2000652	71.77	91.68	67.82	1.28	0.94
NT2RP2000656	59.78	67.92	61.23	1.14	1.02
NT2RP2000658	23	22.41	22.68	1	1
NT2RP2000663	57.62	52.83	51.3	0.92	0.89
NT2RP2000664	54.56	57.67	56.71	1.06	1.04
NT2RP2000668	100.83	114.72	104.66	1.14	1.04
NT2RP2000678	12.98	11.76	16.71	1	1
NT2RP2000694	29.59	45.34	48.15	1.13	1.2
NT2RP2000704	104.09	134.52	106.78	1.29	1.03
NT2RP2000710	156.08	185.31	148.88	1.19	0.95
NT2RP2000712	51.99	53.24	50.67	1.02	0.97
NT2RP2000715	48.49	44.28	57.77	0.91	1.19
NT2RP2000720	72.51	80.12	92.21	1.1	1.27
NT2RP2000731	28	25.91	39.97	1	1
NT2RP2000739	31.78	42.25	48.64	1.06	1.22
NT2RP2000748	19.44	30.53	26.64	1	1
NT2RP2000749	95.57	150.14	142.03	1.57	1.49
NT2RP2000758	40.33	38.61	44.94	0.99	1.11
NT2RP2000764	30.91	29.01	39.21	1	1
NT2RP2000766	530.95	469.52	443.14	0.88	0.83
NT2RP2000777	215.78	325.19	257.62	1.51	1.19
NT2RP2000786	626.64	648.53	653.05	1.03	1.04
NT2RP2000793	31.55	41.9	34.29	1.05	1
NT2RP2000796	35.64	41.62	34.74	1.04	1
NT2RP2000809	73.76	90.4	88.69	1.23	1.2
NT2RP2000812	86.6	107.35	112	1.24	1.29
NT2RP2000814	32.54	26.25	37.18	1	1
NT2RP2000816	28.77	34.57	46.02	1	1.15
NT2RP2000818	16.31	28.83	27.01	1	1
NT2RP2000819	17.91	18.14	22.4	1	1
NT2RP2000841	15.84	18.02	23.79	1	1
NT2RP2000842	13.54	19.85	21.08	1	1
NT2RP2000845	200.91	327.04	210.09	1.63	1.05

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NT2RP2000863	35.81	37.42	46.19	1	1.15
NT2RP2000880	106.21	138.54	97.19	1.3	0.92
NT2RP2000892	34.73	50.83	43.42	1.27	1.09
NT2RP2000894	17.87	22.02	31.84	1	1
NT2RP2000903	43.14	45.14	47.23	1.05	1.09
NT2RP2000906	36.05	40.87	43.39	1.02	1.08
NT2RP2000910	33.87	47.79	33.18	1.19	1
NT2RP2000931	164.08	245.2	172.77	1.49	1.05
NT2RP2000932	49.96	59.22	47.4	1.19	0.95
NT2RP2000938	259.38	284.26	277.17	1.1	1.07
NT2RP2000943	71.79	93.75	85.33	1.31	1.19
NT2RP2000957	41.84	51.98	48.75	1.24	1.17
NT2RP2000958	41.56	65.07	73.13	1.57	1.76
NT2RP2000959	66.89	98.1	83.34	1.47	1.25
NT2RP2000965	32.95	53.24	33.5	1.33	1
NT2RP2000970	78.91	104.95	77.98	1.33	0.99
NT2RP2000973	24.73	26.04	21.47	1	1
NT2RP2000985	69.65	72.21	56.52	1.04	0.81
NT2RP2000987	87.16	105.78	103.55	1.21	1.19
NT2RP2000997	80.13	97.31	85.89	1.21	1.07
NT2RP2001024	26.03	27.38	33.24	1	1
NT2RP2001028	23.88	34.34	25.24	1	1
NT2RP2001036	101.52	157.59	127.02	1.55	1.25
NT2RP2001039	28.4	27.08	31.1	1	1
NT2RP2001044	32.5	30.5	31.86	1	1
NT2RP2001056	197.79	172.56	161.5	0.87	0.82
NT2RP2001065	29.72	52.45	44.28	1.31	1.11
NT2RP2001067	44.92	62.2	52.32	1.38	1.16
NT2RP2001070	67.19	71.7	54.18	1.07	0.81
NT2RP2001081	61.11	77.87	53.93	1.27	0.88
NT2RP2001087	29.46	35.27	27.31	1	1
NT2RP2001094	22.14	21.26	21.02	1	1
NT2RP2001119	60.33	108.76	69.44	1.8	1.15
NT2RP2001127	17.96	23.72	21.77	1	1
NT2RP2001133	51.16	86.85	45.53	1.7	0.89
NT2RP2001137	16.49	15.74	24.06	1	1
NT2RP2001142	55.69	65.86	38.8	1.18	0.72
NT2RP2001149	31.08	34.73	31.77	1	1
NT2RP2001168	137.71	156.65	102.11	1.14	0.74
NT2RP2001173	21.85	25.99	21.14	1	1
NT2RP2001174	65.71	87.83	55.84	1.34	0.85
NT2RP2001184	23.5	36.7	32.13	1	1
NT2RP2001196	16.1	14.26	18.3	1	1
NT2RP2001200	27.56	32.1	31.09	1	1
NT2RP2001218	20.98	32.05	37.84	1	1
NT2RP2001223	22.29	26.2	27.23	1	1

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NT2RP2001226	65.91	77.59	89	1.18	1.35
NT2RP2001227	45.59	46.61	51.67	1.02	1.13
NT2RP2001232	68.05	93.8	61.11	1.38	0.9
NT2RP2001233	53.55	73.71	61.36	1.38	1.15
NT2RP2001245	44.76	35.18	39.01	0.89	0.89
NT2RP2001246	101.65	87.38	52.21	0.86	0.51
NT2RP2001268	192.08	201.65	225.69	1.05	1.17
NT2RP2001270	74.98	61.33	67.32	0.82	0.9
NT2RP2001276	71.67	76.83	66	1.07	0.92
NT2RP2001277	70.85	93.01	50.66	1.31	0.72
NT2RP2001290	42.28	44.1	39.86	1.04	0.95
NT2RP2001295	47.09	58.11	39.78	1.23	0.85
NT2RP2001297	1492.2	1825.76	1590.79	1.22	1.07
NT2RP2001301	73.04	82.58	89.76	1.13	1.23
NT2RP2001312	58.31	70.8	68.87	1.21	1.18
NT2RP2001327	47.98	37.69	45.13	0.83	0.94
NT2RP2001328	203.35	324.41	217.98	1.6	1.07
NT2RP2001341	65.71	123.95	78.81	1.89	1.2
NT2RP2001347	100.71	147.98	101.33	1.47	1.01
NT2RP2001366	283.83	384.24	262.05	1.35	0.92
NT2RP2001378	29.48	28.52	28.34	1	1
NT2RP2001381	43.91	49.31	38.49	1.12	0.91
NT2RP2001388	75.49	88.23	79.08	1.17	1.05
NT2RP2001391	3023.1	3065.39	3040.78	1.01	1.01
NT2RP2001392	37.81	40.87	35.44	1.02	1
NT2RP2001394	91.01	118.75	81.66	1.3	0.9
NT2RP2001397	34.43	57.87	34.55	1.45	1
NT2RP2001400	36.12	43.72	31.79	1.09	1
NT2RP2001408	39.39	46.53	40.74	1.16	1.02
NT2RP2001420	96.7	111.15	110.76	1.15	1.15
NT2RP2001423	48.5	55.63	47.6	1.15	0.98
NT2RP2001427	83.83	106.22	91.5	1.27	1.09
NT2RP2001428	35.38	51.69	39.75	1.29	1
NT2RP2001436	46.13	61.5	51.99	1.33	1.13
NT2RP2001440	45.28	41.99	38.81	0.93	0.88
NT2RP2001445	27.65	26.71	29.81	1	1
NT2RP2001449	31.5	25.95	25.94	1	1
NT2RP2001450	16.92	19.29	25.33	1	1
NT2RP2001467	56.12	80.05	75.91	1.43	1.35
NT2RP2001469	30.95	39.4	43.54	1	1.09
NT2RP2001480	72.62	86.81	53.54	1.2	0.74
NT2RP2001495	56.55	70.86	63.86	1.25	1.13
NT2RP2001499	41.6	49.33	53.13	1.19	1.28
NT2RP2001506	98.25	103.7	142.28	1.06	1.45
NT2RP2001508	78.08	143.5	117.36	1.84	1.5
NT2RP2001511	38.29	51.12	48.54	1.28	1.21

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NT2RP2001514	24.73	36.73	25	1	1
NT2RP2001520	20.33	33.13	38.1	1	1
NT2RP2001526	85.77	106.09	89.31	1.24	1.04
NT2RP2001529	839.09	1001.49	736.88	1.19	0.88
NT2RP2001536	44.53	33	33.56	0.9	0.9
NT2RP2001538	740.03	1188.36	1695.08	1.61	2.29
NT2RP2001547	84.7	104.03	89.1	1.23	1.05
NT2RP2001560	75.86	98.96	91.38	1.3	1.2
NT2RP2001562	22.85	24.37	34.14	1	1
NT2RP2001566	48.34	68	61.69	1.41	1.28
NT2RP2001569	84.87	109.94	76.89	1.3	0.91
NT2RP2001576	48.42	73.44	60.54	1.52	1.25
NT2RP2001581	1311.9	1436.7	1317.05	1.1	1
NT2RP2001597	57.28	82.47	77.08	1.44	1.35
NT2RP2001601	41.33	55.71	45.21	1.35	1.09
NT2RP2001613	13.04	15.85	15.36	1	1
NT2RP2001628	22.45	26.29	49.39	1	1.23
NT2RP2001634	79.75	93.39	83.02	1.17	1.04
NT2RP2001635	72.52	93.93	69.18	1.3	0.95
NT2RP2001660	62.38	72.11	63.18	1.16	1.01
NT2RP2001662	59.38	63.25	51.42	1.07	0.87
NT2RP2001663	71.4	78.93	99.37	1.11	1.39
NT2RP2001672	47.4	62.87	47.78	1.33	1.01
NT2RP2001675	23.16	31.24	35.49	1	1
NT2RP2001677	83.75	111.47	109.77	1.33	1.31
NT2RP2001678	55.11	84.27	57.36	1.53	1.04
NT2RP2001683	39.21	47.92	55.22	1.2	1.38
NT2RP2001699	52.91	58.99	46.35	1.11	0.88
NT2RP2001707	43.39	51.58	32.94	1.19	0.92
NT2RP2001720	27.62	25.2	25.69	1	1
NT2RP2001721	33.65	34.98	33.17	1	1
NT2RP2001740	1262.4	1117.62	1042.98	0.89	0.83
NT2RP2001748	78.28	86.56	80.46	1.11	1.03
NT2RP2001755	33.84	36.68	27.45	1	1
NT2RP2001762	15.01	16.61	17.23	1	1
NT2RP2001768	37.77	40.08	28.43	1	1
NT2RP2001769	39.18	50.27	43.39	1.26	1.08
NT2RP2001784	42.22	55.78	53.57	1.32	1.27
NT2RP2001805	40.84	59.72	44.26	1.46	1.08
NT2RP2001813	14.21	13.37	11.43	1	1
NT2RP2001817	25.42	23.48	19.69	1	1
NT2RP2001818	23.9	32.55	23.46	1	1
NT2RP2001837	160.74	168.55	135.16	1.05	0.84
NT2RP2001839	1191.8	1454.46	831.23	1.22	0.7
NT2RP2001861	28.92	22.05	35.81	1	1
NT2RP2001869	52.62	52.2	43.83	0.99	0.83

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NT2RP2001876	121.69	138.01	131.81	1.13	1.08
NT2RP2001878	65.54	73.03	77.06	1.11	1.18
NT2RP2001881	19.21	19.69	29.64	1	1
NT2RP2001883	31.68	32.48	31.12	1	1
NT2RP2001884	187.76	287.99	166.33	1.53	0.89
NT2RP2001885	44.26	43.53	31.31	0.98	0.9
NT2RP2001898	1298.8	1258.52	940.64	0.97	0.72
NT2RP2001900	35.86	33.69	28.16	1	1
NT2RP2001903	91.39	85.36	64.96	0.93	0.71
NT2RP2001907	99.79	113.04	85.86	1.13	0.86
NT2RP2001915	38.93	30.02	34.78	1	1
NT2RP2001921	39.71	40.48	39.46	1.01	1
NT2RP2001926	52.33	75.14	41.41	1.44	0.79
NT2RP2001933	576.99	649.24	448.46	1.13	0.78
NT2RP2001936	26.34	26.14	16.67	1	1
NT2RP2001943	590.9	657.39	667.96	1.11	1.13
NT2RP2001946	29.02	28.02	20.74	1	1
NT2RP2001947	39.27	33.3	34.99	1	1
NT2RP2001948	60.31	48.08	67.81	0.8	1.12
NT2RP2001956	68.62	68.35	67.06	1	0.98
NT2RP2001969	74.65	75.59	64.91	1.01	0.87
NT2RP2001976	32.09	39.53	28.48	1	1
NT2RP2001978	28.53	31.94	30.82	1	1
NT2RP2001985	21.9	20.13	21.08	1	1
NT2RP2001991	40.08	26.28	20.41	1	1
NT2RP2001997	105.94	103.53	100.23	0.98	0.95
NT2RP2002015	821.48	1711.17	1530.93	2.08	1.86
NT2RP2002017	29.74	38.94	27.43	1	1
NT2RP2002025	341.78	416.77	315.25	1.22	0.92
NT2RP2002030	101.57	148.39	117.23	1.46	1.15
NT2RP2002032	23.91	19.24	25.48	1	1
NT2RP2002033	74.82	73.01	75.08	0.98	1
NT2RP2002041	17.14	20.2	23.63	1	1
NT2RP2002046	30.72	36.34	47.23	1	1.18
NT2RP2002047	24.84	31.53	53.04	1	1.33
NT2RP2002050	82.49	83.44	74.08	1.01	0.9
NT2RP2002052	52.28	82.95	60.41	1.59	1.16
NT2RP2002058	33.18	26.41	31.07	1	1
NT2RP2002060	15.52	15.12	21.86	1	1
NT2RP2002063	15.14	14.04	17.05	1	1
NT2RP2002066	22.48	30.42	30.04	1	1
NT2RP2002070	22.72	31.55	34.87	1	1
NT2RP2002076	26.78	28.4	39.98	1	1
NT2RP2002078	1200.7	2229.66	1192.69	1.86	0.99
NT2RP2002079	588.78	774.15	612.62	1.31	1.04
NT2RP2002099	36.5	37.9	44.47	1	1.11

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NT2RP2002105	40.34	45.91	45.74	1.14	1.13
NT2RP2002115	11.19	10.9	13.64	1	1
NT2RP2002124	19.15	35.38	32.26	1	1
NT2RP2002137	12.7	15.52	22.2	1	1
NT2RP2002139	53.48	106.56	130.78	1.99	2.45
NT2RP2002154	29.92	33.15	33.08	1	1
NT2RP2002155	2164.1	2639.36	1995.75	1.22	0.92
NT2RP2002172	47.58	50.76	34.01	1.07	0.84
NT2RP2002185	52.76	65.91	86.64	1.25	1.64
NT2RP2002188	51.39	53.53	55.37	1.04	1.08
NT2RP2002192	50.12	67.16	65.14	1.34	1.3
NT2RP2002193	30.64	53.71	46.97	1.34	1.17
NT2RP2002208	42.88	68.79	51.29	1.6	1.2
NT2RP2002219	26.79	33.88	29.03	1	1
NT2RP2002231	33.24	37.31	26.27	1	1
NT2RP2002232	67.25	54.44	41.12	0.81	0.61
NT2RP2002235	68.42	88.3	102.97	1.29	1.5
NT2RP2002239	619.81	776.91	701.1	1.25	1.13
NT2RP2002252	24.98	27.24	31.85	1	1
NT2RP2002256	43.05	42	46.67	0.98	1.08
NT2RP2002257	71.14	74.89	64.42	1.05	0.91
NT2RP2002259	63.77	46.44	70.23	0.73	1.1
NT2RP2002264	30.02	27.26	19.64	1	1
NT2RP2002267	96.98	131.04	84.7	1.35	0.87
NT2RP2002270	50.47	59.39	51.89	1.18	1.03
NT2RP2002281	27.73	34.88	32.38	1	1
NT2RP2002288	27.3	32.17	32.6	1	1
NT2RP2002292	41.61	46.35	48.46	1.11	1.16
NT2RP2002299	65.33	75.85	51.16	1.16	0.78
NT2RP2002304	32.49	34.35	32.4	1	1
NT2RP2002312	36.51	35.37	26.42	1	1
NT2RP2002316	47.69	63.06	36.82	1.32	0.84
NT2RP2002325	21.22	20.96	16.72	1	1
NT2RP2002333	20.84	25.29	19.68	1	1
NT2RP2002371	128.63	185.12	152.89	1.44	1.19
NT2RP2002373	208.95	162.4	202.85	0.78	0.97
NT2RP2002381	32.68	30.46	22.37	1	1
NT2RP2002385	34.61	34.41	33.53	1	1
NT2RP2002394	12.52	14.46	10.52	1	1
NT2RP2002408	28.97	28.37	32.27	1	1
NT2RP2002409	132.02	150.6	114.23	1.14	0.87
NT2RP2002424	24.92	21.51	30.03	1	1
NT2RP2002426	65.62	83.37	65.13	1.27	0.99
NT2RP2002429	124.02	147.39	137.21	1.19	1.11
NT2RP2002437	43.64	41.89	41.16	0.96	0.94
NT2RP2002439	24.73	27.69	24.96	1	1

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NT2RP2002442	660.7	759.24	550.94	1.15	0.83
NT2RP2002457	72.94	92.17	70.47	1.26	0.97
NT2RP2002464	17.75	17.87	18.81	1	1
NT2RP2002475	25.27	24.21	25.51	1	1
NT2RP2002479	20.08	31.58	29.24	1	1
NT2RP2002487	34.97	38.75	63.12	1	1.58
NT2RP2002498	17.19	15.94	23.68	1	1
NT2RP2002503	154.9	165.45	113.68	1.07	0.73
NT2RP2002504	72.83	116.92	70.31	1.61	0.97
NT2RP2002510	92.39	100.07	89.61	1.08	0.97
NT2RP2002520	41.2	49.35	41.7	1.2	1.01
NT2RP2002527	69.28	97.88	80.73	1.41	1.17
NT2RP2002533	100.48	126.02	123.07	1.25	1.22
NT2RP2002537	78.34	73.82	70.73	0.94	0.9
NT2RP2002542	33.08	24.03	28.5	1	1
NT2RP2002546	51.94	60.77	50.59	1.17	0.97
NT2RP2002549	86.01	90.63	56.73	1.05	0.66
NT2RP2002564	88.69	86.65	68.99	0.98	0.78
NT2RP2002591	72.24	76.96	64.74	1.07	0.9
NT2RP2002595	96.19	101.69	99.78	1.06	1.04
NT2RP2002602	35.14	31.51	37.84	1	1
NT2RP2002606	44.26	32.12	43.7	0.9	0.99
NT2RP2002609	30.18	27.25	22.99	1	1
NT2RP2002618	63.84	67.53	58.78	1.06	0.92
NT2RP2002621	137.36	214.21	160.58	1.56	1.17
NT2RP2002643	44.16	52.49	41.44	1.19	0.94
NT2RP2002672	99.27	85.27	88.28	0.86	0.89
NT2RP2002673	33.31	32.54	28.88	1	1
NT2RP2002674	32.48	29.29	27.86	1	1
NT2RP2002686	50.31	32.26	39.23	0.8	0.8
NT2RP2002688	158.27	158.03	142.85	1	0.9
NT2RP2002695	87.2	101.22	68.28	1.16	0.78
NT2RP2002701	60.74	87.97	59.89	1.45	0.99
NT2RP2002706	51.79	61.8	57.31	1.19	1.11
NT2RP2002710	305.22	324.01	248.69	1.06	0.81
NT2RP2002721	45.4	55.03	42.99	1.21	0.95
NT2RP2002727	27.76	36.12	30.72	1	1
NT2RP2002734	68.44	78.74	72.28	1.15	1.06
NT2RP2002736	55.64	65.06	57.01	1.17	1.02
NT2RP2002740	26.5	36.58	32.67	1	1
NT2RP2002741	52.42	68.46	55.61	1.31	1.06
NT2RP2002750	85.97	110.9	78.35	1.29	0.91
NT2RP2002752	58.21	64.55	64.72	1.11	1.11
NT2RP2002753	40.88	43.09	45.13	1.05	1.1
NT2RP2002760	37.65	55.19	59.78	1.38	1.49
NT2RP2002769	27.55	35.44	41.67	1	1.04

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NT2RP2002778	44.68	40.94	46.51	0.92	1.04
NT2RP2002791	766.27	997.1	635.97	1.3	0.83
NT2RP2002800	34.99	37.62	31.89	1	1
NT2RP2002805	33.65	25.88	28.6	1	1
NT2RP2002811	34.37	31.97	33.39	1	1
NT2RP2002824	98.05	141.18	121.34	1.44	1.24
NT2RP2002839	155.27	200.57	268.26	1.29	1.73
NT2RP2002845	24.22	28.92	37.44	1	1
NT2RP2002857	19.63	20.87	21.68	1	1
NT2RP2002862	176.44	252.48	216.13	1.43	1.22
NT2RP2002880	52.52	60	58.59	1.14	1.12
NT2RP2002885	78.31	81.02	77.7	1.03	0.99
NT2RP2002891	25.08	26.01	28.99	1	1
NT2RP2002907	24.05	39.75	49.42	1	1.24
NT2RP2002925	26.85	35.21	40.29	1	1.01
NT2RP2002927	56.54	89.26	99.91	1.58	1.77
NT2RP2002928	26.14	29.56	24.51	1	1
NT2RP2002929	74.77	103.8	67.59	1.39	0.9
NT2RP2002934	23.66	25.16	25.56	1	1
NT2RP2002939	40.73	45.35	50.65	1.11	1.24
NT2RP2002942	62.57	78.9	76.51	1.26	1.22
NT2RP2002954	80.07	96.66	124.85	1.21	1.56
NT2RP2002959	55.79	83.95	113.64	1.5	2.04
NT2RP2002974	23.88	29.28	30.59	1	1
NT2RP2002976	44.68	57.28	42.03	1.28	0.94
NT2RP2002979	129.58	178.79	112.71	1.38	0.87
NT2RP2002980	157.13	220.09	132.9	1.4	0.85
NT2RP2002986	47.4	48.06	35.77	1.01	0.84
NT2RP2002987	132.71	168.89	175.01	1.27	1.32
NT2RP2002988	111.84	214.03	170.35	1.91	1.52
NT2RP2002993	25.5	31.38	37.51	1	1
NT2RP2003000	76.46	106.77	86.36	1.4	1.13
NT2RP2003008	331.55	379.73	303.4	1.15	0.92
NT2RP2003020	181.17	195.62	168.89	1.08	0.93
NT2RP2003032	40.48	47.83	34.78	1.18	0.99
NT2RP2003034	145.28	171.31	96.98	1.18	0.67
NT2RP2003042	21.49	25.05	25.25	1	1
NT2RP2003050	19.58	14.34	15.7	1	1
NT2RP2003060	62.53	101.31	83.93	1.62	1.34
NT2RP2003073	113.84	115.05	121.78	1.01	1.07
NT2RP2003099	41.73	51.13	35.91	1.23	0.96
NT2RP2003108	44.33	51.97	44.37	1.17	1
NT2RP2003115	76.15	72.33	55.39	0.95	0.73
NT2RP2003117	63.11	76.62	44.78	1.21	0.71
NT2RP2003121	26.86	30.76	21.49	1	1
NT2RP2003125	73.09	94.3	80.18	1.29	1.1

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NT2RP2003127	17.75	18.12	20.72	1	1
NT2RP2003129	86.58	130.83	76.65	1.51	0.89
NT2RP2003137	26.04	23.71	26.29	1	1
NT2RP2003138	150.72	165.86	90.56	1.1	0.6
NT2RP2003146	267.55	330.27	259.37	1.23	0.97
NT2RP2003148	51.61	56.74	58.16	1.1	1.13
NT2RP2003150	31.83	25.92	40.12	1	1
NT2RP2003157	374.37	442.24	400.41	1.18	1.07
NT2RP2003158	231.08	288.73	253.69	1.25	1.1
NT2RP2003161	34.77	26.93	44.88	1	1.12
NT2RP2003164	18.05	15.52	15.05	1	1
NT2RP2003165	69.08	79.91	55.2	1.16	0.8
NT2RP2003177	37.26	42.87	32.54	1.07	1
NT2RP2003179	29.18	29.09	29.31	1	1
NT2RP2003194	59.15	54.01	59.89	0.91	1.01
NT2RP2003206	19.76	17.37	20.74	1	1
NT2RP2003210	55.61	57.1	56.95	1.03	1.02
NT2RP2003227	44.26	36.25	42.02	0.9	0.95
NT2RP2003228	316.03	318.05	254.76	1.01	0.81
NT2RP2003230	60.62	70.36	78.27	1.16	1.29
NT2RP2003231	32.24	45.25	30.88	1.13	1
NT2RP2003237	58.21	57.82	43.28	0.99	0.74
NT2RP2003239	38.81	42.21	33.65	1.06	1
NT2RP2003243	31.38	28.21	20.39	1	1
NT2RP2003265	32.54	26.78	29.27	1	1
NT2RP2003267	22.93	16.8	22.9	1	1
NT2RP2003272	68.86	81.67	90.05	1.19	1.31
NT2RP2003277	71.96	63.84	62.77	0.89	0.87
NT2RP2003280	52.54	73.49	53.99	1.4	1.03
NT2RP2003286	28.04	26.78	18.22	1	1
NT2RP2003293	71.28	70.24	67.8	0.99	0.95
NT2RP2003295	36.22	40.22	38	1.01	1
NT2RP2003297	28.34	44.52	29.01	1.11	1
NT2RP2003300	100.95	194.28	183.07	1.92	1.81
NT2RP2003302	32.43	34.18	33.1	1	1
NT2RP2003307	14.7	15.78	14.43	1	1
NT2RP2003308	19.05	28.68	21.62	1	1
NT2RP2003311	44	44.95	40.84	1.02	0.93
NT2RP2003329	30.35	27.96	36.19	1	1
NT2RP2003339	54.66	75.38	65.37	1.38	1.2
NT2RP2003345	26.69	20.05	33.5	1	1
NT2RP2003347	20.75	25.26	28.9	1	1
NT2RP2003367	22.37	24.09	19.78	1	1
NT2RP2003369	14.09	18.3	15.2	1	1
NT2RP2003383	44.77	49.15	38.88	1.1	0.89
NT2RP2003390	74.89	87.87	85.57	1.17	1.14

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NT2RP2003391	78.99	105.52	90.86	1.34	1.15
NT2RP2003393	24.3	31.69	32.88	1	1
NT2RP2003394	61.47	72.93	77.78	1.19	1.27
NT2RP2003401	29.3	36.77	36.33	1	1
NT2RP2003403	29.08	33.77	22	1	1
NT2RP2003433	126.57	190.47	111.81	1.5	0.88
NT2RP2003445	35.12	50.9	41.57	1.27	1.04
NT2RP2003446	36.9	48.42	57.41	1.21	1.44
NT2RP2003456	31.7	32.64	28.61	1	1
NT2RP2003466	78.87	117.72	134.62	1.49	1.71
NT2RP2003469	38.03	54.3	59.81	1.36	1.5
NT2RP2003470	35.93	52.34	56.11	1.31	1.4
NT2RP2003471	20.57	26.71	27.17	1	1
NT2RP2003480	164.12	236.44	184.38	1.44	1.12
NT2RP2003495	44.97	57.24	42.73	1.27	0.95
NT2RP2003499	44.06	53.87	60.23	1.22	1.37
NT2RP2003505	14.12	13.89	18.21	1	1
NT2RP2003506	34.66	42.65	39.19	1.07	1
NT2RP2003511	23.66	27.57	43.98	1	1.1
NT2RP2003513	29.42	35.93	47.77	1	1.19
NT2RP2003517	67.98	73.26	75.36	1.08	1.11
NT2RP2003522	52.41	89.04	51.98	1.7	0.99
NT2RP2003525	108.11	164.83	119.07	1.52	1.1
NT2RP2003533	201.25	193.08	228.66	0.96	1.14
NT2RP2003541	84.18	134.97	112.47	1.6	1.34
NT2RP2003543	23.11	28.22	32.49	1	1
NT2RP2003545	16.01	16.7	19.43	1	1
NT2RP2003559	27.55	32.04	25.17	1	1
NT2RP2003564	26.37	31.93	23.11	1	1
NT2RP2003565	243.91	296.02	240.7	1.21	0.99
NT2RP2003567	105.15	123.48	90.75	1.17	0.86
NT2RP2003575	117.24	116.64	97.59	0.99	0.83
NT2RP2003576	1335.4	1624.36	1570.1	1.22	1.18
NT2RP2003579	144.25	216.38	227.85	1.5	1.58
NT2RP2003581	22.57	23.93	26.52	1	1
NT2RP2003587	57.65	75.04	75.78	1.3	1.31
NT2RP2003590	33.61	40.99	39.73	1.02	1
NT2RP2003593	40.65	40.83	32.51	1	0.98
NT2RP2003596	85.94	88.49	78.27	1.03	0.91
NT2RP2003599	63.51	72.53	57.57	1.14	0.91
NT2RP2003600	18.01	22.12	19.26	1	1
NT2RP2003604	71.68	74.24	71.67	1.04	1
NT2RP2003629	27.67	33.18	30.31	1	1
NT2RP2003630	27.27	32.59	26.93	1	1
NT2RP2003643	36.63	42.84	32.71	1.07	1
NT2RP2003655	27.29	33.03	43.48	1	1.09

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NT2RP2003664	84.04	97.96	100.9	1.17	1.2
NT2RP2003668	52.28	63.41	39.59	1.21	0.77
NT2RP2003687	24.2	28.88	25.33	1	1
NT2RP2003691	56.77	82.94	52.58	1.46	0.93
NT2RP2003702	64.53	67.98	50.67	1.05	0.79
NT2RP2003704	26.94	42.5	33.91	1.06	1
NT2RP2003706	13	9.11	10.47	1	1
NT2RP2003713	43.04	45.12	46.52	1.05	1.08
NT2RP2003714	55.18	63.46	54.83	1.15	0.99
NT2RP2003727	35.65	50.3	39.85	1.26	1
NT2RP2003737	36.19	35.71	38	1	1
NT2RP2003751	9.59	9.78	12	1	1
NT2RP2003760	20.65	30.64	41.59	1	1.04
NT2RP2003764	19.42	17.72	23.37	1	1
NT2RP2003769	28.76	51.41	45.44	1.29	1.14
NT2RP2003770	103.65	132.16	103.55	1.28	1
NT2RP2003777	62.83	65.46	58.85	1.04	0.94
NT2RP2003781	227.22	291.9	218.15	1.28	0.96
NT2RP2003785	54.81	70.13	53.63	1.28	0.98
NT2RP2003793	85.13	76.94	56.98	0.9	0.67
NT2RP2003806	126.94	173.95	142.54	1.37	1.12
NT2RP2003825	940.41	1171.4	949.09	1.25	1.01
NT2RP2003840	42.79	45.82	43.67	1.07	1.02
NT2RP2003857	69.35	92.45	49.99	1.33	0.72
NT2RP2003859	58.26	81.21	62.43	1.39	1.07
NT2RP2003871	67.69	76.14	48.09	1.12	0.71
NT2RP2003876	94.1	107.27	76.29	1.14	0.81
NT2RP2003878	43.62	37.63	32.91	0.92	0.92
NT2RP2003885	39.6	38.43	31.02	1	1
NT2RP2003898	89.31	91.03	71.9	1.02	0.81
NT2RP2003902	87.22	116.73	89.89	1.34	1.03
NT2RP2003912	218.24	415.51	277.31	1.9	1.27
NT2RP2003931	43.93	74.7	45.72	1.7	1.04
NT2RP2003940	119.88	137.38	109.06	1.15	0.91
NT2RP2003950	38.31	57.85	35.05	1.45	1
NT2RP2003952	28.71	33.53	29.19	1	1
NT2RP2003968	49.73	49.91	55.64	1	1.12
NT2RP2003976	98.13	164.52	135.8	1.68	1.38
NT2RP2003981	42.71	53.04	41.23	1.24	0.97
NT2RP2003984	109.81	110.82	82.6	1.01	0.75
NT2RP2003986	78.54	108.52	88.82	1.38	1.13
NT2RP2003988	65.23	94.53	60.15	1.45	0.92
NT2RP2004013	130.66	145.55	116.24	1.11	0.89
NT2RP2004014	51.86	73.02	71.42	1.41	1.38
NT2RP2004036	68.93	91.14	103.6	1.32	1.5
NT2RP2004041	45.87	59.05	64.65	1.29	1.41

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NT2RP2004042	34.34	46.91	35.6	1.17	1
NT2RP2004049	119.18	130.39	119.59	1.09	1
NT2RP2004060	70.38	71.01	84.54	1.01	1.2
NT2RP2004066	38.06	34.52	32.27	1	1
NT2RP2004069	49.12	48.58	57	0.99	1.16
NT2RP2004076	23.86	41.08	29.42	1.03	1
NT2RP2004080	27.93	46.37	33.78	1.16	1
NT2RP2004081	55.35	61.77	59.74	1.12	1.08
NT2RP2004098	62.69	81.12	61.52	1.29	0.98
NT2RP2004108	72.22	96.9	81.64	1.34	1.13
NT2RP2004124	49.6	35.29	41.77	0.81	0.84
NT2RP2004130	71.8	91.11	75.86	1.27	1.06
NT2RP2004133	20.73	33.79	29.88	1	1
NT2RP2004141	19.56	31.55	33.62	1	1
NT2RP2004142	31.72	39.25	57.54	1	1.44
NT2RP2004152	24.6	49.38	64.45	1.23	1.61
NT2RP2004165	108.32	154.96	121.86	1.43	1.13
NT2RP2004170	56.54	70.13	67.06	1.24	1.19
NT2RP2004172	61.22	49.25	68.6	0.8	1.12
NT2RP2004176	63.98	101.82	102.25	1.59	1.6
NT2RP2004179	58.32	66.09	69.19	1.13	1.19
NT2RP2004187	28.59	41.27	46.16	1.03	1.15
NT2RP2004190	27.17	48.72	35.84	1.22	1
NT2RP2004194	64.81	108.51	100.19	1.67	1.55
NT2RP2004196	104.89	117.81	114.03	1.12	1.09
NT2RP2004205	109.68	147.41	120.01	1.34	1.09
NT2RP2004207	54.36	58.36	57.09	1.07	1.05
NT2RP2004226	50.34	75.74	53.61	1.5	1.06
NT2RP2004232	42.66	77.03	51.16	1.81	1.2
NT2RP2004239	33.62	42.45	39.89	1.06	1
NT2RP2004240	65.92	95.42	94.14	1.45	1.43
NT2RP2004242	62.53	72.6	75.6	1.16	1.21
NT2RP2004245	41.83	42.98	43.93	1.03	1.05
NT2RP2004270	278.4	373.76	271.06	1.34	0.97
NT2RP2004300	64.33	61.66	59.1	0.96	0.92
NT2RP2004304	76.09	92.71	93.24	1.22	1.23
NT2RP2004313	27.54	36.3	38.31	1	1
NT2RP2004316	30.95	49.24	54.34	1.23	1.36
NT2RP2004321	18.93	16.67	25.09	1	1
NT2RP2004336	20.6	33.65	24.61	1	1
NT2RP2004339	311.81	337.07	307.51	1.08	0.99
NT2RP2004347	48.43	55.94	43.31	1.16	0.89
NT2RP2004364	75.08	108.43	59.18	1.44	0.79
NT2RP2004365	51.96	58.8	43.87	1.13	0.84
NT2RP2004366	41.94	41.12	46.39	0.98	1.11
NT2RP2004373	40.71	47.24	42.9	1.16	1.05

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NT2RP2004375	98.51	111.3	143.19	1.13	1.45
NT2RP2004389	42.75	40.28	39.3	0.94	0.94
NT2RP2004392	89.75	89.36	121.96	1	1.36
NT2RP2004396	61.99	62.76	50.12	1.01	0.81
NT2RP2004399	72.52	89.89	79.85	1.24	1.1
NT2RP2004400	48.32	52.6	52.35	1.09	1.08
NT2RP2004404	396.79	416.19	339.01	1.05	0.85
NT2RP2004410	163.22	233.14	216.35	1.43	1.33
NT2RP2004412	64.71	80.1	44.89	1.24	0.69
NT2RP2004414	31.14	28.58	27.17	1	1
NT2RP2004425	35.7	44.87	48.55	1.12	1.21
NT2RP2004447	38.86	63.12	34.32	1.58	1
NT2RP2004463	94.93	112.23	118.17	1.18	1.24
NT2RP2004476	75.64	98.89	71.55	1.31	0.95
NT2RP2004488	79.81	72.84	68.49	0.91	0.86
NT2RP2004490	37.8	39.37	54.53	1	1.36
NT2RP2004495	84.15	85.14	105.35	1.01	1.25
NT2RP2004512	41.48	35.29	32.02	0.96	0.96
NT2RP2004523	102.36	129.16	84.93	1.26	0.83
NT2RP2004524	62.59	72.8	55.95	1.16	0.89
NT2RP2004536	96	109.85	106.75	1.14	1.11
NT2RP2004538	449.39	541.51	474.16	1.2	1.06
NT2RP2004548	85.01	94.68	72.7	1.11	0.86
NT2RP2004551	49.09	40.63	35.19	0.83	0.81
NT2RP2004556	217.69	243.78	239.38	1.12	1.1
NT2RP2004568	55.4	52.37	65.01	0.95	1.17
NT2RP2004580	132.2	199.31	114.51	1.51	0.87
NT2RP2004585	461.32	561.13	442.05	1.22	0.96
NT2RP2004587	23.75	26.98	22.99	1	1
NT2RP2004594	42.03	41.58	42.14	0.99	1
NT2RP2004600	29.52	34.64	29.35	1	1
NT2RP2004602	107.98	118.23	110.53	1.09	1.02
NT2RP2004606	113.41	309.16	344.5	2.73	3.04
NT2RP2004614	39.24	52.5	40.85	1.31	1.02
NT2RP2004648	79.05	96.15	60.27	1.22	0.76
NT2RP2004655	57.65	113.56	73.28	1.97	1.27
NT2RP2004664	24.72	29.56	22.85	1	1
NT2RP2004670	19.73	14.6	19.24	1	1
NT2RP2004675	76.38	157.04	101.41	2.06	1.33
NT2RP2004681	31.04	40.56	41.49	1.01	1.04
NT2RP2004689	27.72	52.07	93.09	1.3	2.33
NT2RP2004709	75.75	111.56	76.85	1.47	1.01
NT2RP2004710	97.54	158.81	88.3	1.63	0.91
NT2RP2004721	31.95	30.61	55.3	1	1.38
NT2RP2004736	68.13	74.26	74.84	1.09	1.1
NT2RP2004743	41.11	40.64	45.32	0.99	1.1

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NT2RP2004750	154.05	191.29	169.84	1.24	1.1
NT2RP2004755	86.18	139.62	137.63	1.62	1.6
NT2RP2004767	84.96	116.35	81.79	1.37	0.96
NT2RP2004768	205.54	181.13	187.41	0.88	0.91
NT2RP2004775	26.88	26.12	31.71	1	1
NT2RP2004791	90.76	111.21	98.61	1.23	1.09
NT2RP2004794	334.23	427.5	313.46	1.28	0.94
NT2RP2004795	35.78	41.58	32.71	1.04	1
NT2RP2004799	25.36	38.56	45.53	1	1.14
NT2RP2004802	69.78	119.6	123.46	1.71	1.77
NT2RP2004810	40.66	56.27	56.48	1.38	1.39
NT2RP2004816	66.71	12.93	103.38	0.6	1.55
NT2RP2004837	237.92	200.33	286.67	0.84	1.2
NT2RP2004841	32.71	38.2	39.87	1	1
NT2RP2004847	105.22	108.95	145.54	1.04	1.38
NT2RP2004861	25.01	33.52	32.67	1	1
NT2RP2004897	39.34	43.41	40.84	1.09	1.02
NT2RP2004932	41.03	61.33	67.89	1.49	1.65
NT2RP2004933	22.39	28.26	27.38	1	1
NT2RP2004936	43.54	43.99	42.73	1.01	0.98
NT2RP2004951	185.38	81.65	73.62	0.44	0.4
NT2RP2004959	58.55	45.05	48.85	0.77	0.83
NT2RP2004961	94.11	85.7	89.9	0.91	0.96
NT2RP2004962	51.23	59.02	69.86	1.15	1.36
NT2RP2004966	20.25	34.98	36.05	1	1
NT2RP2004967	41.29	51.32	67.2	1.24	1.63
NT2RP2004974	45.13	62.79	59.54	1.39	1.32
NT2RP2004978	44.07	48.81	38.43	1.11	0.91
NT2RP2004982	20.78	20.62	19.94	1	1
NT2RP2004985	672.08	580.66	656.47	0.86	0.98
NT2RP2004999	52.43	55.62	66.74	1.06	1.27
NT2RP2005000	26.4	29.52	42.85	1	1.07
NT2RP2005001	30.84	37.16	58.32	1	1.46
NT2RP2005003	65.23	79.75	77.59	1.22	1.19
NT2RP2005012	107.84	141.37	112.44	1.31	1.04
NT2RP2005018	37.95	40.01	35.87	1	1
NT2RP2005020	251.16	276.02	272.74	1.1	1.09
NT2RP2005022	40.77	51.66	34.86	1.27	0.98
NT2RP2005027	926.57	526.75	654.59	0.57	0.71
NT2RP2005031	41.97	52.7	45.44	1.26	1.08
NT2RP2005035	147.24	185.36	234.94	1.26	1.6
NT2RP2005037	30.72	30.88	40.89	1	1.02
NT2RP2005038	21.88	24.6	24.7	1	1
NT2RP2005048	176.45	217.51	212.45	1.23	1.2
NT2RP2005069	248.86	285.37	306.23	1.15	1.23
NT2RP2005073	141.4	155.91	141.73	1.1	1

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NT2RP2005097	28.09	32.75	35.64	1	1
NT2RP2005108	22.74	21.34	31.09	1	1
NT2RP2005116	41.15	53.6	66.2	1.3	1.61
NT2RP2005126	34.22	45.45	46.98	1.14	1.17
NT2RP2005135	45.22	36.69	33.16	0.88	0.88
NT2RP2005139	22.74	26.34	20.06	1	1
NT2RP2005140	48.41	57.29	55.09	1.18	1.14
NT2RP2005144	21.68	32.94	33.59	1	1
NT2RP2005147	40.37	42.97	45.35	1.06	1.12
NT2RP2005148	87.61	105.49	92.17	1.2	1.05
NT2RP2005159	28.03	39.54	38.53	1	1
NT2RP2005162	31.98	37.51	36.4	1	1
NT2RP2005163	167.01	208.78	151.85	1.25	0.91
NT2RP2005168	31.92	23.09	32.9	1	1
NT2RP2005181	14.93	18.33	30.3	1	1
NT2RP2005204	42.67	47.92	49.6	1.12	1.16
NT2RP2005219	46.08	56.26	50.65	1.22	1.1
NT2RP2005227	57.52	64.28	70.73	1.12	1.23
NT2RP2005237	702.23	905.03	740.94	1.29	1.06
NT2RP2005239	28.92	28.74	44.51	1	1.11
NT2RP2005247	138.92	131.93	183.86	0.95	1.32
NT2RP2005254	63.06	88.92	52.47	1.41	0.83
NT2RP2005270	131.97	191.63	112.76	1.45	0.85
NT2RP2005276	81.65	121.12	79.55	1.48	0.97
NT2RP2005287	67.92	43.13	32.83	0.64	0.59
NT2RP2005288	30.44	39.24	31.71	1	1
NT2RP2005289	84.29	87.29	89.6	1.04	1.06
NT2RP2005293	67.61	78.8	77.73	1.17	1.15
NT2RP2005315	51.46	52.01	53.23	1.01	1.03
NT2RP2005322	140.57	221.72	142.65	1.58	1.01
NT2RP2005325	265.76	349.61	261.62	1.32	0.98
NT2RP2005336	76.14	114.59	67.05	1.5	0.88
NT2RP2005343	82.67	107.8	84	1.3	1.02
NT2RP2005344	34.14	38.09	26.23	1	1
NT2RP2005347	37.29	34.44	31.68	1	1
NT2RP2005354	144.94	150.58	126.74	1.04	0.87
NT2RP2005358	163.78	159.12	162.88	0.97	0.99
NT2RP2005360	61.87	65.97	76.83	1.07	1.24
NT2RP2005378	89.41	144.38	111.09	1.61	1.24
NT2RP2005391	43.26	47.09	44.17	1.09	1.02
NT2RP2005393	53.51	58.69	61	1.1	1.14
NT2RP2005407	38.21	66.93	41.97	1.67	1.05
NT2RP2005419	50.68	48.42	44.09	0.96	0.87
NT2RP2005425	103.27	111.5	100.61	1.08	0.97
NT2RP2005429	72.81	75.45	65.93	1.04	0.91
NT2RP2005436	125.21	162.3	109.64	1.3	0.88

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NT2RP2005441	44.27	52.4	46.13	1.18	1.04
NT2RP2005442	183.99	203.45	212.98	1.11	1.16
NT2RP2005444	215.8	226.22	205.2	1.05	0.95
NT2RP2005453	22.58	25.84	24	1	1
NT2RP2005457	303.62	358.57	733.13	1.18	2.41
NT2RP2005458	34.34	45.8	57.08	1.15	1.43
NT2RP2005463	37.05	68.68	53.42	1.72	1.34
NT2RP2005464	71.14	97.22	75	1.37	1.05
NT2RP2005465	37.23	41.01	48.27	1.03	1.21
NT2RP2005472	316.48	301.15	300.75	0.95	0.95
NT2RP2005476	61.88	55.38	50.22	0.89	0.81
NT2RP2005490	105.98	89.35	98.88	0.84	0.93
NT2RP2005491	183.15	243.56	243.1	1.33	1.33
NT2RP2005495	19.91	34.79	31.35	1	1
NT2RP2005496	142.7	217.32	177.14	1.52	1.24
NT2RP2005498	52.02	62	74.5	1.19	1.43
NT2RP2005501	39.38	30.34	42.15	1	1.05
NT2RP2005506	633.93	904.6	917.02	1.43	1.45
NT2RP2005509	53.92	87.79	79.5	1.63	1.47
NT2RP2005514	22.97	29.12	35.25	1	1
NT2RP2005520	185.87	205.62	262.07	1.11	1.41
NT2RP2005525	29.54	46.93	41.6	1.17	1.04
NT2RP2005531	11.91	17.6	17.21	1	1
NT2RP2005535	134.74	218.17	148.96	1.62	1.11
NT2RP2005539	57.65	66.12	65.45	1.15	1.14
NT2RP2005540	53.2	43.18	54.64	0.81	1.03
NT2RP2005541	59.67	81.33	131.53	1.36	2.2
NT2RP2005549	26.11	55.11	55.91	1.38	1.4
NT2RP2005555	33.68	53.32	59.54	1.33	1.49
NT2RP2005557	29.84	56.2	63.75	1.41	1.59
NT2RP2005581	86.94	117.21	107.5	1.35	1.24
NT2RP2005586	51.69	52.1	57.81	1.01	1.12
NT2RP2005597	28.12	31.78	34.64	1	1
NT2RP2005600	45.99	40.7	56.39	0.88	1.23
NT2RP2005605	116.87	164.11	152.82	1.4	1.31
NT2RP2005614	34.36	43.77	52.17	1.09	1.3
NT2RP2005620	21.89	34.85	41.84	1	1.05
NT2RP2005622	26.95	46.37	42.12	1.16	1.05
NT2RP2005632	54.99	61.66	57.78	1.12	1.05
NT2RP2005635	104.04	125.02	122.81	1.2	1.18
NT2RP2005637	45.18	50.06	42.63	1.11	0.94
NT2RP2005640	62.65	56.16	59.74	0.9	0.95
NT2RP2005645	146.03	164.72	127.78	1.13	0.88
NT2RP2005651	58.01	101.66	88.08	1.75	1.52
NT2RP2005654	23.16	25.7	33.01	1	1
NT2RP2005666	36.67	48.37	40.73	1.21	1.02

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NT2RP2005669	47.34	59.05	49.02	1.25	1.04
NT2RP2005670	52.01	51.97	54.09	1	1.04
NT2RP2005671	95.07	119.76	105.07	1.26	1.11
NT2RP2005675	197.58	176.4	181.02	0.89	0.92
NT2RP2005683	48.29	60.62	52.6	1.26	1.09
NT2RP2005690	33.84	37.58	34.9	1	1
NT2RP2005694	54.44	71.38	72.87	1.31	1.34
NT2RP2005701	76.91	95.76	132.03	1.25	1.72
NT2RP2005712	29.78	38.68	32.64	1	1
NT2RP2005719	57.22	72.99	64.78	1.28	1.13
NT2RP2005722	136.16	123.02	125.23	0.9	0.92
NT2RP2005723	34.36	38.98	47.87	1	1.2
NT2RP2005726	46.95	66.57	61.94	1.42	1.32
NT2RP2005729	171.5	241.49	211.36	1.41	1.23
NT2RP2005731	14.56	13.03	30.45	1	1
NT2RP2005732	868.97	741.23	787.88	0.85	0.91
NT2RP2005737	139.59	115.62	94.86	0.83	0.68
NT2RP2005741	36.86	62.54	59.92	1.56	1.5
NT2RP2005748	52.58	105.09	63.24	2	1.2
NT2RP2005752	64.62	77.63	68.17	1.2	1.05
NT2RP2005753	221.5	224.22	210.21	1.01	0.95
NT2RP2005763	34.18	42.9	49.48	1.07	1.24
NT2RP2005767	37.91	39.1	38.78	1	1
NT2RP2005773	116.76	136.74	134.79	1.17	1.15
NT2RP2005774	78.66	82.34	92.62	1.05	1.18
NT2RP2005775	63.23	61	41.65	0.96	0.66
NT2RP2005781	94.17	112.61	74.46	1.2	0.79
NT2RP2005784	103.3	110.89	83.89	1.07	0.81
NT2RP2005789	148.94	236.78	176.37	1.59	1.18
NT2RP2005799	42.81	38.02	35.82	0.93	0.93
NT2RP2005804	171.73	210	192.39	1.22	1.12
NT2RP2005812	43.57	34.83	40.3	0.92	0.92
NT2RP2005815	25.47	32.69	28.02	1	1
NT2RP2005835	107.47	78.2	91.26	0.73	0.85
NT2RP2005841	74.08	99.48	70.88	1.34	0.96
NT2RP2005853	58.82	79.9	62.95	1.36	1.07
NT2RP2005857	53.87	55.38	46.1	1.03	0.86
NT2RP2005859	48.7	49.64	35.77	1.02	0.82
NT2RP2005860	12.87	12.08	13.69	1	1
NT2RP2005863	44.24	42.73	44.26	0.97	1
NT2RP2005868	44.91	44.98	55.79	1	1.24
NT2RP2005876	142.24	118.34	91.79	0.83	0.65
NT2RP2005878	94.15	127.41	145.24	1.35	1.54
NT2RP2005883	18.53	22.64	21.79	1	1
NT2RP2005886	385.88	460.71	354.33	1.19	0.92
NT2RP2005887	37.85	52.67	47.08	1.32	1.18

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NT2RP2005890	65.71	67.76	46.75	1.04	0.72
NT2RP2005901	31.88	47.82	52.19	1.2	1.3
NT2RP2005902	39.08	41.4	44.78	1.04	1.12
NT2RP2005908	94.52	122.63	90.38	1.3	0.96
NT2RP2005927	28.69	34.86	50.86	1	1.27
NT2RP2005933	45.99	58.31	46	1.27	1
NT2RP2005941	33.2	30.03	42.83	1	1.07
NT2RP2005942	38.15	33.17	41.95	1	1.05
NT2RP2005946	37.21	47.66	39.56	1.19	1
NT2RP2005970	245.7	415.63	364.95	1.69	1.49
NT2RP2005980	27.57	38.5	27.38	1	1
NT2RP2005994	36.84	36.05	31.75	1	1
NT2RP2006004	31.36	26.47	29.04	1	1
NT2RP2006013	53.52	63.17	62.36	1.19	1.17
NT2RP2006023	254.33	347.97	235.94	1.37	0.93
NT2RP2006028	49.91	74.8	74.09	1.5	1.48
NT2RP2006038	13.94	8.52	15.54	1	1
NT2RP2006042	35.94	48.78	51.87	1.22	1.3
NT2RP2006043	59.25	63.23	69.45	1.07	1.17
NT2RP2006052	70.79	79.56	83.54	1.12	1.18
NT2RP2006057	39.92	37.81	51.12	1	1.28
NT2RP2006064	45.72	51.15	93.1	1.12	2.04
NT2RP2006068	49.33	48.11	65.01	0.98	1.32
NT2RP2006069	22.72	38.94	26.22	1	1
NT2RP2006071	24.66	36.75	31.68	1	1
NT2RP2006090	24.93	30.32	39.46	1	1
NT2RP2006092	26.19	36.84	37.75	1	1
NT2RP2006097	219.08	267.5	241.99	1.22	1.1
NT2RP2006098	45.3	52.22	51.87	1.15	1.15
NT2RP2006099	197.06	245.49	204.73	1.25	1.04
NT2RP2006100	37.38	69.47	54.69	1.74	1.37
NT2RP2006103	16.21	28.89	25.74	1	1
NT2RP2006106	86.36	110.14	91.5	1.28	1.06
NT2RP2006127	25.6	34.92	30.49	1	1
NT2RP2006134	52.79	54.03	56.74	1.02	1.07
NT2RP2006141	35.94	55.67	54.37	1.39	1.36
NT2RP2006166	262.07	343.02	226.5	1.31	0.86
NT2RP2006176	50.98	60.42	59.44	1.19	1.17
NT2RP2006181	20.95	21.64	17.07	1	1
NT2RP2006184	197.6	205.28	255.06	1.04	1.29
NT2RP2006186	29.7	24.02	42.07	1	1.05
NT2RP2006196	49.89	53.73	63.47	1.08	1.27
NT2RP2006199	21.22	30.72	25.43	1	1
NT2RP2006200	20.04	28.02	22.31	1	1
NT2RP2006210	190.3	234.04	331.89	1.23	1.74
NT2RP2006219	50.48	46.6	57.46	0.92	1.14

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NT2RP2006224	82.29	10.86	117.7	0.49	1.43
NT2RP2006237	28.01	7.97	31.4	1	1
NT2RP2006238	24.99	25.85	42.34	1	1.06
NT2RP2006258	27.32	32.4	37.21	1	1
NT2RP2006261	23.2	22.02	19.64	1	1
NT2RP2006269	84.32	79.44	94.33	0.94	1.12
NT2RP2006275	634.19	587.83	548.33	0.93	0.86
NT2RP2006282	51.81	56.22	69.03	1.09	1.33
NT2RP2006302	43.82	58.27	48.33	1.33	1.1
NT2RP2006312	65.66	69.12	77.93	1.05	1.19
NT2RP2006320	117.2	148.71	136.69	1.27	1.17
NT2RP2006321	31.95	40.86	34.44	1.02	1
NT2RP2006323	14.55	12.33	13.57	1	1
NT2RP2006333	25.91	34.1	27.48	1	1
NT2RP2006334	39.84	44.01	39.52	1.1	1
NT2RP2006338	21.12	17.89	28.14	1	1
NT2RP2006339	20.07	27.62	26.34	1	1
NT2RP2006355	19.51	21.32	23.89	1	1
NT2RP2006365	18.25	22.48	24.05	1	1
NT2RP2006374	1613.4	1702.3	1315.57	1.06	0.82
NT2RP2006393	85.47	106.95	75.51	1.25	0.88
NT2RP2006394	122.21	159.9	128.55	1.31	1.05
NT2RP2006400	20.6	26.5	20	1	1
NT2RP2006411	197.03	267.32	183.47	1.36	0.93
NT2RP2006429	30.82	35.16	35.32	1	1
NT2RP2006435	21.54	23.95	20.66	1	1
NT2RP2006436	66.84	99.84	96.48	1.49	1.44
NT2RP2006441	32.83	31.52	39.03	1	1
NT2RP2006447	18.75	52.46	42.47	1.31	1.06
NT2RP2006454	52.32	61.91	39.39	1.18	0.76
NT2RP2006455	33.04	31.77	29.07	1	1
NT2RP2006456	35.17	32.94	27.75	1	1
NT2RP2006464	39.57	38.17	31.58	1	1
NT2RP2006467	75.84	85.6	72.34	1.13	0.95
NT2RP2006472	80.6	53.2	68.52	0.66	0.85
NT2RP2006474	83.9	98.77	100.91	1.18	1.2
NT2RP2006475	54.65	71.19	65.43	1.3	1.2
NT2RP2006476	103.5	167.84	72.43	1.62	0.7
NT2RP2006501	99.95	156.07	85.22	1.56	0.85
NT2RP2006512	165.38	190.13	149.63	1.15	0.9
NT2RP2006526	36.45	44.3	40.42	1.11	1.01
NT2RP2006527	54.43	61.68	41.44	1.13	0.76
NT2RP2006534	44.55	44.67	33.64	1	0.9
NT2RP2006537	135.06	142.12	100.2	1.05	0.74
NT2RP2006543	47.42	61.66	53.93	1.3	1.14
NT2RP2006554	65.01	65.19	63.45	1	0.98

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NT2RP2006565	52.73	87.67	59.28	1.66	1.12
NT2RP2006571	38.64	31.27	38.84	1	1
NT2RP2006573	24.83	26.42	23.35	1	1
NT2RP2006598	44.55	52.74	45.13	1.18	1.01
NT2RP2006601	237.67	316.13	233.77	1.33	0.98
NT2RP3000002	67.75	94.87	81.71	1.4	1.21
NT2RP3000011	40.27	51.27	42.82	1.27	1.06
NT2RP3000014	64.09	82.55	73.26	1.29	1.14
NT2RP3000016	60.25	85.07	65.88	1.41	1.09
NT2RP3000022	18.78	16.29	17.22	1	1
NT2RP3000024	60.82	64.84	56.27	1.07	0.93
NT2RP3000031	38.3	41.53	38.71	1.04	1
NT2RP3000034	33.81	47.03	41.05	1.18	1.03
NT2RP3000037	70.35	102.53	70.81	1.46	1.01
NT2RP3000040	25.42	33.11	22.4	1	1
NT2RP3000041	62.42	82.96	57.52	1.33	0.92
NT2RP3000046	88.1	94.32	83.18	1.07	0.94
NT2RP3000047	33.16	39.38	36.46	1	1
NT2RP3000049	43.85	32.36	34.27	0.91	0.91
NT2RP3000050	74.92	109.54	88.44	1.46	1.18
NT2RP3000051	36.52	53.03	57.07	1.33	1.43
NT2RP3000054	43.15	62.33	58.1	1.44	1.35
NT2RP3000055	76.38	117.85	89.05	1.54	1.17
NT2RP3000056	35.69	49.37	45.76	1.23	1.14
NT2RP3000059	47	43.79	43.08	0.93	0.92
NT2RP3000063	19.09	21.17	27.48	1	1
NT2RP3000068	140.16	115.86	110.27	0.83	0.79
NT2RP3000069	47.2	104.8	81.92	2.22	1.74
NT2RP3000072	19.01	34.64	26.31	1	1
NT2RP3000080	108.69	136.08	120.3	1.25	1.11
NT2RP3000085	37.66	42.46	52.31	1.06	1.31
NT2RP3000087	68.12	112.8	83.78	1.66	1.23
NT2RP3000092	34.57	36.04	30.44	1	1
NT2RP3000109	31.21	58.92	49.26	1.47	1.23
NT2RP3000119	66.51	101.4	93.55	1.52	1.41
NT2RP3000125	26.47	34.21	31.63	1	1
NT2RP3000131	96.79	153.54	126.47	1.59	1.31
NT2RP3000134	73.7	128.98	85.29	1.75	1.16
NT2RP3000137	33.87	41.46	41.02	1.04	1.03
NT2RP3000142	66.91	104.65	79.75	1.56	1.19
NT2RP3000148	42.98	47.6	34.62	1.11	0.93
NT2RP3000149	38.86	41.95	36.76	1.05	1
NT2RP3000163	27.92	43.28	36.72	1.08	1
NT2RP3000168	206.14	331.46	311.86	1.61	1.51
NT2RP3000169	20.2	33.43	21.23	1	1
NT2RP3000171	152.24	223.66	186.39	1.47	1.22

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NT2RP3000172	15.66	19.6	19.47	1	1
NT2RP3000186	167.53	185.71	150.17	1.11	0.9
NT2RP3000197	57.78	61.6	48.89	1.07	0.85
NT2RP3000201	65.28	86.63	74.44	1.33	1.14
NT2RP3000204	24.78	41.51	32.52	1.04	1
NT2RP3000207	21.04	29.95	31.39	1	1
NT2RP3000216	29.88	51.11	48.02	1.28	1.2
NT2RP3000220	28	40	31.27	1	1
NT2RP3000221	37.4	34.17	34.95	1	1
NT2RP3000232	63.74	93.59	56.78	1.47	0.89
NT2RP3000233	58.94	60.98	53.13	1.03	0.9
NT2RP3000234	74.55	103.22	70.55	1.38	0.95
NT2RP3000235	22.77	22.48	30.93	1	1
NT2RP3000239	56.22	74.14	56.24	1.32	1
NT2RP3000247	25.72	32.45	42.68	1	1.07
NT2RP3000251	43.21	46.8	55.31	1.08	1.28
NT2RP3000252	49.63	50.57	61.47	1.02	1.24
NT2RP3000255	27.79	34.54	29.21	1	1
NT2RP3000262	59.53	80.34	75.86	1.35	1.27
NT2RP3000266	59.9	82.94	67.93	1.38	1.13
NT2RP3000267	25.21	40.01	38.53	1	1
NT2RP3000271	42.36	50.94	50.87	1.2	1.2
NT2RP3000278	543	360.96	458.15	0.66	0.84
NT2RP3000281	71.44	90.24	58.34	1.26	0.82
NT2RP3000292	22.85	30.52	25.51	1	1
NT2RP3000299	33.15	49.07	32.5	1.23	1
NT2RP3000304	14	17.39	15.1	1	1
NT2RP3000310	179.44	217.36	201.55	1.21	1.12
NT2RP3000312	61.34	65.35	39.79	1.07	0.65
NT2RP3000320	46.64	50.74	42.76	1.09	0.92
NT2RP3000322	101.41	129.36	124	1.28	1.22
NT2RP3000324	436.61	423.83	377.29	0.97	0.86
NT2RP3000326	82.52	85.59	49.29	1.04	0.6
NT2RP3000329	105.53	122.96	80.04	1.17	0.76
NT2RP3000330	63.66	90.05	62.65	1.41	0.98
NT2RP3000333	36.18	37.73	40.19	1	1
NT2RP3000341	130.95	160.84	102.74	1.23	0.78
NT2RP3000344	38.61	30.01	24.98	1	1
NT2RP3000345	11.45	12.73	11.99	1	1
NT2RP3000348	2990.0	3710.2	3532.53	1.24	1.18
NT2RP3000350	64.9	123.73	71.23	1.91	1.1
NT2RP3000359	129.45	148.27	116.24	1.15	0.9
NT2RP3000361	74.9	74.39	60.63	0.99	0.81
NT2RP3000366	80.12	91.67	80.46	1.14	1
NT2RP3000378	28.68	35.68	30.99	1	1
NT2RP3000384	103.53	140.35	104.74	1.36	1.01

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NT2RP3000389	86.34	115.43	110.69	1.34	1.28
NT2RP3000393	46.18	36.54	41.55	0.87	0.9
NT2RP3000395	1487.7	1930.52	1302.83	1.3	0.88
NT2RP3000397	41.26	78.17	46.55	1.89	1.13
NT2RP3000398	101.17	103.54	69.31	1.02	0.69
NT2RP3000403	53.37	60.29	51.57	1.13	0.97
NT2RP3000418	138.46	342.15	131.25	2.47	0.95
NT2RP3000424	46.53	63.27	52.61	1.36	1.13
NT2RP3000427	111.74	160.26	126.82	1.43	1.13
NT2RP3000431	42.77	57.45	89.68	1.34	2.1
NT2RP3000433	165.2	182.88	144.82	1.11	0.88
NT2RP3000436	162.37	229.73	150.7	1.41	0.93
NT2RP3000439	31.16	31.85	29.55	1	1
NT2RP3000441	29.33	29.53	29.97	1	1
NT2RP3000444	20.03	20.53	32.66	1	1
NT2RP3000448	39.27	55.71	61.53	1.39	1.54
NT2RP3000449	21.53	30.58	29.68	1	1
NT2RP3000451	38.61	39.68	42.1	1	1.05
NT2RP3000456	22.13	25.38	27.56	1	1
NT2RP3000460	132.16	148.64	137.38	1.12	1.04
NT2RP3000471	39.3	28.85	40.65	1	1.02
NT2RP3000477	134.16	173.97	158.72	1.3	1.18
NT2RP3000478	28.88	50.61	51.64	1.27	1.29
NT2RP3000481	9.68	20.25	23	1	1
NT2RP3000484	18.56	28.16	27.44	1	1
NT2RP3000487	61.51	93.97	109.7	1.53	1.78
NT2RP3000512	190.14	179.02	177.79	0.94	0.94
NT2RP3000523	163.67	209.19	215.08	1.28	1.31
NT2RP3000526	36.76	51.79	55.52	1.29	1.39
NT2RP3000527	26.38	35.06	33.72	1	1
NT2RP3000531	142.33	286.35	280.41	2.01	1.97
NT2RP3000532	28.51	61.61	60.03	1.54	1.5
NT2RP3000542	65.84	90.43	67.99	1.37	1.03
NT2RP3000554	72.82	95.45	99.85	1.31	1.37
NT2RP3000561	36.35	53.12	48.46	1.33	1.21
NT2RP3000562	31.74	52.5	41.46	1.31	1.04
NT2RP3000578	16.7	17.6	21.3	1	1
NT2RP3000582	20.22	44.4	35.78	1.11	1
NT2RP3000584	15.57	22.12	28.37	1	1
NT2RP3000586	22.97	34.64	36.11	1	1
NT2RP3000590	22.29	32.06	31.1	1	1
NT2RP3000592	31.04	31.96	38.64	1	1
NT2RP3000596	43.39	66.66	52.02	1.54	1.2
NT2RP3000599	36.27	46.5	38.24	1.16	1
NT2RP3000603	254.68	246.24	240.68	0.97	0.95
NT2RP3000605	26.29	34.62	38.06	1	1

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NT2RP3000607	45.24	75.45	73.14	1.67	1.62
NT2RP3000616	14.82	22.67	23.02	1	1
NT2RP3000621	40.05	58.83	51.69	1.47	1.29
NT2RP3000622	35.05	52.01	57.44	1.3	1.44
NT2RP3000624	33.06	40.36	39.69	1.01	1
NT2RP3000628	109.88	187.26	99.41	1.7	0.9
NT2RP3000631	105.63	150.86	137.01	1.43	1.3
NT2RP3000632	50.33	64.39	57.34	1.28	1.14
NT2RP3000638	23.77	26.57	28.7	1	1
NT2RP3000644	304.7	487.68	550.04	1.6	1.81
NT2RP3000645	111.35	124.28	116.48	1.12	1.05
NT2RP3000652	54.8	68.78	81.88	1.26	1.49
NT2RP3000658	40.23	49.35	33.76	1.23	0.99
NT2RP3000660	83.24	131.51	84.43	1.58	1.01
NT2RP3000661	22.15	37.96	30.79	1	1
NT2RP3000665	137.26	166.58	142.33	1.21	1.04
NT2RP3000676	84.64	116.9	89.47	1.38	1.06
NT2RP3000677	22.74	27.27	20.41	1	1
NT2RP3000681	196.87	214.49	150.67	1.09	0.77
NT2RP3000683	97.61	142.2	92.49	1.46	0.95
NT2RP3000685	88.09	92.27	86.67	1.05	0.98
NT2RP3000690	29.96	34.72	34.86	1	1
NT2RP3000698	109.95	139.48	132.06	1.27	1.2
NT2RP3000708	40.63	47.55	39.95	1.17	0.98
NT2RP3000719	22.91	21.41	20.57	1	1
NT2RP3000721	182.39	189.52	179.24	1.04	0.98
NT2RP3000728	20.38	39.27	18.07	1	1
NT2RP3000730	24.26	46.9	28.5	1.17	1
NT2RP3000733	30.31	40.37	34.99	1.01	1
NT2RP3000735	8.98	20.79	13.81	1	1
NT2RP3000736	32.19	36.56	38.66	1	1
NT2RP3000739	91.45	97.24	83.42	1.06	0.91
NT2RP3000742	44.78	60.15	52.95	1.34	1.18
NT2RP3000753	19.16	23.78	30.61	1	1
NT2RP3000759	56.55	39.39	84.1	0.71	1.49
NT2RP3000789	41.47	50.01	37.17	1.21	0.96
NT2RP3000815	74.5	74.88	59.21	1.01	0.79
NT2RP3000818	77.05	97.43	51.97	1.26	0.67
NT2RP3000820	458.65	642.71	243.3	1.4	0.53
NT2RP3000821	32.87	33.65	31.01	1	1
NT2RP3000825	8.12	18.68	12.05	1	1
NT2RP3000826	138.23	241.44	159.01	1.75	1.15
NT2RP3000836	91.4	98.48	104.79	1.08	1.15
NT2RP3000838	3036.2	4396.79	2294.8	1.45	0.76
NT2RP3000839	26.24	30.54	23.82	1	1
NT2RP3000841	52.39	59.34	51.65	1.13	0.99

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NT2RP3000845	82.27	74.14	60.66	0.9	0.74
NT2RP3000847	46.09	53.16	39.49	1.15	0.87
NT2RP3000848	64.4	70.56	53.77	1.1	0.83
NT2RP3000850	86.99	91.14	75.63	1.05	0.87
NT2RP3000852	26.34	20.61	31.38	1	1
NT2RP3000859	76.26	72.23	61.45	0.95	0.81
NT2RP3000861	100.64	153.08	104.76	1.52	1.04
NT2RP3000862	49.12	44.16	40.64	0.9	0.83
NT2RP3000865	46.47	55.59	50.08	1.2	1.08
NT2RP3000866	25.31	29.98	29.36	1	1
NT2RP3000868	24.4	38.72	29.84	1	1
NT2RP3000869	110.44	100.32	94.76	0.91	0.86
NT2RP3000871	36.79	33.65	34.85	1	1
NT2RP3000875	49.24	40.39	34.03	0.82	0.81
NT2RP3000895	34.75	56.81	38.34	1.42	1
NT2RP3000900	103.64	130.63	118.42	1.26	1.14
NT2RP3000901	42.93	60.7	61.46	1.41	1.43
NT2RP3000903	36.65	34.57	30.27	1	1
NT2RP3000904	32.98	41.59	46.33	1.04	1.16
NT2RP3000907	48.65	84.74	82.16	1.74	1.69
NT2RP3000913	53.18	82.07	83.27	1.54	1.57
NT2RP3000917	53.05	73.11	70.12	1.38	1.32
NT2RP3000919	41.76	44.5	39.12	1.07	0.96
NT2RP3000921	33.94	34.26	37.03	1	1
NT2RP3000942	27.18	20.93	30.01	1	1
NT2RP3000968	869.8	1285.36	1136.31	1.48	1.31
NT2RP3000974	30.7	39.92	43.77	1	1.09
NT2RP3000980	42.53	53.79	45.15	1.26	1.06
NT2RP3000984	42.57	56.36	59.5	1.32	1.4
NT2RP3000994	39.6	38.61	42.48	1	1.06
NT2RP3001001	24.8	27.54	25.51	1	1
NT2RP3001004	34.1	37.28	40.47	1	1.01
NT2RP3001007	60.15	63.56	66.1	1.06	1.1
NT2RP3001012	20.21	34.13	29.36	1	1
NT2RP3001042	19.87	25.66	24.69	1	1
NT2RP3001044	25.25	46.01	39.88	1.15	1
NT2RP3001048	12.35	27.84	24.81	1	1
NT2RP3001050	46.86	69.34	59.69	1.48	1.27
NT2RP3001055	58	84.64	73.94	1.46	1.27
NT2RP3001057	69.56	96.19	79.08	1.38	1.14
NT2RP3001061	26.88	36.71	41.68	1	1.04
NT2RP3001069	70.39	125.35	90.32	1.78	1.28
NT2RP3001074	36.64	75.33	57.67	1.88	1.44
NT2RP3001078	35.32	68.97	43.37	1.72	1.08
NT2RP3001081	26.55	44.42	32.41	1.11	1
NT2RP3001084	168.13	218.74	170.51	1.3	1.01

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NT2RP3001095	29.5	34.98	34.01	1	1
NT2RP3001096	100.39	98.43	119.85	0.98	1.19
NT2RP3001097	66.45	81.24	66.83	1.22	1.01
NT2RP3001107	37.43	48.85	43.79	1.22	1.09
NT2RP3001109	18.5	33.37	29.5	1	1
NT2RP3001111	24.08	34.01	31.73	1	1
NT2RP3001112	48.19	172.37	117.36	3.58	2.44
NT2RP3001113	24.8	26.72	24.29	1	1
NT2RP3001115	28.51	40.16	26.51	1	1
NT2RP3001116	41.86	50.04	51.73	1.2	1.24
NT2RP3001119	51.5	56.72	45.28	1.1	0.88
NT2RP3001120	38.67	61.66	56.73	1.54	1.42
NT2RP3001126	46.96	69.33	67.32	1.48	1.43
NT2RP3001127	26.75	47.69	35.12	1.19	1
NT2RP3001133	41.78	57.01	41.02	1.36	0.98
NT2RP3001140	25.63	27.63	27.41	1	1
NT2RP3001147	28.48	36.63	27.92	1	1
NT2RP3001150	33.05	47.14	36.06	1.18	1
NT2RP3001152	13.69	22.65	17.1	1	1
NT2RP3001155	23.86	31.38	24.03	1	1
NT2RP3001156	31.92	41.8	42.62	1.05	1.07
NT2RP3001159	66.25	122.86	119.5	1.85	1.8
NT2RP3001170	39.22	51.34	41.01	1.28	1.03
NT2RP3001176	97.55	118.18	99.57	1.21	1.02
NT2RP3001195	66.3	63.21	61.54	0.95	0.93
NT2RP3001209	100.55	111.62	103.67	1.11	1.03
NT2RP3001214	26.09	38.15	28.98	1	1
NT2RP3001216	43.2	50.29	34.85	1.16	0.93
NT2RP3001221	22.27	27.72	22.63	1	1
NT2RP3001226	181.61	210.81	147.93	1.16	0.81
NT2RP3001230	19.25	20.95	22.46	1	1
NT2RP3001232	21.69	29.63	29.46	1	1
NT2RP3001236	19.38	44.15	25.82	1.1	1
NT2RP3001239	26.33	25.85	27.18	1	1
NT2RP3001240	63.01	66	66.1	1.05	1.05
NT2RP3001245	33.46	45.33	35.8	1.13	1
NT2RP3001253	26.11	34.25	24.98	1	1
NT2RP3001259	89.06	120.22	77.86	1.35	0.87
NT2RP3001260	24.17	42.19	40.2	1.05	1.01
NT2RP3001264	57.03	63.07	40.15	1.11	0.7
NT2RP3001268	74.96	94.93	54.69	1.27	0.73
NT2RP3001271	301.67	348.16	248.92	1.15	0.83
NT2RP3001272	78.64	96.2	67.24	1.22	0.86
NT2RP3001274	130.1	130.91	111.71	1.01	0.86
NT2RP3001275	29.63	33.27	28.8	1	1
NT2RP3001280	35.94	37.66	34.52	1	1

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NT2RP3001281	65.77	81.47	69.44	1.24	1.06
NT2RP3001288	558.59	612.58	574.08	1.1	1.03
NT2RP3001297	307.15	384.44	295.34	1.25	0.96
NT2RP3001300	119.32	149.14	115.2	1.25	0.97
NT2RP3001301	33.42	30.47	31.83	1	1
NT2RP3001307	30.64	30.12	22.38	1	1
NT2RP3001310	72.46	56.17	58.56	0.78	0.81
NT2RP3001318	24.12	25.36	25.42	1	1
NT2RP3001322	31.14	44.29	48.49	1.11	1.21
NT2RP3001325	85.38	122.67	64.92	1.44	0.76
NT2RP3001338	68.4	85.83	77.72	1.25	1.14
NT2RP3001339	23.23	21.65	26.14	1	1
NT2RP3001340	198.23	172.89	198.06	0.87	1
NT2RP3001341	35.58	49.07	43.7	1.23	1.09
NT2RP3001354	94.02	155.88	119.36	1.66	1.27
NT2RP3001355	47.02	52.67	54.05	1.12	1.15
NT2RP3001356	26.16	37.38	36.67	1	1
NT2RP3001359	23.89	25.98	22.7	1	1
NT2RP3001364	32.71	36.84	35.98	1	1
NT2RP3001373	31.9	34.3	36.07	1	1
NT2RP3001374	21.5	16.73	31.56	1	1
NT2RP3001383	39.64	44.16	45.92	1.1	1.15
NT2RP3001384	36.83	41.97	51.33	1.05	1.28
NT2RP3001388	42.48	75.91	63.11	1.79	1.49
NT2RP3001392	22.24	36.48	37.41	1	1
NT2RP3001396	24.7	34.69	26.74	1	1
NT2RP3001398	52.58	51.11	55.1	0.97	1.05
NT2RP3001399	131.78	142.46	121.9	1.08	0.93
NT2RP3001402	371.01	316.05	304.17	0.85	0.82
NT2RP3001407	103.85	166.37	141.76	1.6	1.37
NT2RP3001416	52.72	79.25	71.82	1.5	1.36
NT2RP3001420	31.21	43.79	48.38	1.09	1.21
NT2RP3001425	21.43	35.63	30.94	1	1
NT2RP3001426	44.27	58.16	52.33	1.31	1.18
NT2RP3001427	35.98	42.28	33.84	1.06	1
NT2RP3001428	75.28	69.54	71.75	0.92	0.95
NT2RP3001429	60.36	77.58	88.17	1.29	1.46
NT2RP3001432	48.5	74.44	64.48	1.53	1.33
NT2RP3001439	16.97	28.34	23.67	1	1
NT2RP3001441	88.9	152.82	135.99	1.72	1.53
NT2RP3001446	28.71	33.07	39.33	1	1
NT2RP3001447	96.93	143.88	92.82	1.48	0.96
NT2RP3001449	69.21	88.15	95.8	1.27	1.38
NT2RP3001453	46.33	42.59	44.38	0.92	0.96
NT2RP3001457	47.17	69.16	63.02	1.47	1.34
NT2RP3001459	27.94	34.42	42.83	1	1.07

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NT2RP3001463	22.38	32.46	29.96	1	1
NT2RP3001466	11.82	16.39	13.98	1	1
NT2RP3001472	40.63	56.11	41.44	1.38	1.02
NT2RP3001475	57.88	101.22	77.68	1.75	1.34
NT2RP3001479	55.51	104.08	68.82	1.87	1.24
NT2RP3001490	56.02	74.52	62.52	1.33	1.12
NT2RP3001492	78.91	120.46	89.46	1.53	1.13
NT2RP3001495	12.05	17.39	29.09	1	1
NT2RP3001497	37.28	54.07	51.53	1.35	1.29
NT2RP3001501	21.98	38.33	27.9	1	1
NT2RP3001527	49.51	76.83	53.06	1.55	1.07
NT2RP3001529	57.45	86.59	53.15	1.51	0.93
NT2RP3001538	43.44	71.62	52.26	1.65	1.2
NT2RP3001539	78.32	103.18	83.32	1.32	1.06
NT2RP3001542	32.18	32.31	29.07	1	1
NT2RP3001549	53.07	75.46	62.95	1.42	1.19
NT2RP3001554	40.08	51.39	49.59	1.28	1.24
NT2RP3001560	22.83	23.45	24.54	1	1
NT2RP3001561	206.83	372.07	339.41	1.8	1.64
NT2RP3001564	86.6	74.78	78.12	0.86	0.9
NT2RP3001568	75.84	74.32	69.6	0.98	0.92
NT2RP3001575	66.07	102.6	65.42	1.55	0.99
NT2RP3001580	35.25	46.28	36.67	1.16	1
NT2RP3001587	92.44	107.61	93.48	1.16	1.01
NT2RP3001589	94.2	111.88	100.95	1.19	1.07
NT2RP3001592	99.98	100.34	80.73	1	0.81
NT2RP3001607	19.48	15.23	19.67	1	1
NT2RP3001608	82.24	99.8	92.98	1.21	1.13
NT2RP3001613	57.64	68.33	52.16	1.19	0.9
NT2RP3001619	62.58	70.06	65.53	1.12	1.05
NT2RP3001621	22.21	27.3	28.56	1	1
NT2RP3001629	16.75	21.07	19.99	1	1
NT2RP3001630	22.39	25.61	21.17	1	1
NT2RP3001631	57.54	26.71	59.03	0.7	1.03
NT2RP3001634	41.35	57.44	39.52	1.39	0.97
NT2RP3001642	56.23	59	47.14	1.05	0.84
NT2RP3001646	15.08	18.89	13.35	1	1
NT2RP3001650	25.48	37.39	30.62	1	1
NT2RP3001667	61.01	80.37	81.51	1.32	1.34
NT2RP3001671	32.95	36.89	35.54	1	1
NT2RP3001672	16.39	20.91	29.58	1	1
NT2RP3001676	31.13	37.65	41.73	1	1.04
NT2RP3001678	66.39	74.45	57.02	1.12	0.86
NT2RP3001679	127.44	158.32	116.19	1.24	0.91
NT2RP3001682	24.29	33.63	28.48	1	1
NT2RP3001685	43.06	49.3	45.22	1.14	1.05

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NT2RP3001688	68.31	66.94	60.62	0.98	0.89
NT2RP3001690	31.58	27.09	23.81	1	1
NT2RP3001693	108.21	129.42	90.94	1.2	0.84
NT2RP3001696	43.91	42.52	44.5	0.97	1.01
NT2RP3001698	315.87	413.64	319.4	1.31	1.01
NT2RP3001708	70.76	92.58	47.94	1.31	0.68
NT2RP3001712	141.63	166.33	105.96	1.17	0.75
NT2RP3001716	51	60.17	43.04	1.18	0.84
NT2RP3001724	46.42	36.68	49.91	0.86	1.08
NT2RP3001727	167.98	226.18	171.88	1.35	1.02
NT2RP3001729	36.78	29.4	30.68	1	1
NT2RP3001730	54.08	54.43	57.54	1.01	1.06
NT2RP3001733	22	77.48	36.88	1.94	1
NT2RP3001737	96.14	129.99	96.82	1.35	1.01
NT2RP3001738	97.03	140.56	100.01	1.45	1.03
NT2RP3001739	33.77	41.79	45.01	1.04	1.13
NT2RP3001742	39	35.48	36.14	1	1
NT2RP3001751	64.33	51.48	62.69	0.8	0.97
NT2RP3001752	64.87	69.71	65.33	1.07	1.01
NT2RP3001753	95.47	97.65	102.48	1.02	1.07
NT2RP3001754	60.23	66.79	62.61	1.11	1.04
NT2RP3001756	77.51	62.2	43.41	0.8	0.56
NT2RP3001764	21.85	27.57	20.25	1	1
NT2RP3001771	18.57	16.36	13.96	1	1
NT2RP3001777	29.07	32.49	38.81	1	1
NT2RP3001782	94.5	100.94	87.81	1.07	0.93
NT2RP3001792	39.09	50.36	43.92	1.26	1.1
NT2RP3001799	36.03	58.62	47.31	1.47	1.18
NT2RP3001819	19.25	22.86	25.6	1	1
NT2RP3001829	284.05	356.88	241.7	1.26	0.85
NT2RP3001836	90.61	99.52	94.93	1.1	1.05
NT2RP3001839	132.95	150.06	158.76	1.13	1.19
NT2RP3001844	58.07	70.34	49.48	1.21	0.85
NT2RP3001848	415.62	351.03	329.58	0.84	0.79
NT2RP3001854	99.59	167.41	125.64	1.68	1.26
NT2RP3001855	7.2	8.51	11.4	1	1
NT2RP3001857	30.69	34.05	33.03	1	1
NT2RP3001858	21.65	23.25	23.96	1	1
NT2RP3001861	64.19	51.03	54.36	0.79	0.85
NT2RP3001866	50.36	66.36	52.2	1.32	1.04
NT2RP3001871	55.46	82.83	70.96	1.49	1.28
NT2RP3001874	19.41	23.41	26.67	1	1
NT2RP3001878	31.75	36.24	40.97	1	1.02
NT2RP3001885	38.84	43.23	66.31	1.08	1.66
NT2RP3001896	27.46	44.72	43.75	1.12	1.09
NT2RP3001898	97.08	137.81	114.53	1.42	1.18

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NT2RP3001899	52.14	40.76	46.67	0.78	0.9
NT2RP3001901	30.36	89.56	80.6	2.24	2.02
NT2RP3001915	24.18	39.41	37.95	1	1
NT2RP3001926	19.34	18.45	21.61	1	1
NT2RP3001929	38.26	54.96	59.89	1.37	1.5
NT2RP3001931	20.96	28.29	20.82	1	1
NT2RP3001938	44.42	42.62	38.19	0.96	0.9
NT2RP3001943	60.19	76.51	52.98	1.27	0.88
NT2RP3001944	62.31	69.42	63.27	1.11	1.02
NT2RP3001945	33.47	48.98	50.44	1.22	1.26
NT2RP3001947	21.68	29.93	32.76	1	1
NT2RP3001949	24.71	38.44	35.87	1	1
NT2RP3001952	247.52	506.54	457.74	2.05	1.85
NT2RP3001954	26.13	37.23	31.49	1	1
NT2RP3001956	110.45	165.87	114.04	1.5	1.03
NT2RP3001967	71.91	108.13	80.44	1.5	1.12
NT2RP3001969	22.97	22.49	25.4	1	1
NT2RP3001976	46.03	54.55	39.68	1.19	0.87
NT2RP3001986	19.38	25.22	27.11	1	1
NT2RP3001989	20.53	24.27	35.87	1	1
NT2RP3002002	133.97	174.37	178.87	1.3	1.34
NT2RP3002004	32.63	37.32	38.91	1	1
NT2RP3002007	26.61	28.38	23.88	1	1
NT2RP3002014	66.64	82.76	68.62	1.24	1.03
NT2RP3002015	44.46	78.33	54.06	1.76	1.22
NT2RP3002033	22.5	29.61	28.22	1	1
NT2RP3002045	35.7	36.02	24.46	1	1
NT2RP3002054	35.32	42.28	44.47	1.06	1.11
NT2RP3002056	30.39	30.77	27.95	1	1
NT2RP3002057	41	22.22	23.49	0.98	0.98
NT2RP3002061	48.21	57.96	63.07	1.2	1.31
NT2RP3002062	20.36	18.59	14.3	1	1
NT2RP3002063	62.31	74.04	63.08	1.19	1.01
NT2RP3002064	21.69	23.07	21.6	1	1
NT2RP3002071	16.75	26.42	20.29	1	1
NT2RP3002073	47.11	46.98	45.61	1	0.97
NT2RP3002074	25.85	32.38	27.78	1	1
NT2RP3002075	46.99	46.84	55.88	1	1.19
NT2RP3002077	31.71	46.31	32.01	1.16	1
NT2RP3002081	46.95	62.53	50.21	1.33	1.07
NT2RP3002086	48.42	51.09	51.82	1.06	1.07
NT2RP3002094	67.28	88.8	66.97	1.32	1
NT2RP3002096	16.52	16.04	19.78	1	1
NT2RP3002097	52.1	55.8	60.63	1.07	1.16
NT2RP3002098	31.09	32.61	34.91	1	1
NT2RP3002102	60.5	83.23	50.82	1.38	0.84

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NT2RP3002106	97.61	114.94	77.8	1.18	0.8
NT2RP3002108	43.54	46.03	33.61	1.06	0.92
NT2RP3002109	252.14	279.15	238.77	1.11	0.95
NT2RP3002110	411.5	436.43	380.83	1.06	0.93
NT2RP3002113	232.35	287.1	156.5	1.24	0.67
NT2RP3002120	31.26	36	32.36	1	1
NT2RP3002121	102.56	118.53	123.14	1.16	1.2
NT2RP3002126	393.73	546.97	401.78	1.39	1.02
NT2RP3002128	49.03	82.04	43.95	1.67	0.9
NT2RP3002130	164.12	202.74	139.49	1.24	0.85
NT2RP3002133	82.45	102.63	77.97	1.24	0.95
NT2RP3002136	117.89	134.21	135.34	1.14	1.15
NT2RP3002140	57.47	59.58	39.82	1.04	0.7
NT2RP3002142	605.88	683.52	499.11	1.13	0.82
NT2RP3002146	94.39	91.48	82.97	0.97	0.88
NT2RP3002147	57.54	61.35	55.31	1.07	0.96
NT2RP3002151	97.79	98.18	67.79	1	0.69
NT2RP3002155	20.54	22.2	19.19	1	1
NT2RP3002156	27.53	30.23	24.57	1	1
NT2RP3002160	22.71	19.76	21.67	1	1
NT2RP3002163	339.08	390.35	313.81	1.15	0.93
NT2RP3002165	50.53	57.64	50.86	1.14	1.01
NT2RP3002166	57.16	79.74	76.2	1.4	1.33
NT2RP3002173	38.16	72.73	50.15	1.82	1.25
NT2RP3002174	73.01	91.41	74.15	1.25	1.02
NT2RP3002181	29.25	36.79	29.92	1	1
NT2RP3002185	23.49	23.58	23.08	1	1
NT2RP3002193	138.23	133.32	139.04	0.96	1.01
NT2RP3002204	23.61	32.9	31.83	1	1
NT2RP3002244	55.17	62.72	66.22	1.14	1.2
NT2RP3002248	68.53	122.32	87.51	1.78	1.28
NT2RP3002253	38.41	31.8	33.77	1	1
NT2RP3002255	168.99	177.9	184.59	1.05	1.09
NT2RP3002264	44.05	40.61	41.69	0.92	0.95
NT2RP3002267	26.06	21.36	23.42	1	1
NT2RP3002273	99.28	132.94	130.53	1.34	1.31
NT2RP3002276	19.53	31.09	30.76	1	1
NT2RP3002281	37.59	50.86	53.47	1.27	1.34
NT2RP3002286	30.42	39.5	37.6	1	1
NT2RP3002297	198.27	289.7	257.61	1.46	1.3
NT2RP3002301	86.53	94.22	91.69	1.09	1.06
NT2RP3002303	53.01	47.85	50.14	0.9	0.95
NT2RP3002304	32.44	42.53	34.81	1.06	1
NT2RP3002309	19.68	25.71	24.33	1	1
NT2RP3002311	29.9	37.26	34.94	1	1
NT2RP3002315	45.62	101.03	87.47	2.21	1.92

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NT2RP3002319	21.78	28.55	29.65	1	1
NT2RP3002324	228.71	219.01	186.33	0.96	0.81
NT2RP3002330	59.33	95.67	65.36	1.61	1.1
NT2RP3002333	242.08	315.68	295.21	1.3	1.22
NT2RP3002337	44.4	51.03	50.85	1.15	1.15
NT2RP3002342	43.55	70.38	61.03	1.62	1.4
NT2RP3002343	34.9	43.73	44.29	1.09	1.11
NT2RP3002351	20.91	31.81	28.59	1	1
NT2RP3002352	30.5	41.78	35.34	1.04	1
NT2RP3002353	71.78	70.35	68.58	0.98	0.96
NT2RP3002362	124.23	142.32	97.17	1.15	0.78
NT2RP3002363	38.11	35.41	34.56	1	1
NT2RP3002377	44.72	46.51	36.3	1.04	0.89
NT2RP3002383	130.04	142.36	151.14	1.09	1.16
NT2RP3002388	35.83	45.72	43.7	1.14	1.09
NT2RP3002394	49.99	61.97	59.21	1.24	1.18
NT2RP3002398	79.21	126.27	128.21	1.59	1.62
NT2RP3002399	93.02	98.05	80.72	1.05	0.87
NT2RP3002402	43.31	44.68	39.43	1.03	0.92
NT2RP3002409	74.15	102.87	56.09	1.39	0.76
NT2RP3002410	68.91	85.11	79.09	1.24	1.15
NT2RP3002411	32.25	28.6	26.33	1	1
NT2RP3002429	19.25	21.69	25	1	1
NT2RP3002448	51.94	66.27	81.82	1.28	1.58
NT2RP3002454	88.96	110.48	87.19	1.24	0.98
NT2RP3002455	92.34	94.51	110.7	1.02	1.2
NT2RP3002456	68.51	124.23	76.15	1.81	1.11
NT2RP3002462	53.07	82.8	54.96	1.56	1.04
NT2RP3002469	30.95	39.55	32.73	1	1
NT2RP3002470	114.41	132.92	111.51	1.16	0.97
NT2RP3002484	201.73	251.05	192.81	1.24	0.96
NT2RP3002491	11.09	11.37	10.09	1	1
NT2RP3002494	1117.6	1441.17	955.22	1.29	0.85
NT2RP3002497	21.38	19.12	19.13	1	1
NT2RP3002500	21.63	21.71	20.45	1	1
NT2RP3002501	46.12	43.86	51.26	0.95	1.11
NT2RP3002512	36.76	30.74	31.49	1	1
NT2RP3002529	32.46	45.21	39.38	1.13	1
NT2RP3002533	52.85	69.58	63.25	1.32	1.2
NT2RP3002539	41.9	51.77	43.9	1.24	1.05
NT2RP3002540	29.69	26.98	24.28	1	1
NT2RP3002543	52.93	51.31	50.86	0.97	0.96
NT2RP3002545	37.88	54.86	29.71	1.37	1
NT2RP3002549	28.09	35.52	29.78	1	1
NT2RP3002552	17.76	17.91	23.08	1	1
NT2RP3002558	25.36	34.12	22.97	1	1

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NT2RP3002565	26.21	34.92	34.73	1	1
NT2RP3002566	20.57	26.5	28.31	1	1
NT2RP3002571	15.34	16.38	21.23	1	1
NT2RP3002572	48.24	58.38	47.95	1.21	0.99
NT2RP3002573	100.25	125.77	76.4	1.25	0.76
NT2RP3002577	28.11	33.52	30.72	1	1
NT2RP3002579	41.49	42.29	43.22	1.02	1.04
NT2RP3002582	62.98	71.25	64.36	1.13	1.02
NT2RP3002587	34.51	38.9	38.19	1	1
NT2RP3002590	53.88	42.52	53.88	0.79	1
NT2RP3002602	44.63	46.13	48.74	1.03	1.09
NT2RP3002603	1050.9	1295.99	742.83	1.23	0.71
NT2RP3002621	27.69	33.93	20.65	1	1
NT2RP3002622	61.52	72.03	58.35	1.17	0.95
NT2RP3002624	34.07	32.98	37.7	1	1
NT2RP3002628	96.65	113.19	105.29	1.17	1.09
NT2RP3002629	102.84	116.31	114.99	1.13	1.12
NT2RP3002631	6.16	5.96	8.23	1	1
NT2RP3002647	33.91	31.82	34.73	1	1
NT2RP3002649	79.36	101.87	79.66	1.28	1
NT2RP3002650	96.33	120.26	88.16	1.25	0.92
NT2RP3002652	44.7	40.97	34.83	0.92	0.89
NT2RP3002654	42.27	42.98	52.06	1.02	1.23
NT2RP3002657	181.9	195.68	181.98	1.08	1
NT2RP3002659	38.26	29.13	38.15	1	1
NT2RP3002660	104.58	100.78	89.16	0.96	0.85
NT2RP3002663	29.93	27.09	32.81	1	1
NT2RP3002664	49.51	57.15	37.69	1.15	0.81
NT2RP3002667	40.39	38.2	33.43	0.99	0.99
NT2RP3002671	21.78	27.84	27.47	1	1
NT2RP3002682	134.94	124.84	125.91	0.93	0.93
NT2RP3002684	20.17	23.55	22.82	1	1
NT2RP3002687	33.43	34.38	30.29	1	1
NT2RP3002688	28.16	40.85	35.15	1.02	1
NT2RP3002698	20.33	29.79	27.84	1	1
NT2RP3002701	37.69	39.18	38.09	1	1
NT2RP3002705	59.73	80.87	53.39	1.35	0.89
NT2RP3002708	58.63	52.06	55.2	0.89	0.94
NT2RP3002711	65.94	42.16	49.17	0.64	0.75
NT2RP3002712	376.94	760.41	522.35	2.02	1.39
NT2RP3002713	17.08	16.65	22.46	1	1
NT2RP3002721	59.3	85.17	77.58	1.44	1.31
NT2RP3002722	75.48	105.19	91.94	1.39	1.22
NT2RP3002723	168.14	249.1	197.12	1.48	1.17
NT2RP3002737	75.56	70.15	69.36	0.93	0.92
NT2RP3002738	43.47	46.17	49.75	1.06	1.14

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NT2RP3002742	91.46	197.54	163.14	2.16	1.78
NT2RP3002744	25.19	23.77	27.75	1	1
NT2RP3002756	20.99	34.1	30.35	1	1
NT2RP3002757	314.6	413.48	473.72	1.31	1.51
NT2RP3002758	316.66	390.6	419.58	1.23	1.33
NT2RP3002762	62.34	88.77	67.06	1.42	1.08
NT2RP3002763	35.64	40.12	38.48	1	1
NT2RP3002770	23.63	14.35	25.47	1	1
NT2RP3002771	64.59	115.02	108.28	1.78	1.68
NT2RP3002785	16.99	22.51	28.08	1	1
NT2RP3002790	17.42	27.12	27.61	1	1
NT2RP3002799	38.43	63.67	47.31	1.59	1.18
NT2RP3002801	36	38.11	37.68	1	1
NT2RP3002802	75.68	104.49	70.89	1.38	0.94
NT2RP3002810	38.43	39.64	45.83	1	1.15
NT2RP3002818	16.71	19.6	20.05	1	1
NT2RP3002821	82.59	111.38	103.63	1.35	1.25
NT2RP3002823	16.14	23.07	23.79	1	1
NT2RP3002825	29.97	42.62	51.52	1.07	1.29
NT2RP3002829	56.67	75.96	64.42	1.34	1.14
NT2RP3002831	39.21	48.28	44.67	1.21	1.12
NT2RP3002836	100.32	151.67	121.88	1.51	1.21
NT2RP3002845	43.58	43.77	37.66	1	0.92
NT2RP3002852	47.35	43.95	45.51	0.93	0.96
NT2RP3002861	24.44	43.68	37.2	1.09	1
NT2RP3002869	21.09	37.96	43.81	1	1.1
NT2RP3002874	114.64	160.28	176.35	1.4	1.54
NT2RP3002876	91.78	124.1	102.42	1.35	1.12
NT2RP3002877	67.53	88.2	58.11	1.31	0.86
NT2RP3002887	15.18	18.03	14.99	1	1
NT2RP3002900	84.61	115	84.7	1.36	1
NT2RP3002902	51.09	63.53	44.04	1.24	0.86
NT2RP3002909	67.02	93.32	90.48	1.39	1.35
NT2RP3002911	51.83	62.4	51.57	1.2	0.99
NT2RP3002948	16.79	27.46	27.85	1	1
NT2RP3002953	34.1	33.67	19.45	1	1
NT2RP3002955	20.72	24.46	21.25	1	1
NT2RP3002958	36.45	33.39	36.88	1	1
NT2RP3002969	103.15	94.02	75.44	0.91	0.73
NT2RP3002972	24.57	29.3	23.42	1	1
NT2RP3002978	43.22	43.59	36.37	1.01	0.93
NT2RP3002983	25.18	27.57	25.24	1	1
NT2RP3002985	230.37	195.06	212.4	0.85	0.92
NT2RP3002988	24.12	36.74	22.84	1	1
NT2RP3003000	32.23	25.03	25.55	1	1
NT2RP3003008	36.94	45.85	39.33	1.15	1

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NT2RP3003012	27.83	41.25	27.29	1.03	1
NT2RP3003015	8.21	8.61	14.36	1	1
NT2RP3003018	43.12	32.66	31.72	0.93	0.93
NT2RP3003028	28.71	27.5	24.44	1	1
NT2RP3003029	200.91	206.52	247.25	1.03	1.23
NT2RP3003032	104.87	104.11	100.21	0.99	0.96
NT2RP3003041	5.2	4.96	6.4	1	1
NT2RP3003044	61.39	53.08	48.13	0.86	0.78
NT2RP3003047	65.05	61.01	50.32	0.94	0.77
NT2RP3003050	81.64	85.12	88.43	1.04	1.08
NT2RP3003053	130.71	148.3	110.46	1.13	0.85
NT2RP3003059	28.51	21.68	24.58	1	1
NT2RP3003061	42.13	49.09	36.07	1.17	0.95
NT2RP3003068	58.02	59.04	59.36	1.02	1.02
NT2RP3003071	58.04	63.86	50.19	1.1	0.86
NT2RP3003076	147.96	137.86	103.49	0.93	0.7
NT2RP3003078	25.58	28.56	23.61	1	1
NT2RP3003081	72.21	77.62	70.95	1.07	0.98
NT2RP3003090	46.8	48.98	48.09	1.05	1.03
NT2RP3003097	57.87	52.69	44.19	0.91	0.76
NT2RP3003098	34.21	30.03	27.19	1	1
NT2RP3003101	50.81	39.38	49.48	0.79	0.97
NT2RP3003109	153.35	166.7	189.83	1.09	1.24
NT2RP3003121	66.63	80.69	55.75	1.21	0.84
NT2RP3003133	46.03	64	88.32	1.39	1.92
NT2RP3003137	28.14	20.96	24.07	1	1
NT2RP3003138	20.01	20.35	22.05	1	1
NT2RP3003139	61.14	61.42	46.51	1	0.76
NT2RP3003145	175.66	184.49	166.63	1.05	0.95
NT2RP3003150	32.52	33.81	37.08	1	1
NT2RP3003157	83.36	102.72	94.03	1.23	1.13
NT2RP3003185	26.09	28.62	23.95	1	1
NT2RP3003193	53.04	78.17	45.99	1.47	0.87
NT2RP3003197	32.62	33.01	27.89	1	1
NT2RP3003203	89.37	91.77	103.1	1.03	1.15
NT2RP3003204	55.93	69.49	59.09	1.24	1.06
NT2RP3003210	1429.8	1457.7	1422.21	1.02	0.99
NT2RP3003212	36.76	46.5	49.94	1.16	1.25
NT2RP3003213	21.73	30.96	31.33	1	1
NT2RP3003224	18.28	25.18	23.12	1	1
NT2RP3003226	59.96	65.81	58.87	1.1	0.98
NT2RP3003230	54.68	54.94	45.65	1	0.83
NT2RP3003235	96.54	103.84	100.17	1.08	1.04
NT2RP3003242	31.19	33.59	46.66	1	1.17
NT2RP3003251	47.34	46.86	51.73	0.99	1.09
NT2RP3003252	29.8	43.11	32.53	1.08	1

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NT2RP3003258	75.96	74.28	84.41	0.98	1.11
NT2RP3003260	43.71	50.04	44.53	1.14	1.02
NT2RP3003264	46.41	49.05	41.66	1.06	0.9
NT2RP3003273	30.87	34.85	36.92	1	1
NT2RP3003278	19.53	21.65	19.18	1	1
NT2RP3003280	70.3	105.23	100.25	1.5	1.43
NT2RP3003282	29.36	37.26	41.52	1	1.04
NT2RP3003290	53.11	79.08	68.22	1.49	1.28
NT2RP3003301	23.63	34.12	34.2	1	1
NT2RP3003302	29.76	36.69	34.81	1	1
NT2RP3003311	33.02	35.19	28.62	1	1
NT2RP3003312	31.95	30.46	25.13	1	1
NT2RP3003313	22.54	26.76	28.64	1	1
NT2RP3003327	28.13	35.45	35.73	1	1
NT2RP3003330	23.97	42.1	39.66	1.05	1
NT2RP3003344	17.95	30.92	31.35	1	1
NT2RP3003346	38.44	40.04	32.22	1	1
NT2RP3003349	60.55	76.46	64.89	1.26	1.07
NT2RP3003353	27.37	36.5	28.9	1	1
NT2RP3003354	161.75	238.83	211.06	1.48	1.3
NT2RP3003368	25.31	26.96	30.07	1	1
NT2RP3003375	19.97	23.49	26.89	1	1
NT2RP3003377	26.74	28.34	31.65	1	1
NT2RP3003384	25.96	27.31	29.85	1	1
NT2RP3003385	11.85	18.33	12.44	1	1
NT2RP3003396	92.34	128.93	97.11	1.4	1.05
NT2RP3003403	30.87	32.28	24.09	1	1
NT2RP3003409	29.46	25.47	25.88	1	1
NT2RP3003411	99.26	102.69	117.35	1.03	1.18
NT2RP3003420	40.59	47.26	50.49	1.16	1.24
NT2RP3003425	27.86	30.03	38.29	1	1
NT2RP3003426	114.22	149.54	110.58	1.31	0.97
NT2RP3003427	29.42	49.96	43.87	1.25	1.1
NT2RP3003433	102.25	116.31	100.86	1.14	0.99
NT2RP3003437	220.13	297.2	298.55	1.35	1.36
NT2RP3003448	59.82	65.11	39.78	1.09	0.67
NT2RP3003455	52.9	66.55	49.25	1.26	0.93
NT2RP3003462	33.11	39.48	32.79	1	1
NT2RP3003464	23.16	21.25	23.09	1	1
NT2RP3003469	33.63	46.93	35.52	1.17	1
NT2RP3003473	150.71	144.82	179.22	0.96	1.19
NT2RP3003474	32.83	24.24	29.87	1	1
NT2RP3003475	29.91	23.56	23.67	1	1
NT2RP3003490	28.42	21.14	23.16	1	1
NT2RP3003491	38.03	41.08	31.03	1.03	1
NT2RP3003493	259.66	299.8	250.81	1.15	0.97

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NT2RP3003500	25.38	26.58	21.77	1	1
NT2RP3003527	20.74	27.88	21.92	1	1
NT2RP3003532	44.02	49.96	37.36	1.13	0.91
NT2RP3003535	29.82	61.91	32.24	1.55	1
NT2RP3003536	40.45	49.94	40.95	1.23	1.01
NT2RP3003543	31.23	31.59	39.97	1	1
NT2RP3003549	16.2	16.71	24.15	1	1
NT2RP3003552	7.61	8.16	10.28	1	1
NT2RP3003555	66.81	99.09	115.8	1.48	1.73
NT2RP3003559	33.68	25.88	37.86	1	1
NT2RP3003564	27.89	49.08	40.34	1.23	1.01
NT2RP3003572	61.68	50.6	49.88	0.82	0.81
NT2RP3003576	197.7	212.18	139.92	1.07	0.71
NT2RP3003587	99.62	121.27	118.07	1.22	1.19
NT2RP3003589	106.69	148.93	135.82	1.4	1.27
NT2RP3003592	48.47	34.93	34.74	0.83	0.83
NT2RP3003593	121.2	89.05	117.85	0.73	0.97
NT2RP3003614	99.68	87.23	62.23	0.88	0.62
NT2RP3003621	41.62	38.54	60.39	0.96	1.45
NT2RP3003625	96.86	121.98	79.4	1.26	0.82
NT2RP3003627	134.8	228.15	118.18	1.69	0.88
NT2RP3003636	51.46	92.4	74.18	1.8	1.44
NT2RP3003642	100.17	79.67	85.03	0.8	0.85
NT2RP3003645	20.8	24.32	24.49	1	1
NT2RP3003648	41.86	25.21	34.05	0.96	0.96
NT2RP3003649	31.16	27.84	32.6	1	1
NT2RP3003650	36.91	39	41.77	1	1.04
NT2RP3003656	49.88	59.39	81.98	1.19	1.64
NT2RP3003659	48.02	47.56	48.36	0.99	1.01
NT2RP3003662	217.13	222.27	231.82	1.02	1.07
NT2RP3003664	48.79	48.51	53.65	0.99	1.1
NT2RP3003665	17.33	25.8	24.55	1	1
NT2RP3003671	37.51	33.34	36.86	1	1
NT2RP3003672	98.67	100.41	122.88	1.02	1.25
NT2RP3003673	54.44	49.04	61.03	0.9	1.12
NT2RP3003679	555.93	677.53	564.6	1.22	1.02
NT2RP3003680	31.86	45.99	36.14	1.15	1
NT2RP3003686	28.07	26.41	27.17	1	1
NT2RP3003689	40.14	43.48	57.49	1.08	1.43
NT2RP3003697	1481.3	1320.42	1671.16	0.89	1.13
NT2RP3003701	38.43	32.9	40.95	1	1.02
NT2RP3003704	71.4	101.56	77.83	1.42	1.09
NT2RP3003714	28.59	35.43	38.46	1	1
NT2RP3003716	27.93	28.85	36.37	1	1
NT2RP3003721	30.86	40	43.6	1.3	1.09
NT2RP3003722	26.43	22.24	30.55	1	1

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NT2RP3003726	20.58	19.68	16.82	1	1
NT2RP3003729	32.82	48.21	50.44	1.21	1.26
NT2RP3003731	31.23	40.64	46.66	1.02	1.17
NT2RP3003740	15.05	22.27	14.47	1	1
NT2RP3003746	38.26	40.22	39.43	1.01	1
NT2RP3003749	5.25	5.71	9.07	1	1
NT2RP3003754	38.81	28.6	33.55	1	1
NT2RP3003759	7.69	6.8	10.74	1	1
NT2RP3003764	30.47	37.74	34.96	1	1
NT2RP3003766	21.34	28.02	25.18	1	1
NT2RP3003767	95.41	149.71	94.89	1.57	0.99
NT2RP3003778	94.67	131.15	98.32	1.39	1.04
NT2RP3003779	119.32	121.27	121.96	1.02	1.02
NT2RP3003783	171.19	219.82	218.95	1.28	1.28
NT2RP3003787	40.38	39.85	40.63	0.99	1.01
NT2RP3003789	28.79	38.93	56	1	1.4
NT2RP3003795	29.47	36.03	39.29	1	1
NT2RP3003799	21.04	28.37	33.72	1	1
NT2RP3003800	32.73	47.39	54.64	1.18	1.37
NT2RP3003805	64.74	94.82	77.32	1.46	1.19
NT2RP3003809	47.93	42.27	42.5	0.88	0.89
NT2RP3003819	126.12	156.3	107.38	1.24	0.85
NT2RP3003824	91.46	122.08	133.15	1.33	1.46
NT2RP3003825	76.73	126.14	85.32	1.64	1.11
NT2RP3003828	56.58	58.09	66.3	1.03	1.17
NT2RP3003831	54.49	93.96	81.03	1.72	1.49
NT2RP3003833	39.47	75.96	64.02	1.9	1.6
NT2RP3003836	74.08	99.63	77.31	1.34	1.04
NT2RP3003842	140.84	181.57	132.26	1.29	0.94
NT2RP3003843	49.42	59.35	42.12	1.2	0.85
NT2RP3003844	257.28	375.6	320.58	1.46	1.25
NT2RP3003846	53.68	58.2	51.75	1.08	0.96
NT2RP3003849	22.13	34.22	28.94	1	1
NT2RP3003862	406.72	847.9	1028.77	2.08	2.53
NT2RP3003870	22.75	34.16	30.63	1	1
NT2RP3003874	35.95	49.65	40.87	1.24	1.02
NT2RP3003876	129.38	131.16	115.94	1.01	0.9
NT2RP3003880	45.82	47.69	44.1	1.04	0.96
NT2RP3003889	23.45	20.52	25.95	1	1
NT2RP3003891	20.78	26.18	19.73	1	1
NT2RP3003914	66.42	72.57	64.07	1.09	0.96
NT2RP3003915	49.11	55.32	70.79	1.13	1.44
NT2RP3003918	50	65.27	55.35	1.31	1.11
NT2RP3003920	178.39	277.64	168.45	1.56	0.94
NT2RP3003924	54.06	70.24	70.33	1.3	1.3
NT2RP3003932	91.65	81.99	67.7	0.89	0.74

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NT2RP3003939	52.16	55.91	69.9	1.07	1.34
NT2RP3003940	97.46	162.65	172.59	1.67	1.77
NT2RP3003943	24.14	24.58	22.04	1	1
NT2RP3003959	23.09	27.92	38.31	1	1
NT2RP3003963	44.65	55.53	37.38	1.24	0.9
NT2RP3003965	43.15	43.18	36.22	1	0.93
NT2RP3003972	168.48	231.15	168.29	1.37	1
NT2RP3003973	31.45	52.09	37.35	1.3	1
NT2RP3003979	85.27	106.87	81.39	1.25	0.95
NT2RP3003980	61.68	69.29	63.49	1.12	1.03
NT2RP3003982	17.84	6.37	19.34	1	1
NT2RP3003989	47.69	54.74	72.28	1.15	1.52
NT2RP3003992	29.53	23.75	36.55	1	1
NT2RP3004000	14.57	13.08	20.27	1	1
NT2RP3004001	177.54	233.79	127.51	1.32	0.72
NT2RP3004005	30.16	35.65	26.42	1	1
NT2RP3004013	46.17	46.65	37.77	1.01	0.87
NT2RP3004016	34.63	35.37	32.09	1	1
NT2RP3004025	60.47	54.61	43.79	0.9	0.72
NT2RP3004030	195.26	248.59	192.14	1.27	0.98
NT2RP3004041	67.7	62.62	78.31	0.92	1.16
NT2RP3004042	1660.0	1724.57	1465.74	1.04	0.88
NT2RP3004044	77.95	89	64.06	1.14	0.82
NT2RP3004051	78.57	96.82	72.26	1.23	0.92
NT2RP3004052	77.19	97.8	81.54	1.27	1.06
NT2RP3004053	253.72	303.58	293.82	1.2	1.16
NT2RP3004055	32.75	27.09	27.66	1	1
NT2RP3004059	65.86	79.05	60.14	1.2	0.91
NT2RP3004063	95.84	90.36	96.87	0.94	1.01
NT2RP3004067	63.43	70.46	80.31	1.11	1.27
NT2RP3004070	127.46	123.32	94.25	0.97	0.74
NT2RP3004075	88.72	117.53	102.4	1.32	1.15
NT2RP3004078	36.66	32.91	32.79	1	1
NT2RP3004083	69.74	97.89	110.43	1.4	1.58
NT2RP3004084	125.88	137.91	59.34	1.1	0.47
NT2RP3004087	96.25	77.81	103.81	0.81	1.08
NT2RP3004090	41.03	90.6	68.84	2.21	1.68
NT2RP3004093	77.28	109.24	81.21	1.41	1.05
NT2RP3004095	210.04	196.1	155.28	0.93	0.74
NT2RP3004102	39.95	47.29	49.64	1.18	1.24
NT2RP3004110	162.98	195.65	190.86	1.2	1.17
NT2RP3004119	48.75	62.19	67.55	1.28	1.39
NT2RP3004125	141.66	179.44	183.5	1.27	1.3
NT2RP3004129	40.03	57.6	59.81	1.44	1.49
NT2RP3004130	57.62	59.13	62.66	1.03	1.09
NT2RP3004133	111	102.14	108.91	0.92	0.98

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NT2RP3004145	27.76	26.25	31.93	1	1
NT2RP3004148	39.07	40.2	36.75	1.01	1
NT2RP3004155	67.78	42.47	67.99	0.63	1
NT2RP3004165	56.72	64.94	60.59	1.14	1.07
NT2RP3004179	22.85	32.11	37.49	1	1
NT2RP3004185	24.36	34.07	37.25	1	1
NT2RP3004188	66.84	96.78	76.48	1.45	1.14
NT2RP3004189	46.23	62.74	67.06	1.36	1.45
NT2RP3004190	42.52	45.07	50.82	1.06	1.2
NT2RP3004191	202.98	249.47	202.1	1.23	1
NT2RP3004202	35.82	33.56	31.45	1	1
NT2RP3004205	43.69	72.12	54.29	1.65	1.24
NT2RP3004206	35.46	49.76	45.93	1.24	1.15
NT2RP3004207	14.22	25.46	28.68	1	1
NT2RP3004209	24.68	41.96	45.58	1.05	1.14
NT2RP3004215	38.32	48.72	44.16	1.22	1.1
NT2RP3004219	80.8	112.37	96.89	1.39	1.2
NT2RP3004242	125.53	171.57	162.67	1.37	1.3
NT2RP3004246	70.46	100.3	94.37	1.42	1.34
NT2RP3004253	33.65	54.54	49.59	1.36	1.24
NT2RP3004258	91.75	179.55	148.48	1.96	1.62
NT2RP3004262	23.52	29.25	32.8	1	1
NT2RP3004275	29.98	36.48	32.64	1	1
NT2RP3004282	730.96	592.26	569.66	0.81	0.78
NT2RP3004289	49.81	56.26	53.86	1.13	1.08
NT2RP3004294	108.56	146.82	109.06	1.35	1
NT2RP3004298	935.9	825.21	946.53	0.88	1.01
NT2RP3004309	87.44	147.81	128	1.69	1.46
NT2RP3004321	27.53	38.48	42.68	1	1.07
NT2RP3004322	37.8	46.62	38.83	1.17	1
NT2RP3004332	2087.9	1664.03	1652.84	0.8	0.79
NT2RP3004334	49.38	35.5	37.15	0.81	0.81
NT2RP3004336	87.29	96.15	72.21	1.1	0.83
NT2RP3004338	237.24	202.64	90.27	0.85	0.38
NT2RP3004341	44.72	50.29	46	1.12	1.03
NT2RP3004345	76.87	96.92	95.62	1.26	1.24
NT2RP3004348	112.27	146.02	129.87	1.3	1.16
NT2RP3004349	102.45	114.73	111.08	1.12	1.08
NT2RP3004355	37.02	42.08	41.04	1.05	1.03
NT2RP3004356	140.31	152.19	165.73	1.08	1.18
NT2RP3004360	36.38	30.03	25.16	1	1
NT2RP3004361	53.41	63.16	34.51	1.18	0.75
NT2RP3004374	49.44	86.1	62	1.74	1.25
NT2RP3004378	91.68	128.91	81.31	1.41	0.89
NT2RP3004399	36.97	46.6	44.13	1.17	1.1
NT2RP3004405	38.9	49.75	45	1.24	1.13

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NT2RP3004406	39.42	49.03	45.23	1.23	1.13
NT2RP3004411	35.17	39.08	32.96	1	1
NT2RP3004424	29.21	29.74	24.33	1	1
NT2RP3004428	34.11	36.54	46.38	1	1.16
NT2RP3004432	36.94	41.96	34.59	1.05	1
NT2RP3004434	60.07	78.53	71.15	1.31	1.18
NT2RP3004446	31.37	39.4	49.98	1	1.25
NT2RP3004451	31.02	39.25	35.59	1	1
NT2RP3004454	25.89	34.31	21.28	1	1
NT2RP3004466	114.95	89.15	70.2	0.78	0.61
NT2RP3004470	144.42	183.37	120.21	1.27	0.83
NT2RP3004472	19.68	23.77	21.01	1	1
NT2RP3004475	23.31	17.7	28.06	1	1
NT2RP3004480	66.73	68.77	58.55	1.03	0.88
NT2RP3004481	35.98	47.95	40.79	1.2	1.02
NT2RP3004490	32.03	26.24	49.69	1	1.24
NT2RP3004496	177.5	89.61	219.13	0.5	1.23
NT2RP3004498	202.13	243.53	170.4	1.2	0.84
NT2RP3004503	122.49	122.68	103.11	1	0.84
NT2RP3004504	65.35	91.18	74.69	1.4	1.14
NT2RP3004505	136.86	160.35	101.46	1.17	0.74
NT2RP3004507	25.93	27.52	24.4	1	1
NT2RP3004519	51.38	54.44	67.23	1.06	1.31
NT2RP3004524	205.07	241.42	169.63	1.18	0.83
NT2RP3004527	25.6	24.92	21.93	1	1
NT2RP3004534	89.99	96.47	70.64	1.07	0.78
NT2RP3004539	92.66	108.27	79.87	1.17	0.86
NT2RP3004541	88.72	110.55	87.51	1.25	0.99
NT2RP3004544	58.56	60.41	57.63	1.03	0.98
NT2RP3004551	65.91	83.35	66.69	1.26	1.01
NT2RP3004552	30.3	31.56	45.37	1	1.13
NT2RP3004557	64.5	47.43	68.3	0.74	1.06
NT2RP3004561	25.53	23.26	25.36	1	1
NT2RP3004566	125.24	173.89	117.93	1.39	0.94
NT2RP3004569	49.16	49.44	60.25	1.01	1.23
NT2RP3004572	55.58	43.31	32.83	0.78	0.72
NT2RP3004578	25.37	26.01	25.04	1	1
NT2RP3004584	359.99	342.69	335.17	0.95	0.93
NT2RP3004588	56.8	34.86	42.32	0.7	0.75
NT2RP3004594	53.96	53.37	68.69	0.99	1.27
NT2RP3004603	655.79	684.48	717.45	1.04	1.09
NT2RP3004612	51.3	60.62	72.09	1.18	1.41
NT2RP3004617	19.42	21.74	17.97	1	1
NT2RP3004618	24.28	27.09	31.21	1	1
NT2RP3004625	76.43	84.31	85.4	1.1	1.12
NT2RP3004635	19.08	22.45	20.58	1	1

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NT2RP3004640	1378.9	1514.12	1303.71	1.1	0.95
NT2RP3004642	182.41	303.56	310.29	1.66	1.7
NT2RP3004647	63.45	83.43	77.11	1.31	1.22
NT2RP3004652	91.53	104.68	89.16	1.14	0.97
NT2RP3004669	39.42	38.2	35.67	1	1
NT2RP3004670	160.62	115.64	117.02	0.72	0.73
NT2RP4000008	222.26	228.43	224.99	1.03	1.01
NT2RP4000018	56.28	93.57	95.69	1.66	1.7
NT2RP4000023	42.37	48.37	49.02	1.14	1.16
NT2RP4000025	80.81	126.58	101.15	1.57	1.25
NT2RP4000035	69.03	82.1	81.16	1.19	1.18
NT2RP4000041	79.1	90.13	80.28	1.14	1.01
NT2RP4000049	147.86	192.41	168.8	1.3	1.14
NT2RP4000050	24.77	31.25	36.38	1	1
NT2RP4000051	75.66	116.42	82.53	1.54	1.09
NT2RP4000063	72.62	100.22	100.15	1.38	1.38
NT2RP4000065	45.24	54.51	49.9	1.2	1.1
NT2RP4000070	31.26	54.15	46.48	1.35	1.16
NT2RP4000074	12.33	16.23	20.29	1	1
NT2RP4000078	75.86	110.9	80.3	1.46	1.06
NT2RP4000080	80.88	93.02	78.58	1.15	0.97
NT2RP4000099	1053.2	1038.5	916.55	0.99	0.87
NT2RP4000102	27.86	29.09	25.75	1	1
NT2RP4000103	21.35	29.48	30.97	1	1
NT2RP4000108	58.21	88.52	86.37	1.52	1.48
NT2RP4000109	69.1	131.83	82.99	1.91	1.2
NT2RP4000111	23.75	22.87	28.88	1	1
NT2RP4000112	114.98	134.89	105.27	1.17	0.92
NT2RP4000115	51.75	65.58	71.79	1.27	1.39
NT2RP4000129	35.57	40.59	48.71	1.01	1.22
NT2RP4000137	63.85	72.79	62.88	1.14	0.98
NT2RP4000138	66.49	121.56	116.38	1.83	1.75
NT2RP4000141	28.94	41.68	52.28	1.04	1.31
NT2RP4000147	26	38	38.92	1	1
NT2RP4000150	88.3	120.98	84.52	1.37	0.96
NT2RP4000151	52.29	63.78	54.84	1.22	1.05
NT2RP4000157	778.86	1091.73	934.87	1.4	1.2
NT2RP4000159	40.74	42.67	33.34	1.05	0.98
NT2RP4000163	52.33	101.29	76.1	1.94	1.45
NT2RP4000167	27.03	44.14	34.24	1.1	1
NT2RP4000171	29.03	45.34	48.5	1.13	1.21
NT2RP4000175	479.51	694.03	732.28	1.45	1.53
NT2RP4000180	785.14	618.3	535.68	0.79	0.68
NT2RP4000185	272.26	311.17	267.89	1.14	0.98
NT2RP4000192	31.33	34.17	36.03	1	1
NT2RP4000194	37.09	47.26	43.63	1.18	1.09

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NT2RP4000196	173.52	187.35	178.79	1.08	1.03
NT2RP4000210	133.92	204.79	148.13	1.53	1.11
NT2RP4000212	102.04	156.41	124.9	1.53	1.22
NT2RP4000214	87.17	120.74	99.23	1.39	1.14
NT2RP4000216	35.45	34.37	27.6	1	1
NT2RP4000218	73.32	77.76	81.62	1.06	1.11
NT2RP4000223	4315.5	3901.66	2653.96	0.9	0.61
NT2RP4000243	283.83	295.67	254	1.04	0.89
NT2RP4000246	63.13	77.18	65.82	1.22	1.04
NT2RP4000250	260.85	369.26	332.3	1.42	1.27
NT2RP4000256	76.14	96.38	74.36	1.27	0.98
NT2RP4000257	304.33	327.37	220.04	1.08	0.72
NT2RP4000259	32.33	31.01	27.68	1	1
NT2RP4000261	33.11	40.88	36.45	1.02	1
NT2RP4000262	70.14	119.93	84.26	1.71	1.2
NT2RP4000263	28.95	33.54	30.35	1	1
NT2RP4000280	95.85	95.01	76.73	0.99	0.8
NT2RP4000286	42	33.11	33.2	0.95	0.95
NT2RP4000290	29.66	23.46	26.81	1	1
NT2RP4000291	463.19	507.14	484.02	1.09	1.04
NT2RP4000301	257.66	256.04	228.34	0.99	0.89
NT2RP4000312	461.34	582.8	330.17	1.26	0.72
NT2RP4000321	102.55	127.18	82.83	1.24	0.81
NT2RP4000323	30.01	38.34	29.69	1	1
NT2RP4000324	133.54	155.56	140.5	1.16	1.05
NT2RP4000334	1073.8	1283.99	936.35	1.2	0.87
NT2RP4000343	27.46	16.41	40.57	1	1.01
NT2RP4000348	50.74	45.93	63.21	0.91	1.25
NT2RP4000349	5.83	4.49	8.42	1	1
NT2RP4000355	139.86	160.15	128.91	1.15	0.92
NT2RP4000356	198.87	233.54	126.23	1.17	0.63
NT2RP4000360	37.61	36.07	38.44	1	1
NT2RP4000367	12.78	12.06	13.14	1	1
NT2RP4000370	48.9	49.45	45.56	1.01	0.93
NT2RP4000373	33.89	24.14	29.92	1	1
NT2RP4000376	41.47	43.67	42.83	1.05	1.03
NT2RP4000381	56.09	61.01	67.82	1.09	1.21
NT2RP4000388	3438.4	5353.31	3404.96	1.56	0.99
NT2RP4000390	2074.8	2579.24	1845.43	1.24	0.89
NT2RP4000393	81.2	47.88	61.2	0.59	0.75
NT2RP4000398	127.57	120.61	95.2	0.95	0.75
NT2RP4000406	102.29	126.61	132.07	1.24	1.29
NT2RP4000407	62.3	104.36	70.03	1.68	1.12
NT2RP4000413	15.84	16.77	26.24	1	1
NT2RP4000415	185.4	198.86	176.36	1.07	0.95
NT2RP4000417	110.32	122.95	109.48	1.11	0.99

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NT2RP4000423	103.64	118.47	113.8	1.14	1.1
NT2RP4000424	72.65	76.73	72.62	1.06	1
NT2RP4000447	924.91	841.74	991.27	0.91	1.07
NT2RP4000448	35.39	34.3	43.57	1	1.09
NT2RP4000449	291.75	289.2	289.47	0.99	0.99
NT2RP4000453	47.87	30.3	38.87	0.84	0.84
NT2RP4000455	19.64	23.84	24.61	1	1
NT2RP4000456	104.61	148.67	142.24	1.42	1.36
NT2RP4000457	35.66	40.6	38.53	1.02	1
NT2RP4000461	52.1	63.3	42.8	1.21	0.82
NT2RP4000462	113.25	177.92	150.14	1.57	1.33
NT2RP4000463	734.32	789.76	803.95	1.08	1.09
NT2RP4000471	33.5	37.42	58.74	1	1.47
NT2RP4000472	12.15	15.6	18.38	1	1
NT2RP4000476	121.76	130.74	160.3	1.07	1.32
NT2RP4000480	66.33	74.9	77.03	1.13	1.16
NT2RP4000481	106.26	128.49	120.91	1.21	1.14
NT2RP4000483	87.45	114.02	116.44	1.3	1.33
NT2RP4000487	20.29	22.04	19.75	1	1
NT2RP4000496	43.59	47.74	44.56	1.1	1.02
NT2RP4000497	117.63	194.85	197.38	1.66	1.68
NT2RP4000498	116.96	129.49	162.43	1.11	1.39
NT2RP4000500	19.89	30.49	27.29	1	1
NT2RP4000507	80.77	132.84	67.15	1.64	0.83
NT2RP4000515	559.2	489.79	440.24	0.88	0.79
NT2RP4000516	160.4	200.17	169.4	1.25	1.06
NT2RP4000517	44.31	66.96	58.88	1.51	1.33
NT2RP4000518	33.71	55.87	41.71	1.4	1.04
NT2RP4000519	14.72	16.89	18.66	1	1
NT2RP4000524	7.68	10.47	12.02	1	1
NT2RP4000528	19.94	15.33	17.45	1	1
NT2RP4000537	282.75	572.44	398.79	2.02	1.41
NT2RP4000541	31.87	58.32	29.64	1.46	1
NT2RP4000543	77.54	95.32	104.85	1.23	1.35
NT2RP4000545	103.35	115.15	95.54	1.11	0.92
NT2RP4000546	46.19	61.68	58.47	1.34	1.27
NT2RP4000549	304.19	447.85	414.46	1.47	1.36
NT2RP4000556	48.61	81.77	75.72	1.68	1.56
NT2RP4000557	17.38	22.38	15.84	1	1
NT2RP4000558	45.51	57.79	56.51	1.27	1.24
NT2RP4000560	611.52	667.32	483.99	1.09	0.79
NT2RP4000568	43.55	46.84	31.83	1.08	0.92
NT2RP4000583	86.28	134.26	106.31	1.56	1.23
NT2RP4000585	23.23	30.42	25.59	1	1
NT2RP4000588	46.67	59.72	62.28	1.28	1.33
NT2RP4000590	127.26	166.02	159.16	1.3	1.25

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NT2RP4000599	18.13	16.03	13.63	1	1
NT2RP4000603	130.22	81.45	133.41	0.63	1.02
NT2RP4000607	78.04	70.81	94.27	0.91	1.21
NT2RP4000614	92.47	158.2	95.17	1.71	1.03
NT2RP4000634	69.96	81.94	62.49	1.17	0.89
NT2RP4000638	58.67	72.69	49.02	1.24	0.84
NT2RP4000648	33.2	36.36	39.64	1	1
NT2RP4000657	93.66	95.51	85.48	1.02	0.91
NT2RP4000691	23.7	19.45	22.58	1	1
NT2RP4000697	38.41	42.61	47.16	1.07	1.18
NT2RP4000704	810.46	704.82	575.86	0.87	0.71
NT2RP4000710	367.63	454.8	327.84	1.24	0.89
NT2RP4000713	92.63	68.41	70.43	0.74	0.76
NT2RP4000724	106.96	105.21	96.63	0.98	0.9
NT2RP4000725	20.25	25.12	19.41	1	1
NT2RP4000728	287.33	290.65	341.19	1.01	1.19
NT2RP4000737	10.12	11.16	13.56	1	1
NT2RP4000739	42.61	65.06	46.86	1.53	1.1
NT2RP4000749	31.27	63.8	41.75	1.6	1.04
NT2RP4000769	68.31	66.92	69.17	0.98	1.01
NT2RP4000774	23.97	38.26	29.18	1	1
NT2RP4000781	24.94	29.69	31.17	1	1
NT2RP4000783	51.2	57.57	59.46	1.12	1.16
NT2RP4000787	17	27.58	21.48	1	1
NT2RP4000788	125.97	134.65	116.73	1.07	0.93
NT2RP4000792	55.44	58.72	56.48	1.06	1.02
NT2RP4000809	336.03	732.64	359.46	2.18	1.07
NT2RP4000817	47.51	58.73	43.28	1.24	0.91
NT2RP4000821	300.32	443.02	292.28	1.48	0.97
NT2RP4000822	55.39	88.08	64.38	1.59	1.16
NT2RP4000823	5437.8	5971.64	4790.62	1.1	0.88
NT2RP4000831	851	1057.83	730.11	1.24	0.86
NT2RP4000833	134.75	216.69	113.96	1.61	0.85
NT2RP4000837	46.6	72.94	46.94	1.57	1.01
NT2RP4000839	2006.7	2613.14	1762.14	1.3	0.88
NT2RP4000846	65.04	80.53	56.91	1.24	0.88
NT2RP4000848	145.99	161.97	115.53	1.11	0.79
NT2RP4000855	39.34	46.96	37.55	1.17	1
NT2RP4000863	44.81	42.62	40.65	0.95	0.91
NT2RP4000865	146.47	174.98	130.7	1.19	0.89
NT2RP4000873	774.7	1139.99	671.45	1.47	0.87
NT2RP4000874	75.53	71.8	70.85	0.95	0.94
NT2RP4000875	89.5	101.82	80.06	1.14	0.89
NT2RP4000878	222.32	278.88	214.52	1.25	0.96
NT2RP4000879	28.33	45.55	28.84	1.14	1
NT2RP4000880	100.18	125.5	89.68	1.25	0.9

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NT2RP4000894	30.55	39.26	35.49	1	1
NT2RP4000899	3146.7	3606.62	2797.64	1.15	0.89
NT2RP4000902	109.71	150.03	110.84	1.37	1.01
NT2RP4000906	16.93	22.99	27.12	1	1
NT2RP4000907	99.06	138.21	92.83	1.4	0.94
NT2RP4000915	20.37	19.75	22.59	1	1
NT2RP4000916	56.93	68.73	49.07	1.21	0.86
NT2RP4000918	3435.5	4116.28	2966.55	1.2	0.86
NT2RP4000925	33.51	43.87	63.22	1.1	1.58
NT2RP4000927	3.9	8	7.28	1	1
NT2RP4000928	62.99	74.46	63.24	1.18	1
NT2RP4000929	26.21	31.88	31.03	1	1
NT2RP4000946	68.51	73.12	65.53	1.07	0.96
NT2RP4000947	7.37	8.2	12.9	1	1
NT2RP4000949	23.12	21.49	20.39	1	1
NT2RP4000955	26.96	41.36	34.45	1.03	1
NT2RP4000959	117.38	165.4	117.82	1.41	1
NT2RP4000962	39.29	61.03	38.49	1.53	1
NT2RP4000973	90.41	148.39	110.47	1.64	1.22
NT2RP4000975	73.27	81.85	70.35	1.12	0.96
NT2RP4000979	62.1	63.6	58.87	1.02	0.95
NT2RP4000984	25.88	36.99	33.5	1	1
NT2RP4000986	36.66	49.16	42.08	1.23	1.05
NT2RP4000988	41.63	62.95	58.42	1.51	1.4
NT2RP4000989	21.43	40.11	38.15	1	1
NT2RP4000990	13.72	19.25	19.83	1	1
NT2RP4000994	52.17	63.22	47.5	1.21	0.91
NT2RP4000996	201.53	260.2	229.02	1.29	1.14
NT2RP4000997	346.37	367.39	323.32	1.06	0.93
NT2RP4001001	65.25	166.28	144.6	2.55	2.22
NT2RP4001004	17.32	29.37	27.23	1	1
NT2RP4001006	37.45	58.38	54.94	1.46	1.37
NT2RP4001009	55.45	74.56	67.53	1.34	1.22
NT2RP4001010	30.61	53.35	38.41	1.33	1
NT2RP4001013	268.97	369.38	269.18	1.37	1
NT2RP4001029	73.73	97.74	73.03	1.33	0.99
NT2RP4001036	45.19	84.59	56.53	1.87	1.25
NT2RP4001041	75.04	123.46	61.45	1.65	0.82
NT2RP4001042	38.75	95.82	83.74	2.4	2.09
NT2RP4001046	57.64	93.13	95.53	1.62	1.66
NT2RP4001050	26.37	40.47	43.52	1.01	1.09
NT2RP4001051	61.42	89.43	62.79	1.46	1.02
NT2RP4001057	32.34	36.04	37.94	1	1
NT2RP4001063	26.25	38.27	24.85	1	1
NT2RP4001064	112.85	167.16	116.14	1.48	1.03
NT2RP4001067	48.35	77.59	57.99	1.6	1.2

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NT2RP4001078	23.84	37.66	31.93	1	1
NT2RP4001079	54.19	92.79	92.06	1.71	1.7
NT2RP4001080	27.34	41.41	40.95	1.04	1.02
NT2RP4001086	25.45	36.17	33.23	1	1
NT2RP4001095	110	130.16	98.11	1.18	0.89
NT2RP4001098	44.54	67.38	48.86	1.51	1.1
NT2RP4001100	227.36	317.35	218.72	1.4	0.96
NT2RP4001105	32.08	54.23	35.25	1.36	1
NT2RP4001110	23.12	25.65	26.96	1	1
NT2RP4001115	103.49	125.37	115.49	1.21	1.12
NT2RP4001117	100.37	139.05	141.24	1.39	1.41
NT2RP4001122	41.76	58.12	44.9	1.39	1.08
NT2RP4001123	46.49	38.53	51.12	0.86	1.1
NT2RP4001126	113.39	125.74	96.58	1.11	0.85
NT2RP4001127	30.82	37.12	29.07	1	1
NT2RP4001138	19.54	32.63	17.23	1	1
NT2RP4001143	65.42	96.6	62.56	1.48	0.96
NT2RP4001148	24.25	33.71	26.53	1	1
NT2RP4001149	46.45	59.14	55.45	1.27	1.19
NT2RP4001150	17.46	20.84	16.58	1	1
NT2RP4001159	69.49	138.7	83.52	2	1.2
NT2RP4001162	49.9	71.52	52.02	1.43	1.04
NT2RP4001170	15.29	26.52	19.13	1	1
NT2RP4001174	109.03	139.36	107.01	1.28	0.98
NT2RP4001175	136.22	158.82	98.36	1.17	0.72
NT2RP4001176	1350.5	1507.62	936.35	1.12	0.69
NT2RP4001184	225.16	301.74	216.76	1.34	0.96
NT2RP4001198	190.18	241.01	162.97	1.27	0.86
NT2RP4001199	124.51	180.43	89.79	1.45	0.72
NT2RP4001206	126.71	162.16	109.3	1.28	0.86
NT2RP4001207	44.09	44.29	32.85	1	0.91
NT2RP4001210	41.63	57.34	38.09	1.38	0.96
NT2RP4001213	49.13	52.04	44.67	1.06	0.91
NT2RP4001214	40.72	43.92	31.78	1.08	0.98
NT2RP4001219	77.06	102.93	93.5	1.34	1.21
NT2RP4001228	152.65	191.14	158.88	1.25	1.04
NT2RP4001235	71.1	125.09	70.42	1.76	0.99
NT2RP4001256	38.96	49.68	32.47	1.24	1
NT2RP4001257	43.79	38.05	35.02	0.91	0.91
NT2RP4001260	44.37	40.62	39.19	0.92	0.9
NT2RP4001261	109.74	125.19	97.42	1.14	0.89
NT2RP4001274	174.28	218	149.42	1.25	0.86
NT2RP4001276	75.37	100.86	92.31	1.34	1.22
NT2RP4001283	2449.5	3070.04	2133.89	1.25	0.87
NT2RP4001299	217.09	268.47	225.62	1.24	1.04
NT2RP4001313	15.11	20.98	23.95	1	1

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NT2RP4001315	37.75	47.79	31.64	1.19	1
NT2RP4001320	261.53	361.67	309.05	1.38	1.18
NT2RP4001325	4020.9	4268.24	4022.07	1.06	1
NT2RP4001336	183.17	202.3	163.1	1.1	0.89
NT2RP4001339	17.85	34.33	28.05	1	1
NT2RP4001343	940.26	1345.48	930.02	1.43	0.99
NT2RP4001344	688.94	857.91	532.27	1.25	0.77
NT2RP4001345	41.74	48.57	35.66	1.16	0.96
NT2RP4001351	185.72	182.8	153.03	0.98	0.82
NT2RP4001353	9.68	14.88	21.08	1	1
NT2RP4001355	18.68	28.42	26.43	1	1
NT2RP4001367	40.52	59.34	51.4	1.46	1.27
NT2RP4001372	17.43	26.27	22.03	1	1
NT2RP4001373	118.63	113.01	134.22	0.95	1.13
NT2RP4001375	26.91	23.36	28.7	1	1
NT2RP4001379	47.86	54.08	42.23	1.13	0.88
NT2RP4001381	122.88	173.12	114.91	1.41	0.94
NT2RP4001386	98.02	158.52	109.53	1.62	1.12
NT2RP4001389	53.66	92.57	79.09	1.73	1.47
NT2RP4001396	22.26	30.58	27.78	1	1
NT2RP4001407	17.41	29.36	20.87	1	1
NT2RP4001409	153.69	174.14	234.02	1.13	1.52
NT2RP4001410	245.64	323.8	262.66	1.32	1.07
NT2RP4001414	74.05	84.98	62.2	1.15	0.84
NT2RP4001424	52.44	70.38	58.47	1.34	1.11
NT2RP4001433	37.84	97.44	73.46	2.44	1.84
NT2RP4001438	174.35	282.89	255.46	1.62	1.47
NT2RP4001442	27.03	42.94	32.47	1.07	1
NT2RP4001447	20.24	35.15	23.88	1	1
NT2RP4001466	44.13	64.61	52.86	1.46	1.2
NT2RP4001467	193.06	274.08	203.3	1.42	1.05
NT2RP4001472	94.33	134.01	96.25	1.42	1.02
NT2RP4001474	29.74	42.59	36.54	1.06	1
NT2RP4001483	19.59	26.66	30.24	1	1
NT2RP4001488	158.69	247.94	222.48	1.56	1.4
NT2RP4001492	39.9	56.53	44.59	1.41	1.11
NT2RP4001498	61.89	85.68	61.94	1.38	1
NT2RP4001502	286.72	459.78	352.7	1.6	1.23
NT2RP4001503	84.47	131.1	92.37	1.55	1.09
NT2RP4001507	79.23	93.24	71.69	1.18	0.9
NT2RP4001510	42.37	61.59	42.79	1.45	1.01
NT2RP4001516	24.03	40.09	37.03	1	1
NT2RP4001520	1023.7	1060.53	1038.31	1.04	1.01
NT2RP4001523	98.86	141.39	105.89	1.43	1.07
NT2RP4001524	53.11	82.9	89.37	1.56	1.68
NT2RP4001529	79.15	88.49	79.76	1.12	1.01

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NT2RP4001531	103.9	127.19	97.8	1.22	0.94
NT2RP4001546	3506.6	4354.44	2937.38	1.24	0.84
NT2RP4001547	124.6	236.33	194.94	1.9	1.56
NT2RP4001551	15.2	20	21.58	1	1
NT2RP4001555	28.11	34.17	31.06	1	1
NT2RP4001567	35.99	57.74	51.94	1.44	1.3
NT2RP4001568	123.92	191.69	129.56	1.55	1.05
NT2RP4001569	147.33	159.03	172.95	1.08	1.17
NT2RP4001571	53.11	49.65	47.15	0.93	0.89
NT2RP4001574	74.62	118.32	95.53	1.59	1.28
NT2RP4001575	30.2	46.35	49.83	1.16	1.25
NT2RP4001578	336.45	444.06	354.09	1.32	1.05
NT2RP4001592	72.42	110.61	85.77	1.53	1.18
NT2RP4001593	109.17	167.02	148.89	1.53	1.36
NT2RP4001605	28.22	33.39	31.79	1	1
NT2RP4001606	57.12	57.27	48.49	1	0.85
NT2RP4001607	38.96	41.95	37.14	1.05	1
NT2RP4001610	20.34	26.24	19.62	1	1
NT2RP4001614	35.87	39.23	40.43	1	1.01
NT2RP4001623	30.16	33.74	31.5	1	1
NT2RP4001626	102.72	107.35	83.38	1.05	0.81
NT2RP4001634	20.93	26.6	22.88	1	1
NT2RP4001638	43.2	39.83	27.98	0.93	0.93
NT2RP4001644	90.89	139.21	128.77	1.53	1.42
NT2RP4001646	74.34	105.54	92.13	1.42	1.24
NT2RP4001656	26.99	27.37	30.84	1	1
NT2RP4001666	27.25	22.39	21.49	1	1
NT2RP4001670	25.82	30.17	27.62	1	1
NT2RP4001677	199.37	254.01	216.26	1.27	1.08
NT2RP4001679	284.9	404.21	255.88	1.42	0.9
NT2RP4001695	60.24	57.95	93.09	0.96	1.55
NT2RP4001696	50.27	69.63	41.59	1.39	0.83
NT2RP4001699	115.88	176.36	99.68	1.52	0.86
NT2RP4001717	42.62	53.66	39.68	1.26	0.94
NT2RP4001719	36.5	50.2	30.94	1.26	1
NT2RP4001725	18.61	25.02	18.94	1	1
NT2RP4001726	66.49	89.94	73.84	1.35	1.11
NT2RP4001730	70.16	63.61	47.29	0.91	0.67
NT2RP4001739	42.06	51.3	49.42	1.22	1.17
NT2RP4001741	180.84	250.66	135.6	1.39	0.75
NT2RP4001753	72.78	104.66	52.65	1.44	0.72
NT2RP4001760	51	52.44	44.59	1.03	0.87
NT2RP4001787	4461.9	5125.17	3639.25	1.15	0.82
NT2RP4001790	46.27	54.59	40.79	1.18	0.88
NT2RP4001795	154.14	189.71	153.64	1.23	1
NT2RP4001803	50.74	51.85	46.05	1.02	0.91

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NT2RP4001805	32.65	36.8	29.6	1	1
NT2RP4001809	191.23	213.41	137.81	1.12	0.72
NT2RP4001817	112.92	162.95	120.23	1.44	1.06
NT2RP4001822	65.32	70.78	65.97	1.08	1.01
NT2RP4001823	21.06	22.44	21.32	1	1
NT2RP4001827	102.8	112	95.96	1.09	0.93
NT2RP4001828	431.57	583.31	473.45	1.35	1.1
NT2RP4001836	146.86	202.66	148.56	1.38	1.01
NT2RP4001838	29.91	43.1	37.71	1.08	1
NT2RP4001841	1549.1	1954.07	1139.77	1.26	0.74
NT2RP4001849	33.35	29.78	25.37	1	1
NT2RP4001861	736.02	720.46	638.48	0.98	0.87
NT2RP4001877	93.22	103.29	93.49	1.11	1
NT2RP4001879	49.34	70.19	54.7	1.42	1.11
NT2RP4001889	103.01	187.69	165.9	1.82	1.61
NT2RP4001893	27.15	40.29	34.35	1.01	1
NT2RP4001896	37.41	97.88	61.56	2.45	1.54
NT2RP4001898	183.3	215.58	185.12	1.18	1.01
NT2RP4001901	60.98	80.96	58.59	1.33	0.96
NT2RP4001910	408.91	559.44	327.12	1.37	0.8
NT2RP4001925	59.81	72.23	51.93	1.21	0.87
NT2RP4001926	46.24	66.65	60.62	1.44	1.31
NT2RP4001927	42.17	51.54	45.85	1.22	1.09
NT2RP4001931	54.82	81.7	62.6	1.49	1.14
NT2RP4001933	181.43	229.76	269.85	1.27	1.49
NT2RP4001938	89.48	111.84	97.72	1.25	1.09
NT2RP4001942	157.21	178.4	186.22	1.13	1.18
NT2RP4001945	23.76	21.74	26.27	1	1
NT2RP4001946	34.33	46.5	40.43	1.16	1.01
NT2RP4001947	18.29	28.67	26.12	1	1
NT2RP4001950	23.81	28.29	30.45	1	1
NT2RP4001953	76.32	134.32	95.15	1.76	1.25
NT2RP4001966	14.53	24.06	18.92	1	1
NT2RP4001970	32.46	66.99	45.62	1.67	1.14
NT2RP4001975	93.45	117.02	108.65	1.25	1.16
NT2RP4001988	103.89	188.4	157.9	1.81	1.52
NT2RP4001996	47.79	87.05	68.23	1.82	1.43
NT2RP4002014	48.78	113.53	89.64	2.33	1.84
NT2RP4002018	50.95	67.62	72.16	1.33	1.42
NT2RP4002035	38.64	83.62	57.12	2.09	1.43
NT2RP4002043	50.55	74.39	61.28	1.47	1.21
NT2RP4002046	113.68	146.69	103.17	1.29	0.91
NT2RP4002047	96.67	132.21	84.39	1.37	0.87
NT2RP4002052	47.17	63.23	54.34	1.34	1.15
NT2RP4002056	350.57	455.24	380.17	1.3	1.08
NT2RP4002057	61.49	117.62	116.72	1.91	1.9

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NT2RP4002058	25.72	47.72	52.24	1.19	1.31
NT2RP4002064	19.42	33.93	26.12	1	1
NT2RP4002071	44.49	82.96	52.47	1.86	1.18
NT2RP4002075	28.6	36.73	33.16	1	1
NT2RP4002078	92.71	143.87	108.63	1.55	1.17
NT2RP4002081	236.65	249.16	249.24	1.05	1.05
NT2RP4002083	17.72	23.02	27.12	1	1
NT2RP4002099	18.6	29.18	27.89	1	1
NT2RP4002106	54.11	107.08	119	1.98	2.2
NT2RP4002111	101.96	200.72	148.95	1.97	1.46
NT2RP4002112	74.68	68.41	53.51	0.92	0.72
NT2RP4002116	379.37	384.55	382.82	1.01	1.01
NT2RP4002122	61.29	75.89	55.81	1.24	0.91
NT2RP4002126	66.06	115.78	77.24	1.75	1.17
NT2RP4002133	124.26	188.7	156.52	1.52	1.26
NT2RP4002136	59.72	83.01	65.67	1.39	1.1
NT2RP4002139	196.25	298.89	317.57	1.52	1.62
NT2RP4002174	47.12	56.4	49.37	1.2	1.05
NT2RP4002185	60.33	83.37	80.31	1.38	1.33
NT2RP4002186	122.78	157.98	101.33	1.29	0.83
NT2RP4002187	105.68	137.58	144.38	1.3	1.37
NT2RP4002188	70.98	106.05	83.05	1.49	1.17
NT2RP4002199	31.14	47.63	46.66	1.19	1.17
NT2RP4002206	39.97	38.91	31.55	1	1
NT2RP4002210	26.97	23.02	24.96	1	1
NT2RP4002222	38.72	58.99	42.3	1.47	1.06
NT2RP4002241	81.81	88.06	74.33	1.08	0.91
NT2RP4002248	85.52	108.46	83.74	1.27	0.98
NT2RP4002250	6.36	20.54	11.35	1	1
NT2RP4002259	29.41	42.66	31.34	1.07	1
NT2RP4002268	159.71	202.23	161.92	1.27	1.01
NT2RP4002288	181.37	257.54	204.61	1.42	1.13
NT2RP4002290	56.9	76.7	71.74	1.35	1.26
NT2RP4002298	53.47	84.08	46.67	1.57	0.87
NT2RP4002306	53.35	84.82	74.88	1.59	1.4
NT2RP4002308	42.24	41.6	33.19	0.98	0.95
NT2RP4002336	68.71	90.07	67.38	1.31	0.98
NT2RP4002340	19.09	13.39	14.64	1	1
NT2RP4002361	40.9	56.53	37.12	1.38	0.98
NT2RP4002367	29.1	25.75	23.97	1	1
NT2RP4002368	94.98	113.04	103.33	1.19	1.09
NT2RP4002377	289.2	315.73	317.74	1.09	1.1
NT2RP4002408	30.29	33.42	32.09	1	1
NT2RP4002425	43.47	72.09	45.88	1.66	1.06
NT2RP4002432	1549.3	2074.3	1253.27	1.34	0.81
NT2RP4002447	99.1	100.15	81.33	1.01	0.82

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NT2RP4002451	55.07	53.75	50.58	0.98	0.92
NT2RP4002461	283.54	296.78	229.24	1.05	0.81
NT2RP4002486	52.21	62.8	51.82	1.2	0.99
NT2RP4002517	86.77	89.86	85.96	1.04	0.99
NT2RP4002556	56.11	73.77	77.16	1.31	1.38
NT2RP4002569	96.58	96.6	81.78	1	0.85
NT2RP4002587	59.69	46.93	47.79	0.79	0.8
NT2RP4002591	59.54	66.69	61.58	1.12	1.03
NT2RP4002607	65.45	67.05	57.12	1.02	0.87
NT2RP4002627	1154.4	1435.6	1039.2	1.24	0.9
NT2RP4002628	89.25	115.91	86.23	1.3	0.97
NT2RP4002630	139.5	192.58	143.27	1.38	1.03
NT2RP4002639	949.82	913.58	777.44	0.96	0.82
NT2RP4002641	57.68	78.81	58.54	1.37	1.01
NT2RP4002658	690.44	903.21	768.32	1.31	1.11
NT2RP4002669	55.37	58.95	55.54	1.06	1
NT2RP4002677	65.98	122.24	115.69	1.85	1.75
NT2RP4002715	160.17	197.94	157.66	1.24	0.98
NT2RP4002750	25.5	31.12	32	1	1
NT2RP4002784	79.32	110.67	79.11	1.4	1
NT2RP4002791	31.48	81.22	60.98	2.03	1.52
NT2RP4002811	30.15	37.16	31.27	1	1
NT2RP4002830	78.6	93.65	83.44	1.19	1.06
NT2RP4002832	26.95	34.45	33.04	1	1
NT2RP4002850	105.03	134.98	121.72	1.29	1.16
NT2RP4002874	14.39	16.4	17.69	1	1
NT2RP4002884	248.98	397.43	368.37	1.6	1.48
NT2RP4002888	22.67	39.71	35.05	1	1
NT2RP4002891	78.58	105.26	101.71	1.34	1.29
NT2RP4002894	157.28	186.39	182.82	1.19	1.16
NT2RP4002896	62.43	72.07	61.47	1.15	0.98
NT2RP4002905	35.39	37.85	36.81	1	1
NT2RP4002907	60.03	78.35	74.11	1.31	1.23
NT2RP5003459	2814.9	3301.39	3101.17	1.17	1.1
NT2RP5003461	46.24	61.77	44.54	1.34	0.96
NT2RP5003471	2383.9	4003.5	2319.1	1.68	0.97
NT2RP5003477	14.46	21.09	22.54	1	1
NT2RP5003487	4297.0	5054.14	3381.8	1.18	0.79
NT2RP5003492	31.05	42.59	32.16	1.06	1
NT2RP5003500	28.6	32.69	26.16	1	1
NT2RP5003506	73.76	122.61	102.08	1.66	1.38
NT2RP5003512	15.54	30.94	28.8	1	1
NT2RP5003522	18.03	33.33	26.71	1	1
NT2RP5003524	17.34	31.72	29.03	1	1
NT2RP5003527	349.06	483.98	393.69	1.39	1.13
NT2RP5003531	75.41	76.61	66.44	1.02	0.88

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NT2RP5003534	52.83	100.86	54.98	1.91	1.04
NT2RP6000020	254.97	316.92	257.92	1.24	1.01
NT2RP6000022	28.24	42.02	41.88	1.05	1.05
NT2RP6000050	21.19	34.01	39.08	1	1
NT2RP6000063	24.89	31.66	29.69	1	1
NT2RP6000074	27.19	40.18	36.98	1	1
NT2RP6000083	68.33	91.18	64.08	1.33	0.94
NT2RP6000100	52.92	50.18	45.21	0.95	0.85
NT2RP6000123	34.42	63.3	47.29	1.58	1.18
NT2RP6000129	40.69	50.73	39.14	1.25	0.98
NT2RP6000147	87.35	87.01	84.55	1	0.97
NT2RP6000163	28.6	34.59	32.31	1	1
NT2RP6000181	69.12	113.55	90.59	1.64	1.31
NT2RP6000182	42.14	68.54	51.62	1.63	1.22
OVARC1000001	49.41	91.19	69.76	1.85	1.41
OVARC1000003	102.25	87.38	70.78	0.85	0.69
OVARC1000004	2892.4	2673.1	1762.66	0.92	0.61
OVARC1000006	42.54	69.38	47.66	1.63	1.12
OVARC1000013	63.38	78.08	67.4	1.23	1.06
OVARC1000014	42.8	52.28	43.62	1.22	1.02
OVARC1000017	36.69	47.86	48.03	1.2	1.2
OVARC1000026	320.47	405.43	316.62	1.27	0.99
OVARC1000035	113.44	134.98	108.81	1.19	0.96
OVARC1000037	134.37	144.88	164.84	1.08	1.23
OVARC1000058	73.52	87.2	80.14	1.19	1.09
OVARC1000060	64.66	84.81	57.28	1.31	0.89
OVARC1000068	38.02	38.3	43.24	1	1.08
OVARC1000069	40.42	57.23	49.59	1.42	1.23
OVARC1000071	32.24	33.2	29.25	1	1
OVARC1000075	2412.8	3591.21	2207.17	1.49	0.91
OVARC1000083	117.97	119.13	69.75	1.01	0.59
OVARC1000085	792.51	498.22	687.24	0.63	0.87
OVARC1000086	69.36	75.22	72.13	1.08	1.04
OVARC1000087	24.26	30.25	33.69	1	1
OVARC1000090	123.62	113.17	136.64	0.92	1.11
OVARC1000091	41.32	40.24	43.17	0.97	1.04
OVARC1000092	59.92	45.23	66.35	0.75	1.11
OVARC1000105	193.62	211.28	213.54	1.09	1.1
OVARC1000106	207.32	203.69	194.81	0.98	0.94
OVARC1000109	95.88	83.7	80.21	0.87	0.84
OVARC1000113	119.41	112.39	127.87	0.94	1.07
OVARC1000114	92.45	81.84	102.21	0.89	1.11
OVARC1000133	40.28	48	69.51	1.19	1.73
OVARC1000137	68.99	58.7	79.44	0.85	1.15
OVARC1000139	1597.0	1399.58	1239.81	0.88	0.78
OVARC1000145	18.41	25.65	25.84	1	1

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OVARC1000148	80.77	84.79	78.69	1.05	0.97
OVARC1000151	38.7	34.81	30.58	1	1
OVARC1000157	126.85	138.69	121.57	1.09	0.96
OVARC1000162	31.19	30.47	41.58	1	1.04
OVARC1000168	60.64	84.53	66.09	1.39	1.09
OVARC1000169	593.72	714.83	894.21	1.2	1.51
OVARC1000178	39.59	38.33	28.67	1	1
OVARC1000182	20.83	21.3	22.61	1	1
OVARC1000186	49.43	45.22	42.58	0.91	0.86
OVARC1000188	29.19	26.83	21.31	1	1
OVARC1000191	26.54	29.18	21.28	1	1
OVARC1000198	62.71	85.36	58.69	1.36	0.94
OVARC1000208	272.18	324.49	263.93	1.19	0.97
OVARC1000209	141.71	150.62	119.37	1.06	0.84
OVARC1000212	47.05	49.04	39.68	1.04	0.85
OVARC1000216	17.93	18.99	19.61	1	1
OVARC1000240	103.46	101.08	71.71	0.98	0.69
OVARC1000241	47.76	37.11	42.61	0.84	0.89
OVARC1000249	34.16	38.99	36.88	1	1
OVARC1000254	1580.5	2172.35	1417.43	1.37	0.9
OVARC1000255	26.25	24.08	22.57	1	1
OVARC1000267	158.61	196.13	154.6	1.24	0.97
OVARC1000275	27.34	25.99	28.89	1	1
OVARC1000287	62.95	64.26	84.75	1.02	1.35
OVARC1000288	64.73	68.75	45.65	1.06	0.71
OVARC1000298	79.52	94.53	100.14	1.19	1.26
OVARC1000302	30.55	38.34	29.12	1	1
OVARC1000304	37.61	40.63	42.47	1.02	1.06
OVARC1000307	36.06	33.36	41.11	1	1.03
OVARC1000309	29.18	27.03	22.21	1	1
OVARC1000312	31.23	38.59	29.77	1	1
OVARC1000313	102.54	157.6	184.77	1.54	1.8
OVARC1000321	152.01	148.5	138.68	0.98	0.91
OVARC1000326	27.03	34.02	23.17	1	1
OVARC1000327	29.37	30.83	26.7	1	1
OVARC1000331	47.64	62.99	51.7	1.32	1.09
OVARC1000335	27.77	28.39	32.55	1	1
OVARC1000347	48.79	55.07	37.14	1.13	0.82
OVARC1000348	17.11	23.34	19.96	1	1
OVARC1000363	42.47	45.27	38.6	1.07	0.94
OVARC1000377	29.55	27.57	31.2	1	1
OVARC1000382	31.12	37.4	34.78	1	1
OVARC1000384	37.91	42.89	31.82	1.07	1
OVARC1000401	27.05	26.01	18.81	1	1
OVARC1000406	1432.1	1992.66	2667.11	1.39	1.86
OVARC1000407	55.42	62.17	49.83	1.12	0.9

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OVARC1000408	521.33	474.3	454.23	0.91	0.87
OVARC1000410	57.23	48.05	63.58	0.84	1.11
OVARC1000411	36.21	41.64	34.64	1.04	1
OVARC1000414	102.21	105.16	89.37	1.03	0.87
OVARC1000420	49.94	53.08	44.19	1.06	0.88
OVARC1000421	47.02	45.9	44.27	0.98	0.94
OVARC1000427	3330.4	3323.93	2479.35	1	0.74
OVARC1000431	163.82	212.48	204.37	1.3	1.25
OVARC1000437	52.04	48.36	47.4	0.93	0.91
OVARC1000439	113.64	76.62	106.88	0.67	0.94
OVARC1000440	71.11	74.54	56.39	1.05	0.79
OVARC1000442	119.54	121.73	109.35	1.02	0.91
OVARC1000443	65.66	52.35	38.24	0.8	0.61
OVARC1000461	29.17	37.12	25	1	1
OVARC1000465	34.43	34.38	43.55	1	1.09
OVARC1000466	46.92	37.83	43.09	0.85	0.92
OVARC1000467	38.38	36.82	38.22	1	1
OVARC1000470	62.44	77.76	68.31	1.25	1.09
OVARC1000473	47.79	41.99	31.39	0.88	0.84
OVARC1000479	83.4	72.71	77.11	0.87	0.92
OVARC1000484	116.94	161.5	98.17	1.38	0.84
OVARC1000486	54.85	62.16	47.76	1.13	0.87
OVARC1000496	18.29	28.12	16.71	1	1
OVARC1000520	24.36	22.81	23.25	1	1
OVARC1000522	64	68.45	54.56	1.07	0.85
OVARC1000526	102.56	106.43	75.86	1.04	0.74
OVARC1000529	54.69	60.42	41.68	1.1	0.76
OVARC1000533	80.21	81.45	73.46	1.02	0.92
OVARC1000543	36.03	34.69	22.16	1	1
OVARC1000550	33.22	39.9	37.09	1	1
OVARC1000553	78.24	110.76	91.37	1.42	1.17
OVARC1000556	68.77	93.52	73.85	1.36	1.07
OVARC1000557	28.95	42.48	33.83	1.06	1
OVARC1000561	257.61	351.52	287.81	1.36	1.12
OVARC1000564	139.65	110.7	130.87	0.79	0.94
OVARC1000573	68.41	59.91	62.83	0.88	0.92
OVARC1000576	2089.9	1861.86	1692.32	0.89	0.81
OVARC1000578	43.7	34.85	48.46	0.92	1.11
OVARC1000581	20.13	21.57	21.97	1	1
OVARC1000586	360.06	393.98	421.49	1.09	1.17
OVARC1000588	27.3	24.22	27.51	1	1
OVARC1000605	48.33	40.91	46.84	0.85	0.97
OVARC1000622	225.87	248.61	210.75	1.1	0.93
OVARC1000636	31.45	27.78	33.66	1	1
OVARC1000640	51.97	54.12	101.55	1.04	1.95
OVARC1000649	1164.0	1285.41	980.59	1.1	0.84

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OVARC1000661	50.99	49.55	47.02	0.97	0.92
OVARC1000677	132.42	141.8	167.49	1.07	1.26
OVARC1000678	54.44	54.52	57.5	1	1.06
OVARC1000679	51.06	54.02	40.27	1.06	0.79
OVARC1000681	38.25	27.56	28.08	1	1
OVARC1000682	341.04	412.78	251.86	1.21	0.74
OVARC1000689	99.5	105.11	89.74	1.06	0.9
OVARC1000700	58.34	75.6	60.57	1.3	1.04
OVARC1000703	73.66	74.87	53.93	1.02	0.73
OVARC1000722	715.27	635.83	473.66	0.89	0.66
OVARC1000726	38.23	28.7	25.99	1	1
OVARC1000727	48.09	50.07	40.26	1.04	0.84
OVARC1000730	73.44	74.87	80.56	1.02	1.1
OVARC1000741	73.45	80.84	89.53	1.1	1.22
OVARC1000746	26.64	30	28.58	1	1
OVARC1000764	88.26	97.96	68.38	1.11	0.77
OVARC1000769	101.98	141.42	90.47	1.39	0.89
OVARC1000771	40.54	47.82	40.96	1.18	1.01
OVARC1000773	255.51	361.9	494.36	1.42	1.93
OVARC1000775	115.23	107.57	86.04	0.93	0.75
OVARC1000778	55.18	60.68	47.93	1.1	0.87
OVARC1000779	15.03	16.56	13.23	1	1
OVARC1000781	33.98	45.89	37.86	1.15	1
OVARC1000787	35.99	33.77	27.66	1	1
OVARC1000789	112.59	74.08	135.19	0.66	1.2
OVARC1000800	85.36	118.32	95.97	1.39	1.12
OVARC1000802	39.52	39.36	32.48	1	1
OVARC1000810	119.13	160.74	97.12	1.35	0.82
OVARC1000811	39.94	51.48	34.85	1.29	1
OVARC1000814	174.62	239.67	149.65	1.37	0.86
OVARC1000816	47.23	66.84	64.23	1.42	1.36
OVARC1000817	22.37	20.91	18.09	1	1
OVARC1000834	26.16	25	26.88	1	1
OVARC1000846	73.93	93.47	72.32	1.26	0.98
OVARC1000850	31.18	37.53	39.12	1	1
OVARC1000853	171.25	177.98	145.03	1.04	0.85
OVARC1000862	37.1	42.09	43.93	1.05	1.1
OVARC1000873	60.05	84.54	94.75	1.41	1.58
OVARC1000875	36.96	37.79	30.93	1	1
OVARC1000876	32.05	23.99	36.5	1	1
OVARC1000883	49.62	61.62	63.13	1.24	1.27
OVARC1000885	34.95	40.51	53.3	1.01	1.33
OVARC1000886	44.21	43.73	64.9	0.99	1.47
OVARC1000890	1660.8	1784.57	1371.74	1.07	0.83
OVARC1000891	40.25	41.98	35.62	1.04	0.99
OVARC1000897	25.06	19.74	16.49	1	1

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OVARC1000912	59.56	69.38	47.1	1.16	0.79
OVARC1000914	40.41	41.76	36	1.03	0.99
OVARC1000915	49.67	62.61	41.44	1.26	0.83
OVARC1000916	47.9	43.94	45.57	0.92	0.95
OVARC1000924	29.28	34.41	30.96	1	1
OVARC1000928	35.01	25.29	28.53	1	1
OVARC1000936	34.94	26.94	36.31	1	1
OVARC1000937	52.14	62.32	40.83	1.2	0.78
OVARC1000945	27.17	35.2	26.08	1	1
OVARC1000948	19.22	16.97	17.07	1	1
OVARC1000956	65.96	70.99	47.84	1.08	0.73
OVARC1000959	52.49	59.37	43.22	1.13	0.82
OVARC1000960	280.28	287.82	206.56	1.03	0.74
OVARC1000964	2736	2613.45	1992.33	0.96	0.73
OVARC1000971	38.12	24.33	25.94	1	1
OVARC1000975	690.45	651.91	484.63	0.94	0.7
OVARC1000976	29.45	24.47	22.17	1	1
OVARC1000981	83.75	91.8	88.53	1.1	1.06
OVARC1000982	37.13	52.8	53.82	1.32	1.35
OVARC1000984	30.78	45.59	31.16	1.14	1
OVARC1000995	92.52	90.12	82.09	0.97	0.89
OVARC1000996	43.55	41.13	31.11	0.94	0.92
OVARC1000999	190.43	223.74	180.73	1.17	0.95
OVARC1001000	124.54	163.65	103.45	1.31	0.83
OVARC1001004	20.37	19.73	11.87	1	1
OVARC1001010	28.12	28.13	20.21	1	1
OVARC1001011	53.64	75.49	55.27	1.41	1.03
OVARC1001030	785.13	981.64	1153.75	1.25	1.47
OVARC1001032	39.89	55.5	33.14	1.39	1
OVARC1001034	32.15	37.76	26.08	1	1
OVARC1001038	57.97	61.91	47.15	1.07	0.81
OVARC1001040	161.02	206.83	134.77	1.28	0.84
OVARC1001041	89.09	128.8	96.87	1.45	1.09
OVARC1001044	26.96	24.74	22.65	1	1
OVARC1001049	102.73	174.76	131.25	1.7	1.28
OVARC1001051	824.36	715.74	791.3	0.87	0.96
OVARC1001054	22.98	27.27	27.9	1	1
OVARC1001055	53.59	60.1	38.64	1.12	0.75
OVARC1001062	59.15	51.97	63.58	0.88	1.07
OVARC1001065	428.98	431.9	407.39	1.01	0.95
OVARC1001068	34.9	33.41	45.49	1	1.14
OVARC1001072	26.92	24.25	32.9	1	1
OVARC1001073	36.02	34.51	45.07	1	1.13
OVARC1001074	25.32	30.81	29.07	1	1
OVARC1001078	39.03	51.19	54.45	1.28	1.36
OVARC1001085	47.8	50.43	44.75	1.06	0.94

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OVARC1001086	45.34	42.19	44.01	0.93	0.97
OVARC1001091	2172.5	1902.95	1634.39	0.88	0.75
OVARC1001092	41.59	40.51	44.8	0.97	1.08
OVARC1001104	43.01	47.57	49.82	1.11	1.16
OVARC1001107	313.26	304.53	294.7	0.97	0.94
OVARC1001113	24.12	21.01	23.72	1	1
OVARC1001117	73.35	65.99	75.97	0.9	1.04
OVARC1001118	88.32	80.99	78.51	0.92	0.89
OVARC1001125	66.79	70.91	67.69	1.06	1.01
OVARC1001129	39.94	40.36	41.27	1.01	1.03
OVARC1001132	50.72	51.63	68.85	1.02	1.36
OVARC1001138	229.26	273.54	263.88	1.19	1.15
OVARC1001141	50.72	57.25	57.84	1.13	1.14
OVARC1001154	776.93	774.37	672.45	1	0.87
OVARC1001161	64.57	91.5	118.13	1.42	1.83
OVARC1001162	67.07	66.3	60.17	0.99	0.9
OVARC1001163	44.06	41.7	37.81	0.95	0.91
OVARC1001167	131.97	178.27	124.95	1.35	0.95
OVARC1001169	36.78	27.43	38.99	1	1
OVARC1001170	65.61	77.2	57.31	1.18	0.87
OVARC1001171	222.01	381.42	266.16	1.72	1.2
OVARC1001173	106.94	98.98	64.05	0.93	0.6
OVARC1001176	1738.1	1365.32	1450.41	0.79	0.83
OVARC1001180	170.76	219.17	160.37	1.28	0.94
OVARC1001188	43.78	31.39	45.77	0.91	1.05
OVARC1001200	30.93	28.46	25.56	1	1
OVARC1001202	89.8	109.06	76.14	1.21	0.85
OVARC1001206	25.21	19.96	14.96	1	1
OVARC1001209	135.99	167.39	86.92	1.23	0.64
OVARC1001219	43.42	67.27	69.27	1.55	1.6
OVARC1001222	51.14	44.76	64.42	0.88	1.26
OVARC1001232	87.58	109.93	82.19	1.26	0.94
OVARC1001240	62.57	67.43	59.2	1.08	0.95
OVARC1001243	31.53	23.79	40.34	1	1.01
OVARC1001244	71.67	92.27	74.16	1.29	1.03
OVARC1001246	183.36	317.23	328.1	1.73	1.79
OVARC1001247	38.53	38.34	42.68	1	1.07
OVARC1001260	40.46	31.35	41.53	0.99	1.03
OVARC1001261	29.3	27.69	37.42	1	1
OVARC1001268	156.38	139.16	131.87	0.89	0.84
OVARC1001270	29.69	25.77	25.2	1	1
OVARC1001271	61.41	90.42	61.05	1.47	0.99
OVARC1001282	21.59	10.83	20.59	1	1
OVARC1001296	23.87	32.76	62.54	1	1.56
OVARC1001306	17.53	22.01	16.97	1	1
OVARC1001314	28.21	26.99	26.93	1	1

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OVARC1001316	34.31	39.56	30.84	1	1
OVARC1001329	232.27	293.46	231.75	1.26	1
OVARC1001330	21.47	21.46	24.72	1	1
OVARC1001336	68.81	83.92	59.46	1.22	0.86
OVARC1001338	23.84	21.6	27.85	1	1
OVARC1001339	166.35	209.33	201.15	1.26	1.21
OVARC1001340	24.69	30.23	15.34	1	1
OVARC1001341	83.51	53.41	58.61	0.64	0.7
OVARC1001342	906.51	940.44	1162.95	1.04	1.28
OVARC1001344	94.29	91.84	76.48	0.97	0.81
OVARC1001357	126.87	158.79	126.06	1.25	0.99
OVARC1001359	113.44	108.4	117.25	0.96	1.03
OVARC1001360	19.59	16.38	16.06	1	1
OVARC1001369	28.67	25.63	26.87	1	1
OVARC1001372	21.27	23.59	22.3	1	1
OVARC1001376	126.95	164.03	103.11	1.29	0.81
OVARC1001381	165.56	191.26	187.13	1.16	1.13
OVARC1001391	28.04	23.78	24.37	1	1
OVARC1001392	68.38	51.48	63.08	0.75	0.92
OVARC1001399	37.81	45.74	27	1.14	1
OVARC1001417	24.23	25.39	31.54	1	1
OVARC1001419	37.58	35.05	29.67	1	1
OVARC1001425	27.94	32.96	24.18	1	1
OVARC1001436	40.42	36.41	41.11	0.99	1.02
OVARC1001442	33.01	24.02	27.31	1	1
OVARC1001451	84.3	90.12	71.71	1.07	0.85
OVARC1001452	38.24	38.53	36.34	1	1
OVARC1001453	38.85	54.09	45.75	1.35	1.14
OVARC1001476	60.15	81.57	84.23	1.36	1.4
OVARC1001480	26.66	26.16	25.2	1	1
OVARC1001489	48.15	49.45	101.95	1.03	2.12
OVARC1001493	41.75	42.93	31.69	1.03	0.96
OVARC1001496	60.58	93.19	72.72	1.54	1.2
OVARC1001499	73.29	81.63	65.54	1.11	0.89
OVARC1001506	64.89	70.58	57.55	1.09	0.89
OVARC1001509	55.61	77.79	48.65	1.4	0.87
OVARC1001510	26.95	24.97	15.31	1	1
OVARC1001516	38.07	44.29	47.82	1.11	1.2
OVARC1001525	23.96	35.03	30.42	1	1
OVARC1001542	67.08	99.57	88.99	1.48	1.33
OVARC1001544	95.76	116.73	98.74	1.22	1.03
OVARC1001546	49.52	43.47	38.3	0.88	0.81
OVARC1001547	23.53	18.95	25.34	1	1
OVARC1001555	1367.8	1096.38	1129.08	0.8	0.83
OVARC1001560	35.41	34.45	42.68	1	1.07
OVARC1001569	40.02	36.25	49.64	1	1.24

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OVARC1001570	118.3	90.82	109:86	0.77	0.93
OVARC1001577	67.37	61.81	65.57	0.92	0.97
OVARC1001578	7.12	4.31	2.89	1	1
OVARC1001596	109.11	98.02	100.15	0.9	0.92
OVARC1001600	44.91	38.21	38.78	0.89	0.89
OVARC1001607	103.19	103.55	104.7	1	1.01
OVARC1001610	27.23	22.39	29.89	1	1
OVARC1001611	23.95	21.82	23.28	1	1
OVARC1001615	28.78	30.41	29.35	1	1
OVARC1001636	22.06	26.91	22.4	1	1
OVARC1001668	157.38	182.92	190.28	1.16	1.21
OVARC1001702	29.08	33.35	21.23	1	1
OVARC1001703	34.64	34.78	32.94	1	1
OVARC1001710	37	45.21	35.64	1.13	1
OVARC1001711	65.82	54.04	68.29	0.82	1.04
OVARC1001713	759.21	796.63	608.51	1.05	0.8
OVARC1001725	31.93	66.38	76.74	1.66	1.92
OVARC1001726	33.71	25.68	31.15	1	1
OVARC1001727	18.56	15.27	18.96	1	1
OVARC1001731	644.04	686.39	701.99	1.07	1.09
OVARC1001735	29.65	26.69	27.96	1	1
OVARC1001741	116.98	138.87	99.12	1.19	0.85
OVARC1001745	124.72	141.59	108.68	1.14	0.87
OVARC1001759	24.68	39.22	19.11	1	1
OVARC1001762	34.59	36.76	38.56	1	1
OVARC1001766	94.02	119.94	112.17	1.28	1.19
OVARC1001767	20.16	18.06	19.11	1	1
OVARC1001768	46.1	47.08	41.89	1.02	0.91
OVARC1001770	105.44	120.44	96.89	1.14	0.92
OVARC1001776	23.68	21.65	15.61	1	1
OVARC1001791	28.43	27.18	17.64	1	1
OVARC1001795	19.53	18.07	13.49	1	1
OVARC1001798	101.84	142.85	110.21	1.4	1.08
OVARC1001802	65.06	78	62.46	1.2	0.96
OVARC1001805	35.52	48.94	64.35	1.22	1.61
OVARC1001807	56.61	69.76	47.03	1.23	0.83
OVARC1001809	1088.9	1547.3	919.46	1.42	0.84
OVARC1001812	39.57	54.09	36.17	1.35	1
OVARC1001813	58.4	60.12	50.34	1.03	0.86
OVARC1001820	46.93	54.05	53.52	1.15	1.14
OVARC1001828	22.82	20.17	17.42	1	1
OVARC1001833	23.13	23.75	22.25	1	1
OVARC1001839	25.87	24.28	22.99	1	1
OVARC1001846	32.88	39.67	35.78	1	1
OVARC1001849	42.93	45.6	36.21	1.06	0.93
OVARC1001861	38.57	44.42	39.11	1.11	1

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OVARC1001873	21.53	26.72	31.29	1	1
OVARC1001879	31.66	30.09	34.2	1	1
OVARC1001880	41.78	56.41	43.72	1.35	1.05
OVARC1001883	54.76	53.84	51.98	0.98	0.95
OVARC1001900	41.08	39.22	37.45	0.97	0.97
OVARC1001901	32.69	29.55	28.05	1	1
OVARC1001911	24.17	21.88	19.26	1	1
OVARC1001916	40.38	47.57	41.31	1.18	1.02
OVARC1001928	23.54	15.33	21.01	1	1
OVARC1001937	116.75	121.57	137.57	1.04	1.18
OVARC1001940	27.84	23.38	26.49	1	1
OVARC1001942	51.05	48.07	54.43	0.94	1.07
OVARC1001943	55.91	66.85	90.22	1.2	1.61
OVARC1001949	49.03	55.03	45.81	1.12	0.93
OVARC1001950	111.23	119.03	88.58	1.07	0.8
OVARC1001952	925.52	837.31	491.71	0.9	0.53
OVARC1001954	22.54	22.58	19	1	1
OVARC1001963	39.61	39.13	33.68	1	1
OVARC1001983	156.69	178.79	170.9	1.14	1.09
OVARC1001987	47.79	48.7	50.85	1.02	1.06
OVARC1001989	115.86	105.75	98.03	0.91	0.85
OVARC1001991	52.33	46.51	46.57	0.89	0.89
OVARC1002005	125.8	138.41	116.88	1.1	0.93
OVARC1002044	114.35	98.85	116.74	0.86	1.02
OVARC1002046	159.32	196.2	173.16	1.23	1.09
OVARC1002050	40.99	40.28	45.96	0.98	1.12
OVARC1002058	37.98	49.57	48.1	1.24	1.2
OVARC1002066	144.74	132.59	118.22	0.92	0.82
OVARC1002082	144.14	154.11	143.8	1.07	1
OVARC1002091	52.45	54.17	45.92	1.03	0.88
OVARC1002092	32.76	33.97	32.14	1	1
OVARC1002093	66.9	77.69	43.57	1.16	0.65
OVARC1002094	25.97	23.94	18.11	1	1
OVARC1002107	64.72	70.55	54.95	1.09	0.85
OVARC1002112	139.28	159.48	161.25	1.15	1.16
OVARC1002126	66.61	75.47	60.09	1.13	0.9
OVARC1002127	29.37	25.6	25.54	1	1
OVARC1002138	29.78	31.03	19.45	1	1
OVARC1002143	30.33	31.42	29.88	1	1
OVARC1002156	75.57	70.21	66.57	0.93	0.88
OVARC1002158	37.42	53.19	43.69	1.33	1.09
OVARC1002165	185.67	208.93	182.03	1.13	0.98
OVARC1002176	41.55	53.57	41.99	1.29	1.01
OVARC1002178	28.75	31.58	27.65	1	1
OVARC1002182	30.31	30.67	27.5	1	1
OVARC1002185	396.64	424.71	346.26	1.07	0.87

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PLACE1000004	24.76	25.81	21.48	1	1
PLACE1000005	72.22	70.74	69.75	0.98	0.97
PLACE1000006	27.37	33.84	25.89	1	1
PLACE1000007	21.99	20.68	18.2	1	1
PLACE1000014	46.45	37.66	44.52	0.86	0.96
PLACE1000031	34.07	28.46	37.07	1	1
PLACE1000033	24.31	26.29	25.62	1	1
PLACE1000040	80.02	61.14	61.85	0.76	0.77
PLACE1000048	49.01	44.9	46.33	0.92	0.95
PLACE1000050	76.92	79.6	76.6	1.03	1
PLACE1000061	1833.7	1628.1	1862.77	0.89	1.02
PLACE1000066	100.49	137.52	143.02	1.37	1.42
PLACE1000075	27.62	28.66	37.82	1	1
PLACE1000078	108.32	94.57	102.84	0.87	0.95
PLACE1000081	22.97	26.54	22.74	1	1
PLACE1000086	55.62	56.11	45.41	1.01	0.82
PLACE1000094	22.42	45.59	26.18	1.14	1
PLACE1000101	70.88	63.96	84.2	0.9	1.19
PLACE1000121	24.82	20.96	22.84	1	1
PLACE1000133	96.36	136.13	146.32	1.41	1.52
PLACE1000142	38.87	34.64	40.54	1	1.01
PLACE1000146	23.88	32.9	31.49	1	1
PLACE1000163	55.99	61.61	42.54	1.1	0.76
PLACE1000172	34.86	30.15	28.35	1	1
PLACE1000181	28.93	39.59	30.35	1	1
PLACE1000184	31.13	34.98	39.62	1	1
PLACE1000185	59.19	53.44	60.92	0.9	1.03
PLACE1000198	30.12	40.19	26.16	1	1
PLACE1000213	38.99	48.17	37.26	1.2	1
PLACE1000214	34.7	46.78	49.53	1.17	1.24
PLACE1000220	73.76	70.27	66.16	0.95	0.9
PLACE1000231	95.59	80.27	84.2	0.84	0.88
PLACE1000236	39.98	42.02	37.68	1.05	1
PLACE1000245	82.41	100.11	79.89	1.21	0.97
PLACE1000246	40.74	34.37	31.89	0.98	0.98
PLACE1000258	130.7	150.85	139.27	1.15	1.07
PLACE1000288	24.77	24.09	32.17	1	1
PLACE1000292	106.53	113.38	98.12	1.06	0.92
PLACE1000302	18.27	27.21	15.42	1	1
PLACE1000304	65.7	62.07	62.7	0.94	0.95
PLACE1000308	32.53	34.89	34.8	1	1
PLACE1000309	58.44	64.89	69.33	1.11	1.19
PLACE1000312	26.22	23.84	24.8	1	1
PLACE1000330	24.35	26.43	20.16	1	1
PLACE1000332	35.75	32.57	26.57	1	1
PLACE1000347	42.57	48.19	57.82	1.13	1.36

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PLACE1000351	31.19	20.96	22.08	1	1
PLACE1000374	85.05	103.62	71.9	1.22	0.85
PLACE1000380	36.69	40.89	43.75	1.02	1.09
PLACE1000383	27.18	37.69	30.62	1	1
PLACE1000397	29.25	23.24	30.83	1	1
PLACE1000401	38.53	42.86	33.59	1.07	1
PLACE1000406	33.82	36.73	38.14	1	1
PLACE1000412	36.43	38.07	40.64	1	1.02
PLACE1000420	89.72	84	76.38	0.94	0.85
PLACE1000421	48.98	53.73	40.47	1.1	0.83
PLACE1000423	289.62	300.74	318.77	1.04	1.1
PLACE1000424	47.59	56.91	37.74	1.2	0.84
PLACE1000430	35.21	29.9	25.42	1	1
PLACE1000433	31.4	33.71	27.27	1	1
PLACE1000435	67.53	71.28	61.52	1.06	0.91
PLACE1000437	85.98	76.05	90.26	0.88	1.05
PLACE1000442	71.69	83.76	65.33	1.17	0.91
PLACE1000444	281.96	322.3	237.42	1.14	0.84
PLACE1000453	93.48	96.07	86.64	1.03	0.93
PLACE1000456	155.96	197.31	251.5	1.27	1.61
PLACE1000465	88.14	80.44	56.34	0.91	0.64
PLACE1000481	60.69	64.48	61.62	1.06	1.02
PLACE1000492	29.41	31.26	28.26	1	1
PLACE1000508	43.75	36.51	33.48	0.91	0.91
PLACE1000512	43.13	37.22	29.76	0.93	0.93
PLACE1000540	60.89	54.69	53.42	0.9	0.88
PLACE1000541	194.23	186.38	150.17	0.96	0.77
PLACE1000546	58.5	58.41	50.88	1	0.87
PLACE1000547	62.12	74.88	58.14	1.21	0.94
PLACE1000560	27.65	32.31	26.9	1	1
PLACE1000562	68.1	102.88	93.56	1.51	1.37
PLACE1000564	32.94	44.95	38.66	1.12	1
PLACE1000583	129.86	146.67	93.02	1.13	0.72
PLACE1000587	76.59	77.27	62.7	1.01	0.82
PLACE1000588	44.17	50.72	31.24	1.15	0.91
PLACE1000596	64.54	70.96	67.19	1.1	1.04
PLACE1000599	121.52	140.66	95.47	1.16	0.79
PLACE1000605	111.2	111.23	135.21	1	1.22
PLACE1000610	36.84	46.4	33.01	1.16	1
PLACE1000611	88.85	115.78	96.74	1.3	1.09
PLACE1000626	81.31	97.7	63.54	1.2	0.78
PLACE1000633	89.73	103.53	69	1.15	0.77
PLACE1000636	43.66	38.64	31.59	0.92	0.92
PLACE1000653	48.6	59.21	37.82	1.22	0.82
PLACE1000656	76.78	115.05	89.87	1.5	1.17
PLACE1000663	22.81	25.89	22.83	1	1

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PLACE1000706	47.62	68.55	44.03	1.44	0.92
PLACE1000712	42.96	41.85	44.5	0.97	1.04
PLACE1000716	36.32	30.57	37.12	1	1
PLACE1000740	74.99	71.02	72.48	0.95	0.97
PLACE1000748	59.7	44.52	53.83	0.75	0.9
PLACE1000749	69.67	71.54	88.13	1.03	1.26
PLACE1000751	90.04	63.66	96.59	0.71	1.07
PLACE1000755	28.06	18.71	33.71	1	1
PLACE1000769	28.38	22.38	36.57	1	1
PLACE1000778	309.15	302.88	359.07	0.98	1.16
PLACE1000785	281.33	264.97	226.92	0.94	0.81
PLACE1000786	44.9	51.88	43.46	1.16	0.97
PLACE1000793	49.42	67.76	62.97	1.37	1.27
PLACE1000795	44.34	51.39	45.61	1.16	1.03
PLACE1000798	56	57.48	53.18	1.03	0.95
PLACE1000812	50.83	52.85	42.72	1.04	0.84
PLACE1000823	67.58	81.4	78.53	1.2	1.16
PLACE1000825	292.82	278.76	227.12	0.95	0.78
PLACE1000838	117.7	102.23	110.08	0.87	0.94
PLACE1000841	40.32	63.69	47.74	1.58	1.18
PLACE1000843	46.51	40.25	48.16	0.87	1.04
PLACE1000849	46.45	41.04	46.47	0.88	1
PLACE1000856	36.71	40.33	41.25	1.01	1.03
PLACE1000863	62.44	65.02	86.88	1.04	1.39
PLACE1000876	51.73	69.32	56.48	1.34	1.09
PLACE1000899	40.08	45.46	36.02	1.13	1
PLACE1000907	121.51	131.23	137.97	1.08	1.14
PLACE1000909	64.51	62.85	76.14	0.97	1.18
PLACE1000912	17.7	22.05	17.88	1	1
PLACE1000914	32.84	31.69	26.59	1	1
PLACE1000918	23.6	42.91	25.79	1.07	1
PLACE1000927	92.92	134.99	144.28	1.45	1.55
PLACE1000931	43.54	48.87	49.05	1.12	1.13
PLACE1000944	46.12	56.25	42.79	1.22	0.93
PLACE1000948	31.87	30.6	29.54	1	1
PLACE1000958	26.58	22.19	27.28	1	1
PLACE1000972	77.78	102.18	78.45	1.31	1.01
PLACE1000977	37.49	43.04	37.27	1.08	1
PLACE1000979	56.17	42.68	63.84	0.76	1.14
PLACE1000986	25.37	30.46	29.36	1	1
PLACE1000987	31.24	34.96	33.17	1	1
PLACE1001000	60.23	87.53	55.33	1.45	0.92
PLACE1001007	62.89	63.91	57.94	1.02	0.92
PLACE1001010	32.73	43.47	36.9	1.09	1
PLACE1001015	25.94	37.23	23.1	1	1
PLACE1001016	67.56	68.13	64.74	1.01	0.96

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PLACE1001022	24.1	29.77	22.61	1	1
PLACE1001024	24.54	28.89	23.58	1	1
PLACE1001036	52.29	53.52	38.48	1.02	0.76
PLACE1001038	253.42	281.94	250.92	1.11	0.99
PLACE1001048	26.43	26.89	24.61	1	1
PLACE1001054	1175.5	1243.17	853.43	1.06	0.73
PLACE1001062	65.69	88.71	61.11	1.35	0.93
PLACE1001063	22.22	18.82	21.06	1	1
PLACE1001076	23.43	22.79	18.47	1	1
PLACE1001081	72.77	65.53	103.11	0.9	1.42
PLACE1001088	32.05	30.28	39.19	1	1
PLACE1001092	53.83	55.44	46.76	1.03	0.87
PLACE1001098	151.65	175.93	181.39	1.16	1.2
PLACE1001100	54.47	53.59	38.53	0.98	0.73
PLACE1001104	32.63	33.73	33.87	1	1
PLACE1001114	46.98	47.37	50.39	1.01	1.07
PLACE1001118	53.9	66.84	51.97	1.24	0.96
PLACE1001123	66.86	69.57	68.68	1.04	1.03
PLACE1001136	65.85	79.52	60.64	1.21	0.92
PLACE1001144	90.6	79.44	58.29	0.88	0.64
PLACE1001147	55.83	58.23	55.99	1.04	1
PLACE1001148	41.47	34.75	55.19	0.96	1.33
PLACE1001159	31.15	31.69	25.91	1	1
PLACE1001168	41.99	53.56	68.74	1.28	1.64
PLACE1001171	18.09	17.01	11.3	1	1
PLACE1001183	25.6	35.65	26.27	1	1
PLACE1001185	74.4	83.96	71.65	1.13	0.96
PLACE1001201	65.89	45.96	32.25	0.7	0.61
PLACE1001229	79.77	73.37	75.05	0.92	0.94
PLACE1001231	49.09	70.09	47.97	1.43	0.98
PLACE1001238	59	59.58	44.13	1.01	0.75
PLACE1001241	37.8	28.25	39	1	1
PLACE1001242	212.52	280.16	306.05	1.32	1.44
PLACE1001247	39.43	48.02	40.05	1.2	1
PLACE1001250	43.9	48.93	49.67	1.11	1.13
PLACE1001257	69.88	87.14	49.9	1.25	0.71
PLACE1001272	62.08	59.2	49.01	0.95	0.79
PLACE1001279	36.9	28.46	28.45	1	1
PLACE1001280	59.82	68.95	57.17	1.15	0.96
PLACE1001294	55.4	76.7	58.04	1.38	1.05
PLACE1001295	37.73	42.1	34.43	1.05	1
PLACE1001300	38.62	81.94	59.07	2.05	1.48
PLACE1001304	76.32	107.22	96.84	1.4	1.27
PLACE1001311	71.6	81.41	59.85	1.14	0.84
PLACE1001323	72.17	76.01	59.14	1.05	0.82
PLACE1001325	59.21	89.16	52.84	1.51	0.89

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PLACE1001340	59.98	70.04	68.95	1.17	1.15
PLACE1001344	16.91	17.79	16.63	1	1
PLACE1001351	37.9	35.39	36.71	1	1
PLACE1001366	39.46	53.03	43.75	1.33	1.09
PLACE1001377	39.42	36.27	35.5	1	1
PLACE1001383	50.96	69.88	43.67	1.37	0.86
PLACE1001384	29.93	24.61	29.44	1	1
PLACE1001387	19.84	23.39	22.61	1	1
PLACE1001395	48.1	54.54	59.91	1.13	1.25
PLACE1001399	73	89.28	87.29	1.22	1.2
PLACE1001401	17.36	10.16	14.75	1	1
PLACE1001407	173.32	153.48	184.52	0.89	1.06
PLACE1001412	28.36	51.42	50.36	1.29	1.26
PLACE1001414	103.73	119.31	104.84	1.15	1.01
PLACE1001416	45.34	37.52	46.55	0.88	1.03
PLACE1001433	686.08	633.61	710.08	0.92	1.03
PLACE1001440	31.5	30.51	37.83	1	1
PLACE1001456	93.44	86.92	92.14	0.93	0.99
PLACE1001464	144.35	156.63	222.58	1.09	1.54
PLACE1001468	21.17	20.97	23.23	1	1
PLACE1001484	39.26	44.3	44.46	1.11	1.11
PLACE1001500	29.64	27.34	25.08	1	1
PLACE1001502	44.35	52.36	37.68	1.18	0.9
PLACE1001503	106.67	108.23	94.51	1.01	0.89
PLACE1001505	107.02	84.34	109.11	0.79	1.02
PLACE1001513	59.63	60.93	69.28	1.02	1.16
PLACE1001516	46.89	44.32	37.19	0.95	0.85
PLACE1001517	67.5	61.74	72.29	0.91	1.07
PLACE1001523	35.36	145.54	176.62	3.64	4.42
PLACE1001526	67.64	68.66	60.16	1.02	0.89
PLACE1001534	59.24	49.05	59.78	0.83	1.01
PLACE1001536	21.36	23	24.62	1	1
PLACE1001545	299.5	242.39	336.18	0.81	1.12
PLACE1001551	52.49	59.71	48.37	1.14	0.92
PLACE1001564	32.98	43.9	34.74	1.1	1
PLACE1001570	37.67	45.32	43.97	1.13	1.1
PLACE1001571	60.72	58.01	57.65	0.96	0.95
PLACE1001595	131.76	206.77	116.03	1.57	0.88
PLACE1001602	140.17	124.26	134.66	0.89	0.96
PLACE1001603	106.03	99.78	98.98	0.94	0.93
PLACE1001608	50.87	50.16	41.39	0.99	0.81
PLACE1001610	152.25	167.91	138.81	1.1	0.91
PLACE1001611	23.89	32.27	24.71	1	1
PLACE1001629	26.65	29.58	37.06	1	1
PLACE1001632	30.66	37.71	44.36	1	1.11
PLACE1001634	172.71	157.55	99.09	0.91	0.57

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PLACE1001637	25.7	21.53	18.93	1	1
PLACE1001640	57.73	81.27	57.98	1.41	1
PLACE1001655	20.38	17.61	16.27	1	1
PLACE1001672	36.77	44.13	45.88	1.1	1.15
PLACE1001676	61.14	47.49	68.28	0.78	1.12
PLACE1001683	130.38	163.09	126.67	1.25	0.97
PLACE1001691	66.24	137.29	148.77	2.07	2.25
PLACE1001692	107.1	130.47	90.19	1.22	0.84
PLACE1001705	103	105.83	98.71	1.03	0.96
PLACE1001716	34.04	37.84	33.36	1	1
PLACE1001720	22.82	19.21	23.04	1	1
PLACE1001728	23.74	33.98	26.51	1	1
PLACE1001729	42.25	41.32	31.82	0.98	0.95
PLACE1001739	27.27	36.66	35.51	1	1
PLACE1001740	41.28	37.48	41.21	0.97	1
PLACE1001745	33.2	30.85	25.22	1	1
PLACE1001746	58.49	62.26	51.19	1.06	0.88
PLACE1001748	91.44	111.27	90.04	1.22	0.98
PLACE1001753	46.48	41.49	42.81	0.89	0.92
PLACE1001756	206.24	206.45	146.37	1	0.71
PLACE1001761	105	105.33	114.94	1	1.09
PLACE1001767	906.39	1018.83	646.39	1.12	0.71
PLACE1001771	50.78	47.05	50.31	0.93	0.99
PLACE1001775	56.72	58.09	52.35	1.02	0.92
PLACE1001777	250.62	301.05	385.02	1.2	1.54
PLACE1001781	47.54	45.66	50.36	0.96	1.06
PLACE1001783	25.79	23.91	24.74	1	1
PLACE1001786	27.32	22.95	23.3	1	1
PLACE1001788	63.8	50.58	49.3	0.79	0.77
PLACE1001795	55.25	47.94	42.33	0.87	0.77
PLACE1001799	19.31	21.26	19.78	1	1
PLACE1001810	37.78	34	28.42	1	1
PLACE1001817	51.28	35.63	49.47	0.78	0.96
PLACE1001821	90.72	88.49	68.61	0.98	0.76
PLACE1001836	40.93	47.62	45.4	1.16	1.11
PLACE1001844	50.7	52.62	49.15	1.04	0.97
PLACE1001845	114.64	148.46	138.06	1.3	1.2
PLACE1001858	39.69	37.7	45.91	1	1.15
PLACE1001869	66.67	56.7	50.32	0.85	0.75
PLACE1001890	139.54	181.8	133.9	1.3	0.96
PLACE1001897	103.15	90.08	92.86	0.87	0.9
PLACE1001902	132.93	111.17	101.84	0.84	0.77
PLACE1001904	21.63	26.18	17.37	1	1
PLACE1001907	51.16	54.84	43.55	1.07	0.85
PLACE1001910	4125.5	5812.98	5956.63	1.41	1.44
PLACE1001912	98.39	125.69	81.71	1.28	0.83

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PLACE1001918	75.3	178.35	171.51	2.37	2.28
PLACE1001920	38.58	44.62	25.77	1.12	1
PLACE1001928	59.67	54.32	45.81	0.91	0.77
PLACE1001930	42.5	39.89	29.86	0.94	0.94
PLACE1001949	30.76	31.17	25.06	1	1
PLACE1001959	30.92	27.74	44.02	1	1.1
PLACE1001969	43.67	68.4	60.61	1.57	1.39
PLACE1001974	58.47	87.97	70.98	1.5	1.21
PLACE1001981	20.55	19.1	19.17	1	1
PLACE1001983	50.42	56.62	39.13	1.12	0.79
PLACE1001989	64.23	61.57	57.16	0.96	0.89
PLACE1002004	138.52	136.78	156.35	0.99	1.13
PLACE1002008	78.06	75.77	80.18	0.97	1.03
PLACE1002015	397.49	417.71	445.16	1.05	1.12
PLACE1002044	41.16	31.51	40.22	0.97	0.98
PLACE1002046	44.29	35.77	47.55	0.9	1.07
PLACE1002052	20.68	23.54	25.31	1	1
PLACE1002066	178.37	183.05	183.25	1.03	1.03
PLACE1002072	78.28	81.5	77.13	1.04	0.99
PLACE1002073	27.9	28.71	34.29	1	1
PLACE1002080	61.82	72.61	63.14	1.17	1.02
PLACE1002081	40.52	38.51	38.8	0.99	0.99
PLACE1002090	79.31	102.85	131.29	1.3	1.66
PLACE1002095	63.25	73	81.15	1.15	1.28
PLACE1002102	47.9	64.22	87.09	1.34	1.82
PLACE1002109	121.13	154.2	113.37	1.27	0.94
PLACE1002115	47.16	53.43	44.36	1.13	0.94
PLACE1002119	220.58	222	254.75	1.01	1.15
PLACE1002140	224.21	154.92	220.12	0.69	0.98
PLACE1002150	46.55	38.95	33.85	0.86	0.86
PLACE1002153	34.37	46.95	43.15	1.17	1.08
PLACE1002157	36.71	37.17	35.5	1	1
PLACE1002163	41.57	43.98	53.8	1.06	1.29
PLACE1002168	80.08	72.26	77.83	0.9	0.97
PLACE1002170	32.62	28.6	31.69	1	1
PLACE1002171	54.23	42.59	50.12	0.79	0.92
PLACE1002180	55.02	46.62	41.61	0.85	0.76
PLACE1002184	117.06	172.52	143.25	1.47	1.22
PLACE1002200	33.2	36.06	34.77	1	1
PLACE1002205	93.98	75.49	65.05	0.8	0.69
PLACE1002213	49.41	60.19	55.06	1.22	1.11
PLACE1002219	32.08	34.58	42.83	1	1.07
PLACE1002227	39.22	41.44	39.22	1.04	1
PLACE1002253	13.18	15.01	11.64	1	1
PLACE1002256	36.08	42.07	41.31	1.05	1.03
PLACE1002259	35.42	38.71	28.99	1	1

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PLACE1002285	21.44	22.04	22.02	1	1
PLACE1002301	39.97	51.82	47.69	1.3	1.19
PLACE1002310	38.3	53.71	59.83	1.34	1.5
PLACE1002311	32.31	31.35	21.52	1	1
PLACE1002319	39.1	37.88	38.01	1	1
PLACE1002329	42.35	45.03	28.89	1.06	0.94
PLACE1002333	22.15	21.3	18.15	1	1
PLACE1002342	57.91	78.12	77.69	1.35	1.34
PLACE1002343	24.89	27.37	21.38	1	1
PLACE1002355	29.14	51.73	37.92	1.29	1
PLACE1002358	35.63	34.51	30.06	1	1
PLACE1002359	59.86	66.1	56.59	1.1	0.95
PLACE1002374	108.32	173.07	169.76	1.6	1.57
PLACE1002376	123.21	156.84	143.37	1.27	1.16
PLACE1002379	56.01	73.79	77.99	1.32	1.39
PLACE1002386	18.78	17.51	20.81	1	1
PLACE1002395	131.23	134.81	90.74	1.03	0.69
PLACE1002399	33.82	41.2	50.11	1.03	1.25
PLACE1002407	28.08	24.72	32.3	1	1
PLACE1002433	39.73	34.06	26.39	1	1
PLACE1002437	28.87	27.38	24.22	1	1
PLACE1002438	27.94	29.9	24.65	1	1
PLACE1002446	31.05	33.92	52.9	1	1.32
PLACE1002447	38.57	23.64	33.34	1	1
PLACE1002450	31.98	40.64	39.26	1.02	1
PLACE1002462	34	36.24	27.07	1	1
PLACE1002465	37.59	32.41	32.62	1	1
PLACE1002474	34.19	30.1	31.83	1	1
PLACE1002477	215.53	256.98	192.24	1.19	0.89
PLACE1002493	117.08	120.94	66.9	1.03	0.57
PLACE1002497	22.96	20.27	15.65	1	1
PLACE1002499	50.73	58.7	59.23	1.16	1.17
PLACE1002500	96.27	147.8	112.4	1.54	1.17
PLACE1002514	33.61	26.45	23.6	1	1
PLACE1002518	41.61	56.08	61.21	1.35	1.47
PLACE1002529	35.95	30.55	27.67	1	1
PLACE1002532	111.18	127.2	70.27	1.14	0.63
PLACE1002536	154.38	153.55	128.51	0.99	0.83
PLACE1002537	61.55	59.88	57.19	0.97	0.93
PLACE1002539	37.9	30.66	31.19	1	1
PLACE1002547	67.73	93.86	89.6	1.39	1.32
PLACE1002571	63.4	74.13	58.68	1.17	0.93
PLACE1002578	132.43	150.29	116.55	1.13	0.88
PLACE1002583	32.14	34.49	24.56	1	1
PLACE1002591	37.57	41	27.91	1.03	1
PLACE1002598	96.18	87.39	79.55	0.91	0.83

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PLACE1002604	54.28	66.18	49.22	1.22	0.91
PLACE1002612	95.35	95.19	103.19	1	1.08
PLACE1002625	35.29	35.5	37.17	1	1
PLACE1002638	36.08	51.42	37.95	1.29	1
PLACE1002655	77.69	90.45	87.49	1.16	1.13
PLACE1002665	31.49	32.82	23.4	1	1
PLACE1002685	17.89	18.59	13.37	1	1
PLACE1002692	127.12	135.43	105.27	1.07	0.83
PLACE1002714	19.26	20.24	19.68	1	1
PLACE1002721	34.62	40.72	46.88	1.02	1.17
PLACE1002722	19.06	20.66	14.68	1	1
PLACE1002726	40.31	30.8	31.87	0.99	0.99
PLACE1002756	78.21	83.19	71.78	1.06	0.92
PLACE1002768	25.22	31.86	26.26	1	1
PLACE1002772	20.72	18	15.78	1	1
PLACE1002775	68.56	83.59	84.85	1.22	1.24
PLACE1002780	19.13	20.21	19.82	1	1
PLACE1002782	14.99	11.76	15.12	1	1
PLACE1002794	26.71	32.3	25.11	1	1
PLACE1002795	51.53	51.44	55.42	1	1.08
PLACE1002811	19.7	15.5	14.68	1	1
PLACE1002815	51.13	46.51	44.21	0.91	0.86
PLACE1002816	144.66	145.59	134.13	1.01	0.93
PLACE1002822	37.08	39.75	33.18	1	1
PLACE1002833	99.65	99.15	105.52	0.99	1.06
PLACE1002834	90.65	105.86	92.19	1.17	1.02
PLACE1002835	21.6	20.73	17.21	1	1
PLACE1002839	35.83	40.12	42.4	1	1.06
PLACE1002851	37.62	50.62	39.26	1.27	1
PLACE1002853	77.21	86.13	73.13	1.12	0.95
PLACE1002881	178.57	217.28	143.56	1.22	0.8
PLACE1002901	162.03	130.28	155.87	0.8	0.96
PLACE1002904	41.21	32.91	35.47	0.97	0.97
PLACE1002905	60.55	65.83	58.21	1.09	0.96
PLACE1002908	37.5	41.43	40.54	1.04	1.01
PLACE1002911	50.17	67.78	80.71	1.35	1.61
PLACE1002941	41.63	57.62	41.65	1.38	1
PLACE1002950	60.18	35.74	54.95	0.66	0.91
PLACE1002955	500.04	509.35	572.07	1.02	1.14
PLACE1002958	300.19	264.52	323.01	0.88	1.08
PLACE1002962	31.57	28.46	29.19	1	1
PLACE1002967	58.45	68.94	55.81	1.18	0.95
PLACE1002968	74.85	90.97	72.09	1.22	0.96
PLACE1002976	111.45	136.26	171.19	1.22	1.54
PLACE1002991	68.54	89.4	62.41	1.3	0.91
PLACE1002993	109.46	111.94	93.86	1.02	0.86

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PLACE1002996	52.75	45.18	57.04	0.86	1.08
PLACE1003010	227.78	176.08	214.3	0.77	0.94
PLACE1003025	82.24	84.89	67.49	1.03	0.82
PLACE1003027	43.36	36.79	58.67	0.92	1.35
PLACE1003044	27.11	31.6	30.76	1	1
PLACE1003045	28.39	20.72	24.75	1	1
PLACE1003052	46.7	55.42	35.28	1.19	0.86
PLACE1003083	39.42	35.4	30.63	1	1
PLACE1003085	105.31	95.13	165.83	0.9	1.57
PLACE1003092	53.65	49.63	61.79	0.93	1.15
PLACE1003097	19.84	17.97	16.61	1	1
PLACE1003100	43.48	42.63	54.49	0.98	1.25
PLACE1003108	67.4	69.86	56.14	1.04	0.83
PLACE1003115	2429.8	1938.41	1364	0.8	0.56
PLACE1003120	190.38	186.69	172.7	0.98	0.91
PLACE1003135	22.74	21.24	19.25	1	1
PLACE1003136	66.07	82.56	84.67	1.25	1.28
PLACE1003141	38.76	48.18	41.93	1.2	1.05
PLACE1003145	39.3	41.02	42.47	1.03	1.06
PLACE1003147	32.84	46.21	44.01	1.16	1.1
PLACE1003153	55.32	63.18	48.47	1.14	0.88
PLACE1003163	87.96	126.75	137.45	1.44	1.56
PLACE1003172	292.86	334.87	290.66	1.14	0.99
PLACE1003174	44.47	47.73	42.71	1.07	0.96
PLACE1003176	35.28	43.34	27.58	1.08	1
PLACE1003181	44.5	38.93	34.82	0.9	0.9
PLACE1003184	21.75	19.42	16.07	1	1
PLACE1003190	53.54	44.24	78.5	0.83	1.47
PLACE1003200	19.44	17.3	16.03	1	1
PLACE1003205	149.26	188.41	143.32	1.26	0.96
PLACE1003209	24.57	23.64	19.44	1	1
PLACE1003214	29.44	37.32	25.25	1	1
PLACE1003229	58.97	74.77	48.92	1.27	0.83
PLACE1003238	23.79	31.2	22.95	1	1
PLACE1003249	76.24	88.55	60.02	1.16	0.79
PLACE1003256	136.88	173.8	158.56	1.27	1.16
PLACE1003258	26.94	29.08	19.67	1	1
PLACE1003279	289.62	288.28	218.59	1	0.75
PLACE1003294	40.84	31.78	29.14	0.98	0.98
PLACE1003296	50.97	44.86	42.34	0.88	0.83
PLACE1003297	368.37	299.91	291.38	0.81	0.79
PLACE1003302	113.04	132.54	114.02	1.17	1.01
PLACE1003334	41.77	44.78	39.07	1.07	0.96
PLACE1003337	313.35	296.56	240.71	0.95	0.77
PLACE1003342	22.4	35.38	23.63	1	1
PLACE1003343	30.97	30.24	26.77	1	1

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PLACE1003344	199.37	235.82	176.95	1.18	0.89
PLACE1003353	498.58	500.44	453.52	1	0.91
PLACE1003361	93.89	106.31	91.43	1.13	0.97
PLACE1003366	78.26	94.5	66.92	1.21	0.86
PLACE1003369	5.77	2.72	5.34	1	1
PLACE1003372	57.21	51.02	82.26	0.89	1.44
PLACE1003373	193.53	234.31	178.93	1.21	0.92
PLACE1003375	31.83	33.45	28.49	1	1
PLACE1003378	14.4	11.05	6.95	1	1
PLACE1003383	35.89	36.91	29.46	1	1
PLACE1003394	68.37	65.46	64.47	0.96	0.94
PLACE1003401	9.48	14.44	5.74	1	1
PLACE1003405	31.77	38.58	39.98	1	1
PLACE1003407	47.62	69.36	59.4	1.46	1.25
PLACE1003420	97.91	112.98	116.4	1.15	1.19
PLACE1003428	14.9	21.6	14.87	1	1
PLACE1003432	54.93	40.52	47.7	0.74	0.87
PLACE1003438	32.24	30.44	24.69	1	1
PLACE1003452	46.53	35.85	47.65	0.86	1.02
PLACE1003454	39.61	50.18	45.74	1.25	1.14
PLACE1003455	36.33	33.93	32.61	1	1
PLACE1003456	108.71	98.84	105.2	0.91	0.97
PLACE1003460	102.86	100.68	102.3	0.98	0.99
PLACE1003478	21.22	36.98	21.27	1	1
PLACE1003484	350.57	284.4	235.73	0.81	0.67
PLACE1003493	206.05	248.77	248.38	1.21	1.21
PLACE1003503	782.31	770.43	847.28	0.98	1.08
PLACE1003505	183.24	231.77	199.38	1.26	1.09
PLACE1003516	45.11	53.26	56.23	1.18	1.25
PLACE1003519	314.62	383.46	434.26	1.22	1.38
PLACE1003520	262.65	580.45	525.45	2.21	2
PLACE1003521	49.86	76.87	55.98	1.54	1.12
PLACE1003525	125.96	134.81	112.91	1.07	0.9
PLACE1003528	1564.6	1648.77	1526.57	1.05	0.98
PLACE1003529	41.65	28.28	28.22	0.96	0.96
PLACE1003537	58.26	41.57	70.53	0.71	1.21
PLACE1003549	71.19	60.94	46.62	0.86	0.65
PLACE1003553	33.32	33.26	30.39	1	1
PLACE1003566	129.04	183.13	165.12	1.42	1.28
PLACE1003568	25.89	43.04	31.17	1.08	1
PLACE1003573	50.28	42.88	45.95	0.85	0.91
PLACE1003575	122.7	135.29	90.48	1.1	0.74
PLACE1003583	35.13	38.24	32.11	1	1
PLACE1003584	68.08	74.06	61.63	1.09	0.91
PLACE1003592	130.19	171.31	138.87	1.32	1.07
PLACE1003593	31.68	37.2	39.66	1	1

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PLACE1003594	71.43	93.99	104.68	1.32	1.47
PLACE1003596	150.3	154.27	135.36	1.03	0.9
PLACE1003598	100.52	98.24	96.34	0.98	0.96
PLACE1003602	52.87	50.33	60.7	0.95	1.15
PLACE1003605	467.51	490.79	396.84	1.05	0.85
PLACE1003611	89.33	110.21	81.69	1.23	0.91
PLACE1003618	28.29	31.43	27.78	1	1
PLACE1003625	31.69	39.67	45.94	1	1.15
PLACE1003626	283.72	224.78	209.61	0.79	0.74
PLACE1003630	54.08	63.75	40.92	1.18	0.76
PLACE1003635	39.71	34.86	29.62	1	1
PLACE1003638	65.67	77.09	51.77	1.17	0.79
PLACE1003644	148.25	167.05	116.51	1.13	0.79
PLACE1003654	29.17	27.24	37.13	1	1
PLACE1003656	45.98	64.88	74.77	1.41	1.63
PLACE1003660	69.53	86.73	71.97	1.25	1.04
PLACE1003669	32.51	45.27	35.34	1.13	1
PLACE1003670	155.29	157.75	143.9	1.02	0.93
PLACE1003671	29.58	31.07	29.68	1	1
PLACE1003697	32.77	42.06	124.21	1.05	3.11
PLACE1003704	46.2	53.43	49.07	1.16	1.06
PLACE1003709	21.1	22.79	22.2	1	1
PLACE1003711	57.95	44.93	49.55	0.78	0.86
PLACE1003723	64.95	63.87	54.85	0.98	0.84
PLACE1003724	126.19	128.74	117.29	1.02	0.93
PLACE1003737	33.88	40.76	32.52	1.02	1
PLACE1003738	56.01	62.95	50.36	1.12	0.9
PLACE1003742	59.61	66.3	57.81	1.11	0.97
PLACE1003744	87.46	98.48	85.09	1.13	0.97
PLACE1003758	26.25	23.92	30.05	1	1
PLACE1003760	198.63	264.05	284.47	1.33	1.43
PLACE1003762	48.59	59.1	41.22	1.22	0.85
PLACE1003765	72.13	74.99	56.69	1.04	0.79
PLACE1003768	52.93	50.85	38.01	0.96	0.76
PLACE1003771	156.89	168.16	133.56	1.07	0.85
PLACE1003772	1326.1	1338.01	1235.63	1.01	0.93
PLACE1003783	40.78	42.6	38.87	1.04	0.98
PLACE1003784	35.32	31.33	31.62	1	1
PLACE1003788	16.15	15.6	13.57	1	1
PLACE1003795	69.33	75.16	71.21	1.08	1.03
PLACE1003827	74.21	106.07	131.59	1.43	1.77
PLACE1003833	40.41	38.8	30.6	0.99	0.99
PLACE1003839	564.98	498.2	452.27	0.88	0.8
PLACE1003845	107.06	114.29	87.76	1.07	0.82
PLACE1003850	63.8	58.95	53.45	0.92	0.84
PLACE1003852	24.02	15.1	18.58	1	1

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PLACE1003858	29.1	40.09	42.99	1	1.07
PLACE1003861	112.21	124.5	120.75	1.11	1.08
PLACE1003864	40.19	41.75	36.75	1.04	1
PLACE1003870	266.48	329.04	207.77	1.23	0.78
PLACE1003885	25.52	42.25	33.9	1.06	1
PLACE1003886	81.35	79.28	74.9	0.97	0.92
PLACE1003888	39.04	47.84	30.42	1.2	1
PLACE1003892	206.13	289.84	210.39	1.41	1.02
PLACE1003900	57.88	76.01	53.39	1.31	0.92
PLACE1003902	40.78	41.51	43.92	1.02	1.08
PLACE1003903	28.5	35.54	27.43	1	1
PLACE1003915	40.52	47.1	35.74	1.16	0.99
PLACE1003918	52.38	76.45	47.24	1.46	0.9
PLACE1003923	53.3	58.03	49.05	1.09	0.92
PLACE1003932	49.92	74.44	58.48	1.49	1.17
PLACE1003936	29.36	44.28	34.72	1.11	1
PLACE1003966	46.44	61.08	55.25	1.32	1.19
PLACE1003968	62.13	67.95	76.19	1.09	1.23
PLACE1004018	65.03	72.67	69.12	1.12	1.06
PLACE1004020	100.08	107.43	83.05	1.07	0.83
PLACE1004028	14.25	14.56	14.5	1	1
PLACE1004034	37.37	40.65	43.69	1.02	1.09
PLACE1004042	347.79	322.05	361.95	0.93	1.04
PLACE1004078	43.15	47.81	51.52	1.11	1.19
PLACE1004103	74.8	77.55	95.57	1.04	1.28
PLACE1004104	204.1	203.04	177.57	0.99	0.87
PLACE1004113	51.84	54.36	57.12	1.05	1.1
PLACE1004114	73.67	91.18	74.31	1.24	1.01
PLACE1004118	28.97	31.53	31.34	1	1
PLACE1004128	64.64	48.58	71.02	0.75	1.1
PLACE1004130	63.87	69.03	63.79	1.08	1
PLACE1004149	177.55	168.78	207.8	0.95	1.17
PLACE1004156	114.58	150.12	132.43	1.31	1.16
PLACE1004160	244.43	317.97	314.18	1.3	1.29
PLACE1004161	21.36	26.5	25.84	1	1
PLACE1004166	46.55	64.11	41.06	1.38	0.88
PLACE1004168	43.73	52.05	49.77	1.19	1.14
PLACE1004170	43.27	46.37	37.07	1.07	0.92
PLACE1004178	33.77	30.19	46.55	1	1.16
PLACE1004183	51.1	50.95	56.22	1	1.1
PLACE1004197	31.08	38.77	28.52	1	1
PLACE1004199	111.09	132.66	120.97	1.19	1.09
PLACE1004203	18.22	21.91	21.51	1	1
PLACE1004242	163.08	167.98	126.69	1.03	0.78
PLACE1004249	435.63	372.66	433.16	0.86	0.99
PLACE1004255	32.74	27.54	29.86	1	1

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PLACE1004256	108	91.63	125.22	0.85	1.16
PLACE1004257	53.87	62.72	62.43	1.16	1.16
PLACE1004258	34.99	40.17	32.95	1	1
PLACE1004270	44.65	40.89	34.69	0.92	0.9
PLACE1004272	27.85	29.4	37.92	1	1
PLACE1004273	2399.9	2465.86	2118.46	1.03	0.88
PLACE1004274	92.87	93.1	85.05	1	0.92
PLACE1004277	91.27	98.55	65.14	1.08	0.71
PLACE1004279	59.07	54.01	41.5	0.91	0.7
PLACE1004282	61.13	67.16	45.79	1.1	0.75
PLACE1004284	43.87	53.56	64.09	1.22	1.46
PLACE1004289	94.78	95.17	83.09	1	0.88
PLACE1004299	58.09	235	267.04	4.05	4.6
PLACE1004302	35.49	35.83	21.22	1	1
PLACE1004305	35.37	24.85	23.42	1	1
PLACE1004316	44.19	41.05	43.26	0.93	0.98
PLACE1004322	21.55	19.73	14.91	1	1
PLACE1004325	48.04	49	55.01	1.02	1.15
PLACE1004332	69.17	53.73	54.6	0.78	0.79
PLACE1004336	120.69	133.2	92.79	1.1	0.77
PLACE1004346	24.94	22.62	24.96	1	1
PLACE1004358	60.72	45.68	58.37	0.75	0.96
PLACE1004376	199.94	252.27	215.24	1.26	1.08
PLACE1004384	60.23	55.46	45.37	0.92	0.75
PLACE1004385	16.39	12.29	13.4	1	1
PLACE1004388	31.51	33.43	37.36	1	1
PLACE1004405	26.54	39.85	27.89	1	1
PLACE1004407	166.24	172.82	137.19	1.04	0.83
PLACE1004424	26.57	21.02	21.24	1	1
PLACE1004425	60.07	75.63	53.78	1.26	0.9
PLACE1004427	65.17	71.34	56.67	1.09	0.87
PLACE1004428	57.76	61.38	49.93	1.06	0.86
PLACE1004433	117.69	111.26	87.78	0.95	0.75
PLACE1004435	46.62	46.49	64.22	1	1.38
PLACE1004437	90.85	88.51	97.35	0.97	1.07
PLACE1004441	202.84	222.16	156.5	1.1	0.77
PLACE1004446	21.83	23.05	23.83	1	1
PLACE1004450	28.93	29.69	29.16	1	1
PLACE1004451	43.89	47.63	37.97	1.09	0.91
PLACE1004456	93.62	99.48	112.04	1.06	1.2
PLACE1004458	172.89	222.87	311.93	1.29	1.8
PLACE1004460	17.84	22.83	21.38	1	1
PLACE1004467	105.43	114.12	107.7	1.08	1.02
PLACE1004471	151.27	148.35	121.95	0.98	0.81
PLACE1004473	32.88	24.89	24.19	1	1
PLACE1004475	311.31	286.34	295.05	0.92	0.95

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PLACE1004482	58.85	50.7	45.07	0.86	0.77
PLACE1004491	50.15	31.42	45.64	0.8	0.91
PLACE1004492	574.64	611.87	545	1.06	0.95
PLACE1004506	55.23	43.9	63.47	0.79	1.15
PLACE1004507	36.91	51.87	51.67	1.3	1.29
PLACE1004510	46.45	58.12	43.51	1.25	0.94
PLACE1004516	35.91	31.26	35.07	1	1
PLACE1004518	40.44	46.56	32.76	1.15	0.99
PLACE1004519	29.69	34.96	23.94	1	1
PLACE1004520	39.35	54.81	32.81	1.37	1
PLACE1004530	81.51	148.47	119.38	1.82	1.46
PLACE1004545	26.79	37.64	25.2	1	1
PLACE1004547	76.6	72.83	116.41	0.95	1.52
PLACE1004548	71.71	95.33	72.11	1.33	1.01
PLACE1004550	45.22	45.8	43.85	1.01	0.97
PLACE1004551	32.29	37.21	26.81	1	1
PLACE1004559	44.74	33.16	37.64	0.89	0.89
PLACE1004562	28.12	38.37	24.76	1	1
PLACE1004564	37.79	44.05	36.38	1.1	1
PLACE1004604	69.46	43.79	70.41	0.63	1.01
PLACE1004611	81.59	120.14	93.91	1.47	1.15
PLACE1004629	53.91	94.48	58.88	1.75	1.09
PLACE1004630	24.94	28.66	24.06	1	1
PLACE1004637	82.97	92.18	76.13	1.11	0.92
PLACE1004645	705.25	678.73	617.05	0.96	0.87
PLACE1004646	36.08	34.75	34.74	1	1
PLACE1004648	29.15	23.9	22.52	1	1
PLACE1004655	782.3	922.68	842.27	1.18	1.08
PLACE1004658	68.23	66.04	70.48	0.97	1.03
PLACE1004664	29.86	25.07	23.6	1	1
PLACE1004672	117.85	116.26	135.22	0.99	1.15
PLACE1004674	135.11	150.95	123.26	1.12	0.91
PLACE1004681	76.94	79.8	70.45	1.04	0.92
PLACE1004686	164.64	180.61	159.85	1.1	0.97
PLACE1004690	138.95	137.9	160.53	0.99	1.16
PLACE1004691	47.58	44.73	44.23	0.94	0.93
PLACE1004693	44.67	55.19	52.33	1.24	1.17
PLACE1004701	51.89	124.32	146.8	2.4	2.83
PLACE1004705	24.89	32.52	25.9	1	1
PLACE1004708	207.22	227.65	205.56	1.1	0.99
PLACE1004716	158.09	131.22	159.6	0.83	1.01
PLACE1004722	39.69	47.66	34.38	1.19	1
PLACE1004736	103.31	78.43	109.86	0.76	1.06
PLACE1004737	37.33	40.44	27.74	1.01	1
PLACE1004740	70.48	106.24	121.63	1.51	1.73
PLACE1004743	35.03	27.05	25.32	1	1

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PLACE1004751	54.43	69.55	64.09	1.28	1.18
PLACE1004757	177.06	181.12	169.77	1.02	0.96
PLACE1004761	34	31.06	35.86	1	1
PLACE1004773	30.98	28.52	30.42	1	1
PLACE1004775	14.4	16.78	10.02	1	1
PLACE1004777	26.78	34.18	24.46	1	1
PLACE1004793	30.43	36.04	28.51	1	1
PLACE1004796	46.08	51.98	46.13	1.13	1
PLACE1004804	21.4	25.53	29.44	1	1
PLACE1004813	108.55	112.81	78.88	1.04	0.73
PLACE1004814	217.28	198.39	234.28	0.91	1.08
PLACE1004815	41.79	44.51	36.77	1.07	0.96
PLACE1004816	25.64	24.95	18.01	1	1
PLACE1004824	94.12	86.16	80.67	0.92	0.86
PLACE1004827	42.22	37.37	43.88	0.95	1.04
PLACE1004836	53.01	50.84	41.19	0.96	0.78
PLACE1004838	25.58	24.86	26.19	1	1
PLACE1004840	32.92	31.37	23.93	1	1
PLACE1004842	37.6	33.39	23.96	1	1
PLACE1004850	27.87	30.65	23.65	1	1
PLACE1004868	31.05	27.28	32.01	1	1
PLACE1004885	41.35	54.34	36.85	1.31	0.97
PLACE1004886	26.38	36.64	32.21	1	1
PLACE1004887	265.33	679.13	511.75	2.56	1.93
PLACE1004896	35.15	55.19	48.06	1.38	1.2
PLACE1004900	110.48	137.06	104.42	1.24	0.95
PLACE1004902	56.18	63.04	62.72	1.12	1.12
PLACE1004904	35.56	41.39	44.64	1.03	1.12
PLACE1004911	101.01	83.57	101.41	0.83	1
PLACE1004913	33.78	28.38	26.83	1	1
PLACE1004918	28.12	30.06	20.87	1	1
PLACE1004930	44.21	39.5	43.9	0.9	0.99
PLACE1004934	30.02	33.97	36.31	1	1
PLACE1004937	41.99	43.62	36.19	1.04	0.95
PLACE1004949	387.69	536.79	490.03	1.38	1.26
PLACE1004969	30.07	28.59	21.77	1	1
PLACE1004970	17.22	12.03	17.88	1	1
PLACE1004972	37.41	41.08	40.74	1.03	1.02
PLACE1004974	22.2	26.49	24.87	1	1
PLACE1004975	25.19	26.69	21.49	1	1
PLACE1004979	99.07	105.39	101.37	1.06	1.02
PLACE1004982	87.22	92.31	86.84	1.06	1
PLACE1004985	29.21	28.18	25.76	1	1
PLACE1005003	75.58	71.91	54.65	0.95	0.72
PLACE1005004	23.89	17.83	12.04	1	1
PLACE1005005	82.75	84.73	71.73	1.02	0.87

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PLACE1005011	778.5	847.92	631.14	1.09	0.81
PLACE1005026	28.8	40.65	36.67	1.02	1
PLACE1005027	49.51	56.36	53.55	1.14	1.08
PLACE1005031	62.85	74.25	45.61	1.18	0.73
PLACE1005036	143.79	167.62	129.45	1.17	0.9
PLACE1005041	49.86	45.09	51.96	0.9	1.04
PLACE1005046	84.21	112.84	82.55	1.34	0.98
PLACE1005047	22.51	27.41	16.71	1	1
PLACE1005052	90.85	113.45	114.68	1.25	1.26
PLACE1005055	50.92	76.6	52.3	1.5	1.03
PLACE1005066	75.14	83.4	86.5	1.11	1.15
PLACE1005077	30.3	30.8	20.94	1	1
PLACE1005085	83.67	127.5	74.04	1.52	0.88
PLACE1005086	101.48	119.52	84.13	1.18	0.83
PLACE1005088	357.2	403.63	377.94	1.13	1.06
PLACE1005089	37.14	48.9	29.41	1.22	1
PLACE1005101	42.93	53.29	78.3	1.24	1.82
PLACE1005102	56.52	82.2	74.5	1.45	1.32
PLACE1005108	72.54	88.83	80.32	1.22	1.11
PLACE1005110	13.81	14.71	11.43	1	1
PLACE1005111	20.64	21.67	18.57	1	1
PLACE1005123	123.7	108.42	108.63	0.88	0.88
PLACE1005124	43.31	45.57	29.89	1.05	0.92
PLACE1005128	132.8	180.99	174.06	1.36	1.31
PLACE1005130	38.65	55.88	39.43	1.4	1
PLACE1005141	130.79	134.07	116.15	1.03	0.89
PLACE1005146	25.44	35.02	27.31	1	1
PLACE1005152	54.53	46.52	69.96	0.85	1.28
PLACE1005157	30.2	33.7	30.13	1	1
PLACE1005162	62.82	53.03	59.26	0.84	0.94
PLACE1005170	49.13	37.62	40.27	0.81	0.82
PLACE1005176	17.88	22.59	17.36	1	1
PLACE1005181	15.51	13.04	18.65	1	1
PLACE1005184	89.71	87.43	97.88	0.97	1.09
PLACE1005186	68.29	59.84	58.49	0.88	0.86
PLACE1005187	43.18	43.45	28.94	1.01	0.93
PLACE1005189	93.46	75.94	97.23	0.81	1.04
PLACE1005193	27.01	24.91	29.9	1	1
PLACE1005200	90.96	100.02	104.26	1.1	1.15
PLACE1005206	35.25	30.09	34.22	1	1
PLACE1005216	72.34	62.49	46.77	0.86	0.65
PLACE1005223	56.97	70.55	66.1	1.24	1.16
PLACE1005225	30.95	34.01	22.19	1	1
PLACE1005232	93.45	98.34	74.05	1.05	0.79
PLACE1005239	27.92	29.83	20.54	1	1
PLACE1005243	46.36	51.14	47.55	1.1	1.03

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PLACE1005250	63.7	64.27	69.23	1.01	1.09
PLACE1005261	39.94	47.49	45.93	1.19	1.15
PLACE1005266	50.13	47.62	41.62	0.95	0.83
PLACE1005271	105.46	119.85	107.51	1.14	1.02
PLACE1005277	23.12	23.98	23.79	1	1
PLACE1005287	34.49	30.55	24.59	1	1
PLACE1005299	227.75	244.53	240.7	1.07	1.06
PLACE1005305	69.35	58.03	70.36	0.84	1.01
PLACE1005307	47.35	45	36.3	0.95	0.84
PLACE1005308	69.41	60.66	61.59	0.87	0.89
PLACE1005313	30.06	30.16	21.98	1	1
PLACE1005320	23.98	27.05	34.24	1	1
PLACE1005327	115.46	121.53	98.08	1.05	0.85
PLACE1005331	30.68	23.63	27.98	1	1
PLACE1005335	21.07	19.09	21.14	1	1
PLACE1005336	59.36	64.07	46.08	1.08	0.78
PLACE1005351	214.19	250.8	232.92	1.17	1.09
PLACE1005366	40.76	25.34	38.17	0.98	0.98
PLACE1005373	39.99	49.78	40.8	1.24	1.02
PLACE1005374	72.3	70.1	60.1	0.97	0.83
PLACE1005383	28.31	37.28	28.35	1	1
PLACE1005388	20.09	15.33	18.44	1	1
PLACE1005409	41.93	44.79	33.57	1.07	0.95
PLACE1005410	88.35	94.3	106.85	1.07	1.21
PLACE1005426	19.09	18.98	20.59	1	1
PLACE1005431	88.69	108.82	135.42	1.23	1.53
PLACE1005453	71.2	88.48	54.16	1.24	0.76
PLACE1005467	77.47	67.27	64.65	0.87	0.83
PLACE1005471	25.1	22.55	17.51	1	1
PLACE1005476	18.71	20.07	18.3	1	1
PLACE1005477	41.23	32.25	32.73	0.97	0.97
PLACE1005480	17.77	14.42	12.46	1	1
PLACE1005481	50.84	54.24	40.04	1.07	0.79
PLACE1005494	20.43	21.23	13.29	1	1
PLACE1005495	40.63	117.46	154.7	2.89	3.81
PLACE1005497	42.63	75.44	65.24	1.77	1.53
PLACE1005499	80.45	84.52	88.63	1.05	1.1
PLACE1005502	27.31	28.42	23.04	1	1
PLACE1005513	23.38	27.63	25.62	1	1
PLACE1005515	17.68	23.24	12.33	1	1
PLACE1005519	52.35	24.62	32.27	0.76	0.76
PLACE1005526	20.49	19.76	12.62	1	1
PLACE1005528	99.57	107.34	90.46	1.08	0.91
PLACE1005530	107.92	99.06	99.36	0.92	0.92
PLACE1005536	27.52	29.04	23.69	1	1
PLACE1005539	22.2	17.91	26.37	1	1

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PLACE1005543	39.44	35.71	33.19	1	1
PLACE1005544	43.12	40.95	42.44	0.95	0.98
PLACE1005550	66.14	57.67	48.6	0.87	0.73
PLACE1005554	23.4	23.49	18.53	1	1
PLACE1005557	36.97	33.18	33	1	1
PLACE1005563	30.06	22.35	18.23	1	1
PLACE1005569	18.5	16.08	13.5	1	1
PLACE1005574	40.77	30.21	35.7	0.98	0.98
PLACE1005584	53.92	36.99	33.41	0.74	0.74
PLACE1005590	68.27	70.39	50.66	1.03	0.74
PLACE1005595	47.62	51.56	48.11	1.08	1.01
PLACE1005601	32.77	30.9	27.67	1	1
PLACE1005603	32.65	27.59	23.46	1	1
PLACE1005604	67.16	64.62	58.72	0.96	0.87
PLACE1005611	31.91	31.2	21.85	1	1
PLACE1005622	27.53	25.29	20.54	1	1
PLACE1005623	69.61	74.43	44.64	1.07	0.64
PLACE1005630	57.78	77.87	63.31	1.35	1.1
PLACE1005639	23.29	30.52	21.47	1	1
PLACE1005646	54.09	58.74	66.48	1.09	1.23
PLACE1005647	31.24	27.78	22.16	1	1
PLACE1005648	174.8	182.82	151.55	1.05	0.87
PLACE1005653	40.53	53.46	41.03	1.32	1.01
PLACE1005656	34.66	27.91	19.94	1	1
PLACE1005659	27.58	27.75	20.25	1	1
PLACE1005660	65.26	79.83	68.7	1.22	1.05
PLACE1005664	68.48	102.48	82.87	1.5	1.21
PLACE1005666	67.44	89.33	65.27	1.32	0.97
PLACE1005669	68.49	89.01	66.6	1.3	0.97
PLACE1005682	42.95	56.26	53.91	1.31	1.26
PLACE1005698	26.95	22.03	29.51	1	1
PLACE1005708	524.06	409.37	510.49	0.78	0.97
PLACE1005725	84.61	74.38	60.65	0.88	0.72
PLACE1005727	39.57	43.65	52.09	1.09	1.3
PLACE1005730	21.15	15.02	28.98	1	1
PLACE1005736	91.38	85.92	104.25	0.94	1.14
PLACE1005739	19.52	17.35	20.44	1	1
PLACE1005745	87.46	101.97	90.38	1.17	1.03
PLACE1005752	40	32.42	36.99	0.81	0.92
PLACE1005755	22.36	23.11	27.42	1	1
PLACE1005756	819	846.51	766.08	1.03	0.94
PLACE1005760	1062.4	953.29	852.14	0.9	0.8
PLACE1005763	95.45	96.07	92.3	1.01	0.97
PLACE1005768	58.28	58.42	49.18	1	0.84
PLACE1005771	65.24	83.61	81.92	1.28	1.26
PLACE1005783	56.7	49.41	41.56	0.87	0.73

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PLACE1005799	84.34	62.07	66.02	0.74	0.78
PLACE1005802	40.45	36.71	22.56	0.99	0.99
PLACE1005803	52.4	52.65	55.01	1	1.05
PLACE1005804	30.97	22.7	26.77	1	1
PLACE1005813	1808.1	1743.44	1328.93	0.96	0.73
PLACE1005815	95.63	82.59	64.07	0.86	0.67
PLACE1005828	66.49	73.06	63.39	1.1	0.95
PLACE1005833	643.83	631.1	507.77	0.98	0.79
PLACE1005834	48.61	47.74	45.99	0.98	0.95
PLACE1005835	360.43	407.67	352.53	1.13	0.98
PLACE1005836	15.6	19.62	14.08	1	1
PLACE1005845	29.39	26.53	21.53	1	1
PLACE1005850	43.16	48.82	40.66	1.13	0.94
PLACE1005851	24.59	29.45	23.01	1	1
PLACE1005856	31.36	36.06	38.2	1	1
PLACE1005875	28.19	27.56	23.48	1	1
PLACE1005876	38.64	32.99	39.6	1	1
PLACE1005878	28.58	30.51	22.54	1	1
PLACE1005880	32.67	30.18	23.51	1	1
PLACE1005884	26.98	25.83	20.75	1	1
PLACE1005890	35.41	31.1	33.76	1	1
PLACE1005898	102.07	112.8	93.03	1.11	0.91
PLACE1005913	94.01	97.52	77.21	1.04	0.82
PLACE1005921	32.53	33.54	19.76	1	1
PLACE1005923	19.81	19.65	16.69	1	1
PLACE1005925	35.08	37.64	17.11	1	1
PLACE1005927	20.75	20.69	18.83	1	1
PLACE1005932	24.82	24	17.52	1	1
PLACE1005934	42.12	41.03	39.84	0.97	0.95
PLACE1005936	27.74	24.68	25.54	1	1
PLACE1005939	241.35	526.2	524.44	2.18	2.17
PLACE1005951	29.76	26.23	25.81	1	1
PLACE1005953	22.65	23.03	23.62	1	1
PLACE1005955	32.99	32.9	28.43	1	1
PLACE1005966	34.05	28.76	23.82	1	1
PLACE1005968	32.82	26.94	42.21	1	1.06
PLACE1005975	56.15	93.88	70.1	1.67	1.25
PLACE1005990	17.45	27.59	15.96	1	1
PLACE1005997	978.15	2219.43	3051.68	2.27	3.12
PLACE1006002	130.64	147.49	122.1	1.13	0.93
PLACE1006003	47.98	54.08	51.82	1.13	1.08
PLACE1006011	43.98	54.19	44.58	1.23	1.01
PLACE1006017	38.94	43.81	30.38	1.1	1
PLACE1006037	26.17	24.55	38.53	1	1
PLACE1006040	37.97	39.89	41.47	1	1.04
PLACE1006063	58.1	43.53	43.45	0.75	0.75

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PLACE1006071	41.95	35.58	31.87	0.95	0.95
PLACE1006073	59.05	60.62	48.62	1.03	0.82
PLACE1006074	46.55	44.08	45.19	0.95	0.97
PLACE1006076	60.92	62.26	43.74	1.02	0.72
PLACE1006079	26.25	30.84	17.99	1	1
PLACE1006093	21.09	19.72	15.98	1	1
PLACE1006116	33.38	37.02	38.15	1	1
PLACE1006119	72.16	83.88	61.88	1.16	0.86
PLACE1006129	37	24.91	26.66	1	1
PLACE1006139	103.34	92.13	64.98	0.89	0.63
PLACE1006143	77.31	82.9	55.21	1.07	0.71
PLACE1006157	73.63	59.36	39.19	0.81	0.54
PLACE1006159	50.76	58.41	56	1.15	1.1
PLACE1006164	38.42	29.2	24.79	1	1
PLACE1006167	30.05	34.28	28.7	1	1
PLACE1006170	54.12	53.86	45.69	1	0.84
PLACE1006181	51.85	61.22	75.19	1.18	1.45
PLACE1006187	20.35	22.27	11.76	1	1
PLACE1006195	36.98	41.33	31.38	1.03	1
PLACE1006196	46.25	49.99	34.23	1.08	0.86
PLACE1006197	35.41	80.45	36.64	2.01	1
PLACE1006198	20.33	24.15	10.65	1	1
PLACE1006205	27.04	30.33	47.81	1	1.2
PLACE1006208	166.18	160.11	155.9	0.96	0.94
PLACE1006211	81.85	110.21	141.57	1.35	1.73
PLACE1006219	43.13	49.69	43.38	1.15	1.01
PLACE1006223	18.71	20.08	11.24	1	1
PLACE1006225	26.16	18.15	12.96	1	1
PLACE1006236	38.99	51.3	34.8	1.28	1
PLACE1006239	21.14	21.54	22.6	1	1
PLACE1006245	32.35	38.28	31.77	1	1
PLACE1006246	41.33	40.97	38.4	0.99	0.97
PLACE1006248	29.34	37.42	27.46	1	1
PLACE1006262	27.21	37.14	22.75	1	1
PLACE1006269	14.07	11.07	12.08	1	1
PLACE1006275	32.47	29.42	27.81	1	1
PLACE1006277	14.32	12.83	14.05	1	1
PLACE1006288	121.68	126.55	150.05	1.04	1.23
PLACE1006290	44.54	37.22	52.02	0.9	1.17
PLACE1006298	24.6	18.55	24.34	1	1
PLACE1006311	224.76	362.9	478.96	1.61	2.13
PLACE1006318	39.28	35.78	29.29	1	1
PLACE1006325	104.31	87.97	80.82	0.84	0.77
PLACE1006331	63.21	61.33	59.62	0.97	0.94
PLACE1006335	50.13	45.24	37.81	0.9	0.8
PLACE1006357	27.55	22.91	22.51	1	1

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PLACE1006360	31.91	28.01	32.95	1	1
PLACE1006364	34.98	32.36	36.01	1	1
PLACE1006365	16.88	20.54	23.57	1	1
PLACE1006368	35.92	33.82	27.34	1	1
PLACE1006371	33.44	37.43	26.91	1	1
PLACE1006373	87.74	94.97	83.52	1.08	0.95
PLACE1006382	33.59	26.24	29.91	1	1
PLACE1006385	26.01	27.2	27.21	1	1
PLACE1006391	67.93	81.48	92.19	1.2	1.36
PLACE1006412	89.26	93.45	99.21	1.05	1.11
PLACE1006414	18.25	22.77	19.71	1	1
PLACE1006419	42.52	42.88	32.14	1.01	0.94
PLACE1006438	60	55.71	43.01	0.93	0.72
PLACE1006443	64.71	77.33	79.64	1.2	1.23
PLACE1006445	34.57	26.21	29.93	1	1
PLACE1006447	46.13	47.27	45.94	1.02	1
PLACE1006466	30.92	25.74	21.02	1	1
PLACE1006469	28.34	25.31	26.97	1	1
PLACE1006470	71.3	79.67	74.87	1.12	1.05
PLACE1006472	247.42	236.96	256.25	0.96	1.04
PLACE1006476	66.33	66.38	56.39	1	0.85
PLACE1006482	55.71	67.95	39.62	1.22	0.72
PLACE1006488	263.14	243.49	211.79	0.93	0.8
PLACE1006492	74.4	85.96	60.14	1.16	0.81
PLACE1006506	39.87	39.23	42.33	1	1.06
PLACE1006515	31.54	34.21	43.45	1	1.09
PLACE1006516	28.57	28.1	32.19	1	1
PLACE1006520	50.97	51.84	36.08	1.02	0.78
PLACE1006521	91.91	93.22	93.9	1.01	1.02
PLACE1006529	77.96	70.96	85.63	0.91	1.1
PLACE1006531	17.55	16.72	17.3	1	1
PLACE1006534	28.78	26.63	23.78	1	1
PLACE1006540	97.91	113.43	90.41	1.16	0.92
PLACE1006549	24.66	26.8	21.47	1	1
PLACE1006550	30.72	30.14	34.44	1	1
PLACE1006552	25.88	21.37	17.37	1	1
PLACE1006557	20.03	20.85	22.74	1	1
PLACE1006563	32.75	38.63	32.31	1	1
PLACE1006579	38.36	50.2	53.09	1.26	1.33
PLACE1006594	1470.4	2343.7	2977.72	1.59	2.03
PLACE1006598	25.17	28.2	20.86	1	1
PLACE1006607	102.62	96.98	63.83	0.95	0.62
PLACE1006610	161.44	157.4	158.37	0.97	0.98
PLACE1006615	170.53	230.37	181.33	1.35	1.06
PLACE1006617	41.36	52.47	40.33	1.27	0.98
PLACE1006618	61.9	63.49	60.92	1.03	0.98

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PLACE1006626	18.78	18.58	15.81	1	1
PLACE1006629	39.09	28.14	26.39	1	1
PLACE1006637	47.74	54.16	45.68	1.13	0.96
PLACE1006640	19.56	21.49	18.75	1	1
PLACE1006644	34.47	24.66	38.52	1	1
PLACE1006657	36.76	43.91	33.57	1.1	1
PLACE1006673	105.75	118.39	90.89	1.12	0.86
PLACE1006678	25.26	26.33	21.23	1	1
PLACE1006682	32.57	35.48	39.14	1	1
PLACE1006684	24.76	15.56	12.72	1	1
PLACE1006698	21.9	21.87	19.07	1	1
PLACE1006704	29.17	27.59	21.49	1	1
PLACE1006708	52.21	56.79	44.42	1.09	0.85
PLACE1006711	90.49	83.29	83.69	0.92	0.92
PLACE1006714	61.05	49.27	37.68	0.81	0.66
PLACE1006716	23.05	15.83	18.42	1	1
PLACE1006731	38.28	45.12	38.86	1.13	1
PLACE1006754	18.26	15.48	13.94	1	1
PLACE1006760	54.5	61.53	57.07	1.13	1.05
PLACE1006779	32.63	28.19	24.73	1	1
PLACE1006782	22.28	17.96	16.97	1	1
PLACE1006783	26.21	29.78	19.3	1	1
PLACE1006786	30.43	23.44	19.4	1	1
PLACE1006792	96.99	109.36	85.04	1.13	0.88
PLACE1006795	21.7	18.73	12.96	1	1
PLACE1006800	32.54	34.66	29.4	1	1
PLACE1006805	65	91.51	86.82	1.41	1.34
PLACE1006809	55.84	58.93	56.4	1.06	1.01
PLACE1006815	38.62	40.32	33.93	1.01	1
PLACE1006819	11.29	13.41	5.54	1	1
PLACE1006820	132.74	162.76	119.25	1.23	0.9
PLACE1006826	49.88	87.77	43.48	1.76	0.87
PLACE1006829	123.27	130.22	102.14	1.06	0.83
PLACE1006853	29.17	41.16	32.7	1.03	1
PLACE1006860	17.5	23.58	21.3	1	1
PLACE1006867	66.64	94.76	67.34	1.42	1.01
PLACE1006875	43.58	44.55	38.5	1.02	0.92
PLACE1006878	49.53	49.03	45.07	0.99	0.91
PLACE1006883	76.12	68.45	71.78	0.9	0.94
PLACE1006898	46.07	40.11	68.46	0.87	1.49
PLACE1006901	31.34	33.46	37.51	1	1
PLACE1006904	58.07	68.41	69.27	1.18	1.19
PLACE1006917	60.31	46.57	73.27	0.77	1.21
PLACE1006932	25.98	21.08	20.62	1	1
PLACE1006935	14.99	15.43	17.56	1	1
PLACE1006956	33.28	22.73	21.83	1	1

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PLACE1006958	26.5	20.75	19.07	1	1
PLACE1006959	67.11	66.82	64.38	1	0.96
PLACE1006961	90.14	97.32	90.46	1.08	1
PLACE1006962	92.89	89.3	88.91	0.96	0.96
PLACE1006966	35.53	38.49	39.19	1	1
PLACE1006979	25.57	36.6	24.14	1	1
PLACE1006989	29.39	43.87	33.32	1.1	1
PLACE1007001	64.69	60.54	57.94	0.94	0.9
PLACE1007014	34.47	27.4	25.01	1	1
PLACE1007021	37.43	35.79	26.42	1	1
PLACE1007026	33.55	27.29	38.92	1	1
PLACE1007028	70.75	79.26	68.52	1.12	0.97
PLACE1007038	905.48	1441.98	1352.28	1.59	1.49
PLACE1007040	42	29.8	29.82	0.95	0.95
PLACE1007045	36.67	50.06	37.33	1.25	1
PLACE1007048	679.34	713.4	741.8	1.05	1.09
PLACE1007053	31.94	30.93	29.32	1	1
PLACE1007068	860.62	1042.12	659.27	1.21	0.77
PLACE1007070	71.9	54.02	58.47	0.75	0.81
PLACE1007076	146.49	190.93	165.54	1.3	1.13
PLACE1007077	32.04	29.37	39.47	1	1
PLACE1007081	29.72	27.35	21.94	1	1
PLACE1007082	23.97	23.42	30.77	1	1
PLACE1007092	69.29	69.41	61.52	1	0.89
PLACE1007096	21.59	22.38	18.71	1	1
PLACE1007097	29.53	26.42	24.05	1	1
PLACE1007099	31.63	31.56	22.21	1	1
PLACE1007105	20	18.95	19.48	1	1
PLACE1007108	38.02	33.29	48.92	1	1.22
PLACE1007111	23.6	19.67	22.41	1	1
PLACE1007112	19.93	23.21	22.24	1	1
PLACE1007130	24.68	18.62	16.94	1	1
PLACE1007132	57.55	73.92	47.55	1.28	0.83
PLACE1007140	18.39	18.58	14.36	1	1
PLACE1007143	35.84	33.62	34.44	1	1
PLACE1007169	34.92	47.03	50.92	1.18	1.27
PLACE1007178	19.73	19.53	17.73	1	1
PLACE1007190	28	37.16	35.42	1	1
PLACE1007201	18.63	16.17	17.55	1	1
PLACE1007202	677.92	712.91	790.84	1.05	1.17
PLACE1007226	24.8	33.84	26.76	1	1
PLACE1007238	33.43	38.99	29.72	1	1
PLACE1007239	20.1	18.41	23.99	1	1
PLACE1007242	16.1	16.07	12.84	1	1
PLACE1007243	24.97	28.75	26.19	1	1
PLACE1007247	51.59	68.41	90.72	1.33	1.76

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PLACE1007257	42.7	49.42	38.19	1.16	0.94
PLACE1007274	69.44	86.8	65.54	1.25	0.94
PLACE1007276	48.55	59.63	39.58	1.23	0.82
PLACE1007282	43.99	53.32	49.34	1.21	1.12
PLACE1007286	134.31	145.39	129.15	1.08	0.96
PLACE1007296	123.21	122.62	140.64	1	1.14
PLACE1007301	28.54	25.3	16.19	1	1
PLACE1007314	44.52	56.15	56.98	1.26	1.28
PLACE1007317	27.02	28.27	23.95	1	1
PLACE1007329	37.74	46.99	36.74	1.17	1
PLACE1007338	74.91	71.97	76.65	0.96	1.02
PLACE1007342	23.57	21.57	14.99	1	1
PLACE1007345	23.84	16.63	15.18	1	1
PLACE1007346	63.49	71.76	66.56	1.13	1.05
PLACE1007359	28.39	32.41	26.65	1	1
PLACE1007367	159.7	186.86	156.38	1.17	0.98
PLACE1007375	19.55	21.28	14.79	1	1
PLACE1007377	32.15	26.06	26.24	1	1
PLACE1007386	51.65	39.6	35.88	0.77	0.77
PLACE1007392	57.87	39.48	53.45	0.69	0.92
PLACE1007402	24.24	21.89	19.65	1	1
PLACE1007409	26.87	31.02	20.7	1	1
PLACE1007416	42.3	50.8	46.06	1.2	1.09
PLACE1007420	157.5	187.73	170.92	1.19	1.09
PLACE1007431	53.07	48.14	51.76	0.91	0.98
PLACE1007450	57.18	56.14	36.36	0.98	0.7
PLACE1007452	47.38	52.61	44.05	1.11	0.93
PLACE1007454	808.25	1172.33	677.25	1.45	0.84
PLACE1007460	22.94	51.42	18.14	1.29	1
PLACE1007478	23.46	29.22	21.9	1	1
PLACE1007484	32.11	29.62	26.58	1	1
PLACE1007488	23.81	42.75	27.1	1.07	1
PLACE1007507	32.1	37.71	39.41	1	1
PLACE1007511	15.76	5.91	8.15	1	1
PLACE1007513	161.99	171.44	146.12	1.06	0.9
PLACE1007524	34.31	42.75	22.87	1.07	1
PLACE1007525	33.3	38.5	31.23	1	1
PLACE1007537	522.32	806.81	756.73	1.54	1.45
PLACE1007544	45.92	59.57	40.41	1.3	0.88
PLACE1007547	12.49	11.54	10.46	1	1
PLACE1007557	26.79	35.05	25.91	1	1
PLACE1007560	85.37	83.75	89.1	0.98	1.04
PLACE1007565	13.72	11.48	11.24	1	1
PLACE1007580	15.6	17.77	13.42	1	1
PLACE1007583	13.03	11.45	11.12	1	1
PLACE1007591	23.16	24.73	22.04	1	1

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PLACE1007598	34.82	41.77	40.76	1.04	1.02
PLACE1007610	15.71	17.8	14.41	1	1
PLACE1007618	16.96	14.76	19.7	1	1
PLACE1007621	49.66	63.38	47.91	1.28	0.96
PLACE1007626	206.41	191.62	205.95	0.93	1
PLACE1007632	25.71	33.13	22.35	1	1
PLACE1007635	28.76	44.58	32.88	1.11	1
PLACE1007645	66.33	65.83	72.06	0.99	1.09
PLACE1007649	29.1	34.68	30.47	1	1
PLACE1007659	90.42	97.9	99.72	1.08	1.1
PLACE1007669	49.54	52.01	42.57	1.05	0.86
PLACE1007677	63.65	59.05	51.58	0.93	0.81
PLACE1007688	17.33	19.31	18.55	1	1
PLACE1007690	36.16	45.58	38.69	1.14	1
PLACE1007697	19.44	27.63	18.31	1	1
PLACE1007702	45.14	50.45	48.08	1.12	1.07
PLACE1007705	24.22	28.63	23.9	1	1
PLACE1007706	30.37	61.24	54.39	1.53	1.36
PLACE1007725	24.61	34.48	29.15	1	1
PLACE1007729	34.14	33.58	29.39	1	1
PLACE1007730	39.03	48.12	36.63	1.2	1
PLACE1007737	66.18	62.59	60.25	0.95	0.91
PLACE1007743	29.65	29.57	22.91	1	1
PLACE1007746	39.86	55.92	40.38	1.4	1.01
PLACE1007753	45.77	33.19	32.84	0.87	0.87
PLACE1007769	19.02	23.08	24.56	1	1
PLACE1007780	27.07	28.18	15.2	1	1
PLACE1007791	47.86	33.55	52.91	0.84	1.11
PLACE1007807	33.91	38.21	30.23	1	1
PLACE1007810	39.2	33.89	26.94	1	1
PLACE1007814	46.48	47.22	43.65	1.02	0.94
PLACE1007828	22.07	33.44	22.21	1	1
PLACE1007829	48.99	63.25	55.56	1.29	1.13
PLACE1007841	53.22	51.05	50.01	0.96	0.94
PLACE1007842	26.23	28.98	21.18	1	1
PLACE1007843	25.1	23.19	23.9	1	1
PLACE1007845	43.72	36.46	48.07	0.91	1.1
PLACE1007846	28.86	32.03	27.2	1	1
PLACE1007848	29.19	38.01	26.21	1	1
PLACE1007852	32.2	42.4	27.49	1.06	1
PLACE1007858	48.92	70.66	50.24	1.44	1.03
PLACE1007866	332.62	421.67	403.75	1.27	1.21
PLACE1007871	133.08	126.7	134.77	0.95	1.01
PLACE1007877	41.18	51.83	34.76	1.26	0.97
PLACE1007878	126.48	142.52	119.91	1.13	0.95
PLACE1007881	19.21	19.92	18.79	1	1

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PLACE1007885	45.12	41.68	42.69	0.92	0.95
PLACE1007897	24.63	23.73	16.27	1	1
PLACE1007908	63.89	82.77	86.71	1.3	1.36
PLACE1007922	66.14	60.47	54.63	0.91	0.83
PLACE1007946	24.76	34.34	26.2	1	1
PLACE1007950	89.89	101.23	70.71	1.13	0.79
PLACE1007954	22.84	24.75	19.71	1	1
PLACE1007955	37.84	43.08	42.66	1.08	1.07
PLACE1007956	23.21	22.74	25.64	1	1
PLACE1007958	12.85	11.41	9.59	1	1
PLACE1007965	42.59	44.77	32.57	1.05	0.94
PLACE1007969	77.66	66.93	64.71	0.86	0.83
PLACE1007971	32.43	45.19	31.39	1.13	1
PLACE1007990	38.68	34.43	34.99	1	1
PLACE1008000	20.44	19.44	11.18	1	1
PLACE1008002	22.17	33.99	22.75	1	1
PLACE1008037	16.65	21.52	14.26	1	1
PLACE1008044	37.14	25.78	26.62	1	1
PLACE1008045	36.38	23.24	30.44	1	1
PLACE1008080	29.7	29.28	28.28	1	1
PLACE1008092	24.71	24.17	18.05	1	1
PLACE1008095	34.48	41.13	26.09	1.03	1
PLACE1008105	143.94	109.41	100.26	0.76	0.7
PLACE1008107	19.18	21.02	17.6	1	1
PLACE1008111	29.75	32.08	29.35	1	1
PLACE1008113	122.11	147.06	134.03	1.2	1.1
PLACE1008122	16.38	26.8	19.23	1	1
PLACE1008129	64.74	50.69	63.95	0.78	0.99
PLACE1008132	57.78	63.8	38.67	1.1	0.69
PLACE1008137	32.83	28.72	29.18	1	1
PLACE1008174	68.35	62.42	52.45	0.91	0.77
PLACE1008177	22.86	29.48	15	1	1
PLACE1008181	21.43	22.51	16.17	1	1
PLACE1008195	34.63	40.85	43	1.02	1.08
PLACE1008198	29.8	35.31	22.76	1	1
PLACE1008201	29.51	41.32	24.42	1.03	1
PLACE1008209	40.18	38.31	21.63	1	1
PLACE1008226	100.46	120.86	72.39	1.2	0.72
PLACE1008227	65.63	79.11	45.82	1.21	0.7
PLACE1008231	20.91	25.23	20.05	1	1
PLACE1008238	43.7	29.4	37.16	0.92	0.92
PLACE1008244	24.28	34.12	24.16	1	1
PLACE1008249	39.57	40.74	20.42	1.02	1
PLACE1008266	192.68	238.99	221.82	1.24	1.15
PLACE1008273	45.14	34.93	35.3	0.89	0.89
PLACE1008275	29.89	24.58	30.57	1	1

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PLACE1008280	31.84	26.17	33.13	1	1
PLACE1008282	46.39	42.02	55.69	0.91	1.2
PLACE1008297	27.1	23.76	23.37	1	1
PLACE1008303	36.02	27.9	38.59	1	1
PLACE1008309	12.82	20.09	21.46	1	1
PLACE1008315	44.1	71.28	50.84	1.62	1.15
PLACE1008329	47.26	31.28	40.19	0.85	0.85
PLACE1008330	56.78	50.96	52.48	0.9	0.92
PLACE1008331	36.09	39.1	38.37	1	1
PLACE1008351	46.98	54.09	52.87	1.15	1.13
PLACE1008356	37.43	38.51	35.78	1	1
PLACE1008359	25.5	36.61	27.97	1	1
PLACE1008368	33.84	39.35	44.68	1	1.12
PLACE1008369	26.62	38.18	22.53	1	1
PLACE1008392	39.26	40.96	41.66	1.02	1.04
PLACE1008394	64.15	72.39	65.77	1.13	1.03
PLACE1008398	117.87	78.09	88.46	0.66	0.75
PLACE1008401	74.59	80.4	77.01	1.08	1.03
PLACE1008402	46.76	45.46	31	0.97	0.86
PLACE1008405	294.38	355.09	299.1	1.21	1.02
PLACE1008409	49.91	58.05	61.69	1.16	1.24
PLACE1008420	36.85	25.34	18.93	1	1
PLACE1008424	31.93	31.73	34.57	1	1
PLACE1008426	128.65	104.91	110.1	0.82	0.86
PLACE1008429	26.12	36.14	18.71	1	1
PLACE1008430	31.14	27.16	21.39	1	1
PLACE1008437	27.95	26.66	26.19	1	1
PLACE1008453	19.74	23.38	20.36	1	1
PLACE1008454	59.11	47.29	55.88	0.8	0.95
PLACE1008455	104.77	114.22	86.16	1.09	0.82
PLACE1008457	105.89	110.43	74.5	1.04	0.7
PLACE1008465	19.49	16.22	15.38	1	1
PLACE1008469	49.11	61.84	63.6	1.26	1.3
PLACE1008488	25.09	39.82	22.71	1	1
PLACE1008519	43.53	37.61	28.61	0.92	0.92
PLACE1008524	24.48	26.12	28.78	1	1
PLACE1008531	34.75	30.13	30.84	1	1
PLACE1008532	53.96	74.15	45.05	1.37	0.83
PLACE1008533	36.34	37.3	30.27	1	1
PLACE1008542	24.41	34.57	31.42	1	1
PLACE1008549	28.54	28.54	20.08	1	1
PLACE1008560	18.37	27.73	27.3	1	1
PLACE1008567	48.98	39.86	41.78	0.82	0.85
PLACE1008568	28.33	33.4	37.15	1	1
PLACE1008569	36.53	70.51	67.9	1.76	1.7
PLACE1008584	33.63	55.99	53.83	1.4	1.35

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PLACE1008585	58.8	75.59	59.76	1.29	1.02
PLACE1008603	581.28	561.11	342.21	0.97	0.59
PLACE1008621	24.79	24.25	20.06	1	1
PLACE1008625	11.5	11.09	11.98	1	1
PLACE1008626	16.22	13.49	12.11	1	1
PLACE1008627	29.28	30.91	37.43	1	1
PLACE1008629	65.18	56.54	148.28	0.87	2.27
PLACE1008630	22.18	21.25	23.79	1	1
PLACE1008643	34.29	35.04	29.44	1	1
PLACE1008650	14.74	15.41	13.33	1	1
PLACE1008657	55.09	57.36	43.89	1.04	0.8
PLACE1008664	23.34	23.64	24.27	1	1
PLACE1008693	43.13	41.51	30.19	0.96	0.93
PLACE1008696	31.94	34.65	25.43	1	1
PLACE1008715	47.85	46.82	42.88	0.98	0.9
PLACE1008716	41.71	53.61	31.3	1.29	0.96
PLACE1008722	54.61	45.03	44.82	0.82	0.82
PLACE1008738	88.36	84.43	83.28	0.96	0.94
PLACE1008742	162.86	160.2	161.81	0.98	0.99
PLACE1008744	14.14	22.94	12.18	1	1
PLACE1008748	22.27	24.48	14.44	1	1
PLACE1008757	34.6	42.71	27.87	1.07	1
PLACE1008766	32.11	27.78	28.26	1	1
PLACE1008785	49.07	59.73	41.43	1.22	0.84
PLACE1008790	33.27	33.02	29.64	1	1
PLACE1008798	63.72	66.89	67.61	1.05	1.06
PLACE1008807	22.01	22.03	19.94	1	1
PLACE1008808	32.24	18.82	19.03	1	1
PLACE1008813	29.43	35.83	35.39	1	1
PLACE1008836	79.18	55.11	47.12	0.7	0.6
PLACE1008851	115.23	81.63	55.52	0.71	0.48
PLACE1008854	20.39	26.55	11.71	1	1
PLACE1008864	48.15	54.26	72.45	1.13	1.5
PLACE1008867	56.85	58.24	33.04	1.02	0.7
PLACE1008876	549.37	600.39	469.11	1.09	0.85
PLACE1008887	41.83	58.22	24.8	1.39	0.96
PLACE1008902	25.21	36.34	34.18	1	1
PLACE1008911	55.54	65.78	52.58	1.18	0.95
PLACE1008917	19.14	25.45	24.12	1	1
PLACE1008920	11.29	12.12	6.23	1	1
PLACE1008925	13.83	16.73	10.48	1	1
PLACE1008930	27.53	23.49	18.05	1	1
PLACE1008934	28.64	34.88	18.8	1	1
PLACE1008941	17.54	24.91	22.06	1	1
PLACE1008947	37.22	51.14	43.96	1.28	1.1
PLACE1008984	23.24	34.33	21.6	1	1

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PLACE1008985	19.99	29.03	21.28	1	1
PLACE1008994	10.53	10.54	7.43	1	1
PLACE1009020	20.44	34.43	21.28	1	1
PLACE1009027	14.33	10.59	13.29	1	1
PLACE1009039	12.51	12.97	9.67	1	1
PLACE1009045	25.26	34.62	28.65	1	1
PLACE1009048	11.07	6.67	9.57	1	1
PLACE1009050	16.3	17.99	13.91	1	1
PLACE1009060	52.29	76.48	76.13	1.46	1.46
PLACE1009067	63.86	53.76	34.08	0.84	0.63
PLACE1009071	54.23	73.27	59.81	1.35	1.1
PLACE1009090	29.1	39.11	39.61	1	1
PLACE1009091	739.81	739.41	547.06	1	0.74
PLACE1009094	19.97	28.69	21.59	1	1
PLACE1009099	36.64	45.19	48.83	1.13	1.22
PLACE1009110	20.35	18.46	20.9	1	1
PLACE1009111	18.51	23.09	18.16	1	1
PLACE1009113	53.98	42.76	37.35	0.79	0.74
PLACE1009130	41.39	52.31	43.13	1.26	1.04
PLACE1009150	39.25	37.55	32.77	1	1
PLACE1009155	69.35	94.89	74.07	1.37	1.07
PLACE1009158	21.91	26.54	18.92	1	1
PLACE1009166	50.25	51.72	46.79	1.03	0.93
PLACE1009172	22.82	29.53	36.75	1	1
PLACE1009174	34.79	36.37	30.96	1	1
PLACE1009183	94.37	89.34	64.66	0.95	0.69
PLACE1009186	20.43	20.53	17.56	1	1
PLACE1009190	20.48	35.41	18.66	1	1
PLACE1009196	54.35	52.71	38.66	0.97	0.74
PLACE1009200	58.25	76.13	58.44	1.31	1
PLACE1009217	42.05	46.24	41.71	1.1	0.99
PLACE1009230	144.11	204.77	153.75	1.42	1.07
PLACE1009236	24.31	27.66	29.72	1	1
PLACE1009246	158.99	139.66	83.91	0.88	0.53
PLACE1009265	66.52	42.3	71.65	0.64	1.08
PLACE1009279	34.59	34.51	23.57	1	1
PLACE1009298	79.99	77.85	81.83	0.97	1.02
PLACE1009308	33.45	27.01	16.14	1	1
PLACE1009319	65.4	73.56	77.72	1.12	1.19
PLACE1009328	49.82	47.34	43.67	0.95	0.88
PLACE1009335	19.74	18.97	16.42	1	1
PLACE1009338	46.74	52.39	38.16	1.12	0.86
PLACE1009344	19.93	16.12	20.93	1	1
PLACE1009355	147.61	162.58	173.91	1.1	1.18
PLACE1009368	17.87	20.22	16.8	1	1
PLACE1009375	22.61	32.24	29.19	1	1

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PLACE1009388	49.9	74.96	45.01	1.5	0.9
PLACE1009398	35.17	53.79	43.1	1.34	1.08
PLACE1009404	34.21	46.04	38.16	1.15	1
PLACE1009410	26.75	35.99	28.94	1	1
PLACE1009417	58.32	67.04	42.72	1.15	0.73
PLACE1009424	34.63	42.13	42.37	1.05	1.06
PLACE1009434	24.85	24.58	24.73	1	1
PLACE1009443	47.53	48.97	35.82	1.03	0.84
PLACE1009444	31.89	50.08	34.61	1.25	1
PLACE1009459	18.43	17.86	18.01	1	1
PLACE1009460	67.87	55.15	59.2	0.81	0.87
PLACE1009468	61.44	73.54	56.01	1.2	0.91
PLACE1009476	18.42	23.28	12.77	1	1
PLACE1009477	38.48	38.41	40.05	1	1
PLACE1009493	14.61	13.38	11.75	1	1
PLACE1009502	24.2	18.19	17.23	1	1
PLACE1009524	18.39	17.32	15.6	1	1
PLACE1009527	34.8	37.6	27.86	1	1
PLACE1009531	202.28	205.54	217.56	1.02	1.08
PLACE1009535	41.74	48.48	38.26	1.16	0.96
PLACE1009539	52.88	57.83	52.55	1.09	0.99
PLACE1009540	74.03	82.77	96.82	1.12	1.31
PLACE1009542	20.3	17.51	18.66	1	1
PLACE1009546	26.64	16.94	13.4	1	1
PLACE1009556	19.56	22.58	16.96	1	1
PLACE1009569	42.87	51.18	43.48	1.19	1.01
PLACE1009571	28.33	26.69	25.34	1	1
PLACE1009573	55.23	54.49	56.76	0.99	1.03
PLACE1009576	43.33	35.6	25.18	0.92	0.92
PLACE1009580	66.98	54.33	52.85	0.81	0.79
PLACE1009581	35.02	40.73	37.32	1.02	1
PLACE1009587	21.2	22.71	17.17	1	1
PLACE1009593	69.23	95.74	64.2	1.38	0.93
PLACE1009595	67.55	60.93	55.12	0.9	0.82
PLACE1009596	31.43	27.75	24.05	1	1
PLACE1009600	76.24	87.08	68	1.14	0.89
PLACE1009604	51.17	39.11	25.77	0.78	0.78
PLACE1009607	105.68	136.82	84.46	1.29	0.8
PLACE1009613	27.91	34.76	27.43	1	1
PLACE1009621	70.93	83.59	74.98	1.18	1.06
PLACE1009622	51.58	101.79	73.07	1.97	1.42
PLACE1009624	36.65	51.5	30.53	1.29	1
PLACE1009637	14.3	19.67	15.18	1	1
PLACE1009639	60.81	23.05	18.6	0.66	0.66
PLACE1009654	29.81	37.96	30.06	1	1
PLACE1009659	49.17	66.83	38.29	1.36	0.81

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PLACE1009665	36.25	41.13	28.7	1.03	1
PLACE1009669	20.88	23.64	26.93	1	1
PLACE1009670	27.37	30.25	30.27	1	1
PLACE1009708	24.07	37.18	35.56	1	1
PLACE1009721	28.98	18.31	19.77	1	1
PLACE1009731	35.52	28.93	25.46	1	1
PLACE1009735	40.83	32.49	55.08	0.98	1.35
PLACE1009737	35.2	30.66	37.3	1	1
PLACE1009741	18.21	26.46	34.29	1	1
PLACE1009752	40.61	30.49	23.87	0.98	0.98
PLACE1009763	49.08	51.16	54.68	1.04	1.11
PLACE1009766	41.6	36.03	39.03	0.96	0.96
PLACE1009772	17.1	38.53	32.16	1	1
PLACE1009782	44.04	32.84	31.11	0.91	0.91
PLACE1009794	37.6	36.48	30.69	1	1
PLACE1009798	43.74	40.97	39.06	0.94	0.91
PLACE1009845	17.16	29.15	19.05	1	1
PLACE1009849	18.1	25.14	34.22	1	1
PLACE1009857	24.47	21.19	22.73	1	1
PLACE1009861	157.04	147.3	184.61	0.94	1.18
PLACE1009872	183.78	532.08	595.65	2.9	3.24
PLACE1009877	88.74	127.12	82	1.43	0.92
PLACE1009879	50.78	61.76	51.43	1.22	1.01
PLACE1009886	26.47	30.9	26.46	1	1
PLACE1009888	40.97	27.49	37.88	0.98	0.98
PLACE1009908	38.76	52.68	31.63	1.32	1
PLACE1009919	72.43	157.7	91.06	2.18	1.26
PLACE1009921	33.92	34.44	25.56	1	1
PLACE1009923	30.5	44.49	36.52	1.11	1
PLACE1009924	99.41	54.1	55.42	0.54	0.56
PLACE1009925	35.65	20.58	22.27	1	1
PLACE1009931	90.33	98.46	76.54	1.09	0.85
PLACE1009935	25.18	24.01	15.51	1	1
PLACE1009947	27.03	27.39	20.09	1	1
PLACE1009961	24.51	25.25	21.83	1	1
PLACE1009971	24.03	25.77	25.6	1	1
PLACE1009982	18.22	39.31	15.49	1	1
PLACE1009992	9.19	11.11	8.64	1	1
PLACE1009995	63.3	51.96	56.69	0.82	0.9
PLACE1009997	43.45	50.16	41.93	1.15	0.97
PLACE1010002	32.44	23.09	16.62	1	1
PLACE1010011	25.99	24.02	19.6	1	1
PLACE1010013	15.52	18.47	13.26	1	1
PLACE1010021	24.58	36.88	37.14	1	1
PLACE1010023	43.52	60.71	61.14	1.39	1.4
PLACE1010031	52.61	51.96	38.23	0.99	0.76

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PLACE1010039	19.95	22.68	18.66	1	1
PLACE1010045	36.67	47.27	35.84	1.18	1
PLACE1010053	21.58	20.14	20.04	1	1
PLACE1010060	38.71	56.37	32.78	1.41	1
PLACE1010069	19.39	23.73	18.91	1	1
PLACE1010070	20.01	20.72	21.19	1	1
PLACE1010074	165.08	128.25	150.68	0.78	0.91
PLACE1010076	230.47	311.86	258.06	1.35	1.12
PLACE1010078	31.79	36.25	37	1	1
PLACE1010081	76.83	74.34	52.61	0.97	0.68
PLACE1010083	17.09	21.13	24.34	1	1
PLACE1010089	20.95	24.75	17.3	1	1
PLACE1010096	70.55	70.61	54.95	1	0.78
PLACE1010102	39.64	55.68	62.77	1.39	1.57
PLACE1010105	47.44	49.6	48.65	1.05	1.03
PLACE1010106	40.34	52.34	43.81	1.3	1.09
PLACE1010130	40.29	44.66	30.55	1.11	0.99
PLACE1010132	56.7	85.85	65.52	1.51	1.16
PLACE1010134	20.51	15.99	20.46	1	1
PLACE1010139	415.41	498.57	421.38	1.2	1.01
PLACE1010148	39.47	45.32	27.49	1.13	1
PLACE1010152	29.32	28.44	29.8	1	1
PLACE1010155	330.96	335.95	408.91	1.02	1.24
PLACE1010156	356.21	422.83	469.57	1.19	1.32
PLACE1010161	37.57	44.88	36.68	1.12	1
PLACE1010181	34.13	35.33	27.84	1	1
PLACE1010194	24.35	22.48	25.49	1	1
PLACE1010202	18.23	20.58	13.78	1	1
PLACE1010231	31.51	46.67	24.45	1.17	1
PLACE1010235	45.66	38.3	32.66	0.88	0.88
PLACE1010237	15.65	11.4	11.73	1	1
PLACE1010251	45.81	45.52	23.23	0.99	0.87
PLACE1010261	32.21	38.4	27.38	1	1
PLACE1010270	25.56	34.7	21.54	1	1
PLACE1010273	20.85	22.99	16.74	1	1
PLACE1010274	54.13	47.79	55.26	0.88	1.02
PLACE1010277	71.1	82.25	73.8	1.16	1.04
PLACE1010293	66.72	98.76	53.8	1.48	0.81
PLACE1010297	190.1	248.33	202.48	1.31	1.07
PLACE1010300	45.22	39.59	27.21	0.88	0.88
PLACE1010310	424.98	529.37	453.64	1.25	1.07
PLACE1010321	55.25	72.06	55.13	1.3	1
PLACE1010324	25.61	25.41	17.98	1	1
PLACE1010329	50.18	65.57	47.53	1.31	0.95
PLACE1010330	55.1	76.67	55.02	1.39	1
PLACE1010335	77.42	150.11	159.9	1.94	2.07

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PLACE1010341	14.28	17.1	15.38	1	1
PLACE1010342	9.17	10.68	6.34	1	1
PLACE1010346	.25	30.67	21.84	1	1
PLACE1010362	35.78	48.63	28.59	1.22	1
PLACE1010364	19.36	14.8	13.85	1	1
PLACE1010368	32.4	36.5	44.4	1	1.11
PLACE1010373	55.73	66.05	70.87	1.19	1.27
PLACE1010383	105.68	48.05	71.29	0.45	0.67
PLACE1010385	6.58	5.18	2.96	1	1
PLACE1010389	149.57	123.41	125.82	0.83	0.84
PLACE1010401	15.79	15.26	16.26	1	1
PLACE1010410	28.15	37.81	34.22	1	1
PLACE1010418	36.95	33.69	39.07	1	1
PLACE1010425	16.45	18.69	17.64	1	1
PLACE1010443	273.44	343.89	242.35	1.26	0.89
PLACE1010445	32.75	43.52	36.7	1.09	1
PLACE1010481	19.87	17.5	20.62	1	1
PLACE1010482	24.01	33.97	24.55	1	1
PLACE1010491	35.66	27.01	27.99	1	1
PLACE1010492	97.73	111.42	92.48	1.14	0.95
PLACE1010509	28.13	32.42	36.16	1	1
PLACE1010518	98.12	123.6	114.12	1.26	1.16
PLACE1010522	100.54	105.4	126.63	1.05	1.26
PLACE1010529	32.36	59.45	68.71	1.49	1.72
PLACE1010547	21.89	34.68	16.06	1	1
PLACE1010560	29.41	35.2	34.06	1	1
PLACE1010562	23.25	30	23.72	1	1
PLACE1010579	38.25	33.08	29.89	1	1
PLACE1010580	37.66	33.68	35.77	1	1
PLACE1010599	92.73	121.5	90.34	1.31	0.97
PLACE1010606	30.04	34.79	22.32	1	1
PLACE1010616	46.86	69.11	81.69	1.47	1.74
PLACE1010622	28.24	38.42	25.03	1	1
PLACE1010624	51.97	49.53	49.27	0.95	0.95
PLACE1010628	40.93	49.51	35.73	1.21	0.98
PLACE1010629	35.56	41.65	35.77	1.04	1
PLACE1010630	44.56	38.38	46.6	0.9	1.05
PLACE1010631	27.36	20.75	17.51	1	1
PLACE1010651	233.15	363.62	282.49	1.56	1.21
PLACE1010661	22.85	27.37	31.66	1	1
PLACE1010662	26.01	24.27	21.39	1	1
PLACE1010668	190.83	153.29	181.8	0.8	0.95
PLACE1010702	59.8	61.23	55.06	1.02	0.92
PLACE1010709	513.52	534.45	611.18	1.04	1.19
PLACE1010713	60.05	51.29	72.19	0.85	1.2
PLACE1010714	19.13	16.92	16.72	1	1

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PLACE1010716	26.71	33.85	35.18	1	1
PLACE1010717	42.47	35.58	37.32	0.94	0.94
PLACE1010720	229.86	278.82	183.49	1.21	0.8
PLACE1010739	32.44	33.25	22.11	1	1
PLACE1010743	22.46	29.9	23.34	1	1
PLACE1010752	18.27	19.55	21.76	1	1
PLACE1010761	104.86	122.36	130.93	1.17	1.25
PLACE1010771	45.25	59.5	57.83	1.31	1.28
PLACE1010784	20.56	18.65	15.58	1	1
PLACE1010786	40.55	56.08	27.24	1.38	0.99
PLACE1010789	27.09	24.19	22.66	1	1
PLACE1010800	34.72	39.52	36.8	1	1
PLACE1010802	35.51	47.64	36.65	1.19	1
PLACE1010811	21.55	29.77	27	1	1
PLACE1010813	1287.7	1414.73	856.15	1.1	0.66
PLACE1010827	23	21.43	17.87	1	1
PLACE1010833	33.54	35.98	30.25	1	1
PLACE1010839	72	85.27	69.36	1.18	0.96
PLACE1010856	86.05	87.34	90.48	1.01	1.05
PLACE1010857	57.56	61.88	60.74	1.08	1.06
PLACE1010870	40.96	50.46	29.36	1.23	0.98
PLACE1010877	46.38	39.36	49.51	0.86	1.07
PLACE1010882	16.02	15.31	13.01	1	1
PLACE1010891	16.64	15.08	17.9	1	1
PLACE1010896	30.16	23.93	23.2	1	1
PLACE1010900	323.44	310.25	341.11	0.96	1.05
PLACE1010916	20.94	23.68	16.14	1	1
PLACE1010917	8.78	12.15	5.58	1	1
PLACE1010924	28.2	31.02	20.59	1	1
PLACE1010925	59.4	63.62	79.68	1.07	1.34
PLACE1010926	26.05	25.68	21.29	1	1
PLACE1010942	73.09	63.9	54.96	0.87	0.75
PLACE1010943	114.11	144.64	114	1.27	1
PLACE1010944	34.71	34.89	33.54	1	1
PLACE1010947	50.97	56.41	46.75	1.11	0.92
PLACE1010954	179.34	191.9	149.28	1.07	0.83
PLACE1010960	63.89	65.16	57.38	1.02	0.9
PLACE1010965	63.35	54.39	57.39	0.86	0.91
PLACE1010968	20	25	20.64	1	1
PLACE1010978	52.43	69.4	55.7	1.32	1.06
PLACE1010982	40.37	51.27	37.65	1.27	0.99
PLACE1010990	34.79	33.81	43.07	1	1.08
PLACE1011017	114.63	113.45	90.55	0.99	0.79
PLACE1011019	66.26	57.22	82.98	0.86	1.25
PLACE1011026	61.83	68.6	53.2	1.11	0.86
PLACE1011032	44.7	54.48	36.43	1.22	0.89

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PLACE1011041	31.57	35.69	21.03	1	1
PLACE1011045	35.8	33.36	50.66	1	1.27
PLACE1011046	34.53	36.4	27.94	1	1
PLACE1011054	87.07	91.74	90.14	1.05	1.04
PLACE1011056	234.93	341.05	191.57	1.45	0.82
PLACE1011057	50.32	61.94	47.85	1.23	0.95
PLACE1011059	28.75	30.18	17.75	1	1
PLACE1011066	40.74	45.85	31.71	1.13	0.98
PLACE1011087	126.9	97.7	103.08	0.77	0.81
PLACE1011090	43.14	63.67	54.04	1.48	1.25
PLACE1011109	72.28	109.31	75.78	1.51	1.05
PLACE1011114	40.38	55.61	44.13	1.38	1.09
PLACE1011116	59.89	60.46	61.74	1.01	1.03
PLACE1011122	23.85	22.65	27.32	1	1
PLACE1011133	29.8	25.5	32.54	1	1
PLACE1011134	702.54	855.96	742.75	1.22	1.06
PLACE1011143	18.05	26.08	15.76	1	1
PLACE1011146	27.97	31.76	30.52	1	1
PLACE1011160	27.65	29.84	36.02	1	1
PLACE1011165	29.12	25.53	32.58	1	1
PLACE1011181	719.05	676.22	532.05	0.94	0.74
PLACE1011185	128.61	184.54	128.11	1.43	1
PLACE1011186	161.64	160.59	193.09	0.99	1.19
PLACE1011203	26.77	26.81	25.39	1	1
PLACE1011214	745.48	767.22	632.47	1.03	0.85
PLACE1011219	38.42	58.33	37.91	1.46	1
PLACE1011221	31.09	40.42	44.12	1.01	1.1
PLACE1011229	20.84	29.07	17.82	1	1
PLACE1011231	20.61	29.22	21.09	1	1
PLACE1011236	553.05	663.66	472.59	1.2	0.85
PLACE1011247	162.35	152.62	169.63	0.94	1.04
PLACE1011263	28.78	26.07	29.73	1	1
PLACE1011273	22.76	23.17	22.03	1	1
PLACE1011278	72.55	79.44	63.03	1.09	0.87
PLACE1011289	23.79	33.63	31.25	1	1
PLACE1011291	134.38	169.36	147.47	1.26	1.1
PLACE1011296	30.64	34.19	32.38	1	1
PLACE1011310	29.41	24.49	28.94	1	1
PLACE1011311	80.01	83.34	61.28	1.04	0.77
PLACE1011321	63.79	59.32	62.43	0.93	0.98
PLACE1011325	21.43	25.41	19.82	1	1
PLACE1011332	46.92	65.48	63.02	1.4	1.34
PLACE1011340	96.73	105.33	93.22	1.09	0.96
PLACE1011353	87.13	92.87	77.19	1.07	0.89
PLACE1011360	73.75	62.56	56.98	0.85	0.77
PLACE1011364	40.61	42.21	47	1.04	1.16

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PLACE1011365	31.47	37.76	31.3	1	1
PLACE1011371	1393.0	1511.96	1103.92	1.09	0.79
PLACE1011375	21.17	21.56	18.08	1	1
PLACE1011386	52.19	45.65	48.93	0.87	0.94
PLACE1011399	34.74	30.13	32.85	1	1
PLACE1011406	30.27	36.26	23.82	1	1
PLACE1011407	36.4	42.05	33.38	1.05	1
PLACE1011419	27.2	44.71	42.78	1.12	1.07
PLACE1011433	37.98	29.32	35.67	1	1
PLACE1011440	18.75	14.39	23.74	1	1
PLACE1011452	52.41	64.26	64.32	1.23	1.23
PLACE1011465	25.85	23.7	25.01	1	1
PLACE1011472	25.31	25.72	28.29	1	1
PLACE1011477	589.52	635.4	447.32	1.08	0.76
PLACE1011478	115.07	140.27	106.64	1.22	0.93
PLACE1011492	72	97.27	57.14	1.35	0.79
PLACE1011498	17.1	22.26	16.32	1	1
PLACE1011501	17.79	17.26	18.01	1	1
PLACE1011503	9.79	7.51	7.6	1	1
PLACE1011509	34.49	28.69	32.22	1	1
PLACE1011514	223.19	247.57	222.01	1.11	0.99
PLACE1011516	101.6	143.7	107.63	1.41	1.06
PLACE1011520	27.41	24.9	24.32	1	1
PLACE1011538	29.14	23.25	16.78	1	1
PLACE1011555	23.6	20.53	25.6	1	1
PLACE1011561	24.88	25.71	37.82	1	1
PLACE1011563	37.3	42.35	32.36	1.06	1
PLACE1011567	59.12	55.36	61.57	0.94	1.04
PLACE1011569	110.07	98.25	92.78	0.89	0.84
PLACE1011576	107.13	119.56	82.05	1.12	0.77
PLACE1011586	58.35	60.15	53.06	1.03	0.91
PLACE1011635	126.85	122.41	79.4	0.96	0.63
PLACE1011641	21.95	15.08	12	1	1
PLACE1011642	96.47	131.07	98.89	1.36	1.03
PLACE1011643	27.01	32.97	23.44	1	1
PLACE1011646	311.38	371.3	292.59	1.19	0.94
PLACE1011649	39.42	40.05	38.15	1	1
PLACE1011650	23.59	25.05	20.03	1	1
PLACE1011661	92.23	95.48	84.22	1.04	0.91
PLACE1011664	62.94	63.99	43.95	1.02	0.7
PLACE1011672	22.5	26.83	22.49	1	1
PLACE1011675	20.43	16.82	14.39	1	1
PLACE1011682	34.22	33.4	46.45	1	1.16
PLACE1011708	80.24	92.72	58.81	1.16	0.73
PLACE1011719	61.08	68.74	59.57	1.13	0.98
PLACE1011725	39.29	49.72	30.96	1.24	1

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PLACE1011729	48.33	49.66	37.62	1.03	0.83
PLACE1011741	42.11	42.21	26.14	1	0.95
PLACE1011749	98.54	120.28	81.54	1.22	0.83
PLACE1011757	200.1	214.18	192.99	1.07	0.96
PLACE1011762	31.14	34.16	27.67	1	1
PLACE1011778	20.12	27.07	17.12	1	1
PLACE1011783	79.37	103.33	80.61	1.3	1.02
PLACE1011795	62.52	74.53	49.61	1.19	0.79
PLACE1011810	26.95	35.71	25.38	1	1
PLACE1011824	94.06	261.39	163.66	2.78	1.74
PLACE1011825	152.66	173.17	154.8	1.13	1.01
PLACE1011835	23.8	27.8	43.04	1	1.08
PLACE1011836	120.62	135.76	141.71	1.13	1.17
PLACE1011847	285.54	294.38	284.53	1.03	1
PLACE1011855	22.68	27.11	28.04	1	1
PLACE1011858	36.79	39.34	31.86	1	1
PLACE1011874	45.52	57.52	57.05	1.26	1.25
PLACE1011875	21.91	19.56	19.38	1	1
PLACE1011877	31.1	30.5	28.95	1	1
PLACE1011891	17.01	14.38	16	1	1
PLACE1011896	9.03	4.47	5.22	1	1
PLACE1011920	17.59	18.35	15.64	1	1
PLACE1011922	14.43	22.14	26.94	1	1
PLACE1011923	318.75	346.7	273.3	1.09	0.86
PLACE1011937	47.17	42.55	44.49	0.9	0.94
PLACE1011939	72	86.06	70.82	1.2	0.98
PLACE1011940	48.98	53.18	48.23	1.09	0.98
PLACE1011962	47.89	49.93	54.67	1.04	1.14
PLACE1011964	25.14	30.6	30.08	1	1
PLACE1011978	45.43	47.26	54.6	1.04	1.2
PLACE1011980	45.74	54.67	59.79	1.2	1.31
PLACE1011981	248.01	278.49	169.77	1.12	0.68
PLACE1011982	22.97	26.02	26.36	1	1
PLACE1011995	53.57	49.73	50.05	0.93	0.93
PLACE1012023	21.43	23.58	20.15	1	1
PLACE1012026	22.39	20.44	21.38	1	1
PLACE1012031	29.21	36.05	24.28	1	1
PLACE2000003	171.38	188.33	175.86	1.1	1.03
PLACE2000005	17.08	13.58	14.3	1	1
PLACE2000006	215.06	220.3	169.37	1.02	0.79
PLACE2000007	32.91	35.43	30.39	1	1
PLACE2000011	77.03	82.84	64.01	1.08	0.83
PLACE2000014	635.17	607.14	482.26	0.96	0.76
PLACE2000015	37.29	41.56	31.59	1.04	1
PLACE2000017	14.69	19.74	13.51	1	1
PLACE2000021	44.21	63.31	49.29	1.43	1.11

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PLACE2000022	46.15	49.28	51.9	1.07	1.12
PLACE2000030	1694.2	2013.81	1419.12	1.19	0.84
PLACE2000032	60.37	68.14	58.24	1.13	0.96
PLACE2000033	110.17	111.61	98.7	1.01	0.9
PLACE2000034	57.78	58.66	54.29	1.02	0.94
PLACE2000039	120.07	145.25	131.21	1.21	1.09
PLACE2000043	346.07	354.6	252.31	1.02	0.73
PLACE2000044	23.97	29.58	29.62	1	1
PLACE2000047	102.56	112.06	113.24	1.09	1.1
PLACE2000050	71.89	90.85	58.04	1.26	0.81
PLACE2000061	17.86	20.56	15.09	1	1
PLACE2000062	66.1	72.31	49.98	1.09	0.76
PLACE2000072	17.99	18.55	16.31	1	1
PLACE2000073	15.95	15.72	13.57	1	1
PLACE2000097	213.87	252.44	257.53	1.18	1.2
PLACE2000100	78.87	88.68	57.86	1.12	0.73
PLACE2000103	54.73	54.47	56.01	1	1.02
PLACE2000106	135.55	158.65	131.58	1.17	0.97
PLACE2000111	87.67	97.31	56.96	1.11	0.65
PLACE2000115	17.7	16.8	12.26	1	1
PLACE2000118	108.86	115.04	163.24	1.06	1.5
PLACE2000124	816.3	718.85	492.7	0.88	0.6
PLACE2000132	13.87	16.39	13.31	1	1
PLACE2000136	13.17	14.88	13.46	1	1
PLACE2000137	22.14	19.06	19.32	1	1
PLACE2000140	98.61	148.4	126.8	1.5	1.29
PLACE2000147	21.9	25.66	17.02	1	1
PLACE2000153	14.7	11.12	14.66	1	1
PLACE2000164	20.49	18.37	20.21	1	1
PLACE2000170	125.31	145.03	117.3	1.16	0.94
PLACE2000172	17.54	16.31	16.59	1	1
PLACE2000173	70.78	80.23	58.69	1.13	0.83
PLACE2000174	57.95	64.79	58.03	1.12	1
PLACE2000176	43.43	41.92	40.16	0.97	0.92
PLACE2000187	60.61	54.14	36.42	0.89	0.66
PLACE2000216	59.22	72.23	56.49	1.22	0.95
PLACE2000219	39.68	48.98	40.11	1.22	1
PLACE2000221	135.95	164.16	158.94	1.21	1.17
PLACE2000223	5.6	6.49	3.36	1	1
PLACE2000231	33.93	38.68	26.47	1	1
PLACE2000235	98.28	112.79	92.76	1.15	0.94
PLACE2000246	94.02	98.46	83.22	1.05	0.89
PLACE2000264	79.88	92.69	64.8	1.16	0.81
PLACE2000274	35.59	37.8	39.08	1	1
PLACE2000287	20.39	20.25	23.46	1	1
PLACE2000296	18.03	15.38	14.93	1	1

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PLACE2000302	45.55	58.9	46:59	1.29	1.02
PLACE2000305	155.84	169.39	135.63	1.09	0.87
PLACE2000317	32.82	20.28	20.47	1	1
PLACE2000324	41.35	38.7	36.15	0.97	0.97
PLACE2000334	183.82	175.14	175.68	0.95	0.96
PLACE2000335	136	196.92	135.48	1.45	1
PLACE2000340	16.11	18.58	11.97	1	1
PLACE2000341	210.96	277.16	209.16	1.31	0.99
PLACE2000342	166.99	114.91	107.63	0.69	0.64
PLACE2000347	154.45	189.66	153.52	1.23	0.99
PLACE2000357	79.73	96.17	102.29	1.21	1.28
PLACE2000358	256.57	305.62	211.22	1.19	0.82
PLACE2000359	3.81	4.5	1.37	1	1
PLACE2000366	99.02	132.98	84.55	1.34	0.85
PLACE2000371	68.55	85.66	71.92	1.25	1.05
PLACE2000373	43.55	47.22	46.75	1.08	1.07
PLACE2000374	23.53	32.86	28.16	1	1
PLACE2000379	16.39	17.7	16.49	1	1
PLACE2000386	1286.2	1518.95	1572.54	1.18	1.22
PLACE2000388	50.87	49.22	36.25	0.97	0.79
PLACE2000392	319.51	348.31	353.39	1.09	1.11
PLACE2000394	71.84	67.92	78.67	0.95	1.1
PLACE2000398	30.22	38.93	35.07	1	1
PLACE2000399	42.9	34.91	50.88	0.93	1.19
PLACE2000402	32.87	31.76	32.88	1	1
PLACE2000404	58.57	67.45	73.86	1.15	1.26
PLACE2000411	52.82	83.73	115.98	1.59	2.2
PLACE2000418	50.46	65.86	56.08	1.31	1.11
PLACE2000419	102.69	137.4	124.2	1.34	1.21
PLACE2000425	37.31	40.72	33.56	1.02	1
PLACE2000427	21.66	25.88	27.14	1	1
PLACE2000433	50.87	47.44	43.55	0.93	0.86
PLACE2000435	21.67	16.61	17.84	1	1
PLACE2000438	19.41	25.68	29.91	1	1
PLACE2000450	81.66	92.34	97.83	1.13	1.2
PLACE2000455	18.01	22.78	20.07	1	1
PLACE2000458	55.64	68.4	59.18	1.23	1.06
PLACE2000464	29.94	27.76	24.02	1	1
PLACE2000465	213.81	251.88	207.06	1.18	0.97
PLACE2000473	836.58	983.57	806.98	1.18	0.96
PLACE2000477	16.45	29.51	16.05	1	1
PLACE3000004	87.82	83.69	80.62	0.95	0.92
PLACE3000009	1606.2	1262.54	1148.63	0.79	0.72
PLACE3000020	760.66	812.44	697.12	1.07	0.92
PLACE3000029	217.19	259.74	201.46	1.2	0.93
PLACE3000038	41.85	54.63	40.3	1.31	0.96

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PLACE3000052	367.89	489.29	371.66	1.33	1.01
PLACE3000059	24.83	27.37	23.53	1	1
PLACE3000067	59.74	70.09	61.55	1.17	1.03
PLACE3000069	93.54	91.2	73.59	0.97	0.79
PLACE3000070	185.28	188.38	229.21	1.02	1.24
PLACE3000103	65.17	61.33	54.93	0.94	0.84
PLACE3000119	3.61	113.76	2.84	2.84	1
PLACE3000121	1345.4	1349.82	1036.69	1	0.77
PLACE3000124	97.43	115.22	90.24	1.18	0.93
PLACE3000135	11.35	10.57	7.29	1	1
PLACE3000136	28.24	30.03	24.93	1	1
PLACE3000142	21.84	22.96	23.32	1	1
PLACE3000145	738.49	611.83	451.51	0.83	0.61
PLACE3000147	176.32	164.52	132.27	0.93	0.75
PLACE3000148	4.21	2.12	1.47	1	1
PLACE3000154	35.29	60.89	56.38	1.52	1.41
PLACE3000155	66.71	65.47	53.88	0.98	0.81
PLACE3000156	18.22	36.57	17.58	1	1
PLACE3000157	26.5	33.22	27.53	1	1
PLACE3000158	115.37	133.81	102.19	1.16	0.89
PLACE3000160	136.75	99.83	114.37	0.73	0.84
PLACE3000169	165.8	195.53	168.21	1.18	1.01
PLACE3000181	127.79	141.83	120.13	1.11	0.94
PLACE3000194	49.19	48.32	44.38	0.98	0.9
PLACE3000197	12.91	14.38	16.78	1	1
PLACE3000199	14.71	10.56	10.36	1	1
PLACE3000205	868.43	1057.62	753.31	1.22	0.87
PLACE3000207	216.92	252.67	191.1	1.16	0.88
PLACE3000208	54.89	54.23	48.79	0.99	0.89
PLACE3000213	33.26	40.23	30.49	1.01	1
PLACE3000215	21.84	17.5	13.39	1	1
PLACE3000218	13.41	11.66	9.09	1	1
PLACE3000220	114.32	105.77	107.52	0.93	0.94
PLACE3000221	437.38	475.47	358.38	1.09	0.82
PLACE3000225	48.79	61.71	52.94	1.26	1.09
PLACE3000226	89.7	98.83	76.04	1.1	0.85
PLACE3000230	26.28	30.38	53.41	1	1.34
PLACE3000231	34.3	53.63	46.02	1.34	1.15
PLACE3000235	105.91	116.52	94.01	1.1	0.89
PLACE3000242	62.07	67.67	62.09	1.09	1
PLACE3000244	26.87	27.09	18.22	1	1
PLACE3000253	20.69	18.14	18.91	1	1
PLACE3000254	59.24	71.24	61.14	1.2	1.03
PLACE3000271	210.99	227.81	179.99	1.08	0.85
PLACE3000276	22.03	19.83	15.86	1	1
PLACE3000304	283.54	350.52	301.89	1.24	1.06

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PLACE3000309	48.91	70.41	44.97	1.44	0.92
PLACE3000310	42.78	41.15	34.91	0.96	0.94
PLACE3000320	49.02	51.22	40.77	1.04	0.83
PLACE3000322	3.16	0.57	1.79	1	1
PLACE3000330	221.71	298.07	276.82	1.34	1.25
PLACE3000331	138.49	160.45	123.87	1.16	0.89
PLACE3000336	37.63	52.57	39.67	1.31	1
PLACE3000339	104.65	114.64	90.45	1.1	0.86
PLACE3000341	114.82	141.48	110.97	1.23	0.97
PLACE3000350	160.43	173.42	121.49	1.08	0.76
PLACE3000352	47.6	57.89	40.6	1.22	0.85
PLACE3000353	61.18	67.39	56.69	1.1	0.93
PLACE3000362	76	90.79	76.16	1.19	1
PLACE3000363	16.4	27.93	15.48	1	1
PLACE3000365	27.86	33.26	31.95	1	1
PLACE3000373	21.61	21.8	22.19	1	1
PLACE3000374	31.32	41.25	22.3	1.03	1
PLACE3000387	8.25	9.82	6.88	1	1
PLACE3000388	64.69	77.9	44.31	1.2	0.68
PLACE3000399	112.65	133.33	109.36	1.18	0.97
PLACE3000400	44.55	49.98	41.2	1.12	0.92
PLACE3000401	490.44	600.16	510.14	1.22	1.04
PLACE3000402	32.95	41.75	27.52	1.04	1
PLACE3000405	53.52	61.97	62.72	1.16	1.17
PLACE3000406	35.93	38.71	42.23	1	1.06
PLACE3000413	18.05	16.88	18	1	1
PLACE3000416	29.64	28.6	31.16	1	1
PLACE3000425	50.28	54.42	57.61	1.08	1.15
PLACE3000437	204.43	214.99	215.82	1.05	1.06
PLACE3000455	70.16	96.18	109.86	1.37	1.57
PLACE3000475	146.58	174.44	167.87	1.19	1.15
PLACE3000477	71.98	48.83	46.22	0.68	0.64
PLACE4000003	23.25	25.51	19.95	1	1
PLACE4000008	70.24	63.65	74.26	0.91	1.06
PLACE4000009	43.12	37.54	47.82	0.93	1.11
PLACE4000014	21.64	19.96	21.69	1	1
PLACE4000029	445.92	441.3	386.76	0.99	0.87
PLACE4000034	90.28	104.98	136.62	1.16	1.51
PLACE4000049	80.02	77.88	91.08	0.97	1.14
PLACE4000052	28.33	17.89	22.57	1	1
PLACE4000062	33.61	37.15	30.93	1	1
PLACE4000063	43.96	48.75	45.39	1.11	1.03
PLACE4000089	59.97	63.79	58.77	1.06	0.98
PLACE4000093	19.92	15.59	24.78	1	1
PLACE4000100	59.02	65.05	68.87	1.1	1.17
PLACE4000103	23.19	22.13	16.6	1	1

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PLACE4000106	42.56	54.08	43.9	1.27	1.03
PLACE4000128	67.58	75.38	71.3	1.12	1.06
PLACE4000129	29.93	24.81	23.87	1	1
PLACE4000131	782.86	711.57	587.61	0.91	0.75
PLACE4000147	14.59	9.44	6.98	1	1
PLACE4000156	163.18	267.14	159.69	1.64	0.98
PLACE4000175	14.89	13.1	10.66	1	1
PLACE4000190	628.33	504.54	459.39	0.8	0.73
PLACE4000192	28.59	35.85	25.67	1	1
PLACE4000206	77.21	57.16	80.21	0.74	1.04
PLACE4000211	79.65	101.47	63.07	1.27	0.79
PLACE4000214	26	17.61	16.37	1	1
PLACE4000222	84.71	90.07	69.78	1.06	0.82
PLACE4000223	22.62	14.09	14.21	1	1
PLACE4000229	33.82	41.71	44.09	1.04	1.1
PLACE4000230	85.95	57.35	62.17	0.67	0.72
PLACE4000233	73.47	68.6	63.73	0.93	0.87
PLACE4000239	100.72	94.05	95.4	0.93	0.95
PLACE4000247	34.55	28.2	23.03	1	1
PLACE4000250	51.35	59.3	45.61	1.15	0.89
PLACE4000252	20.75	19.51	18.21	1	1
PLACE4000259	250.69	228.39	179.09	0.91	0.71
PLACE4000261	21.5	12.14	17.49	1	1
PLACE4000264	38.97	41.66	55.02	1.04	1.38
PLACE4000269	47.1	37.8	32.16	0.85	0.85
PLACE4000270	24.24	29.97	22.47	1	1
PLACE4000281	211.22	274.25	267.89	1.3	1.27
PLACE4000300	24.03	26.73	16.79	1	1
PLACE4000320	47.61	52.92	41.99	1.11	0.88
PLACE4000323	70.64	77.63	73.66	1.1	1.04
PLACE4000326	17.15	19.53	21.91	1	1
PLACE4000344	20.15	17.55	19.07	1	1
PLACE4000347	42.11	35.66	37.07	0.95	0.95
PLACE4000354	20.54	16.97	13.97	1	1
PLACE4000367	19.08	21.62	13.54	1	1
PLACE4000369	18.56	16.86	16.32	1	1
PLACE4000379	44.93	48.22	35.27	1.07	0.89
PLACE4000387	28.48	18.41	23.23	1	1
PLACE4000392	18.72	23.43	16.99	1	1
PLACE4000399	417.14	435.88	349.26	1.04	0.84
PLACE4000401	13.12	19.41	12.77	1	1
PLACE4000403	72.03	64.17	68.86	0.89	0.96
PLACE4000411	59.36	51.92	41.47	0.87	0.7
PLACE4000415	23.89	20.82	25.63	1	1
PLACE4000416	174.35	147.12	179.04	0.84	1.03
PLACE4000424	19.71	16.25	17.79	1	1

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PLACE4000431	263.83	293	219.65	1.11	0.83
PLACE4000443	20.1	8.3	13.07	1	1
PLACE4000445	71.62	72.15	70.79	1.01	0.99
PLACE4000450	147.23	126.29	117.48	0.86	0.8
PLACE4000455	62.39	48.46	44.08	0.78	0.71
PLACE4000465	135.53	132.4	107.77	0.98	0.8
PLACE4000466	1046.6	1140.39	799.29	1.09	0.76
PLACE4000472	121.8	126.78	113.94	1.04	0.94
PLACE4000487	264.78	281.84	202.36	1.06	0.76
PLACE4000489	48.45	36.77	38.35	0.83	0.83
PLACE4000494	23.84	20.8	21.4	1	1
PLACE4000502	88.64	86.75	81.9	0.98	0.92
PLACE4000521	323.04	404.56	285.14	1.25	0.88
PLACE4000522	30.08	33.41	25.49	1	1
PLACE4000537	29.74	23.24	26.85	1	1
PLACE4000548	42.55	40.31	87.2	0.95	2.05
PLACE4000558	23.58	23.82	17.37	1	1
PLACE4000581	61.42	69.56	63.92	1.13	1.04
PLACE4000590	8.23	5	6.05	1	1
PLACE4000593	18.6	17.3	14.81	1	1
PLACE4000612	41.95	53.37	32.82	1.27	0.95
PLACE4000638	26.8	37.75	22.79	1	1
PLACE4000650	27.3	16.4	33.1	1	1
PLACE4000651	36.82	39.3	38.22	1	1
PLACE4000654	16.89	15.19	15.24	1	1
PLACE4000670	16.92	13.19	15.71	1	1
PLACE4000685	187.86	211.77	202.76	1.13	1.08
PLACE4000687	16.21	22.59	13.56	1	1
PLACE5000003	21.87	28.54	21.39	1	1
PLACE5000005	110.24	120.37	147.87	1.09	1.34
PLACE5000019	13.52	8.92	10.26	1	1
PLACE5000021	13.23	15.67	10.24	1	1
PLACE5000022	19.05	19.6	21.59	1	1
PLACE5000024	34.25	21.2	21.25	1	1
PLACE5000036	40.53	31.28	35.69	0.99	0.99
PLACE5000059	352.37	319.61	357.62	0.91	1.01
PLACE5000076	47.21	58.74	32.77	1.24	0.85
PLACE5000117	84.84	102.57	87.82	1.21	1.04
PLACE5000143	23.5	22.78	23.28	1	1
PLACE5000152	15.35	12.76	11.52	1	1
PLACE5000154	144.51	199.46	237.34	1.38	1.64
PLACE5000155	89.36	81.41	79.91	0.91	0.89
PLACE5000165	78.93	76.87	88.02	0.97	1.12
SKNMC1000004	101.25	99.46	95.02	0.98	0.94
SKNMC1000011	46.1	44.65	56.16	0.97	1.22
SKNMC1000013	16.47	25.9	14.18	1	1

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SKNMC1000014	92.84	113.71	75.96	1.22	0.82
SKNMC1000018	54.44	47.21	45.13	0.87	0.83
SKNMC1000020	21.7	28.63	29.3	1	1
SKNMC1000046	26.3	28.76	16.18	1	1
SKNMC1000050	62.13	60.84	53.16	0.98	0.86
SKNMC1000062	330.04	282.45	310.59	0.86	0.94
SKNMC1000075	17.55	17.79	15.1	1	1
SKNMC1000082	22.09	43.54	26.48	1.09	1
SKNMC1000091	55.45	72.12	67.23	1.3	1.21
SKNMC1000099	15.48	12.31	17.8	1	1
SKNMC1000104	19.72	17.77	17.75	1	1
SKNMC1000113	25.72	23.37	13.13	1	1
SKNMC1000119	31.7	33.07	28.84	1	1
SKNMC1000142	13.17	9.46	8.15	1	1
SKNMC1000170	18.9	35.22	13.42	1	1
SKNMC1000178	36.62	37.44	34.52	1	1
SKNMC1000194	30.86	16.71	25.89	1	1
SKNMC1000198	34.11	45.61	47.99	1.14	1.2
SKNMC1000225	26.81	26.95	26.7	1	1
SKNMC1000249	8.56	7.08	5.55	1	1
SPLEN1000007	23.41	31.55	22.1	1	1
SPLEN1000012	12.79	13.7	8.13	1	1
SPLEN1000014	70.11	67.87	59.13	0.97	0.84
SPLEN1000036	594.83	558.47	477.44	0.94	0.8
SPLEN1000059	18.59	12.25	11.97	1	1
SPLEN1000068	70.13	64.3	54.94	0.92	0.78
SPLEN1000072	32.05	40.98	29.41	1.02	1
SPLEN1000101	192.61	203.71	206.97	1.06	1.07
SPLEN1000108	11.49	13.35	11.51	1	1
SPLEN1000113	34.46	41.39	30.71	1.03	1
SPLEN1000114	45.22	48.21	35.95	1.07	0.88
SPLEN1000132	34.95	36.95	42.28	1	1.06
SPLEN1000135	343.33	311.82	277.27	0.91	0.81
SPLEN1000136	66.82	82.96	80.88	1.24	1.21
SPLEN1000141	76.01	69.18	98.16	0.91	1.29
SPLEN1000164	30.6	24.91	22.66	1	1
SPLEN1000166	23.21	20.04	14.17	1	1
SPLEN1000175	139.17	239.48	209	1.72	1.5
SPLEN1000182	14.94	11.84	11.7	1	1
SPLEN1000185	55.33	55.69	40.97	1.01	0.74
THYMU1000004	71.72	74.9	83.41	1.04	1.16
THYMU1000009	94.13	77.8	90.28	0.83	0.96
THYMU1000015	228.36	266.58	260.48	1.17	1.14
THYMU1000016	85.88	95.7	65.55	1.11	0.76
THYMU1000023	20.69	15.9	18.99	1	1
THYMU1000034	24.06	21.75	16.17	1	1

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THYMU1000035	16.7	12.77	9.02	1	1
THYMU1000037	19.37	14.84	13.58	1	1
THYMU1000042	79.95	82.87	68.39	1.04	0.86
THYMU1000047	89.91	103.09	89.83	1.15	1
THYMU1000080	40.1	18.75	23.34	1	1
THYMU1000094	100.33	88.03	83.95	0.88	0.84
THYMU1000109	3394.6	3204.08	2476.84	0.94	0.73
THYMU1000127	149.43	302.07	224.65	2.02	1.5
THYMU1000130	50.99	54.49	39.21	1.07	0.78
THYMU1000137	89.89	98.22	85.61	1.09	0.95
THYMU1000146	41.95	48.71	54.46	1.16	1.3
THYMU1000159	75.18	54.17	55.6	0.72	0.74
THYMU1000163	1438.2	1056.73	808.48	0.73	0.56
THYMU1000167	37.01	32.25	20.73	1	1
THYMU1000186	41.69	49.31	32.2	1.18	0.96
THYRO1000017	64.39	60.8	44.03	0.94	0.68
THYRO1000026	34.47	79.34	36.05	1.98	1
THYRO1000034	27.76	31.8	20.76	1	1
THYRO1000035	35.4	40.29	62.06	1.01	1.55
THYRO1000036	23.43	26.13	14.41	1	1
THYRO1000040	29.81	42.36	39.84	1.06	1
THYRO1000061	37.9	51.34	31.21	1.28	1
THYRO1000067	72.96	86.57	57.57	1.19	0.79
THYRO1000070	21.53	26.8	23.38	1	1
THYRO1000072	36.97	46.63	32.18	1.17	1
THYRO1000084	44.96	56.29	56.67	1.25	1.26
THYRO1000085	49.35	66.17	67.44	1.34	1.37
THYRO1000086	11.1	15.74	10.31	1	1
THYRO1000087	8.58	16.78	5.64	1	1
THYRO1000092	52.96	62.53	59.75	1.18	1.13
THYRO1000093	8.63	7.64	6.15	1	1
THYRO1000099	37.27	32.4	28.52	1	1
THYRO1000107	24.41	21.8	26.8	1	1
THYRO1000111	21.9	17.22	25.47	1	1
THYRO1000121	20.79	17.72	18.35	1	1
THYRO1000124	8.23	6.71	9.71	1	1
THYRO1000129	6.81	8.74	7.68	1	1
THYRO1000130	37.8	41.72	38.31	1.04	1
THYRO1000132	98.28	111.98	107.16	1.14	1.09
THYRO1000134	27.46	37.47	27.29	1	1
THYRO1000144	28.27	22.09	27.89	1	1
THYRO1000155	12.36	10.14	12.44	1	1
THYRO1000156	51.42	49.18	46.2	0.96	0.9
THYRO1000163	65.44	73.1	64.89	1.12	0.99
THYRO1000173	15.15	16	17.87	1	1
THYRO1000186	210.15	248.49	187.91	1.18	0.89

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THYR01000187	77.72	82.92	67.1	1.07	0.86
THYR01000190	75.91	65.3	68.76	0.86	0.91
THYR01000196	10.19	6.64	5.51	1	1
THYR01000197	74.14	96.54	82.33	1.3	1.11
THYR01000199	18.64	18.82	15.04	1	1
THYR01000206	29.32	53.8	59.34	1.35	1.48
THYR01000221	53.54	70.47	61.06	1.32	1.14
THYR01000222	38.81	43.06	43.08	1.08	1.08
THYR01000228	45.93	36.69	32.8	0.87	0.87
THYR01000241	97.96	115.66	91.36	1.18	0.93
THYR01000242	39.55	36.22	38.32	1	1
THYR01000246	34.94	38.43	32.03	1	1
THYR01000253	62.15	52.77	55.94	0.85	0.9
THYR01000270	25.94	22.66	21.26	1	1
THYR01000279	10.27	4.06	5.62	1	1
THYR01000285	91.85	96.96	103.11	1.06	1.12
THYR01000288	44.89	35.11	51.9	0.89	1.16
THYR01000296	51.1	53.97	49.14	1.06	0.96
THYR01000320	52.48	54.06	54.2	1.03	1.03
THYR01000322	33.96	29.37	30.02	1	1
THYR01000327	29.34	27.31	29.2	1	1
THYR01000343	27.82	34.09	28.73	1	1
THYR01000345	55.7	46.72	51.21	0.84	0.92
THYR01000358	9.41	7.7	6.57	1	1
THYR01000368	19.77	17.83	17.93	1	1
THYR01000375	67.03	68.23	60.2	1.02	0.9
THYR01000381	15.46	15.89	24.65	1	1
THYR01000387	36.11	33.07	29.39	1	1
THYR01000394	57.36	48.17	50.67	0.84	0.88
THYR01000395	28.97	30.24	27.58	1	1
THYR01000400	17.65	26.72	35.19	1	1
THYR01000401	24.4	25.58	18.17	1	1
THYR01000407	16.4	16.1	17.58	1	1
THYR01000420	46.85	54.92	41.53	1.17	0.89
THYR01000438	50.01	46.6	46.81	0.93	0.94
THYR01000452	42.1	54.28	49.65	1.29	1.18
THYR01000455	8.03	4.68	3.86	1	1
THYR01000471	40.24	41.92	30.96	1.04	0.99
THYR01000481	30.3	21.61	26.84	1	1
THYR01000484	61.87	67.03	50.17	1.08	0.81
THYR01000488	20.11	25.07	21.14	1	1
THYR01000501	22.62	16.34	20.31	1	1
THYR01000502	16.19	23.43	22.05	1	1
THYR01000505	13.77	12.09	10.63	1	1
THYR01000535	225.34	256.48	247.53	1.14	1.1
THYR01000556	55.39	56.81	48.63	1.03	0.88

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THYRO1000558	23.81	19.28	21.37	1	1
THYRO1000569	74.05	68.57	73.64	0.93	0.99
THYRO1000570	41.62	41.36	28.83	0.99	0.96
THYRO1000572	21.39	7.23	11.72	1	1
THYRO1000573	19.98	17.86	16.98	1	1
THYRO1000577	14.92	4.37	7.74	1	1
THYRO1000580	35.2	44.75	27.1	1.12	1
THYRO1000584	51.21	39.64	46.27	0.78	0.9
THYRO1000585	22.9	30.19	25.55	1	1
THYRO1000596	13.06	12.04	12.16	1	1
THYRO1000602	221.44	258.24	175.93	1.17	0.79
THYRO1000605	22.69	14.45	17	1	1
THYRO1000615	20.64	20.24	22.7	1	1
THYRO1000625	55.48	53.13	39.91	0.96	0.72
THYRO1000636	67.42	74.2	69.95	1.1	1.04
THYRO1000637	28.99	27.15	20.45	1	1
THYRO1000641	27.36	20.13	13.73	1	1
THYRO1000657	25.52	29.79	32.29	1	1
THYRO1000658	144.83	157.65	111.64	1.09	0.77
THYRO1000662	39.96	34.34	26.55	1	1
THYRO1000666	35.48	38.48	23.93	1	1
THYRO1000676	55.83	49.12	51.23	0.88	0.92
THYRO1000678	17.96	23.23	20.9	1	1
THYRO1000684	19.12	21.46	17.53	1	1
THYRO1000694	27.86	22.19	23.82	1	1
THYRO1000699	89.92	90.86	76.51	1.01	0.85
THYRO1000712	184.29	270.08	170.04	1.47	0.92
THYRO1000715	143.06	353.21	194.25	2.47	1.36
THYRO1000716	33.56	44.54	28.99	1.11	1
THYRO1000717	77.22	110.47	65.42	1.43	0.85
THYRO1000723	11.31	19.35	9.86	1	1
THYRO1000734	23.48	18.16	13.64	1	1
THYRO1000748	16.72	20.76	14.58	1	1
THYRO1000755	58.84	52.18	63.38	0.89	1.08
THYRO1000756	33.49	31	34.07	1	1
THYRO1000776	50.16	42.39	50.04	0.85	1
THYRO1000777	23.87	35.27	19.82	1	1
THYRO1000779	6.32	4.93	6.1	1	1
THYRO1000782	117.27	125.31	142.84	1.07	1.22
THYRO1000783	12.02	9.07	10.19	1	1
THYRO1000786	55.04	58.8	55.91	1.07	1.02
THYRO1000787	19.96	12.46	13.7	1	1
THYRO1000792	38.21	33.39	36.86	1	1
THYRO1000793	17.33	13.84	12.2	1	1
THYRO1000795	28.83	24.46	21.51	1	1
THYRO1000796	42.19	47.03	31.27	1.11	0.95

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THYRO1000798	21.24	23.63	18.2	1	1
THYRO1000800	117.04	315.89	252.61	2.7	2.16
THYRO1000805	16.57	11.21	16.09	1	1
THYRO1000815	65.07	58.64	52.6	0.9	0.81
THYRO1000829	58.28	53.39	49.78	0.92	0.85
THYRO1000835	27.36	30.54	24.1	1	1
THYRO1000843	62.82	52.11	57.79	0.83	0.92
THYRO1000846	26.19	21.19	19.35	1	1
THYRO1000852	31.05	29.41	35.84	1	1
THYRO1000855	75.51	92.14	58.07	1.22	0.77
THYRO1000865	102.88	116.21	119.95	1.13	1.17
THYRO1000866	45.28	32.65	45.38	0.88	1
THYRO1000881	89.25	87.76	93.28	0.98	1.05
THYRO1000894	19.5	18.71	15.61	1	1
THYRO1000895	24.84	14.82	13.39	1	1
THYRO1000916	86.36	104.38	80.99	1.21	0.94
THYRO1000917	1332.1	1907.82	1793.1	1.43	1.35
THYRO1000926	21.25	19.37	21.25	1	1
THYRO1000934	13.71	17.06	13.29	1	1
THYRO1000951	18.61	27.82	26.82	1	1
THYRO1000952	28.39	29.36	28.1	1	1
THYRO1000956	15.25	6.93	8.82	1	1
THYRO1000960	12.17	13.58	16.76	1	1
THYRO1000961	37.05	31.39	30.86	1	1
THYRO1000964	13.96	17.88	15.56	1	1
THYRO1000971	22.43	35.29	29.46	1	1
THYRO1000974	81.82	86.36	97.53	1.06	1.19
THYRO1000975	77.2	76.65	60.02	0.99	0.78
THYRO1000983	57.05	64.85	57.92	1.14	1.02
THYRO1000984	51.78	47.85	48	0.92	0.93
THYRO1000988	57.88	51.98	58.3	0.9	1.01
THYRO1000991	14.79	9	10.42	1	1
THYRO1000999	30.62	26.66	22.67	1	1
THYRO1001003	51.62	45.23	52.45	0.88	1.02
THYRO1001015	19.88	10.58	15.95	1	1
THYRO1001016	67.86	67.9	60.96	1	0.9
THYRO1001022	19.18	19.19	16	1	1
THYRO1001031	157.9	113.8	73.39	0.72	0.46
THYRO1001033	20.62	16.08	14.67	1	1
THYRO1001062	38.12	38.16	24.23	1	1
THYRO1001063	41.75	35.16	36.06	0.96	0.96
THYRO1001071	7.28	6.77	9.2	1	1
THYRO1001080	43.21	35.05	40.67	0.93	0.94
THYRO1001093	71.48	81.87	63.33	1.15	0.89
THYRO1001100	20.18	16.25	13.76	1	1
THYRO1001102	36.88	35.13	38.38	1	1

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THYR01001104	49.54	71.39	81.87	1.44	1.65
THYR01001109	26.9	24.31	17.57	1	1
THYR01001113	124.88	144.83	163.96	1.16	1.31
THYR01001120	31.33	42.01	28.69	1.05	1
THYR01001121	28.39	26.15	21.16	1	1
THYR01001128	56.44	105.01	71.13	1.86	1.26
THYR01001133	129.29	141.09	109.23	1.09	0.84
THYR01001134	6.12	48.8	3.2	1.22	1
THYR01001142	13.49	9.24	6.46	1	1
THYR01001173	69.76	76.75	76.64	1.1	1.1
THYR01001175	18.21	19.94	20.86	1	1
THYR01001177	136.34	154.56	107.81	1.13	0.79
THYR01001189	76.97	101.83	89.67	1.32	1.16
THYR01001194	105.93	107.92	103.06	1.02	0.97
THYR01001204	63.61	57.71	51.46	0.91	0.81
THYR01001205	351.28	452.06	359.35	1.29	1.02
THYR01001213	77.39	103.68	84.02	1.34	1.09
THYR01001224	136.69	152.12	149.46	1.11	1.09
THYR01001237	40.47	50.92	42.87	1.26	1.06
THYR01001242	115.84	153.83	147.74	1.33	1.28
THYR01001258	40.94	31.04	30.95	0.98	0.98
THYR01001262	26.89	27.89	19.46	1	1
THYR01001266	24.21	23.01	18.49	1	1
THYR01001271	33.6	39.06	47.64	1	1.19
THYR01001287	618.09	675.7	490.75	1.09	0.79
THYR01001290	8.16	5.43	5.68	1	1
THYR01001291	59.43	91.42	60.21	1.54	1.01
THYR01001297	36.39	49.57	53.18	1.24	1.33
THYR01001302	16.1	15.52	13.89	1	1
THYR01001313	12.16	11.5	7.09	1	1
THYR01001320	67.67	100.5	55.72	1.49	0.82
THYR01001321	47.21	52.86	37.77	1.12	0.85
THYR01001322	24.97	27.56	20.65	1	1
THYR01001327	22.74	18.51	20.74	1	1
THYR01001336	67.89	117.68	67.41	1.73	0.99
THYR01001347	30.07	15.91	22.89	1	1
THYR01001358	33.4	31.77	32.94	1	1
THYR01001363	29.1	29.57	27.89	1	1
THYR01001365	22.72	20.54	17.71	1	1
THYR01001374	55.89	36.19	39.41	0.72	0.72
THYR01001401	67.18	66.1	79.9	0.98	1.19
THYR01001403	36.96	35.79	36.33	1	1
THYR01001405	60.25	66.49	51.3	1.1	0.85
THYR01001406	99.99	118.14	125.66	1.18	1.26
THYR01001411	162.66	177.91	174.09	1.09	1.07
THYR01001420	281.42	206.35	163.61	0.73	0.58

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THYR01001426	295.65	347.22	278.53	1.17	0.94
THYR01001430	66.13	74.19	77.05	1.12	1.17
THYR01001434	32.32	68.71	43.27	1.72	1.08
THYR01001456	36.49	32.57	41.27	1	1.03
THYR01001457	45.96	55.07	45.99	1.2	1
THYR01001458	37.02	45.23	50.19	1.13	1.25
THYR01001459	169.67	160.28	164.66	0.94	0.97
THYR01001471	33.1	25.58	22.4	1	1
THYR01001478	23.72	21.89	21.41	1	1
THYR01001480	332.7	411.76	349.43	1.24	1.05
THYR01001481	120.8	159.14	137.5	1.32	1.14
THYR01001487	120.62	158.11	135.86	1.31	1.13
THYR01001495	82.69	84.53	88.63	1.02	1.07
THYR01001498	24.31	46.88	45.76	1.17	1.14
THYR01001510	26.13	19.03	19.35	1	1
THYR01001512	1869.6	2049.81	1317.06	1.1	0.7
THYR01001519	79.4	79.3	75.14	1	0.95
THYR01001522	89.46	101.52	59.9	1.13	0.67
THYR01001523	71.35	72.38	74.09	1.01	1.04
THYR01001526	240.13	365.08	318.05	1.52	1.32
THYR01001529	90.07	80.02	57.67	0.89	0.64
THYR01001534	50.65	49.31	81.97	0.97	1.62
THYR01001537	166.69	165.39	144.11	0.99	0.86
THYR01001541	177.91	167.08	139.4	0.94	0.78
THYR01001545	51.89	36.64	42.95	0.77	0.83
THYR01001559	145.05	146.22	132.42	1.01	0.91
THYR01001563	183.92	184.36	182.85	1	0.99
THYR01001570	30.95	31.51	31.27	1	1
THYR01001573	65.95	39.85	42.27	0.61	0.64
THYR01001584	47.65	49.27	53.94	1.03	1.13
THYR01001593	82.04	72.74	68.9	0.89	0.84
THYR01001595	103.98	110.51	102.49	1.06	0.99
THYR01001596	58.19	51.42	63.84	0.88	1.1
THYR01001602	87.72	85.88	72.86	0.98	0.83
THYR01001605	42.84	41.69	43.2	0.97	1.01
THYR01001608	121.51	57.35	96.56	0.47	0.79
THYR01001617	117.84	136.24	110.76	1.16	0.94
THYR01001634	47.62	45.6	45.24	0.96	0.95
THYR01001637	208.17	214.42	182.7	1.03	0.88
THYR01001641	27.43	33.65	36.4	1	1
THYR01001656	59.41	54.94	78.81	0.92	1.33
THYR01001658	164.89	276.29	264.03	1.68	1.6
THYR01001661	26.03	22.14	26.37	1	1
THYR01001671	40.07	38.84	37.89	1	1
THYR01001672	15.08	14.64	16.68	1	1
THYR01001673	142.06	146.64	96.74	1.03	0.68

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THYR01001677	67.29	78.89	67.23	1.17	1
THYR01001683	134.37	158.27	162.12	1.18	1.21
THYR01001700	20.47	19.37	14.84	1	1
THYR01001702	116	117.84	102.88	1.02	0.89
THYR01001703	48.06	45.1	43.24	0.94	0.9
THYR01001706	82.92	111.31	83.86	1.34	1.01
THYR01001721	34.49	36.81	37.64	1	1
THYR01001725	156.38	135.31	116.05	0.87	0.74
THYR01001730	439.5	509.26	459.36	1.16	1.05
THYR01001738	45.7	45.43	46.39	0.99	1.02
THYR01001743	28.14	23.08	20.97	1	1
THYR01001745	17.14	21.06	16.26	1	1
THYR01001746	31.83	30.99	31.95	1	1
THYR01001770	365.71	367.44	345.23	1	0.94
THYR01001772	123.83	151.39	150.86	1.22	1.22
THYR01001778	125.3	136.46	114.03	1.09	0.91
THYR01001793	118.26	92.44	95.51	0.78	0.81
THYR01001796	35.4	35.03	31.41	1	1
THYR01001800	138.35	110.54	85.07	0.8	0.61
THYR01001803	54.17	51.87	51.91	0.96	0.96
THYR01001809	68.41	58.62	37.24	0.86	0.58
THYR01001817	108.47	135.8	146.32	1.25	1.35
THYR01001819	52.11	82.26	80.67	1.58	1.55
THYR01001828	4332.9	3758.25	2993.64	0.87	0.69
THYR01001854	310.97	325.29	244.91	1.05	0.79
THYR01001895	50.43	53.8	41.92	1.07	0.83
THYR01001907	95.74	95.16	76.26	0.99	0.8
TRACH1000006	28.12	33.72	27.35	1	1
TRACH1000013	14.62	17.35	10.88	1	1
TRACH1000074	91.95	104.52	91.83	1.14	1
TRACH1000095	24.29	25.7	21.89	1	1
TRACH1000102	89.04	112.46	84.84	1.26	0.95
TRACH1000108	18.93	22.62	9.17	1	1
TRACH1000126	56.02	51.95	46.03	0.93	0.82
TRACH1000146	55.68	61.38	44.09	1.1	0.79
TRACH1000160	6.99	1.98	2.87	1	1
TRACH1000184	135.47	176.97	305.52	1.31	2.26
VESEN1000004	30.77	39.29	26.61	1	1
VESEN1000007	47.71	47.56	40.32	1	0.85
VESEN1000013	92.2	108.84	158.66	1.18	1.72
VESEN1000028	152.94	139.07	153.59	0.91	1
VESEN1000059	47.54	41	36.63	0.86	0.84
VESEN1000100	43.33	51.75	59.44	1.19	1.37
VESEN1000107	36.45	39.21	41.9	1	1.05
VESEN1000117	36.31	35.07	40.25	1	1.01
VESEN1000122	47.58	33.92	57.09	0.84	1.2

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VESEN1000137	54.08	51.03	54.97	0.94	1.02
VESEN1000195	59.79	53.87	60.72	0.9	1.02
VESEN1000215	20.64	18.66	18.03	1	1
VESEN1000279	182.2	194.3	161.47	1.07	0.89
VESEN1000363	130.95	132.52	120.92	1.01	0.92
VESEN1000388	47.19	34.28	39.83	0.85	0.85
VESEN1000394	45.79	54.32	54.41	1.19	1.19
VESEN1000410	33.77	24.94	18.14	1	1
VESEN1000411	40.62	43.06	55.86	1.06	1.38
VESEN1000415	44.83	38.74	34.12	0.89	0.89
VESEN1000440	77.99	76.99	81.63	0.99	1.05
VESEN1000452	55.97	59.97	56.08	1.07	1
VESEN1000539	2520.3	1514.24	2475.51	0.6	0.98
VESEN1000554	23.28	20.08	20.19	1	1
VESEN1000557	65.42	99.26	91.48	1.52	1.4
VESEN1000575	33	42.85	36.23	1.07	1
VESEN1000585	33.26	35.72	48.21	1	1.21
VESEN1000592	14.7	10.84	12.9	1	1
VESEN1000658	53.11	50.87	53.69	0.96	1.01
VESEN1000669	156.32	171.85	194.32	1.1	1.24
VESEN1000743	30.01	26.82	23.72	1	1
VESEN1000752	616.05	621.22	670.66	1.01	1.09
VESEN1000761	102.22	128.97	144.62	1.26	1.41
VESEN2000039	76.51	106.05	108.81	1.39	1.42
VESEN2000102	27.9	33.4	39.37	1	1
VESEN2000164	75.95	85.45	57.77	1.13	0.76
VESEN2000175	16.91	16.81	13.67	1	1
VESEN2000186	47.71	41.92	47.45	0.88	0.99
VESEN2000199	210.67	251.42	274.58	1.19	1.3
VESEN2000200	31.77	34.78	30.5	1	1
VESEN2000204	42.87	27.57	46.4	0.93	1.08
VESEN2000218	233.2	310.25	266.85	1.33	1.14
VESEN2000230	51.87	57.61	55.03	1.11	1.06
VESEN2000272	66.18	71.44	47.62	1.08	0.72
VESEN2000299	33.39	36.15	34.44	1	1
VESEN2000323	122.34	153.67	120.03	1.26	0.98
VESEN2000327	25.64	38.53	30.18	1	1
VESEN2000328	287.92	426.6	459.49	1.48	1.6
VESEN2000330	210.17	635.42	400.1	3.02	1.9
VESEN2000336	19.26	21	30.8	1	1
VESEN2000354	29.98	44.87	45.25	1.12	1.13
VESEN2000378	214.41	200.95	233.25	0.94	1.09
VESEN2000379	637.63	734.74	663.65	1.15	1.04
VESEN2000397	33.94	34.23	25.21	1	1
VESEN2000416	33.88	35.1	24.86	1	1
VESEN2000420	13.29	9.98	11.98	1	1

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VESEN2000430	82.14	123.46	143.79	1.5	1.75
VESEN2000448	13.1	15.75	14.63	1	1
VESEN2000449	77.75	116.78	106.38	1.5	1.37
VESEN2000456	16.97	16.07	16.5	1	1
VESEN2000562	141.49	130.91	105.14	0.93	0.74
VESEN2000573	8.91	8.61	6.79	1	1
VESEN2000604	13.88	12.29	11.35	1	1
VESEN2000614	226.89	314.06	318.98	1.38	1.41
VESEN2000638	17.11	18.86	13.45	1	1
VESEN2000641	30.44	33.47	35.1	1	1
VESEN2000645	114.84	103.19	111.61	0.9	0.97
Y79AA1000013	23.65	28.36	17.86	1	1
Y79AA1000030	54.3	54.62	46.92	1.01	0.86
Y79AA1000033	111.64	118.12	102.03	1.06	0.91
Y79AA1000037	88.44	96.39	66.63	1.09	0.75
Y79AA1000041	30.18	31.51	34.51	1	1
Y79AA1000059	55.17	55.82	52.18	1.01	0.95
Y79AA1000065	270.08	316.25	285.13	1.17	1.06
Y79AA1000081	261.42	374.34	508.29	1.43	1.94
Y79AA1000127	107.56	107.37	68.62	1	0.64
Y79AA1000130	127.02	147.17	116.76	1.16	0.92
Y79AA1000131	6111.2	5656.63	5788.88	0.93	0.95
Y79AA1000134	52.82	69.93	53.91	1.32	1.02
Y79AA1000143	117.86	127.82	125.02	1.08	1.06
Y79AA1000144	74.35	76.59	74.72	1.03	1
Y79AA1000150	2545.9	2718.65	2054.54	1.07	0.81
Y79AA1000153	5666.0	5284.5	5846.98	0.93	1.03
Y79AA1000166	55.33	54.66	50.83	0.99	0.92
Y79AA1000179	91.15	94.27	64.88	1.03	0.71
Y79AA1000181	46.14	50.95	39.78	1.1	0.87
Y79AA1000202	588.9	770.83	565.25	1.31	0.96
Y79AA1000207	188.44	235.03	155.99	1.25	0.83
Y79AA1000214	266.68	298.79	319.39	1.12	1.2
Y79AA1000222	86.44	101.81	106.59	1.18	1.23
Y79AA1000226	82.03	161.73	169.02	1.97	2.06
Y79AA1000227	48.01	65.96	45.99	1.37	0.96
Y79AA1000230	31.14	25.61	22.03	1	1
Y79AA1000231	118.41	136.39	99.08	1.15	0.84
Y79AA1000239	151.15	168.81	146.2	1.12	0.97
Y79AA1000258	29.42	44.77	54.63	1.12	1.37
Y79AA1000268	43.67	51.54	45.57	1.18	1.04
Y79AA1000269	47.5	40.64	44.86	0.86	0.94
Y79AA1000270	130.55	110.71	113.31	0.85	0.87
Y79AA1000280	70.79	81.14	73.63	1.15	1.04
Y79AA1000285	29.49	30.14	27.66	1	1
Y79AA1000295	35.22	30.73	33.72	1	1

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Y79AA1000307	18.53	20.75	18	1	1
Y79AA1000313	49.32	51.4	49.22	1.04	1
Y79AA1000314	75.77	84.06	101.41	1.11	1.34
Y79AA1000328	29.85	29.66	36.26	1	1
Y79AA1000334	23.99	28.51	35.56	1	1
Y79AA1000342	327.09	366.24	329.71	1.12	1.01
Y79AA1000346	81.6	47.85	70.26	0.59	0.86
Y79AA1000347	133.77	102.63	126.89	0.77	0.95
Y79AA1000349	108.67	107.41	141.16	0.99	1.3
Y79AA1000355	162.38	124.35	158.8	0.77	0.98
Y79AA1000368	300.14	326.89	275.96	1.09	0.92
Y79AA1000388	264.81	244.65	255.31	0.92	0.96
Y79AA1000392	29.82	42.96	63.94	1.07	1.6
Y79AA1000405	76.52	90.11	72.49	1.18	0.95
Y79AA1000410	344.28	441.37	334.83	1.28	0.97
Y79AA1000420	51.5	55.34	53.93	1.07	1.05
Y79AA1000423	99.42	111.57	110.84	1.12	1.11
Y79AA1000426	48.92	57.41	47.33	1.17	0.97
Y79AA1000432	31.27	26.61	25.92	1	1
Y79AA1000453	79.54	259.3	206.07	3.26	2.59
Y79AA1000465	17.15	42	49.86	1.05	1.25
Y79AA1000469	168.58	190.42	171.96	1.13	1.02
Y79AA1000480	43.91	47.71	38.1	1.09	0.91
Y79AA1000502	92.82	78.1	86.82	0.84	0.94
Y79AA1000521	41.82	34.78	40.15	0.96	0.96
Y79AA1000534	82.06	125.38	113.59	1.53	1.38
Y79AA1000538	184.83	261.28	173.89	1.41	0.94
Y79AA1000539	354.26	344.61	222.22	0.97	0.63
Y79AA1000540	26.42	33.12	31.6	1	1
Y79AA1000560	1601.9	1282.77	1345.84	0.8	0.84
Y79AA1000574	24.19	29.5	35.63	1	1
Y79AA1000584	48.15	39.35	38.38	0.83	0.83
Y79AA1000589	2778.1	2470.28	1588.55	0.89	0.57
Y79AA1000598	29.48	26.04	21.58	1	1
Y79AA1000600	114.94	209.4	237.16	1.82	2.06
Y79AA1000609	31.84	21.28	28.15	1	1
Y79AA1000618	63.61	66.01	76.25	1.04	1.2
Y79AA1000627	62.01	61.57	49.97	0.99	0.81
Y79AA1000636	92.84	80.65	118.18	0.87	1.27
Y79AA1000649	96.75	123.64	122.08	1.28	1.26
Y79AA1000656	1766.0	1687.12	1253.96	0.96	0.71
Y79AA1000673	27.77	24.97	21.2	1	1
Y79AA1000674	1171.6	1373.94	651.44	1.17	0.56
Y79AA1000678	36.94	44.09	34.34	1.1	1
Y79AA1000682	1983.1	1699.68	1530.39	0.86	0.77
Y79AA1000683	49.85	42.48	43.56	0.85	0.87

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Y79AA1000697	242.38	296.34	355.35	1.22	1.47
Y79AA1000700	43.92	66.94	58.24	1.52	1.33
Y79AA1000702	139.07	146.21	285.74	1.05	2.05
Y79AA1000704	18.66	25.29	15.37	1	1
Y79AA1000705	44.31	44.51	31.94	1	0.9
Y79AA1000717	75.03	98.74	86.2	1.32	1.15
Y79AA1000722	41.86	34.12	41.61	0.96	0.99
Y79AA1000724	72.99	67.48	66.4	0.92	0.91
Y79AA1000726	33.66	36.24	29.59	1	1
Y79AA1000734	44.87	42.21	66.46	0.94	1.48
Y79AA1000748	31.18	25.23	28.06	1	1
Y79AA1000750	122.85	138.64	121.01	1.13	0.99
Y79AA1000752	32.8	31.76	33.14	1	1
Y79AA1000774	66.23	53.85	62.7	0.81	0.95
Y79AA1000776	26.59	22.27	24.72	1	1
Y79AA1000777	129.38	122.4	131.92	0.95	1.02
Y79AA1000778	51.22	36.45	32.48	0.78	0.78
Y79AA1000782	63.92	63.79	87.96	1	1.38
Y79AA1000784	52.79	64.69	85.36	1.23	1.62
Y79AA1000794	23.36	22.73	19.03	1	1
Y79AA1000800	29.75	32.72	33.2	1	1
Y79AA1000802	30.35	26.74	20.73	1	1
Y79AA1000805	19.03	22.52	16.55	1	1
Y79AA1000814	106.9	114.58	89.95	1.07	0.84
Y79AA1000823	158.18	147.37	123.66	0.93	0.78
Y79AA1000824	36.55	29.44	33.27	1	1
Y79AA1000827	72.11	68.69	52.85	0.95	0.73
Y79AA1000831	100.55	112.39	119.5	1.12	1.19
Y79AA1000833	2837.1	2936.23	2467.7	1.03	0.87
Y79AA1000850	56.14	49.87	45.58	0.89	0.81
Y79AA1000856	86.17	85.24	87.41	0.99	1.01
Y79AA1000862	21.4	15.44	14.93	1	1
Y79AA1000876	126.25	128.25	138.28	1.02	1.1
Y79AA1000888	391.22	560.15	327.4	1.43	0.84
Y79AA1000902	91.22	102.61	97.33	1.12	1.07
Y79AA1000935	63.3	75.01	65.76	1.18	1.04
Y79AA1000959	59.37	76.73	60.41	1.29	1.02
Y79AA1000962	36.15	37.57	34.42	1	1
Y79AA1000963	96.8	192.62	232.02	1.99	2.4
Y79AA1000966	519	651.66	477.36	1.26	0.92
Y79AA1000967	19.89	292.47	251.96	7.31	6.3
Y79AA1000968	80.03	76.94	75.11	0.96	0.94
Y79AA1000969	37.01	40.02	31.68	1	1
Y79AA1000976	14.88	17.75	13.35	1	1
Y79AA1000978	51.09	73.65	56.87	1.44	1.11
Y79AA1000985	236.63	273.81	258.11	1.16	1.09

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Y79AA1000989	119.43	125.67	133.77	1.05	1.12
Y79AA1000991	1240.5	994.5	880.71	0.8	0.71
Y79AA1001013	1435.4	1460.4	1293.41	1.02	0.9
Y79AA1001014	59.34	57.2	61.99	0.96	1.04
Y79AA1001019	50.26	49.6	55.51	0.99	1.1
Y79AA1001020	77.34	83.75	108.42	1.08	1.4
Y79AA1001023	30.63	37.84	28.21	1	1
Y79AA1001030	54.37	72.86	67.84	1.34	1.25
Y79AA1001035	36.18	52.22	60.57	1.31	1.51
Y79AA1001041	34.02	26.39	39.75	1	1
Y79AA1001043	104.7	132.62	114.65	1.27	1.1
Y79AA1001048	36.81	40.02	39.21	1	1
Y79AA1001056	83.24	70.9	78.16	0.85	0.94
Y79AA1001061	109.03	110.8	115.01	1.02	1.05
Y79AA1001062	29.05	40.37	33.85	1.01	1
Y79AA1001068	155.79	171.69	179.73	1.1	1.15
Y79AA1001073	63.42	240.36	260.57	3.79	4.11
Y79AA1001077	141.08	122.58	123.69	0.87	0.88
Y79AA1001078	89.83	99.86	113.12	1.11	1.26
Y79AA1001081	52.76	53.5	48.66	1.01	0.92
Y79AA1001088	430.32	406.89	460.33	0.95	1.07
Y79AA1001089	92.85	116.61	115.46	1.26	1.24
Y79AA1001090	67.22	69.72	59.84	1.04	0.89
Y79AA1001105	122.65	110.5	72.39	0.9	0.59
Y79AA1001142	62.73	127.62	148.35	2.03	2.36
Y79AA1001145	99.57	109.62	105.59	1.1	1.06
Y79AA1001162	61.53	55.57	54.52	0.9	0.89
Y79AA1001167	22.2	27.76	22.05	1	1
Y79AA1001176	22.58	13.4	14.3	1	1
Y79AA1001177	33.47	34.18	31.87	1	1
Y79AA1001179	172.36	288.96	209.97	1.68	1.22
Y79AA1001185	4.57	59.88	4.92	1.5	1
Y79AA1001201	75.33	82.93	99.95	1.1	1.33
Y79AA1001205	37.54	42.63	48.27	1.07	1.21
Y79AA1001211	97.72	107.77	98.62	1.1	1.01
Y79AA1001212	95.32	102.86	78.99	1.08	0.83
Y79AA1001216	650.81	671.69	747.64	1.03	1.15
Y79AA1001228	81.54	86.06	78.83	1.06	0.97
Y79AA1001233	24.91	19.52	21.84	1	1
Y79AA1001236	41.43	68.09	69.24	1.64	1.67
Y79AA1001239	66.08	63.52	79.5	0.96	1.2
Y79AA1001240	40.45	44.69	30.33	1.1	0.99
Y79AA1001255	209.03	243.4	327.16	1.16	1.57
Y79AA1001264	77.47	114.96	155.28	1.48	2
Y79AA1001272	94.67	108.27	133.39	1.14	1.41
Y79AA1001281	18.21	17.06	16.63	1	1

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Y79AA1001299	84.16	104.65	104.16	1.24	1.24
Y79AA1001312	29.58	27.93	24.52	1	1
Y79AA1001319	50.23	74.51	92.58	1.48	1.84
Y79AA1001323	29.99	42.34	39.19	1.06	1
Y79AA1001328	54.08	55.7	41.63	1.03	0.77
Y79AA1001343	4712.6	5708.31	5950.25	1.21	1.26
Y79AA1001351	30.34	22.22	24.29	1	1
Y79AA1001364	57.23	72.81	54.68	1.27	0.96
Y79AA1001367	33.46	28.07	29.13	1	1
Y79AA1001384	16.59	11.98	21.5	1	1
Y79AA1001391	22.75	18.1	18.89	1	1
Y79AA1001394	107.41	106.15	85.41	0.99	0.8
Y79AA1001402	88.44	106.63	80.2	1.21	0.91
Y79AA1001410	31.55	32.32	27.63	1	1
Y79AA1001414	89.66	99.17	102.16	1.11	1.14
Y79AA1001426	26.19	30.96	29.42	1	1
Y79AA1001427	944.35	1175.39	818.75	1.24	0.87
Y79AA1001430	62.12	77.68	66.7	1.25	1.07
Y79AA1001439	106.67	110.26	142.44	1.03	1.34
Y79AA1001485	46.51	42.89	31.32	0.92	0.86
Y79AA1001493	35.54	24.61	23.88	1	1
Y79AA1001511	57.74	65.35	93.44	1.13	1.62
Y79AA1001523	37.34	66.39	30.87	1.66	1
Y79AA1001530	106.49	109.86	93.6	1.03	0.88
Y79AA1001532	99.42	111.62	100.16	1.12	1.01
Y79AA1001533	64.49	53.61	44.36	0.83	0.69
Y79AA1001541	23.65	33.4	31.44	1	1
Y79AA1001548	180.15	182.1	165.86	1.01	0.92
Y79AA1001555	57.85	54.82	39.03	0.95	0.69
Y79AA1001562	159.81	149.99	152.18	0.94	0.95
Y79AA1001581	54.55	60.53	50.36	1.11	0.92
Y79AA1001585	96.52	98.24	79.13	1.02	0.82
Y79AA1001592	62.47	74.66	67.17	1.2	1.08
Y79AA1001594	6.58	7.46	4.36	1	1
Y79AA1001603	1371.8	1354.64	1311.51	0.99	0.96
Y79AA1001613	41.9	47.86	41.96	1.14	1
Y79AA1001630	21.43	17.4	21.48	1	1
Y79AA1001647	76.41	83.21	65.45	1.09	0.86
Y79AA1001664	87	149.39	85.61	1.72	0.98
Y79AA1001665	46.95	45.27	52.61	0.96	1.12
Y79AA1001679	226.19	250.68	232.31	1.11	1.03
Y79AA1001692	36.23	50.52	46.28	1.26	1.16
Y79AA1001696	14.49	20.08	15.55	1	1
Y79AA1001705	28.44	37.49	24.51	1	1
Y79AA1001711	93.7	115.28	83.78	1.23	0.89
Y79AA1001717	21.82	24.44	17.74	1	1

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Y79AA1001719	56.65	50.42	51.8	0.89	0.91
Y79AA1001727	63.97	82.15	75.03	1.28	1.17
Y79AA1001750	201.52	244.27	213.32	1.21	1.06
Y79AA1001760	1525.1	1826.08	1836.66	1.2	1.2
Y79AA1001777	27.57	22.01	20.75	1	1
Y79AA1001781	14.2	10.34	11.67	1	1
Y79AA1001787	34.67	32.77	31.46	1	1
Y79AA1001793	490.12	500.64	415.02	1.02	0.85
Y79AA1001795	20.82	15.64	16.66	1	1
Y79AA1001799	63.3	90.19	82.19	1.42	1.3
Y79AA1001800	206.49	248.75	358.98	1.2	1.74
Y79AA1001801	59.81	46	44.71	0.77	0.75
Y79AA1001803	32.78	24.73	24.59	1	1
Y79AA1001805	93.54	111.29	88.98	1.19	0.95
Y79AA1001807	156.64	104.4	119.1	0.67	0.76
Y79AA1001827	54.55	36.34	49.28	0.73	0.9
Y79AA1001846	90.02	81.03	88.49	0.9	0.98
Y79AA1001848	46.02	35.28	38.62	0.87	0.87
Y79AA1001853	54.99	60.14	72.48	1.09	1.32
Y79AA1001863	55.19	71.44	82.39	1.29	1.49
Y79AA1001866	73	77.51	62.79	1.06	0.86
Y79AA1001874	12.88	7.85	8.7	1	1
Y79AA1001875	92.9	99.69	99.18	1.07	1.07
Y79AA1001907	1093.8	755.57	1038.49	0.69	0.95
Y79AA1001908	28.59	18.2	21.42	1	1
Y79AA1001923	40.94	40.51	35.36	0.99	0.98
Y79AA1001927	54.84	54.43	48.17	0.99	0.88
Y79AA1001930	25.74	40.86	42.58	1.02	1.06
Y79AA1001932	97.69	98.39	84.63	1.01	0.87
Y79AA1001933	57.63	46.41	44	0.81	0.76
Y79AA1001942	37.83	42.2	33.88	1.06	1
Y79AA1001963	342.06	324.07	294.47	0.95	0.86
Y79AA1001968	133.87	148.65	174	1.11	1.3
Y79AA1001983	31.53	29.07	29.92	1	1
Y79AA1002000	38.81	38.99	47.02	1	1.18
Y79AA1002004	37.99	102.36	131.4	2.56	3.29
Y79AA1002008	90.25	65.44	54.66	0.73	0.61
Y79AA1002012	127.69	126.92	98.41	0.99	0.77
Y79AA1002017	12.63	3.46	2.78	1	1
Y79AA1002022	130.63	151.97	106.29	1.16	0.81
Y79AA1002027	31.61	32.98	29.25	1	1
Y79AA1002050	45.8	38.26	51.32	0.87	1.12
Y79AA1002058	1897.1	1240.87	921.95	0.65	0.49
Y79AA1002060	63.24	95.77	121.69	1.51	1.92
Y79AA1002062	138.95	173.15	116.65	1.25	0.84
Y79AA1002065	241.79	213.59	256.71	0.88	1.06

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Y79AA1002067	69.44	85.04	88.86	1.22	1.28
Y79AA1002069	22.45	14.55	11.72	1	1
Y79AA1002070	290.21	261.7	420.51	0.9	1.45
Y79AA1002074	4784.8	4322.02	3500.57	0.9	0.73
Y79AA1002076	23.92	22.89	30.01	1	1
Y79AA1002083	32.64	25.47	18.78	1	1
Y79AA1002084	56.93	47.45	58.61	0.83	1.03
Y79AA1002086	29.98	30.26	23.7	1	1
Y79AA1002087	339.84	473.89	305.27	1.39	0.9
Y79AA1002089	63.57	68.96	66.81	1.08	1.05
Y79AA1002093	45.69	38.45	36.91	0.88	0.88
Y79AA1002101	19.61	22.84	19.2	1	1
Y79AA1002103	37.61	37.75	35.74	1	1
Y79AA1002115	48.3	60.52	68.39	1.25	1.42
Y79AA1002121	50.52	36.73	32.42	0.79	0.79
Y79AA1002125	81.65	86.76	79.2	1.06	0.97
Y79AA1002129	33.63	31.52	18.59	1	1
Y79AA1002131	20.65	14.34	20.31	1	1
Y79AA1002139	31.44	25.87	27.48	1	1
Y79AA1002144	138.16	90.77	145.45	0.66	1.05
Y79AA1002177	53.67	57.36	47.56	1.07	0.89
Y79AA1002183	168.93	154.43	165.5	0.91	0.98
Y79AA1002202	111.2	133.56	100.48	1.2	0.9
Y79AA1002204	35.34	28.87	17.92	1	1
Y79AA1002206	28.51	22.35	18.61	1	1
Y79AA1002208	36.92	36.47	44.08	1	1.1
Y79AA1002209	48.12	45.04	49.5	0.94	1.03
Y79AA1002210	29.11	36.94	29.41	1	1
Y79AA1002211	57.36	63.16	52.25	1.1	0.91
Y79AA1002213	133.51	136.73	123.74	1.02	0.93
Y79AA1002215	139.31	112.01	119.56	0.8	0.86
Y79AA1002220	69.79	59.74	58.27	0.86	0.83
Y79AA1002226	91.29	74.46	87.97	0.82	0.96
Y79AA1002229	34.29	24.76	28.27	1	1
Y79AA1002234	34.52	56.44	51.95	1.41	1.3
Y79AA1002235	73.58	67.73	74.78	0.92	1.02
Y79AA1002246	50.76	51.58	35.73	1.02	0.79
Y79AA1002258	63.15	82.64	90.15	1.31	1.43
Y79AA1002279	122.18	148.88	110.84	1.22	0.91
Y79AA1002292	61.42	72.22	67.83	1.18	1.1
Y79AA1002298	39.81	43.55	30.57	1.09	1
Y79AA1002307	32.77	30.65	23.26	1	1
Y79AA1002309	18.06	24.11	13.63	1	1
Y79AA1002311	53.31	57.19	84.46	1.07	1.58
Y79AA1002334	35.05	38.07	31.31	1	1
Y79AA1002351	42.13	61.09	58.56	1.45	1.39

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Y79AA1002355	48.88	42.39	40.68	0.87	0.83
Y79AA1002361	87.11	88.66	76.9	1.02	0.88
Y79AA1002365	38.75	24.26	20.53	1	1
Y79AA1002373	43.96	55.06	28.34	1.25	0.91
Y79AA1002376	3080.7	3824.05	4481.1	1.24	1.45
Y79AA1002378	73.33	93.61	68.22	1.28	0.93
Y79AA1002381	248.36	288.51	304.13	1.16	1.22
Y79AA1002388	118.82	135.82	129.37	1.14	1.09
Y79AA1002399	36.12	30.1	32.87	1	1
Y79AA1002407	57.84	42.82	52.54	0.74	0.91
Y79AA1002413	78.77	81.36	87.31	1.03	1.11
Y79AA1002416	34.3	30.2	51.99	1	1.3
Y79AA1002429	67.91	69.81	80.19	1.03	1.18
Y79AA1002431	24.66	21.16	23.98	1	1
Y79AA1002433	27.12	18.11	23.63	1	1
Y79AA1002445	78.66	54.58	73.75	0.69	0.94
Y79AA1002461	29.04	24.84	32	1	1
Y79AA1002466	882.69	904.65	782.53	1.02	0.89
Y79AA1002471	53.74	51.26	68.91	0.95	1.28
Y79AA1002472	121.95	127.4	127.11	1.04	1.04
Y79AA1002474	53.33	40.85	47.18	0.77	0.88
Y79AA1002482	103.36	111.11	116.07	1.07	1.12
Y79AA1002487	30.92	25.8	32.51	1	1
Y79AA1002490	101.4	90.92	90.54	0.9	0.89
Y79AA1002493	107.88	125.54	105.75	1.16	0.98
ZRV6C1006278	46.63	30.08	32.23	0.86	0.86

Table 170

Expression of each cDNA in undifferentiated NT2 cells, in NT2 cells cultured in the presence of retinoic acid, or in NT2 cells that were cultured in the presence of retinoic acid and then further cultured in the presence of cell-division inhibitor added (This table also contains clones without description in Examples)

In the table, NT2, NT2_RA, and NT2_RA_INHIB represent untreated NT2 cells, retinoic acid-treated NT2 cells, and retinoic acid/inhibitor-treated NT2 cells, respectively. The assay was performed in triplicate (n=3), and each result was shown in the column of exp.1, exp.2, or exp.3. In addition, "t-test N/R" and "t-test N/I" represent results of test for significance of difference between the untreated cells and the retinoic acid-treated cells, and between the untreated cells and the retinoic acid/inhibitor-treated cells, respectively. The results of the test are shown in the columns of *:$p<0.05$ and **:$p<0.01$.

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Clone	NT2			NT2 RA			NT2 RA INHIB			ttest N/R	+ −	ttest N/I	+ −
	exp.1	exp.2	exp.3	exp.1	exp. 2	exp.3	exp.1	exp.2	exp.3				
GAPDH(Cr1)	3.53	1.08	0.98	2.92	2.49	2.8	1.76	2.59	1.52				
β actin(Cr2)	155.4	118	99.68	148.5	110.7	101.3	114.7	105.8	151.1				
ADRGL1000005	4.01	2.03	1.55	4.05	3.65	3.6	2.27	2.93	4.24				
ADRGL1000007	11.08	5.73	7.92	15.42	10.6	13.87	8.99	8.17	9.15				
ADRGL1000009	1.11	0.72	1.04	1.66	1.89	1.03	1.22	1.62	1.58			*	+
ADRGL1000011	4.27	2.7	2.85	4.32	4.35	3.38	2.76	3.27	3.06				
ADRGL1000027	1.83	0.38	0.56	0.97	0.62	0.99	0.92	1.33	1.5				
ADRGL1000058	3.65	2.58	1.37	2.92	3.36	2.75	2.25	3.51	2.7				
ADRGL1000069	3.25	1.85	3.28	1.86	2.53	2.85	2.01	2.89	2.7				
ADRGL1000077	13.48	10.41	6.71	19.62	17.92	22.59	11.6	16.66	19.34	*	+		
ADRGL1000092	5.73	2.8	4.51	7.31	5.01	4.83	3.24	6.16	7.22				
ADRGL1000099	5.64	3.42	2.08	5.59	3.73	4.24	3.98	3.98	4.06				
ADRGL1000136	9.97	3.52	4.19	5.77	4.73	5.86	6.61	5.16	5.49				
ADRGL1000147	23.09	13.85	11.7	14.77	14.96	14.89	17.7	13.3	19.47				
ADRGL1000159	6.11	2.22	3.37	5.24	2.88	4.15	2.76	2.93	3.59				
ADRGL1000160	7.16	3.48	4.19	5.94	4.59	3.41	3.95	4.67	4.25				
ADRGL1000171	4.84	2.99	3.23	3.52	4.19	4.37	2.55	3.88	3.45				
ADRGL1000181	5.1	3.65	2.6	3.16	4.06	2.97	2.64	3.06	3.44				
BGGI11000015	13.95	6.83	6.72	9.61	9.19	10.24	9.94	10.66	10.13				
BGGI11000016	15.49	5.92	7.09	11.88	11.38	8.72	11.82	10.98	10.51				
BGGI11000017	7.89	2.99	3.25	4.94	4.94	4.93	3.55	4.27	3.52				
BGGI11000022	8.77	5.14	5.91	7.12	7.05	4.54	5.71	5.59	5.9				
BGGI11000031	4.71	2.16	2.74	4.09	3.29	3.96	4.02	3.67	2.33				
BGGI11000042	6.37	5.24	3.74	5.63	6.22	4.36	4.66	5.2	4.04				
BGGI11000046	19.01	12.57	9.23	12.39	15.7	12.37	8.8	10.92	9.17				
BNGH41000020	859	910.1	603	164	319.2	267.4	638.2	771.6	845.4	**	-		
BNGH41000025	5.35	2.06	2.09	2.76	2.76	3.77	4.23	2.01	3.06				
BNGH41000026	16.2	7.69	7.05	9.34	11.37	9.66	10.13	7.16	10.71				
BNGH41000027	2.31	2.18	2.5	2.9	3.01	2.82	3.68	3.48	4.21	**	+	**	+
BNGH41000035	14.57	8.83	9.36	10.92	9.55	14.75	15.02	15.18	12.2				
BNGH41000037	10.56	7.46	6.2	8.16	9.21	6.42	3.37	5.45	4.98				
BNGH41000042	77.1	50.85	58.45	47.64	53.39	62.67	28.12	35.48	23.44			*	-
BNGH41000048	3.5	2.19	1.91	4.28	2.87	2.4	1.63	3.01	1.78				
BNGH41000056	2.57	2.01	1	1.91	2.63	2.15	1.41	2.4	1.79				
BNGH41000087	9.84	5.84	5.53	12.49	10.24	10.25	11.74	9.68	8.53				
BNGH41000091	3.37	2.59	1.21	3.29	3.01	1.55	2.95	2.57	2.13				
BNGH41000157	10.63	5.64	6.15	8.53	9.05	7.74	6.38	6.68	5.75				
BNGH41000169	3.77	4.34	3.82	4.9	3.48	3.32	3.4	4.16	4.19				
BNGH41000181	2.47	1.59	1.84	2.93	2.1	1.8	1.7	2.66	1.59				
BNGH41000198	8.13	4.64	3.79	5.48	4.35	5.59	4.3	4.15	4.35				
BNGH41000219	9.61	3.92	4.87	4.17	5.29	5.45	5.24	7.12	7.13				
BNGH41000229	19.61	13.28	8.68	10.86	11.27	9.36	7.9	9.5	10.85				
BNGH41000237	10.9	5.47	6.45	6.65	6.97	7.79	6.36	6.25	5.44				
BNGH41000238	4.58	7	3.45	5.91	4.68	4.34	4.33	5.44	4.22				
BNGH41000243	13.85	8.69	8.48	10.19	9.71	8.97	8.23	4.87	5.54				
BNGH41000270	5.83	2.62	2.35	2.3	3.05	3.44	2.59	3.49	1.3				
BRAWH1000004	4.19	2.83	2.48	5.04	3.15	3.26	1.44	3.45	2.05				
BRAWH1000018	4.85	1.95	2.29	7.47	8.8	8.85	8.68	6.61	7.96	**	+	*	+
BRAWH1000021	6.52	5.06	5.87	5.09	6.94	6.44	2.89	6.23	4.28				
BRAWH1000027	11.64	8.86	7.19	8.24	10.39	11.51	5.58	7.13	8.24				
BRAWH1000029	9.58	5.15	3.52	6.01	6.72	6	5.08	5.12	5.84				
BRAWH1000040	4.6	1.89	2.14	2.92	2.71	2.7	2.92	2.5	3.01				
BRAWH1000050	11.48	4.95	5.19	9.74	7.25	8.62	8.25	8.09	8.93				
BRAWH1000051	8.18	3.93	3.19	6.15	5.72	6.02	5.01	4.25	4.44				

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Table 171

BRAWH1000060	2.9	2.93	1.8	3.46	3.35	2.78	2.07	3.22	2.32				
BRAWH1000075	2.06	1.78	1.17	2.08	2.99	2.28	1.92	2.13	2.14				
BRAWH1000081	4.56	1.87	2.1	2.75	2.22	2.25	1.42	2.46	1.85				
BRAWH1000084	26.93	16.26	13.57	23.37	33.3	27.71	19.86	27.26	24.74				
BRAWH1000095	11.47	5.88	3.86	6.15	6.04	6.04	6.03	4.2	5.03				
BRAWH1000096	7.17	5.2	3.04	5.76	6.13	4.73	6.35	5.93	7.43				
BRAWH1000097	7.61	5.42	4.3	8.36	9.37	10.77	5.92	6.56	7.12	*	+		
BRAWH1000100	2.35	1.26	1.29	3.27	4.09	3.18	3.47	3.17	3.82	*	+	*	+
BRAWH1000101	15.93	5.73	7.58	15.78	16.69	15.33	10.38	7.98	10.75				
BRAWH1000104	1.83	1.99	1.25	3.05	2.31	2.64	0.9	2.83	2.28	*	+		
BRAWH1000107	5.24	3.06	2.55	3.69	4.48	3.14	2.51	6.62	2.54				
BRAWH1000110	37.02	23.89	17.95	52.01	48.45	48.78	25.83	19.88	30.82	*	+		
BRAWH1000111	13.78	8.87	6.05	12.15	10.84	10.06	10.64	8.06	9.74				
BRAWH1000135	11.51	6.6	6.16	7.34	6.27	6.18	7.86	5.16	9.04				
BRAWH1000190	5.57	3.61	3.06	4.88	4.05	4.63	4.28	3.62	5.01				
HEMBA1000005	2.17	2.36	2.39	3.59	3.26	3.09	2.51	1.69	3.76	**	+		
HEMBA1000006	4.88	4.08	3.07	5.64	5.07	4.69	3.89	4.34	3.69				
HEMBA1000012	7.67	9.97	9.83	7.99	7.06	6.98	3.55	5.22	3.46			**	-
HEMBA1000020	27.06	14.56	16.3	24.94	23.65	29.76	15.51	14.38	17.35				
HEMBA1000030	7.2	6.04	4.37	4.93	6.66	4.71	4.8	4.96	7.17				
HEMBA1000034	5.42	3.03	3.13	3.92	5.81	5.55	2.45	2.65	5.55				
HEMBA1000042	10.53	5.34	5.29	12.34	15.71	15.33	6.74	5.14	8.81	*	+		
HEMBA1000045	3.35	1.45	2	3.11	2.27	3.63	2.78	2.42	2.82				
HEMBA1000046	4.44	3.21	3.62	6.34	8.01	11.1	5.61	5.39	6.03	*	+	**	+
HEMBA1000047	3.38	2.86	1.36	3.03	2.25	2.95	2.29	1.9	1.25				
HEMBA1000048	6.35	3.98	4.34	16.75	14.72	14.62	7.09	8.13	7.75	**	+	*	+
HEMBA1000050	1.73	0.67	0.56	1.86	1.47	1.56	1.52	2.71	1.56				
HEMBA1000053	2.66	1.5	1.58	2.81	3.5	3.13	2.37	1.92	3.37	*	+		
HEMBA1000060	4.78	3.18	2.77	4.56	4.67	4.59	3.9	4.27	4.27				
HEMBA1000072	71.82	55.54	44.63	47.17	62.62	63.43	25.66	24.24	32.66			*	-
HEMBA1000073	2.41	1.46	1.48	2.36	2.35	2.6	1.84	2.72	2.72				
HEMBA1000076	10.02	11.17	8.35	27.94	21.02	20.27	16.4	9.49	15.31	**	+		
HEMBA1000084	3.64	2.86	3.72	4.85	4.96	4.11	5.09	5.98	4.83	*	+	*	+
HEMBA1000087	3.12	2.56	2.1	4.7	3.46	2.58	2.59	4.09	3.28				
HEMBA1000088	1.57	0.55	0.65	1.47	0.74	0.92	1.69	2.19	2.78			*	+
HEMBA1000091	7.82	3.65	3.58	5.14	4.68	5.32	5.87	2.69	5.02				
HEMBA1000111	3.34	2.33	2.42	4.87	5.39	5.9	3.66	3.37	3.36	**	+		
HEMBA1000121	3.69	2.19	1.8	4.54	7.02	6.59	3.95	3.3	4.32	*	+		
HEMBA1000128	4.07	1.73	1.88	3.07	3.61	4.19	4.82	5.85	5.45			*	+
HEMBA1000129	4.83	2.28	2.77	2.81	3.65	3.39	2.57	2.73	3.94				
HEMBA1000141	2.71	2.09	1.62	4.16	2.77	4.01	2.77	3.67	1.66	*	+		
HEMBA1000146	2.9	1.3	1.8	2.65	2.28	1.73	1.61	3.65	1.85				
HEMBA1000150	26.65	13.33	17.02	31.39	35.61	38.63	19.78	16.66	26.75	*	+		
HEMBA1000154	36.53	16.72	17.93	24.12	23.55	16.21	9	9.29	13.92				
HEMBA1000156	12.63	7.55	7.2	12.13	11.18	10.85	5.44	6.27	10.52				
HEMBA1000158	14.24	5.92	4.83	15.57	17.46	14.26	10.9	12.16	12.71				
HEMBA1000168	10.07	5.72	5.58	8.47	10.06	8.07	7.36	7.05	5.56				
HEMBA1000180	3.67	1.14	1.34	3.4	2.55	2.88	1.78	2.08	2.49				
HEMBA1000185	9.44	4.05	4.26	11.55	10.93	10.36	7.42	5.5	5.94	*	+		
HEMBA1000188	2.86	1.61	0.93	2.94	2.35	3.1	1.57	1.58	1.71				
HEMBA1000193	1.27	0.58	0.24	1.37	0.89	0.82	0.26	0.53	0.45				
HEMBA1000194	11.09	4.55	5.41	17.15	17.6	13.81	11.08	8.03	17.29	*	+		
HEMBA1000201	3.51	1.9	1.75	4.07	2.62	2.46	2.06	2.69	2.83				
HEMBA1000213	2.2	0.91	0.97	1.85	2.66	1.89	1.72	1.64	1.67				
HEMBA1000216	4.38	3.53	3.49	7.1	6.02	3.1	3.46	3.84	4.14				
HEMBA1000227	6.93	1.95	2.95	5.37	3.71	3.99	3.84	2.55	3.65				

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Table 172

HEMBA1000231	5.77	4.79	1.39	5.73	5.06	5.05	2.57	4.02	3.83				
HEMBA1000237	10.5	9.41	7.28	13.8	14.47	14.03	8.59	13.21	9.08	**	+		
HEMBA1000243	4.4	2.18	1.57	4.11	5.36	4.88	3.72	3.39	3.4				
HEMBA1000244	11.09	6.03	5.16	9.66	7.12	6.2	9.02	6.06	9.63				
HEMBA1000251	2.83	2.17	1.02	2.88	4.48	2.64	1.69	2.92	2.44				
HEMBA1000254	5.6	3.06	2.15	6.61	5.66	5.33	3.44	3.21	4.84				
HEMBA1000264	3.12	2.38	1.29	3	2.42	2.07	2.39	1.18	3.05				
HEMBA1000269	3.15	2.65	1.66	4.09	3.3	1.89	1.88	1.49	1.6				
HEMBA1000275	10.1	8.27	6.59	12.65	12.4	13.32	7.47	7.72	5.65	*	+		
HEMBA1000280	2.4	1.67	1.88	3.2	3.34	2.25	0.92	2.83	1.47				
HEMBA1000282	4.3	2.15	1.99	8.2	7.71	7.54	4.05	3.59	4.68	**	+		
HEMBA1000287	6.5	5	3.8	6.66	6.95	7.33	6.19	6.14	4.66				
HEMBA1000288	4.22	5.47	1.6	5.44	4.7	5.08	3.8	2.7	3.03				
HEMBA1000290	2.44	1.68	1.41	3.3	2.07	2.24	2.46	1.37	1.82				
HEMBA1000296	4.58	3.23	3.04	3.88	4.57	3.87	2.97	3.13	3.49				
HEMBA1000300	7.18	7.47	4.77	15.63	12.41	11.86	8.05	9.96	6.36	**	+		
HEMBA1000302	2.87	1.87	1.42	2.86	2.56	2.8	1.34	2.59	1.57				
HEMBA1000303	12.63	6.43	5.95	8.6	9.24	8.52	6.4	8.51	7.91				
HEMBA1000304	5.94	4.85	2.91	8.58	10.98	8.79	6.22	5.73	5.36	*	+		
HEMBA1000307	3.35	2.83	1.79	7.52	6.27	5.03	5.57	4.79	3.97	*	+	*	+
HEMBA1000312	7.59	5.13	7.25	13.4	9.35	10.01	7.66	6.43	8.25	*	+		
HEMBA1000318	4.73	3.46	2.76	7.07	6.34	4.78	4.52	5.17	4.75				
HEMBA1000327	4.9	14.95	2.36	5.69	8.99	5.72	3.18	5.4	3.63				
HEMBA1000333	2.68	1.29	0.21	2.59	1.6	1.38	2.24	1.33	1.95				
HEMBA1000338	7.1	5.92	3.55	10.42	12.67	10.27	5.82	7.1	5.05	*	+		
HEMBA1000343	4	2.99	2.01	2.63	3.79	2.89	1.22	2.1	1.84				
HEMBA1000349	3.15	2.72	2.94	1.9	3.38	2.84	1.58	1.8	2.44			*	-
HEMBA1000351	12.26	4.06	4.63	9.54	11.2	9.66	5.66	5.25	4.95				
HEMBA1000355	5.83	4.02	3.82	5.03	5.09	4.09	3.9	3.77	4.2				
HEMBA1000356	8.5	4.16	3.88	9.66	6	7.29	7.01	5.23	5.35				
HEMBA1000357	6.36	2.11	3.61	7.55	7.35	8.12	3.8	3.56	3.53	*	+		
HEMBA1000366	2.01	1.56	0.82	2.54	1.86	2.67	1.26	2.04	1.96				
HEMBA1000369	7.61	3.99	4.13	5.06	4.64	5.24	3.29	3.78	3.59				
HEMBA1000370	1.94	1.23	1.23	3.73	3.06	3.01	1.19	2.46	1.97	**	+		
HEMBA1000376	5.48	4.4	4.48	8.19	9.77	8.68	4.81	5.75	4.74	**	+		
HEMBA1000387	6.72	4.8	4.24	12.88	11.31	8.93	7.04	6.86	7.9	*	+		
HEMBA1000389	6.41	4.31	3.18	5.44	5.19	3.87	3.91	4.16	5.13				
HEMBA1000390	2.89	3.46	2.42	2.82	2.5	3.02	2.55	2.1	2.56				
HEMBA1000392	1.66	1.01	0.96	2.76	2.9	2.64	1.17	2.08	1.89	**	+		
HEMBA1000396	2.67	1.46	1.17	3.48	2.29	1.9	2.07	2.04	2.6				
HEMBA1000411	2.73	2.11	2	2.49	2.83	1.98	1.3	2.58	1.84				
HEMBA1000418	2.29	2.59	1.6	3.21	4.57	2.67	2.11	3.04	2.45				
HEMBA1000422	5.88	3.82	2.78	5.71	5.46	6.46	2.91	5	3.36				
HEMBA1000428	2.98	1.47	1	5.92	5.67	4.87	3.36	3.17	3.89	**	+		
HEMBA1000434	0.46	1.18	0.48	1.51	2.2	1.01	1.46	1.36	1.4			*	+
HEMBA1000442	1.91	1.74	2.18	1.99	2.71	2.66	1.77	2.2	1.7				
HEMBA1000443	5.28	4.21	2.77	4.95	5.35	7.43	4.57	4.71	4				
HEMBA1000446	15.47	8.43	7.47	8.86	8.46	9.56	8.97	8.38	10.15				
HEMBA1000456	7.87	3.87	5.62	12.88	11.2	12.65	6.87	8.86	10.32	**	+		
HEMBA1000459	3.86	2.75	1.81	4.89	5.61	4.96	2.29	3.47	3.74	*	+		
HEMBA1000460	2.95	1.91	1.24	1.69	3.46	2.84	3.05	2.46	5.23				
HEMBA1000462	17.16	10.03	4.79	13.14	13.57	10.69	11.49	13.69	11.75				
HEMBA1000464	1.23	1.41	0.6	1.41	1.89	0.9	1.32	1.26	0.96				
HEMBA1000468	1.87	1.63	0.67	3.5	1.61	1.75	2.85	2.43	2.2				
HEMBA1000469	4.36	2.95	2.67	7.93	8.36	9.97	5.39	4.1	4.79	**	+		
HEMBA1000477	6.04	2.58	2.34	5.17	5.61	5.34	6	5.59	6.01				

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Table 173

HEMBA1000481	20.13	11.47	12.73	18.55	18.55	15.53	7.84	7.33	12.91				
HEMBA1000488	7.66	4.44	4.62	7.86	6.19	6.89	3.5	5.38	6.42				
HEMBA1000490	4.18	2.68	1.34	3.95	5.37	3.63	2.12	2.88	4.31				
HEMBA1000491	7.15	3.43	2.52	5.5	6.82	6.64	4.25	3.29	3.33				
HEMBA1000498	10.26	6.11	4.98	10.58	18.06	18.44	9.53	6.44	8.57	*	+		
HEMBA1000501	10.31	9.16	7.08	7.41	5.02	8.46	4.06	4.46	3.72			**	-
HEMBA1000504	0.29	1.06	0.88	2.55	1.79	2.74	3.2	4.91	2.54	*	+	*	+
HEMBA1000505	4	3.11	2.61	4.34	3.87	4.06	3.11	3.95	3.94				
HEMBA1000507	8.99	4.59	6.64	9.35	10.47	8.65	5.55	8.59	7.24				
HEMBA1000508	8.59	6.68	6.07	11.49	13.9	16.57	7.32	8.75	9.79	*	+		
HEMBA1000518	2.98	1.78	1.55	2.04	2.31	1.71	2.15	1.54	1.87				
HEMBA1000519	13.74	9.63	6.41	18.15	26.1	23.45	14.61	12.39	16.75	*	+		
HEMBA1000520	0.74	1.54	1.42	0.53	4.99	5.32	0.3	3.24	3.21				
HEMBA1000523	2.58	1.73	1.85	2.49	2.81	3.42	2.38	3.31	2.63				
HEMBA1000531	5.39	5.46	3.11	3.93	6.67	3.26	3.72	3.54	2.94				
HEMBA1000534	0.79	3.21	2.91	1.73	9.74	6.64	0.85	6.6	3.17				
HEMBA1000538	-0.07	2.6	2.6	0.69	6.28	5.42	0.12	7.11	5.18				
HEMBA1000540	3.94	2.64	3.3	8.03	7.49	8.11	2.04	3.68	2.54	**	+		
HEMBA1000542	5.67	3.4	2.44	3.85	3.5	5.44	3.98	3.82	4.97				
HEMBA1000545	2.41	1.53	0.38	4.15	3.69	3.21	1.98	2.16	2.09	*	+		
HEMBA1000547	1.74	1.59	1.68	5.72	8.77	7.03	3.43	3.74	3.3	**	+	**	+
HEMBA1000551	9.65	6.1	8.03	14.99	17.46	18.61	8.56	8.89	9.19	**	+		
HEMBA1000555	5.3	2	2.07	3.79	6.18	4.25	2.7	2.98	2.37				
HEMBA1000557	4.48	2.92	3.57	7.15	7.8	8.32	4.31	6.14	5.01	**	+		
HEMBA1000561	3.7	1.44	1.77	4.14	3.06	3.15	3.47	4.41	2.34				
HEMBA1000563	1.24	0.37	0.85	2.27	1.82	2.27	0.66	2.98	0.86	*	+		
HEMBA1000567	3.87	1.04	1.51	8.01	8.19	8.67	2.66	3.73	4	**	+		
HEMBA1000568	3.88	2.11	2.05	5.69	5.23	5.4	1.77	2.82	3.91	*	+		
HEMBA1000569	4.97	2.5	2.71	6.85	4.01	5.8	3.46	3.51	4.29				
HEMBA1000575	13.92	7.22	8.43	20.52	24.59	18.68	11.63	11.79	11.04	*	+		
HEMBA1000588	1.28	0.91	1.2	2.91	2.49	2.9	1.78	2.48	2.62	**	+	*	+
HEMBA1000590	3.14	1.5	1.84	3.09	1.65	1.71	1.44	1.82	1.81				
HEMBA1000591	6.68	3.59	4.87	8.78	6.73	9.08	5.54	5.94	6.27				
HEMBA1000592	1.77	1	1.66	2.61	3.4	2.25	1.98	2.18	1.99	*	+		
HEMBA1000594	3.25	0.68	1.19	1.74	3.07	2.12	1.39	1.15	1.72				
HEMBA1000604	5.99	4.47	2.05	8.88	9.05	6.96	6.29	5.91	6.23	*	+		
HEMBA1000607	4.99	3.1	3.35	6.44	6.82	5.81	3.43	4.28	4.42	*	+		
HEMBA1000608	0.99	1.94	0.42	3.85	2.15	1.46	2.61	2.1	3.4				
HEMBA1000622	2.66	1.16	0.99	4.04	3.67	4.04	2.76	3.15	3.26	*	+		
HEMBA1000634	28.82	15.23	16.08	35.62	36.93	32.2	24.35	21.77	26.76	*	+		
HEMBA1000636	10.44	4.41	5.46	7.42	7.72	8.03	6.42	4.97	5.75				
HEMBA1000637	5.28	3.33	4.09	4.63	6.26	5.53	4.14	4.87	4.43				
HEMBA1000655	7.39	4.24	2.84	8.57	9.07	9.85	5.75	6.56	6.78	*	+		
HEMBA1000657	7.14	3.75	3.78	6.89	5.66	6.19	7.09	4.53	7.57				
HEMBA1000662	2.8	1.64	1.1	1.89	1.7	1.33	1.86	1.9	1.81				
HEMBA1000664	2.6	2.45	0.17	3.74	3.57	2.7	2.86	2.52	2.77				
HEMBA1000671	3.69	2.81	2.74	7.05	5.05	5.15	3.14	2.82	3.51	*	+		
HEMBA1000673	5.96	2.79	3.34	9.32	7.79	7.67	4.47	3.8	5.32	*	+		
HEMBA1000675	2.45	2.8	0.77	6.63	4.04	4.43	3.65	3.8	3.87	*	+	*	+
HEMBA1000678	7.03	5.09	6.34	10.12	8.74	9.2	2.93	5.72	5.28	*	+		
HEMBA1000682	5.22	2.07	2.75	12.42	15.95	13.04	14.17	11.88	14.92	**	+	**	+
HEMBA1000686	5.1	3.46	2.35	5.21	4.74	3.32	3.54	2.67	2.25				
HEMBA1000702	9.79	6.15	6.42	10.8	11.22	8.35	8.93	8.45	8.8				
HEMBA1000705	1.79	1.26	0.4	2.12	2.25	1.15	1.75	1.57	2.17				
HEMBA1000713	5.65	3.58	2.89	6.69	5.36	6.21	7.06	6.72	4.64				
HEMBA1000718	4.7	2.67	2.33	5.7	6	5.76	3.69	3.85	2.59	*	+		

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Table 174

HEMBA1000719	4.82	2.97	2.79	3.61	4.58	3.67	3.75	2.77	3.67				
HEMBA1000722	2.03	0.86	1.42	1.98	2.82	1.59	1.34	3.92	2.07				
HEMBA1000726	10.3	9.3	7.72	23.56	26.89	19.83	12.69	13.58	11.3	**	+	*	+
HEMBA1000727	6.04	3.96	3.25	8.14	10.98	7.59	6.32	6.82	2.98	*	+		
HEMBA1000732	3.01	2.28	1.42	2.14	1.87	1.92	2.98	2.21	2.48				
HEMBA1000736	4.72	2.16	2	3.64	1.97	1.99	2.73	2.2	2.64				
HEMBA1000743	0.32	1.05	0.53	1.51	2.41	0.98	0.72	1.22	1.24				
HEMBA1000745	1.74	1.73	1.32	1.18	1.69	2.12	1.96	2.53	1.18				
HEMBA1000747	4.19	1.78	1.08	3.03	2.21	1.78	1.85	3.32	2.09				
HEMBA1000748	2.17	1.28	2.24	2.2	3.52	2.79	1.6	2.38	1.72				
HEMBA1000749	4.95	3.09	2.17	6.45	8.33	7.14	3.25	4.29	3.58	*	+		
HEMBA1000752	4.81	3.6	2.79	5.03	6.01	4.99	3.34	3.06	3.28				
HEMBA1000753	9.91	6.17	6.18	9.28	11.1	8.29	5.77	5.12	5.5				
HEMBA1000757	7.1	7.74	5.44	11.01	14.04	12.37	5.58	4.46	4.75	**	+		
HEMBA1000760	16.78	13.36	13.64	8.72	12.16	6.16	8.22	7.22	7.97			**	-
HEMBA1000769	7.05	2.51	3.23	9	8.67	9.72	4.24	4.83	3.98	*	+		
HEMBA1000773	1.32	0.68	0.25	0.36	1.46	1.1	0.81	1.64	0.68				
HEMBA1000774	8	3.27	7.05	12.39	12.55	13.92	7.51	8.12	7.46	*	+		
HEMBA1000780	2.14	1.77	0.74	2.61	2.17	1.75	1.28	2.13	1.21				
HEMBA1000783	1.08	1.96	1.07	2.21	1.08	2.2	1.9	1.74	1.44				
HEMBA1000791	3.14	3.15	3.13	6.58	7.55	5.76	3.73	3.72	6.22	**	+		
HEMBA1000793	9.3	4	3.98	5.49	6.95	5.86	5.38	4.76	5.7				
HEMBA1000802	3.76	2.25	1.22	2.43	3.6	2.62	0.88	2.18	1.88				
HEMBA1000813	9.81	3.16	4.27	6.99	7.53	7.12	3.67	6.02	6.65				
HEMBA1000817	2.66	1.43	0.92	2.74	3.08	2.72	1.26	2.52	1.67				
HEMBA1000822	0.99	1.09	0.85	1.62	3.22	2.71	1.22	1.82	0.71	*	+		
HEMBA1000827	7.7	6.4	3.84	6.01	6.66	6.53	3.91	3.03	4.64				
HEMBA1000833	5.1	2.66	2.23	8.93	7.69	7.93	7.69	5.86	6.86	**	+	*	+
HEMBA1000835	5.71	3.29	3.29	5.75	3.34	4.85	2.51	3.39	3.41				
HEMBA1000843	6.36	5.57	5.21	6.61	9.85	9.29	4.9	5.64	10.02				
HEMBA1000851	4.2	1.79	2.1	3.58	3.85	2.86	2.91	1.96	2.78				
HEMBA1000852	5.4	3.22	2.28	5.81	4.07	5.82	2.77	3.99	3.71				
HEMBA1000867	1.61	2.47	1.06	2.17	3.19	2.37	0.68	2.24	0.83				
HEMBA1000869	1.82	1.11	0.72	0.98	2.58	1.99	0.79	2.22	0.83				
HEMBA1000870	6.82	3.33	3.67	6.25	6.67	4.52	3.47	4.37	5.69				
HEMBA1000872	4.12	2.25	3.08	4.7	5.64	4.68	3.33	3.29	4.33	*	+		
HEMBA1000875	1.77	1.41	1.93	5.81	7.31	5.85	7.19	6.68	8.14	**	+	**	+
HEMBA1000876	5.86	4.79	3.07	7.1	7.28	6.57	4.55	4.52	6.23	*	+		
HEMBA1000907	2.12	2.01	0.66	2.54	2.27	2.12	2.3	1.55	1.2				
HEMBA1000908	4.73	8.03	3.2	3.97	8	4.77	4.32	3.17	3.88				
HEMBA1000910	4.06	2.39	3.23	5.88	8	5.6	3.31	3.17	3.05	*	+		
HEMBA1000918	3.62	1.79	2.38	3.54	2.97	3.56	2.53	2.34	2.18				
HEMBA1000919	6.44	3.37	2.05	4.74	4.83	4.38	3.75	4.79	3.18				
HEMBA1000934	8.7	4.01	3.95	4.96	5.39	5.6	4.1	3.51	4.76				
HEMBA1000935	2.09	1.32	1.09	2.05	2.33	2	1.1	2.66	1.72				
HEMBA1000940	4.94	2.14	2.53	3.07	4.88	4.53	2.3	2.63	3.13				
HEMBA1000942	6.3	3.89	2.49	7.11	9.28	8.54	5.01	6.29	5.19	*	+		
HEMBA1000943	1.76	1.55	1.49	3.18	2.76	2.23	1.98	2.58	2.05	*	+	*	+
HEMBA1000946	8.15	7.73	6	5.16	5.33	4.88	2.92	2.97	2.91	*	-	**	-
HEMBA1000960	9.59	5.75	7.08	15.65	18.02	18.53	8.6	9.11	11.03	**	+		
HEMBA1000962	6.47	2.77	4.32	4.75	7	7.13	5.16	3.51	7.23				
HEMBA1000968	7	1.7	1.54	3	4.17	3.31	2.23	2.96	3.14				
HEMBA1000971	5.14	1.71	2.36	4.85	4.32	4.5	3.47	4.15	3.21				
HEMBA1000972	3.69	1.13	1.73	5.98	4.9	5.9	2.76	4.55	2.35	*	+		
HEMBA1000974	1.6	0.93	0.68	2.29	1.66	2.44	2.01	3.61	2.23	*	+		
HEMBA1000975	3.28	2	1.5	5.97	3.13	2.57	2.25	4.14	2.32				

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Table 175

HEMBA1000979	5.49	2.18	2.97	6.7	3.77	4.39	3.48	5.27	4.03				
HEMBA1000981	9.63	9.63	8.99	5.49	6.85	5.43	3.2	5.8	4.89	**	-	**	-
HEMBA1000983	6.43	3.92	2.91	5.46	7.35	6.51	4.3	3.18	4.68				
HEMBA1000985	1.63	1.32	0.83	1.53	0.96	1.83	1.43	0.82	1.18				
HEMBA1000986	8.66	3.3	4.89	7.79	10.67	12.32	6.59	5.63	7.52				
HEMBA1000991	3.99	3.51	3.27	7.03	8.03	8.59	3.11	5.46	4.41	**	+		
HEMBA1001007	6.98	3.16	4.1	4.53	6.32	6.25	5.08	5.14	4.03				
HEMBA1001008	3.18	2.08	1.67	6.05	4.43	4.59	2.99	3.85	3.36	*	+		
HEMBA1001009	3.19	2.06	1.89	3	2.73	3.35	2.83	4.13	2.55				
HEMBA1001014	5.39	3.12	5.74	9.86	11.08	12.45	4.65	7.98	7.55	**	+		
HEMBA1001017	7.4	4.83	4.74	5.73	6.28	5.4	4.08	4.41	5.88				
HEMBA1001019	2.85	2.29	1.26	2.91	2.72	2.07	1.51	2.11	2.14				
HEMBA1001020	3.1	1.76	1.25	4.02	4.91	3.89	2.56	2.42	2.65	*	+		
HEMBA1001021	5.67	3.26	3.56	5.27	3.84	4.59	5.11	3.82	6.55				
HEMBA1001022	4.52	3.09	3.23	5.25	4.72	3.27	2.64	3.83	3.89				
HEMBA1001024	1.94	0.42	0.87	1.28	1.11	2.19	1.54	1.4	1.01				
HEMBA1001026	1.87	1.27	0.7	1.76	2.89	2.28	1.38	1.06	1.68				
HEMBA1001043	2.16	1.91	1.95	3.51	4.01	3.96	1.57	1.82	0.63	**	+		
HEMBA1001051	12.22	4.76	5.28	19.03	15.88	16.82	10.42	7.53	10.73	*	+		
HEMBA1001052	1.62	0.97	1.98	2.53	4.21	2.8	2.24	1.49	2.61				
HEMBA1001059	6.89	2.24	2.49	4.96	3.77	4.85	4.31	4.18	4.43				
HEMBA1001060	7.98	3.88	4.72	10.32	9.35	8.51	6.1	5.55	6.56	*	+		
HEMBA1001064	5.36	3.84	3.22	6.43	5.68	4.77	2.55	3.39	3.71				
HEMBA1001071	1.62	1.41	0.32	16	17.18	11.61	12.79	12.04	12.64	**	+	**	+
HEMBA1001077	4.45	3.8	1.96	11.6	9.35	8.57	3.08	5.61	3.95	**	+		
HEMBA1001078	14.1	8.18	8.99	5.43	6.25	7.02	4.32	6.96	5.16				
HEMBA1001080	5.79	3.95	2.49	3.69	5.23	5.89	5.35	4.03	3.93				
HEMBA1001084	5.31	2.86	2.62	7.71	7.07	6.47	5.73	4.4	5.39	*	+		
HEMBA1001085	13.38	7.46	10.01	19.29	18.48	14.18	11.36	11.18	10.99	*	+		
HEMBA1001088	5.8	4.05	4.96	5.45	4.2	4.92	5.6	5.06	6.59				
HEMBA1001093	2.01	1.13	0.59	2.57	2.37	1.64	1.63	2.12	1.53				
HEMBA1001094	0.9	1.06	0.61	2.27	2.81	2.04	1.48	1.38	2.02	**	+	*	+
HEMBA1001099	2.64	3.87	2.39	4.48	2.58	3.18	1.73	2.49	1.54				
HEMBA1001104	4.32	2.56	3.02	5.08	3.19	2.29	3.64	4.68	2.66				
HEMBA1001109	15.93	10.15	10.15	27.48	26.01	22.62	15.71	11.93	11.35	**	+		
HEMBA1001114	8.6	5.78	5.64	9.84	9.77	10.41	14.65	11.13	18.58	*	+	*	+
HEMBA1001121	2.07	1.57	0.99	2.33	3.89	3.11	2.34	1.82	1.7	*	+		
HEMBA1001122	2.51	5.06	1.5	14.85	12.94	9.66	6.46	7.06	7.13	**	+	*	+
HEMBA1001123	10.26	5.27	4.03	8.74	8.81	11.74	6.7	7.3	6.19				
HEMBA1001133	4.14	2.91	3.18	3.04	2.73	4.12	2.58	3.25	4.04				
HEMBA1001137	9.39	4	4.74	6.72	8.14	6.94	3.8	6.14	4.6				
HEMBA1001140	6.82	5.7	6.11	10.25	12.69	12.18	4.71	6.45	5.99	**	+		
HEMBA1001144	14.92	3.84	7.57	18.27	23.75	20.85	12.2	8.33	12.65	*	+		
HEMBA1001145	28.51	33.95	19.22	28.92	30.82	30.17	44.7	41.59	36.72			*	+
HEMBA1001158	5.04	3.15	2.61	5.99	3.8	6.16	5.34	3.86	4.7				
HEMBA1001172	5.81	3.09	2.82	8.57	8.02	8.53	5.72	4.06	4.92	*	+		
HEMBA1001174	2.3	2.42	1	1.59	2.22	1.73	1.99	2.72	1.46				
HEMBA1001175	4.94	2.83	3.63	9.64	8.74	8.9	6.25	5.58	6.09	**	+	*	+
HEMBA1001182	15.48	8.24	12.75	16.98	16.95	14.52	6.34	9.16	8.55				
HEMBA1001184	1.37	1.11	1.17	2.46	2.2	1.94	1.7	1.64	1.09	**	+		
HEMBA1001192	1.14	1.3	0.71	1.4	1.96	2.74	1.17	1.75	1.29				
HEMBA1001196	9.67	6.82	7.53	12.04	9.93	10.61	8.76	5.56	6.62				
HEMBA1001197	26.77	18.72	19.29	43.93	39.7	25.47	17.6	13.26	17.88				
HEMBA1001208	4.45	2.51	2.06	2.43	4.11	3.2	2.93	2.71	2.12				
HEMBA1001213	4.18	2.48	2.29	4.96	5.22	3.94	3.68	3.27	5.1				
HEMBA1001214	28.24	15.89	17.42	11.21	10.37	12.48	8.74	7.69	7.51			*	-

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Table 176

HEMBA1001221	2.19	1.18	0.78	2.28	2.36	2.53	2.4	3.63	1.51				
HEMBA1001225	1.21	1.77	1.22	2.62	2.13	1.37	0.82	1.74	2.82				
HEMBA1001226	13.52	10.49	8.9	18.36	20	19.62	7.7	10.44	7.45	**	+		
HEMBA1001228	13.05	5.12	4.29	9.55	8.22	7.69	6.04	7.48	7.86				
HEMBA1001229	12.71	9.28	6.69	8.25	7.48	7.38	10.2	8.81	12.42				
HEMBA1001235	4.86	4.97	4.74	7.89	8.06	6.71	5.12	7.06	11.33	**	+		
HEMBA1001238	5.14	3.54	3.32	7.04	6.92	8.57	3.98	4.55	5.25	*	+		
HEMBA1001242	9.9	9.56	8.33	13.88	6.68	13.26	5.82	6.16	5.11			**	-
HEMBA1001247	4.46	1.61	1.9	3.57	3.49	3.72	3.78	3.48	3.42				
HEMBA1001253	5.27	3.3	2.61	4.73	4.85	2.62	2.61	2.92	2.88				
HEMBA1001257	3.88	2.26	2.32	3.08	5.15	4.69	1.41	2.58	1.9				
HEMBA1001261	30.79	16.66	18.37	18.07	18.08	21.82	20.19	23.46	27.67				
HEMBA1001262	2.76	4.04	1.52	6.54	5.42	3.57	2.84	3.16	4.61				
HEMBA1001265	5.3	6.7	4.27	9.23	8.19	10.09	4.34	5.27	5.82	*	+		
HEMBA1001266	7.76	6.62	6.38	9.89	9.6	8.87	6.28	5.38	7.65	**	+		
HEMBA1001269	37.26	20.56	22.9	18.88	18.77	19.35	8.45	11.29	14.06			*	-
HEMBA1001272	1.9	1.41	1.17	1.81	2.19	2.98	1.62	1.83	1.14				
HEMBA1001279	7.18	4.55	5.66	6.03	6.98	6.47	3.39	5.47	3.9				
HEMBA1001281	5.42	5.55	6.33	11.93	16.02	13.78	5.82	4.84	7.89	**	+		
HEMBA1001286	25.93	14.58	10.17	19.52	21.27	19.41	15.05	12.01	17.84				
HEMBA1001289	4.9	3.9	2.72	4.42	4.59	5.54	4.24	2.99	5.3				
HEMBA1001291	12.14	5.79	5.07	8.25	5.62	6.51	5.37	5.12	8.98				
HEMBA1001294	3.24	2.44	2.03	4.94	4.48	4.82	2.73	2.45	3.08	**	+		
HEMBA1001296	3.68	1.37	1.28	2.91	2.24	3.02	2.56	2.34	2.65				
HEMBA1001297	5.4	4.74	4.72	5.79	6.42	4.8	3.21	2.6	2.27			**	-
HEMBA1001299	6.03	3.81	4.28	7.69	11.74	10.72	5.99	5.39	5.03	*	+		
HEMBA1001302	6.53	3.1	5.55	4.99	5.75	7.13	4.2	5.14	4.56				
HEMBA1001303	3.57	2.21	0.92	2.41	4.91	3.42	1.52	2.66	2.14				
HEMBA1001306	22.18	12.36	12.24	18.89	23.21	22.17	16.22	12.41	17.9				
HEMBA1001308	11.41	6.87	7.33	12.58	12.35	13.73	8.36	8.24	9.57	*	+		
HEMBA1001310	7.91	5.67	6.18	9.02	7.1	8.4	7.65	6.89	8.59				
HEMBA1001312	6.83	4.78	4.59	4.91	5.69	6.9	6.83	6.24	6.66				
HEMBA1001319	0.37	0.17	0.45	0.79	0.92	1.12	0.66	2.44	0.75	**	+		
HEMBA1001321	7.21	5.19	6.74	8.06	10.08	9.08	6.21	7.42	7.75	*	+		
HEMBA1001323	4.23	3.25	2.82	10.32	10.14	7.03	8.56	8.82	9.24	**	+	**	+
HEMBA1001326	5.74	3.25	2.25	3.17	5.59	5.42	5.13	3.49	5.64				
HEMBA1001327	2.36	2.51	1.03	2	2.41	3.09	2.74	2.46	3.87				
HEMBA1001330	5.82	5.46	4.35	11.86	14.54	13.29	6.08	7.36	9.3	**	+		
HEMBA1001348	3.13	2.19	2.78	4.2	2.23	2.88	1.71	2.63	2.74				
HEMBA1001350	12.36	10.68	7.51	15.66	13.69	14.52	11.25	9.44	10.45	*	+		
HEMBA1001351	8.18	6.48	5.91	13	14.47	12.39	10.67	8.35	8.14	**	+		
HEMBA1001352	7.26	6.11	6.06	7.73	6.7	6.17	5.26	7.29	6.09				
HEMBA1001353	31.3	26.87	27.53	25.75	22.23	20.82	12.94	17.74	19.72	*	-	**	-
HEMBA1001358	34.05	17.05	14.31	20.81	35.28	26	9.32	9.14	12.44				
HEMBA1001361	1.82	1.14	2.1	2.53	3.2	3.65	3	2.26	2.92	*	+	*	+
HEMBA1001364	1.53	0.54	0.65	1.45	1.91	1.58	2.49	1.92	1.51				
HEMBA1001375	3.85	2.39	2.36	2.46	4.27	4.44	3.43	3.13	3.87				
HEMBA1001377	8.53	6.83	5.73	14.04	14.14	13.21	6.15	8.25	6.71	**	+		
HEMBA1001383	2.54	1.25	1.73	3.25	2.57	3.3	1.34	2.99	1.96				
HEMBA1001387	4.07	1.84	3.25	5.31	4.33	4.27	3.43	4.91	3.24				
HEMBA1001388	4.68	4.67	4.87	6.78	7.58	7.44	4.52	4.77	5.63	**	+		
HEMBA1001390	7.44	5.12	5.37	11.6	11.73	11.98	10.29	9.6	11.06	**	+	**	+
HEMBA1001391	1.33	1.22	1.11	3.9	2.02	2.65	2.4	1.36	1.99	*	+		
HEMBA1001398	5.47	2.84	3.19	6.23	6.58	7.24	3.41	4.42	5.15	*	+		
HEMBA1001405	5.26	1.42	2.09	2.65	2.11	2.81	3.1	2.12	3.28				
HEMBA1001406	3.16	2.03	2.11	4.74	3.74	4.54	2.55	3.04	2.7	*	+		

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Table 177

HEMBA1001407	5.43	1.65	2.98	3.95	4.01	3.47	2.95	2.92	2.93				
HEMBA1001411	2.17	0.69	0.63	2.51	1.83	3.63	1.29	1.35	1.63				
HEMBA1001413	5.49	2.49	2.2	4.28	3.2	3.97	3.24	2.49	2.68				
HEMBA1001414	3.79	2.32	2.38	3.06	1.8	2.44	2.65	3.55	3.21				
HEMBA1001415	6.49	2.16	2.76	5.46	6.84	6.46	4.32	4.17	5.11				
HEMBA1001416	6.22	3.74	3.23	8.62	6.54	6.82	5.91	4.3	6.02				
HEMBA1001432	5.37	2.98	3.43	7.69	6.86	7.06	3.39	4.18	4.43	*	+		
HEMBA1001433	4.8	2.47	2.21	6.26	5.3	4.79	3.29	2.49	2.37				
HEMBA1001435	8.18	4.71	5.41	14.34	11.54	13.2	6.78	6.29	7.26	**	+		
HEMBA1001442	1.65	1.46	0.73	2.67	3.31	2.57	0.77	1.88	2.03	*	+		
HEMBA1001446	9.08	2.53	3.23	6.88	6.71	6.42	5.95	6.22	6.04				
HEMBA1001450	7.08	5.32	4.43	8.06	5.46	8.96	5.99	5.4	5.68				
HEMBA1001454	10.16	4.17	5.03	16.08	14.78	15.21	9.95	9.22	10.42	**	+		
HEMBA1001455	1.25	1.28	0.63	2.33	2.23	1.74	2.53	2.34	2.01	*	+	**	+
HEMBA1001459	3.35	1.42	1.26	1.85	2.02	1.94	1.14	1.39	2.31				
HEMBA1001461	8.81	3.16	4.05	10.82	10.26	6.95	6	5.33	4.95				
HEMBA1001462	2.66	2.42	2.15	2.1	1.78	2.07	1.34	1.53	2.31				
HEMBA1001463	7.17	2.73	3.52	7.24	7.08	8.95	4.33	5.14	4.39				
HEMBA1001469	7.79	8.03	2.81	8.15	8.71	7.67	5.88	4.2	6.47				
HEMBA1001473	2.06	0.9	0.31	1.64	1.59	1.3	1.54	1.11	1.32				
HEMBA1001477	1.25	0.8	0.62	0.91	1.28	0.76	1.34	2.38	1.44				
HEMBA1001478	2.09	0.93	1.34	1.5	1.78	0.98	1.62	2.3	1.59				
HEMBA1001480	12.07	6.47	7.53	8.82	7.12	9.89	6	6.87	5.33				
HEMBA1001483	4.46	3.27	2.35	2.86	3.34	4.48	1.86	2.27	1.82				
HEMBA1001490	1.81	1.4	1.03	1.82	1.46	1.52	1.48	2.37	1.32				
HEMBA1001495	36.22	21.61	21.87	15.42	21.1	17.04	16.21	19.62	20.73				
HEMBA1001497	7.26	3.96	4.28	11.8	9.61	9.85	5.21	4.28	5.2	*	+		
HEMBA1001510	13.72	5.93	6.56	13.7	15.62	12.58	10.78	9.6	9.58				
HEMBA1001515	2.6	2	0.87	2.75	3.2	2.93	2.35	3.19	2.52				
HEMBA1001517	1.89	1.95	1.22	2.95	2.33	2.76	1.72	1.66	2.42	*	+		
HEMBA1001522	3.61	1.7	1.12	1.99	2.84	1.73	1.04	1.87	1.3				
HEMBA1001526	5.16	2.43	3.68	6.63	4.1	5.88	3.55	3.16	3.42				
HEMBA1001533	8.95	4.93	4.41	7.97	8.75	10.67	4.59	5.06	4.92				
HEMBA1001547	35.19	25.44	22.4	15.45	14.19	13.27	6.7	4.99	4.47	*	-	**	-
HEMBA1001552	8.07	6.24	3.86	9.62	10.94	7.97	8.18	5.74	5.97				
HEMBA1001553	16.17	10.48	11.7	14.97	19.64	15.26	19.38	22.7	26.62			*	+
HEMBA1001557	8.77	5.74	4.35	8.02	8.99	7.7	7.33	5.59	10.39				
HEMBA1001563	3.9	1.92	1.89	5.08	3.9	4.71	2.33	3.96	2.78				
HEMBA1001566	3.98	2.49	2.79	5.22	9.83	5.76	3.59	4.31	4.01				
HEMBA1001569	8.8	4.36	5.19	13.14	14.49	14.76	6.66	7.84	10.58	**	+		
HEMBA1001570	10.01	5.49	7.22	16.18	15.76	21.41	6.88	8.18	7.08	*	+		
HEMBA1001579	14.95	9.44	8.88	11.45	10.82	11.3	6.85	6.64	9.61				
HEMBA1001581	6.6	2.62	2.74	9.65	8.35	7.34	4.2	4.87	7.29	*	+		
HEMBA1001582	1.39	1.89	0.99	1.46	1.52	1.21	1.87	1.43	1.14				
HEMBA1001585	3.5	1.76	2.06	4.04	4.61	4.34	2.06	2.32	2.78	*	+		
HEMBA1001589	5.07	3.16	2.15	3.41	3.1	3.21	3.05	2.93	3.94				
HEMBA1001595	13.49	4.3	6.8	10.71	10.28	9.89	6.83	8.2	8.67				
HEMBA1001604	5.72	2.28	3.75	6.52	7.03	5.34	2.89	3.22	3.58				
HEMBA1001608	8.03	3.96	3.18	8.15	6.4	9.15	2.3	4.25	3.65				
HEMBA1001615	46.6	32.92	22.49	33.05	34.32	33.44	126.5	104.9	149.7			**	+
HEMBA1001620	14.48	8.32	7.64	17.62	16.71	15.28	9.29	10.91	11.09	*	+		
HEMBA1001621	9.93	5.63	3.68	7.55	6.93	6.59	5	4.37	6.21				
HEMBA1001635	5.73	3.82	2.42	4.14	4.05	5.67	2.93	3.94	3.69				
HEMBA1001636	4.39	1.44	3.08	3.97	3.02	3.88	3.71	3.49	4.55				
HEMBA1001640	3.49	0.97	1.46	3.57	2.02	3.07	2.4	3.06	2.05				
HEMBA1001647	6.4	2.49	4.47	3.2	5.99	5.63	2.28	4.03	4.16				

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Table 178

HEMBA1001651	21.79	9.98	12.75	16.31	17.89	15.92	12.62	14.58	15.88				
HEMBA1001655	4.81	3.57	3.37	4.17	7.59	5.82	3.99	4.47	4.7				
HEMBA1001658	2.18	2.11	2.13	1.33	1.53	2.6	1.84	1.15	1.86				
HEMBA1001661	8.45	3.05	2.97	4.66	4.8	5.77	3.88	4.28	4.23				
HEMBA1001665	5.86	2.62	4.27	4.6	3.94	3.51	4.69	4.17	4.52				
HEMBA1001670	4.7	2.98	3.53	6.5	7.04	7.21	4.56	5.94	4.89	**	+		
HEMBA1001672	2.9	1.62	1.17	2.74	2.64	2.91	2.23	3.35	2.84				
HEMBA1001673	9.39	3.95	5.37	12.29	9.95	9.16	6.04	3.4	6.06				
HEMBA1001675	2.77	1.09	1.9	3.14	3.42	1.99	2.07	3.04	2.09				
HEMBA1001676	66.2	42	41.28	59.83	62.25	61.28	35.33	41.76	48.98				
HEMBA1001678	23.82	16.82	12.46	26.08	27.44	24.59	15.29	14.2	16.03				
HEMBA1001680	7.07	3.71	3.69	6.51	7.15	6.71	4.41	4.86	5.34				
HEMBA1001681	1.95	0.92	1.52	1.86	1.78	2.38	1.26	2.56	1.49				
HEMBA1001684	10.32	4.07	5.37	13.29	14.64	14.01	8.6	7.77	8.12	*	+		
HEMBA1001695	1.84	2.2	0.62	1.62	1.54	2.31	1.72	2.13	0.77				
HEMBA1001702	3.21	1.66	2.35	4.83	3.35	4.17	3.17	4.1	3.6				
HEMBA1001709	3.9	1.96	2.65	5.53	4.06	6.56	5.94	7.83	7.54			**	+
HEMBA1001711	2.38	2.81	1.61	5.64	7.85	8.65	3.33	2.8	5.34	**	+		
HEMBA1001712	2.87	1.69	2.03	2.84	2.47	3.33	3.23	2.26	2.84				
HEMBA1001714	27.51	15.33	17.22	17.64	16.58	15.17	22.02	17.65	27.85				
HEMBA1001717	1.6	0.57	0.95	1.72	1.13	1.76	8.51	5.96	6.55			**	+
HEMBA1001718	3.34	3.04	3.56	7.23	5.88	7.76	3.79	4.78	3.44	**	+		
HEMBA1001723	3.28	1.43	2.31	5.16	4.28	5.3	2.9	4.31	2.84	*	+		
HEMBA1001731	2.16	1.22	2.13	2.79	1.84	2.37	1.77	2.95	2.23				
HEMBA1001734	2.33	0.57	2.06	3.71	2.97	2.91	2.16	2.87	2.2				
HEMBA1001736	8.5	4.87	4.76	7.17	7.6	9.06	7.56	6.14	10.7				
HEMBA1001741	1.43	1.25	0.91	2.83	2.87	2.84	0.76	1.93	1.43	**	+		
HEMBA1001744	1.28	0.91	0.85	1.4	1.01	1.73	0.65	1.88	1.22				
HEMBA1001745	3.12	1.1	1.48	2.46	2.57	2.63	2.55	3.03	2.51				
HEMBA1001746	1.85	2.08	1.47	2.46	2.29	3.39	2.8	3.77	3.54			*	+
HEMBA1001761	4.88	2.73	3.04	7.7	5.44	7.35	2.96	5.66	4.32	*	+		
HEMBA1001762	1.84	0.76	1.19	2.52	2.18	2.84	1.18	3.82	1	*	+		
HEMBA1001781	3.69	1.25	2.05	4.27	2.77	4.83	2.36	3.3	2.22				
HEMBA1001784	5.2	3.84	2.76	3.59	2.92	3.32	3.06	2.91	4.28				
HEMBA1001791	11.2	5.23	3.55	8.42	10	8.96	7.67	7.29	10.19				
HEMBA1001794	16.08	14.18	10.1	17.79	20.03	18.56	11.08	17.68	19.33	*	+		
HEMBA1001800	3.13	2.01	2.42	2.99	2.87	3.62	3.26	1.68	2.16				
HEMBA1001803	1.53	0.75	0.44	1.21	1.11	1.38	1.41	1.74	1.3				
HEMBA1001804	13.32	7.17	6.9	11.34	8.08	9.13	6.64	6.79	7.2				
HEMBA1001808	2.99	2.64	1.45	3.65	1.42	1.93	2.32	1.6	1.79				
HEMBA1001809	8.19	6.19	4.29	9.5	5.47	7.96	5.87	6.3	5.81				
HEMBA1001811	22.78	13.64	9.05	9.98	11.16	7.43	11.09	9.04	12.53				
HEMBA1001815	6.31	3.66	3.82	9.75	9.09	7.86	4.84	3.89	4.99	*	+		
HEMBA1001816	2.42	2.34	2.86	3.29	2.61	3.73	2.83	1.8	2.99				
HEMBA1001819	6.29	5.74	3.76	9.76	8.91	7.84	4.59	4.2	3.42	*	+		
HEMBA1001820	0.7	1.31	0.35	1.28	0.85	0.69	1	1.34	0.88				
HEMBA1001822	14.41	5.14	6.88	15.5	12.29	15.38	7.82	5.44	7.89				
HEMBA1001824	8.95	4.75	6.46	8.72	13.86	15.64	6.51	9.15	7.54				
HEMBA1001835	1.68	1.35	0.6	1.34	1.74	3.48	1.4	1.22	1.48				
HEMBA1001844	7.57	4.41	3.42	10.11	10.97	6.9	6.82	4.22	6.02				
HEMBA1001847	7.9	4.44	3.77	6.2	5.53	6.41	3.82	3.06	3.92				
HEMBA1001849	8.79	2.94	4.27	12.39	11.89	10.26	7.27	5.07	7.41	*	+		
HEMBA1001850	7.06	2.55	2.83	6.48	6.52	7.6	4.57	4.3	4.89				
HEMBA1001861	1.79	0.52	1.23	3.32	3.68	4.21	1.63	1.37	1.83	**	+		
HEMBA1001862	20.07	14.3	16.51	10.49	11.03	16.7	24.43	27.68	20.89			*	+
HEMBA1001864	1.89	1.29	0.85	2.99	3	2.74	1.08	1.87	1.04	**	+		

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Table 179

HEMBA1001866	3.9	2.3	1.44	4.16	4.87	4.12	3.87	2.04	2.67				
HEMBA1001869	9.74	8.73	4.94	27.07	27.58	25.58	12.15	11.95	13.97	**	+	*	+
HEMBA1001871	74.25	58.85	43.65	34.31	39.06	32.3	22.21	20.99	22.52			*	-
HEMBA1001876	3.15	3.01	2.05	6.71	7.01	5.67	24.3	20.84	22.31	**	+	**	+
HEMBA1001878	8.91	7.59	5.14	7.69	6.34	6.19	2.57	4.4	3.62			*	-
HEMBA1001879	6.77	3.64	3.77	7.79	7.79	8.38	5.4	7.09	7.12	*	+		
HEMBA1001884	8.03	4.66	4.9	8.15	7.93	9.25	2.34	3.47	2.61				
HEMBA1001886	15.37	8.23	7.45	18.06	17.92	20.6	6.22	8.67	8.91	*	+		
HEMBA1001888	4.74	2.28	2.28	8.53	6.01	5.71	3.99	3.23	5.19	*	+		
HEMBA1001890	6.82	5.35	4.39	17.01	13.2	14.58	10.35	9.13	10.28	**	+	**	+
HEMBA1001896	7.21	3.51	4.27	4.48	4.55	6.32	4.5	3.56	4.29				
HEMBA1001899	10.27	5.12	6.13	12.84	16.36	13.59	19.93	20.02	20.79	*	+	**	+
HEMBA1001904	117.8	90.63	69.63	121.8	145.7	135.1	54.06	69.53	68.48				
HEMBA1001910	2.98	1.61	1.31	1.77	1.8	2.33	2.01	1.92	2.16				
HEMBA1001911	24.54	11.64	15.86	17.52	15.24	14.86	10.3	9.59	10.07				
HEMBA1001912	20.82	8.69	15.18	15.64	15.33	18.75	6.84	9.35	7.93				
HEMBA1001913	11.57	4.6	5.78	9.2	8.02	9.12	5.36	7.66	8.31				
HEMBA1001915	2.07	1.75	1.56	2.72	4.13	3.37	2.79	1.65	1.94	*	+		
HEMBA1001918	2.07	1.25	1.13	3.95	3.76	3.13	1.5	2.66	1.53	**	+		
HEMBA1001921	7.05	7.38	3.11	5.25	3.04	7.8	3.53	3.11	2.74				
HEMBA1001931	0.78	1.98	0.41	1.78	1.48	1.79	0.69	1.82	0.96				
HEMBA1001939	2.45	1.1	1.29	2.61	2.56	3.15	2.04	3.08	2.2				
HEMBA1001940	3.74	2.59	1.93	4.33	6.11	5.9	2.78	3.06	3.22	*	+		
HEMBA1001942	3.67	2.27	1.69	2.35	3.04	3.41	1.26	2.11	2.03				
HEMBA1001944	9.44	4.28	2.7	6.72	6.77	6.95	5.78	5.16	5.81				
HEMBA1001945	2.07	0.91	0.94	1.56	3.05	1.77	1.66	1.79	2.71				
HEMBA1001950	4.31	3.64	2.4	3.3	1.98	4.19	2.53	3.33	2.77				
HEMBA1001951	11.47	5.14	7.18	8.76	8.49	10.31	7.11	7.14	6.62				
HEMBA1001958	5.93	3.29	3.76	7.31	5.94	5.87	2.95	3.04	4.22				
HEMBA1001960	5.09	2.29	3.83	2.58	2	3.56	3.69	2.82	3.05				
HEMBA1001962	0.53	0.49	0.61	0.68	0.72	0.97	-0.01	1.07	0.54				
HEMBA1001964	1.04	0.26	1.15	2.39	2.99	2.5	0.67	1.12	1.07	**	+		
HEMBA1001967	5.08	3.46	3.83	6.72	5.35	6.55	3.95	4.57	3.93	*	+		
HEMBA1001979	2.59	1.65	1.24	2.97	3.02	3.75	2.54	2.41	2.4	*	+		
HEMBA1001987	6.47	2.58	3.01	7.96	9.29	7.63	5.55	5.23	5.01	*	+		
HEMBA1001991	7.79	3.05	3.16	10.3	8.9	8.81	6.21	4.84	5.65	*	+		
HEMBA1002003	6.67	2.83	3.92	3.54	4.68	6.3	5.41	4.34	5.17				
HEMBA1002005	4.44	1.76	2.03	5.73	4.88	5.69	3.58	2.87	3.42	*	+		
HEMBA1002008	2.92	0.92	1.99	4.42	4.45	4.33	2.3	2.71	2.6	*	+		
HEMBA1002018	7.24	3.29	3.8	4.79	5.31	4.52	3.14	4.37	3.39				
HEMBA1002022	0.68	0.34	0.54	1.12	1.17	1.66	0.59	0.97	1.25	*	+		
HEMBA1002029	147.9	114.2	64.17	209.3	183.3	187.5	83.85	70.94	83.09	*	+		
HEMBA1002030	3.84	2.17	1.78	2.59	2.01	2.76	1.95	2.52	1.44				
HEMBA1002035	4.53	2.83	2.27	3.74	3.23	4.73	2.32	2.93	2.77				
HEMBA1002037	7.19	3.71	4.11	7.77	6.62	7.18	5.2	4.49	4.12				
HEMBA1002038	5.05	3.39	2	4.89	4.12	6.29	3.56	4.65	2.86				
HEMBA1002039	2.43	1.42	2.68	4.62	4.34	5.48	2.31	3.78	2.6	**	+		
HEMBA1002042	5.07	5.1	4.66	5.37	6.66	7.8	3.75	3.26	4.84				
HEMBA1002043	9.02	4.29	4.09	8.45	7.53	9.32	5.8	6.07	6.51				
HEMBA1002048	3.59	2.88	2.34	3.02	3.12	3.4	3.49	2.47	3.92				
HEMBA1002049	6.44	2.94	4.68	7.87	9.3	8.66	5.4	4.91	5.09	*	+		
HEMBA1002053	6.69	4.81	4.26	7.69	7.89	9.03	5.94	6.61	5.76	*	+		
HEMBA1002055	9.71	8.18	6.93	9.3	5.31	10.84	11.8	6.23	11.57				
HEMBA1002056	10.47	4.85	5.55	4.12	3.5	3.57	2.73	3.84	2.21				
HEMBA1002061	2.87	2.19	2.53	7.31	4.68	4.5	2.4	3.51	2.69	*	+		
HEMBA1002080	60.84	42.27	48.29	35.05	22.5	22.95	22.84	15.7	24.41	*	-	**	-

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Table 180

HEMBA1002084	1.07	0.5	0.79	1.77	1.77	2.12	1.8	1.72	1.8	**	+	**	+
HEMBA1002085	15.53	10.5	9.09	3.93	5.17	5.54	4.22	4.66	4.34	*	-	*	-
HEMBA1002092	6.36	2.95	3.86	3.82	3.84	2.97	3.77	3.66	5.02				
HEMBA1002098	2.76	1.13	1.81	2.4	2.24	2.53	2.57	2.73	1.55				
HEMBA1002100	32.5	21.44	18.67	25.5	28.16	25.35	18.35	13.17	17.71				
HEMBA1002101	14.23	9.44	8.67	29.98	21.28	21.61	20.63	10.83	13.44	*	+		
HEMBA1002102	5.78	2.45	5.61	10.26	9.25	10.76	5.53	7.91	7.68	**	+		
HEMBA1002105	3.54	2.37	3.22	6.12	5.06	5.65	3.82	6.51	5.09	**	+		
HEMBA1002107	11.45	5.11	6.25	8.68	8.52	8.38	12.57	12.66	17.5				
HEMBA1002113	32.25	19.17	17.4	39.34	45.35	45.81	28.29	21.95	34.31	*	+		
HEMBA1002119	2.11	2.17	0.99	2.79	2.14	2.54	2.06	2.87	1.79				
HEMBA1002125	5.95	2.4	2.92	5.45	9.25	7.16	7.44	6.34	6.72				
HEMBA1002131	5.93	2	3.14	4.14	4.06	4.13	3.5	4.3	3.28				
HEMBA1002133	6.81	5.25	2.52	6.36	5.83	7.36	4.72	7.3	4.48				
HEMBA1002139	1.09	0.26	0.36	1.2	0.84	1.33	0.99	2.43	0.56				
HEMBA1002141	1.29	0.49	1.21	2.38	1.03	1.99	0.5	1.42	1.34				
HEMBA1002144	5.69	3.1	2.06	7.29	6.78	8.63	2.59	3.43	5.33	*	+		
HEMBA1002147	21.38	10.63	10.33	16.26	8.66	14.72	7.7	9.8	14.04				
HEMBA1002150	19.09	10.95	13.29	13.45	10.91	11.19	15.49	16.53	17.44				
HEMBA1002151	5.57	4.52	3.73	5.15	5.43	4.75	6.45	4.35	4.86				
HEMBA1002153	2.06	0.67	0.65	2.43	2.33	1.79	1.41	1.49	1.24				
HEMBA1002156	6.64	2.07	2.79	3.49	2.76	4.92	4.24	4.29	3.26				
HEMBA1002160	9.96	4.66	4.52	11.03	12.78	11.54	5.12	4.86	6.62	*	+		
HEMBA1002161	5.93	2.84	3.76	7.56	5.8	7.54	3.32	4.13	3.25				
HEMBA1002162	7.92	3.54	4.29	9.23	12.27	9.59	6.96	4.68	6.43	*	+		
HEMBA1002163	16.52	8.9	8.29	30.66	23.8	18.1	23.47	24.41	36.58	*	+	*	+
HEMBA1002164	6.58	3.37	3.2	7.61	7.12	6.96	5.68	4.84	5.16				
HEMBA1002166	39.64	27.28	27.86	36.11	45.05	43.8	20.24	20.85	22.71				
HEMBA1002167	4.76	1.86	1.62	2.99	2.78	2.27	3.13	3.05	2.27				
HEMBA1002173	5.99	4.25	4.52	7.86	9.55	7.59	5.43	4.55	6.47	*	+		
HEMBA1002177	7.43	2.78	2.92	3.23	3.61	5.94	3.11	3.88	4.09				
HEMBA1002178	5.72	4.28	4.98	4.38	4.69	4.23	3.54	5.04	4.32				
HEMBA1002179	38.56	31.74	22.53	17.89	19.71	18.71	27.72	23.97	26.16				
HEMBA1002185	6.54	3.16	3.12	9.32	10.15	8.6	6.14	5.78	6.76	*	+		
HEMBA1002188	8.98	4.74	6.39	7.79	6.15	7.58	6.43	5.81	6.6				
HEMBA1002189	3.48	3.26	1.78	4.27	5.47	4.09	2.69	3.88	3.54				
HEMBA1002191	8.3	3.89	4.67	8.84	6.83	6.19	5.91	5.98	6.36				
HEMBA1002192	5.28	4.26	4.29	8.27	6.01	5.9	2.94	2.49	2.82			**	-
HEMBA1002195	5.98	3.67	4.11	6.21	5.77	4.89	3.93	4.26	3.98				
HEMBA1002196	1.16	1.29	1.53	2.22	2.69	3.34	2.25	2.29	2.94	*	+	**	+
HEMBA1002199	2.9	1.1	2.41	4.59	4.69	3.07	3.88	2.62	3.82				
HEMBA1002204	3.61	1.66	0.98	2.22	2.66	1.99	3.47	1.11	1.87				
HEMBA1002208	48.26	35.92	30.61	48.99	56.44	45.32	18.77	22.83	23.91			*	-
HEMBA1002212	1.63	2.93	1.64	4.46	4.61	4.63	3.31	1.91	1.67	**	+		
HEMBA1002215	6.24	3.92	3.6	5.45	4.91	5.62	4.3	4.83	3.3				
HEMBA1002217	18.63	10.54	10.96	10.92	19.47	21.75	8.18	9.72	7.73				
HEMBA1002220	2.36	1.42	1.13	2.73	2.21	2.69	1.63	2.43	2.05				
HEMBA1002226	7.06	3.57	4.14	9.44	8.41	9.81	3.48	7.93	5.79	*	+		
HEMBA1002227	23.89	11.28	12.65	63.81	64.96	61.28	43.22	41.38	46.55	**	+	**	+
HEMBA1002229	12.93	9.6	8.96	22.59	17.4	16.24	11.18	9.43	9.71	*	+		
HEMBA1002237	2.73	1.56	1.22	2.88	3.54	2.57	2.65	2.19	1.5				
HEMBA1002239	9.11	4.97	3.45	14.42	9.61	11	4.46	5.84	6.91				
HEMBA1002241	4.16	2.92	3.35	4.29	3.16	4.98	3.45	3.5	3.33				
HEMBA1002253	2	1.21	0.86	1.18	1.75	2.13	1.77	1.87	1.29				
HEMBA1002257	2.5	1.06	1.11	1.47	1.72	1.38	1.46	2.73	1.02				
HEMBA1002259	3.93	2.57	3.46	3.84	3.35	3.79	1.58	3.6	2.24				

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Table 181

HEMBA1002262	19.33	13.63	11.06	41.08	43.27	39.59	22.08	18	19.52	**	+		
HEMBA1002265	5.77	2.24	2.87	4.81	4.22	4.54	5.24	3.12	3.12				
HEMBA1002267	6.66	4.16	4.1	9.3	9.47	10.3	6.16	5.48	5.21	**	+		
HEMBA1002270	6.24	3.34	3.58	7.78	8.98	7.9	3.76	4.01	4.91	*	+		
HEMBA1002286	2.71	2.63	1.38	2.66	4.03	3.95	2.71	3.54	3.82				
HEMBA1002290	7.29	3.76	4.66	10.41	13.32	10.04	5.97	7.37	8.02	*	+		
HEMBA1002302	11.09	4.74	4.9	14.47	14.16	14.79	5.34	6.14	6.47	*	+		
HEMBA1002304	2.15	1.99	3.2	4.13	2.57	4.4	1.76	2.42	1.31				
HEMBA1002307	20.52	10.07	9.13	9.76	9.15	8.21	13.28	14.24	17.09				
HEMBA1002316	21.96	17.53	15.62	14.66	14.2	13.67	14.54	18.03	17.67				
HEMBA1002319	3.87	2.44	2.95	2.86	3.71	4.51	3	3.92	3.09				
HEMBA1002320	2.67	1.82	1.12	4.11	5.01	6.24	3.84	4.14	3.6	*	+	*	+
HEMBA1002321	1.46	2.38	0.87	3.05	1.97	2.21	1.05	1.18	1.29				
HEMBA1002328	4.66	1.71	1.99	5.92	5.51	4.89	3	3.99	2.69				
HEMBA1002333	4.92	1.14	2.37	2.57	3.45	2.77	2.04	3.2	1.93				
HEMBA1002337	5.38	3.22	4.87	9.22	12.3	11.34	4.19	5.44	4.11	**	+		
HEMBA1002339	23.81	10.43	6.17	11.11	15.1	14.91	11.67	12.27	12.43				
HEMBA1002341	7.39	3.74	4.25	4.55	4.12	3.82	6.09	5.66	5.69				
HEMBA1002348	2.07	1.83	0.9	1.44	1.88	2.08	1.92	2.6	1.34				
HEMBA1002349	1.51	1.42	0.34	1.38	1.3	1.96	1.46	2.19	1.38				
HEMBA1002353	1.79	1.25	2.28	2.64	3.11	3.43	2.11	1.34	1.36	*	+		
HEMBA1002356	13.39	6.02	7.85	8.42	10.26	11	4.88	6.24	6.12				
HEMBA1002357	136.4	89.6	109	142.6	135.4	152.8	57.09	66.8	75.58			*	-
HEMBA1002360	6.54	3.66	5.93	10.16	10.44	10.51	8.07	9.62	8.15	**	+	*	+
HEMBA1002363	9.05	6.26	4.11	8.4	5.32	7.47	3.78	3.67	4.84				
HEMBA1002365	2.33	1.04	1.69	2.69	1.93	1.79	0.53	1.83	2.11				
HEMBA1002370	2.04	0.84	0.68	5.63	6.49	6.21	1.4	3.02	2.46	**	+		
HEMBA1002374	8.05	4.75	3.85	6.96	7.96	4.55	6.91	5.19	7.37				
HEMBA1002376	22.58	10.7	11.64	20.42	22.01	21.09	9.22	9.95	12.27				
HEMBA1002377	22.23	20.26	24.74	17.13	16.56	16.97	12.65	5.84	13.5	*	-	*	-
HEMBA1002380	10.33	4.73	6.12	25.3	20.75	23.1	10.39	11.3	10.43	**	+		
HEMBA1002381	6.11	3.6	4.83	7.07	8.7	10.4	3.87	4.54	4.53	*	+		
HEMBA1002384	15.5	10.84	6.42	29.27	32.78	29.1	8.58	9.53	10.47	**	+		
HEMBA1002389	4.27	1.82	1.04	3.34	2.49	2.48	1.75	2.27	2.21				
HEMBA1002396	5.31	1.45	2.21	3.61	3.86	4.27	4.37	4.75	6.22				
HEMBA1002402	4.83	1.75	1.81	2.54	2.69	3.67	3.46	2.38	3.41				
HEMBA1002417	10.95	4.91	5.09	7.22	6.91	7.47	6.16	5.78	7.28				
HEMBA1002419	5.08	2.09	1.3	5.6	4.81	5.12	3.66	3.43	3.31				
HEMBA1002420	9.17	4.99	7.48	15.98	15.18	16.1	7.55	7.5	9.4	**	+		
HEMBA1002421	3.35	2.15	2.59	6.22	6.03	5.26	6.83	6.92	8.74	**	+	**	+
HEMBA1002423	1.54	0.63	0.83	2.44	3.48	3.88	1.7	2.52	2.63	*	+	*	+
HEMBA1002424	8.4	2.37	3.82	4.43	5.04	5.22	3.68	2.96	3.47				
HEMBA1002426	6.49	3.96	3.42	4.7	3.88	6.41	6.1	4.1	4.43				
HEMBA1002430	2.26	0.52	0.37	1.48	0.95	2.01	1.47	2.19	1.34				
HEMBA1002439	5.88	2.46	3.67	5.4	4.16	4.53	3.95	4.58	3.74				
HEMBA1002441	9.17	5.14	6.07	34.35	24.41	25.8	23.81	16.3	21.56	**	+	**	+
HEMBA1002454	5.79	2.67	3.42	5.87	3.7	3.81	3.97	3.14	3.78				
HEMBA1002458	25.18	17.65	26.81	56.49	54.86	61.69	25.04	31.59	38.07	**	+		
HEMBA1002460	13.9	7.3	5.63	4.27	4.5	4.21	3.8	3.84	3.88				
HEMBA1002462	5.97	3.49	2.63	4.68	5.48	5.1	5.76	6.26	5.62				
HEMBA1002465	1.48	0.35	0.87	1.94	1.91	2	2	1.62	1.54	*	+		
HEMBA1002469	10.61	5.54	6.1	9.43	9.29	9.35	6.49	6.37	7.65				
HEMBA1002475	2.44	1.25	1.2	2.62	1.19	1.93	1.75	2.35	1.4				
HEMBA1002477	4.33	2.21	3.54	6.33	6.45	9.03	4.12	5.33	4.08	*	+		
HEMBA1002480	12.76	7.21	8.4	13.9	9.22	9.97	6.6	9.31	9.9				
HEMBA1002481	4.17	1.44	3.57	5.7	5.97	7.71	3.35	4.98	3.12	*	+		

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Table 182

HEMBA1002486	8.76	6.38	4.66	8.52	8.8	10.2	5.18	4.82	7				
HEMBA1002490	4.65	2.87	1.43	3.68	2.57	3.08	3.01	1.75	3.98				
HEMBA1002495	3.72	2.75	1.63	4.11	3.81	4.48	2.24	3.36	3.9				
HEMBA1002498	2.75	1.45	1.13	1.68	1.82	1.19	2.23	1.05	1.96				
HEMBA1002501	4.03	2.44	2.73	2.79	3.44	4.73	2.7	2.56	4.15				
HEMBA1002503	5.04	2.61	2.84	6.45	4.88	5.28	3.23	3.79	3.13				
HEMBA1002504	8.07	4.4	4.13	10.71	10.32	10.08	4.47	6.58	5.92	*	+		
HEMBA1002508	5.99	4.98	4.38	8.82	14.4	16.34	4.8	6.77	5.33	*	+		
HEMBA1002513	8.6	4.28	4.52	7.08	4.68	6.71	4.93	3.86	4.51				
HEMBA1002515	4.33	1.73	2.07	3.29	2.16	3.66	2.65	1.63	3.58				
HEMBA1002524	9.35	6	4.75	8.16	6.47	7.51	5.77	5.05	6.67				
HEMBA1002538	4.58	2.05	1.84	2.98	3.05	4.53	2.16	2.92	2.68				
HEMBA1002542	8.07	5.4	5.41	9.41	8.04	9.27	4.65	5.75	5.16				
HEMBA1002544	3.1	1.76	1.69	4.47	3.6	3.68	2.18	2.17	2.61	*	+		
HEMBA1002546	50.52	34.29	29.94	56.51	60.33	61.14	35.34	44.64	38.68	*	+		
HEMBA1002547	2.2	1.72	2.07	1.6	3.25	2.8	2.97	4.34	2.32				
HEMBA1002550	7.14	5.4	3.96	4.54	4.38	4.87	6.51	4.38	5.24				
HEMBA1002551	5.47	2.09	2.27	5.04	4.39	3.41	4.06	3.2	3.87				
HEMBA1002552	12.19	3.86	6.34	10.16	9.24	10.66	6.5	6.73	6.78				
HEMBA1002555	1.98	0.86	1	1.95	2.49	2.76	2.25	1.97	2.82				
HEMBA1002558	7.34	3.99	4.45	10.47	9.14	11.18	5.75	4.9	5.48	*	+		
HEMBA1002561	1.53	2.23	1.45	3.76	4.16	3.85	2.34	2.9	2.42	**	+		
HEMBA1002562	2.58	1.09	1.24	1.55	1.58	1.46	1.13	1.38	1.77				
HEMBA1002568	4.34	2.05	1.84	2.65	3.18	3.63	2.01	3.91	2.77				
HEMBA1002569	10.12	2.96	3.15	6.04	6.91	7.8	6.66	5.49	5.73				
HEMBA1002570	17.18	8.39	8.43	7.74	7.84	6.32	4.15	4.68	4.47				
HEMBA1002574	9.13	5.2	4.08	4.71	4.69	3.46	6.41	4.34	4.04				
HEMBA1002583	2.63	1.94	1.44	4.35	4.76	4.81	4.07	4.23	4.71	**	+	**	+
HEMBA1002587	9.65	5.73	4.29	5.38	5.09	6.69	6.95	4.55	5.87				
HEMBA1002590	5	2.82	3.17	5.3	7.12	7.9	3.16	4.25	3.45	*	+		
HEMBA1002592	7.22	3.8	5.73	9.2	7.27	11.07	4.7	6.52	5.38				
HEMBA1002595	6.26	2.72	4.83	2.78	4.06	4.2	3.48	5.01	4.73				
HEMBA1002609	4.35	4.09	2.17	4.02	4.01	4.31	3.53	3.64	3.18				
HEMBA1002617	3.95	2.7	1.65	11.81	11.46	11.36	4.49	2.86	3.96	**	+		
HEMBA1002619	6.56	3.72	3.15	6.01	4.48	4.66	4.55	5.76	4.4				
HEMBA1002621	1.33	2.05	0.58	1.87	2.25	1.68	1.25	2.13	1.22				
HEMBA1002624	10.87	5.76	5.5	10.8	7.15	9.93	6.61	9.08	8.33				
HEMBA1002628	2.46	1.89	1.56	8.26	8.9	8.55	6.5	6.76	7.64	**	+	**	+
HEMBA1002629	2.92	1.59	1.72	2.35	1.78	3.13	2.15	2.22	2.55				
HEMBA1002632	3.01	3.25	2.45	3.55	4.56	5.56	2.28	3.32	2.22				
HEMBA1002645	5.23	3.12	3.3	9.71	9.85	8.47	4.08	4.56	3.84	**	+		
HEMBA1002651	2.74	3.3	3.7	3.63	3.14	3.96	3.35	3.43	3.18				
HEMBA1002652	10.09	4.55	2.8	3.94	7.21	6.45	4.43	4.54	4.59				
HEMBA1002659	10	4.51	4.33	9.97	11.66	8.87	6.05	6.33	5.41				
HEMBA1002661	4.42	2.54	1.79	6.87	7.34	8.27	4.97	3.82	3.85	**	+		
HEMBA1002666	3.37	1.93	1.85	2.66	2.68	3.23	2.59	2.71	2.16				
HEMBA1002667	3.38	2.19	2.12	5.95	5.18	5.02	0.91	3	2.2	**	+		
HEMBA1002673	24.31	16.62	13.86	16.81	24.76	24.88	10.84	15.49	10.36				
HEMBA1002678	6.22	4.52	2.39	8.83	7	9.06	5.27	5.81	5.58	*	+		
HEMBA1002679	6.14	2.98	2.3	7.06	5.91	5.92	4.9	4.03	4.55				
HEMBA1002688	2.43	1.85	1.49	1.28	2.14	1.93	0.91	1.94	1.12				
HEMBA1002696	5.94	3.2	2.68	4.46	5.16	4.1	3.48	3.38	3.28				
HEMBA1002703	14.6	8	9.65	11.88	14.48	12.25	7.74	9.23	10.55				
HEMBA1002706	14.74	6.11	9.63	11.39	13.51	13.79	6.16	6.12	6.47				
HEMBA1002712	5.57	3.22	3.91	7.46	9.02	7.13	2.62	3.73	3.7	*	+		
HEMBA1002715	7.56	4.05	6.71	7.13	9.71	10.17	4.38	6.93	5.48				

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Table 183

HEMBA1002716	2.33	1.79	1.1	2.97	1.95	2.33	1.67	1.27	1.06				
HEMBA1002718	16.72	11.81	9.31	17.97	12.98	15.17	10.44	10.19	11.13				
HEMBA1002728	9.67	3.54	5.97	10.6	12.96	15.33	7.76	5.08	9.8	*	+		
HEMBA1002730	7.86	2.52	3.4	5.36	7.91	6.74	6.78	4.96	7.37				
HEMBA1002734	7.73	4.31	3.55	7.93	6.46	7.46	5.62	6.29	6.83				
HEMBA1002742	3.65	1.6	2.01	2.64	2.74	2.6	1.48	2.29	1.92				
HEMBA1002746	6.82	4.06	4.19	4.98	4.66	5.4	2.78	4.2	3.33				
HEMBA1002748	4.16	2.16	3.32	2.53	4.45	4.03	2.42	2.8	3.88				
HEMBA1002750	6.45	3.44	3.09	5.38	6.22	7.28	3.44	2.24	3.97				
HEMBA1002755	6.83	3.3	3.88	9.75	9.18	10.07	4.45	5.29	5.42	*	+		
HEMBA1002759	2.47	0.92	1.55	4.32	3.79	4.12	2.56	2.66	2.65	**	+		
HEMBA1002763	17.79	8.69	9.49	11.93	10.68	12.89	9.46	10.98	11.31				
HEMBA1002767	4.86	3.64	4.15	4.69	4.37	5.27	4.84	4.88	6.63				
HEMBA1002768	7.65	3.89	4.38	7.6	7.36	7.85	6.31	6.75	7.16				
HEMBA1002769	6.55	2.6	4.29	4.3	5.76	5.49	4.08	5.08	4.57				
HEMBA1002770	10.29	6.74	8.19	11.22	11.06	13.4	7.03	6.36	8.42				
HEMBA1002777	9.75	4.7	5.71	8.59	8.79	9.46	6.38	4.3	7.48				
HEMBA1002779	19.22	10.66	6.22	15.16	13.63	10.21	10.37	10.01	10.31				
HEMBA1002780	5.7	2.86	3	6.99	7.8	9.55	4.79	4.73	6.4	*	+		
HEMBA1002790	4.99	2.33	3.07	6.37	8.93	7.96	4.08	3.78	4.9	*	+		
HEMBA1002794	8.37	5.67	4.58	5.78	6.13	8.44	6.79	6.5	6.15				
HEMBA1002798	1.26	0.86	1.65	2.72	2.3	1.86	0.87	2.64	0.77	*	+		
HEMBA1002801	1.99	0.93	1.36	4.21	3.6	1.85	2.71	2.29	3.22			*	+
HEMBA1002810	9.65	4.37	5.68	13.26	12.11	9.75	5.27	6.41	6.28				
HEMBA1002816	9.84	4.52	4.72	9.31	6.58	9.2	5.89	5.54	5.86				
HEMBA1002818	13.95	7.65	7.85	12.57	11.48	11.5	11.94	8.46	10.87				
HEMBA1002820	8.63	4.01	5.8	12.08	16.06	13.75	7.38	6.93	7.73	*	+		
HEMBA1002826	2.06	0.77	0.96	1	0.94	1.69	1.3	2.13	0.88				
HEMBA1002833	9.88	4.57	5.73	7.08	7.89	7.35	7.95	8.57	7.16				
HEMBA1002850	0.76	0.3	1.24	1.8	1.57	1.81	0.67	2.12	1.24	*	+		
HEMBA1002862	2.92	2.24	3.55	9.63	8.86	7.72	5.29	8.86	7.89	**	+	*	+
HEMBA1002863	3.16	2.79	5.23	4.86	5.55	5.31	3.6	5.86	5.95				
HEMBA1002867	3.74	1.09	1.41	1.95	2.42	2.24	1.51	1.85	1.96				
HEMBA1002876	10.81	3.46	4.85	5.22	5.51	6.47	5.11	4.45	5.37				
HEMBA1002886	1.73	1.14	1.2	1.8	3.11	2.84	1.24	1.52	0.93	*	+		
HEMBA1002896	5.56	2.89	2.26	4.16	5.6	6.36	4.43	4.26	5.28				
HEMBA1002913	6.83	3.41	4.1	6.13	4.56	5.54	4.6	4.46	4.22				
HEMBA1002921	5.09	1.35	3.42	4.01	3.76	3.47	2.82	3.68	1.76				
HEMBA1002924	3.44	1.46	2.03	3.99	2.79	5.07	4.7	2.86	2.66				
HEMBA1002934	19.41	10.56	13.01	28.28	26.9	31.77	13.81	10.62	17.37	**	+		
HEMBA1002935	5.64	2.51	3.1	9.39	9.17	8.78	4.05	4.5	6.44	**	+		
HEMBA1002937	2.94	0.97	1.56	5.32	3.72	3.3	4.25	3.23	5.41			*	+
HEMBA1002939	5.23	2.26	1.27	6.12	6.22	7.2	3.36	5.43	4.03	*	+		
HEMBA1002944	2.39	1.05	0.97	2.45	2.94	1.89	1.97	1.66	1.79				
HEMBA1002951	4.82	2.48	2.82	6.08	7.02	6.04	4.67	6.63	5.8	*	+		
HEMBA1002954	3.07	1.62	1.21	5.05	3.53	2.74	1.86	3.21	2.77				
HEMBA1002962	4.7	4.71	2.06	11.63	8.54	7.28	2.97	4.52	4.25	*	+		
HEMBA1002968	7.62	3.18	4.17	11.44	8.51	9.98	4.32	4.58	5.82	*	+		
HEMBA1002970	1.55	2.24	2.05	3.8	4.05	2.91	1.8	3.84	2.44	*	+		
HEMBA1002971	2.55	2.17	1.09	2.11	2.8	2.2	1.84	1.44	2.55				
HEMBA1002973	4.7	1.37	2.41	7.46	7.53	5.02	4.19	3.07	3.54	*	+		
HEMBA1002978	4.6	2.2	2.96	5.07	6.26	5.9	2.87	3.98	1.74	*	+		
HEMBA1002981	10.14	3.92	5.05	6.62	5.73	6.85	4.75	3.37	4.22				
HEMBA1002985	5.65	3.15	2.63	4.75	6.26	6.46	4.22	6.1	4.66				
HEMBA1002986	8.06	6.02	4.91	10.22	16.35	15.33	12.26	16.22	12.17	*	+	*	+
HEMBA1002988	1.58	0.97	1.43	5.23	7.34	7.21	3.78	3.98	3.2	**	+	**	+

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Table 184

HEMBA1002992	9.81	4.26	5.48	8.62	8.82	10.46	6.24	6.81	7.68				
HEMBA1002995	9.95	5.67	5.79	12.67	13.82	15.45	7.42	8.68	5.34	*	+		
HEMBA1002997	5.35	3.23	2.63	6.04	6.82	4.47	3.67	4.27	4.14				
HEMBA1002999	1.41	1.2	1	1.77	1.86	2.15	1.32	1.54	1.79	*	+		
HEMBA1003004	4.4	2.05	2.04	4.44	2.35	3.6	4.34	2.86	3.43				
HEMBA1003006	3.81	3.03	1.95	4.39	5.85	4.42	3.51	4.58	4.16				
HEMBA1003008	3.21	2.19	2.5	3.68	6.17	6.62	2.11	3.8	2.8	*	+		
HEMBA1003021	7.74	5.2	3.87	9.69	18.49	13.68	7.18	7.68	6.46	*	+		
HEMBA1003027	2.46	2.25	2.2	3.48	3.21	5.26	3.71	4.99	5.27			**	+
HEMBA1003029	16.49	15.58	12.66	14.01	22.6	13.51	9.84	22.76	21.22				
HEMBA1003031	7	6.8	4.83	11.72	14.51	12.51	5.21	5.97	6.1	**	+		
HEMBA1003032	8.54	5.52	5.51	6.83	9.05	7.67	7.01	6.8	7.13				
HEMBA1003033	13.69	8.92	7.92	18.19	20.22	19.59	7.06	10.97	9.51	**	+		
HEMBA1003034	10.16	6.76	5.59	16.34	16.21	18.88	7.61	9.38	7.94	**	+		
HEMBA1003035	0.86	0.59	0.52	1.61	1.97	0.55	0.09	2.49	0.47				
HEMBA1003037	14.14	5.43	5.96	7.58	8.71	8.97	7.73	6.56	7.19				
HEMBA1003041	13.54	5.42	7.39	11.23	11.7	11.68	7.62	7.38	7.89				
HEMBA1003046	10.88	8	7.65	10.34	12.65	9.57	6.83	7.13	6.72				
HEMBA1003047	6.06	2.52	2.2	4.15	5.03	5.74	4.14	4.89	5.07				
HEMBA1003048	4.06	2.13	2.64	5.2	6.24	5.07	5.54	7.31	7.12	*	+	**	+
HEMBA1003064	1.85	0.88	1.11	2.44	3.01	2.83	0.75	2.55	1.61	*	+		
HEMBA1003067	3.99	3.75	3.24	6.04	4.55	5.67	2.42	3.41	2.73	*	+		
HEMBA1003071	4.89	2	2.46	3.09	3.36	3.95	2.75	4.15	2.46				
HEMBA1003072	5	3.54	3.49	9.31	7.84	7.21	4.62	3.3	3.28	**	+		
HEMBA1003076	17.78	7.65	8.23	14.31	15.74	15.39	9.87	12.41	9.92				
HEMBA1003077	2.58	1.45	1.89	1.93	2.25	1.91	1.66	2.15	1.57				
HEMBA1003078	2.54	1.51	1.55	3	4.23	3.44	2.66	2.38	2.18	*	+		
HEMBA1003079	1.91	1.85	1.65	2.48	2.95	4.35	2.42	3.49	4.71				
HEMBA1003083	3.9	3.64	3.64	4.53	10.29	6.35	3.33	5.25	3.51				
HEMBA1003086	4.22	1.35	2.59	5.79	6.56	7.76	2.96	3.81	3.22	*	+		
HEMBA1003090	4.24	1.39	3.28	3.62	3.38	4	2.6	2.81	2.75				
HEMBA1003094	7.91	4.48	3.84	6.39	5.65	6.37	3.63	7.81	6.29				
HEMBA1003096	2.55	1.26	1.42	4.86	4.02	4.86	6.22	5.89	7.19	**	+	**	+
HEMBA1003098	13.3	7.22	6.89	14.21	8.08	14.42	7.57	4.87	3.41				
HEMBA1003101	3.86	1.83	2.21	3.42	3.01	2.84	5.05	3.05	3.57				
HEMBA1003109	4.5	2.81	2.78	4.25	4.4	4.14	3.32	3.04	3.75				
HEMBA1003114	4.72	1.49	2.76	4.85	5.37	3.83	2.72	3.02	2.47				
HEMBA1003117	3.34	1.32	1.84	1.94	3.48	3.4	1.15	2.8	1.47				
HEMBA1003120	6.26	3.04	4.46	8.53	11.03	9.87	2.19	4.52	4.23	*	+		
HEMBA1003129	2.92	2.45	1.66	4.57	4.93	4.76	2.42	2.95	3.22	**	+		
HEMBA1003133	3.76	2.75	2.66	4.15	4.94	3.64	3.03	3.83	3.17				
HEMBA1003136	10.1	5.38	5.56	4.76	5.69	3.55	4.84	6.06	5.16				
HEMBA1003142	3.63	2.31	2.57	5.7	6.12	5.75	4.06	4.52	4.11	**	+	*	+
HEMBA1003148	3.76	1.84	1.85	6.57	6.35	7.13	3.78	3.2	3.41	**	+		
HEMBA1003151	3.06	1.21	2.06	3.57	3.12	3.47	1.14	2.71	1.88				
HEMBA1003152	0.94	1.17	1.24	1.37	1.78	3.11	1.18	1.39	0.96				
HEMBA1003157	5.21	1.69	3.38	3.87	2.5	3.42	0.86	1.61	0.57				
HEMBA1003166	16.26	12.43	11.19	32.39	35.71	31.69	16.79	24.31	19.76	**	+		
HEMBA1003171	2.89	0.72	0.57	1.31	1.88	0.92	1.38	1.84	1.16				
HEMBA1003175	2.6	1.51	1.44	3.64	3.88	4.37	1.98	2.4	2.06	**	+		
HEMBA1003179	4.43	2.72	4.24	3.15	2.78	4.29	3.01	4.28	3.14				
HEMBA1003186	8.23	6.45	5.52	11.84	15.62	13.23	6.12	9.01	7.56	**	+		
HEMBA1003196	5.41	2.8	3.15	4.6	6.06	5.01	3.65	4.6	3.58				
HEMBA1003197	1.16	0.72	0.59	1.88	2.27	1.84	1.37	1.38	0.69	**	+		
HEMBA1003199	2.2	0.82	0.97	3.9	3.83	3.59	1.11	2.24	1.33	**	+		
HEMBA1003202	6.51	4.3	4.72	9.3	10.18	10.03	5.76	4.86	4.67	**	+		

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Table 185

HEMBA1003204	4.47	2.88	1.95	6.42	9.31	7.19	4.16	4.11	3.52	*	+		
HEMBA1003210	5.3	3.32	2.57	8.14	10.48	8.37	17.93	9.12	16.05	**	+	*	+
HEMBA1003212	10.06	5.15	6.84	12.91	14.8	18.49	9.01	8.88	9.76	*	+		
HEMBA1003218	1.85	0.63	1.04	1.36	1.25	1.72	1.4	2.5	1.89				
HEMBA1003220	27.66	24	25.44	26.62	36.09	37.79	16.07	14.85	17.5			**	-
HEMBA1003222	2.88	1.72	3.36	3.75	3.58	3.59	2.57	3.59	2.87				
HEMBA1003225	2.92	1.48	2.59	3.07	2.81	2.57	2.42	3.81	3.48				
HEMBA1003229	3.63	1	0.92	4.49	4.02	4.36	4.86	6.18	8.35			*	+
HEMBA1003230	4.81	1.33	1.59	3.63	3.48	2.96	4.65	4.11	4.45				
HEMBA1003235	4.25	2.83	2.72	4.77	5.98	6.44	3.15	3.65	2.94	*	+		
HEMBA1003236	2.61	2.12	2.62	4.85	3.24	5.32	5.66	4.6	3.8	*	+	*	+
HEMBA1003250	1.73	0.34	1.4	2.93	3	2.03	1.83	2.23	1.38	*	+		
HEMBA1003252	5.88	2.96	5.36	7.78	7.79	7.89	4.58	5.63	5.99	*	+		
HEMBA1003257	4.93	1.49	3.88	3.03	4.82	4.08	2.99	3.59	4.04				
HEMBA1003268	0.75	0.26	0.6	2.39	1.18	1.2	0.42	1.31	0.41				
HEMBA1003273	3.46	2.51	1.67	5.94	6.01	5.04	2.19	3.45	3.47	**	+		
HEMBA1003276	1.81	1.29	0.96	4.38	4.69	4.83	2.14	2.73	3.03	**	+	*	+
HEMBA1003277	2.81	1.68	0.99	2.39	2.91	2.66	2.69	2.74	1.67				
HEMBA1003278	1.65	0.9	1.98	2.98	3.92	3.95	2.37	3.01	2.17	**	+		
HEMBA1003280	3.32	1.78	3	4.76	3.3	3.57	2.93	5.18	3.65				
HEMBA1003281	4.06	0.91	2.42	3.46	3.32	3.57	2.53	4.81	3.88				
HEMBA1003284	0.48	0.51	0.58	2.22	0.82	1.41	1.13	2.8	1.15				
HEMBA1003286	3.88	2.4	2.73	5.92	3.88	3.67	2.08	4.79	3.77				
HEMBA1003291	2.38	1.74	0.96	2.57	3.95	3.8	2.72	4.5	5.97	*	+		
HEMBA1003294	5.2	3.14	3.02	8.15	7.24	7.54	4.43	4.64	6.12	**	+		
HEMBA1003296	3.52	1.49	1.47	1.62	2.44	1.83	2.01	2.49	2.5				
HEMBA1003304	1.33	0.87	0.46	1.14	1.8	1.15	0.92	1.05	1.59				
HEMBA1003306	4.82	1.91	2.68	6.16	5.24	6.21	5.8	5.67	6.01	*	+	*	+
HEMBA1003309	0.64	0.18	0.98	3.28	3.28	2.43	1.17	2.04	1.94	**	+	*	+
HEMBA1003314	30.47	18.15	16.33	19.29	25.08	19.75	20.31	20.79	24.11				
HEMBA1003315	10.03	5	5.86	8.82	6.71	8.85	7.02	6.3	8.18				
HEMBA1003322	6.46	2.81	4.38	11.92	11.23	7.71	5.2	4.77	6.83	*	+		
HEMBA1003326	4.18	1.78	2.35	2.75	2.35	2.84	2.28	3.1	3.12				
HEMBA1003327	1.82	3.14	1.29	2.95	3.45	3.27	2.29	2.03	3.08				
HEMBA1003328	4.01	4	2.1	5.29	8.03	6.1	3.75	5.53	3.53	*	+		
HEMBA1003330	11.21	6.43	6.46	11.55	10.31	11.11	5.39	5.56	6.86				
HEMBA1003348	5.75	4.37	3.56	10.47	9.44	9.51	4.42	5.42	4.82	**	+		
HEMBA1003369	3.52	2.39	2.06	5.95	6.68	6.94	3.15	4.91	3.36	**	+		
HEMBA1003370	20.51	11.56	11.02	25.15	23.1	21.13	12.45	14.72	17.99				
HEMBA1003373	3.04	1.4	0.86	3.17	2.01	3.32	2.12	1.4	2.16				
HEMBA1003376	11.18	5.54	7.92	20.96	23.88	21.25	10.64	10.28	11.12	**	+		
HEMBA1003380	2.3	1.46	1.33	2.34	1.63	1.87	2.49	1.54	2.46				
HEMBA1003384	2.29	0.73	1.56	3.93	3.22	3.27	1.72	2.42	3.12	*	+		
HEMBA1003387	1.34	0.55	1.92	1.88	0.47	0.99	1.2	0.99	1.1				
HEMBA1003392	8.27	4.38	5.55	5.24	7.99	8.63	5.42	7.97	6.53				
HEMBA1003395	1.96	1.22	1.19	2.43	3.54	3.02	1.59	5.5	1.02	*	+		
HEMBA1003399	5.58	3.74	3.33	5.08	4.37	5.04	3.4	3.1	3.67				
HEMBA1003400	10.74	5.28	6.5	8.13	8.07	5.69	7.43	7.79	7.28				
HEMBA1003402	4.66	2.07	1.57	4.25	3.02	2.77	2.27	1.71	2.18				
HEMBA1003403	4.57	4.91	4.99	4.14	4.8	3.26	2.96	3.55	2.8			**	-
HEMBA1003408	10.68	7.13	5.44	7.16	7.17	7.67	7.62	9.08	7.52				
HEMBA1003412	6.57	4.94	4.07	6.42	6.27	6.69	3.99	6.63	4.67				
HEMBA1003417	4.27	2.26	3.09	1.9	2.03	2.19	2.24	2.99	2.76				
HEMBA1003418	10.03	4.9	6.22	10.24	12.15	12.3	3.46	6.64	4.53				
HEMBA1003420	1.52	0.53	0.73	7.04	2.2	5.31	11.33	12.68	10.88			**	+
HEMBA1003425	1.37	1.11	1.09	2.68	2.01	2.17	1.69	0.88	0.88	**	+		

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Table 186

HEMBA1003433	2.51	1.64	1.17	2.63	2.77	1.5	2.03	2.04	0.74				
HEMBA1003440	7.38	4.95	3.98	3.59	4.49	2.94	11.67	10.24	9.89			*	+
HEMBA1003442	7.11	3.89	5.36	33.69	44.16	39.43	12.88	14.11	14.92	**	+	**	+
HEMBA1003447	6.43	2.84	5.38	2.86	4.59	3.43	2.19	3.65	2.78				
HEMBA1003453	5.3	2.06	4.2	3.35	2.95	3.68	3.79	4.22	4.22				
HEMBA1003461	4.9	1.85	2.53	3.24	4.51	4.52	2.91	4.48	2.29				
HEMBA1003463	2.07	0.69	1.15	5.59	5.7	5.89	4.6	5.83	5.74	**	+	**	+
HEMBA1003465	9.37	4.59	4.46	10.69	9.03	7.99	6.08	6.86	6.92				
HEMBA1003480	9.33	5.04	6.92	12.74	16.03	14.45	6.27	6.32	7.43	**	+		
HEMBA1003485	20.75	10.29	10.54	10.17	12.27	12.15	10.87	6.69	7.13				
HEMBA1003487	4.58	2.05	1.61	2.41	3.47	2.58	3.04	3.53	2.9				
HEMBA1003492	2.07	1.37	0.95	2.53	2.7	2.94	1.03	2.89	1.4	*	+		
HEMBA1003494	2.49	0.76	1.49	27.92	31.78	20.12	3.6	6.11	5.48	**	+	*	+
HEMBA1003497	3.12	0.78	1.83	3.69	4.28	3.96	1.74	2.6	2.31	*	+		
HEMBA1003503	3.45	2.06	1.43	3.15	2.26	2.25	1.52	3	3.05				
HEMBA1003511	2.69	1.04	0.98	1.76	1.46	1.83	1.71	1.33	0.95				
HEMBA1003528	18.14	11.27	11.45	12.37	19.83	18.44	16.97	12.4	16.79				
HEMBA1003530	2.6	1.44	2.11	2.26	2.64	3.14	2.32	2.96	3.27				
HEMBA1003531	6.99	4.57	4.74	10.98	15.62	10.36	6.08	6.8	4.37	*	+		
HEMBA1003532	13.93	5.28	9.84	12.79	13.95	12.42	7.71	9.02	10.58				
HEMBA1003538	2.36	1.42	1.55	0.71	3.61	2.87	1.32	3.05	1.48				
HEMBA1003545	1.41	0.47	0.87	1.63	1.67	1.35	0.85	1.8	0.86				
HEMBA1003546	6.22	3.88	2.1	11.53	13.41	10.1	6.93	7.89	5.98	**	+		
HEMBA1003548	0.92	0.44	0.29	1.8	1.25	1.92	0.41	1.43	0.38	*	+		
HEMBA1003553	10.98	8.66	9.18	19.1	13.8	21.91	7.81	8.18	9.02	*	+		
HEMBA1003555	3.02	1.7	1.46	1.76	3.2	2.69	2.27	3.4	2.27				
HEMBA1003556	4.32	1.68	2.2	3.83	6.46	5.67	2.71	3.54	2.22				
HEMBA1003560	1.14	1.46	1.03	0.88	1.35	1.08	1.46	2.03	1.63				
HEMBA1003565	4.06	3.07	3.95	3.82	4.6	4.62	4.01	5.7	5.12				
HEMBA1003568	2.91	0.76	1.15	1.22	1.08	1.38	1.05	1.98	0.77				
HEMBA1003569	8.99	12.88	9.75	5.29	6.55	5.16	4.54	5.33	5.68	*	-	*	-
HEMBA1003571	10.48	4.42	3.13	21.11	11.99	10.73	5.96	8.94	7.11				
HEMBA1003579	5.23	2.72	1.87	4.14	3.57	5.4	3.01	3.4	2.79				
HEMBA1003580	11.03	7.36	6.64	6.54	6.56	8.11	7.97	8.17	8.81				
HEMBA1003581	5.6	4.24	4.26	4.68	5.52	5.87	5.47	4.38	5.02				
HEMBA1003591	39.81	31.07	28.74	52.34	52.04	48.99	14.34	10.05	14.79	**	+	**	-
HEMBA1003595	1.99	0.8	1.07	3.33	4.04	3.39	2.08	3.22	1.45	**	+		
HEMBA1003597	1.33	0.63	1.33	3.65	3.35	4.52	1.94	2.9	2.36	**	+	*	+
HEMBA1003598	2.9	0.82	1.41	1.32	2.05	2.83	1.88	0.98	0.49				
HEMBA1003600	5.78	3.55	3.06	6.44	7.48	5.87	4.2	4.07	5.87				
HEMBA1003602	2.69	1.98	1.66	3.29	2.76	2.29	1.48	2.11	2.34				
HEMBA1003604	11.43	8.02	8.72	12.24	9.01	11.87	7.65	8.32	8.25				
HEMBA1003610	8.44	6.02	5.83	14.76	14.29	15.88	13.42	9.31	12.15	**	+	*	+
HEMBA1003615	6.42	3.45	3.87	5.96	5.91	5.22	3.28	5.75	3.48				
HEMBA1003617	3.99	3.24	3.91	16.74	14.07	12.64	7.57	9.08	9.03	**	+	**	+
HEMBA1003620	5.35	2.63	3.62	8.39	6.31	6.44	4.6	5.32	5.6	*	+		
HEMBA1003621	5.01	4.74	3.02	9.46	12.07	10.28	5.9	5.67	5.82	**	+		
HEMBA1003622	1.74	1.02	0.61	2.09	2.03	2.5	0.94	1.66	0.88	*	+		
HEMBA1003630	1.59	0.33	0.75	1.41	1.11	1.15	1.54	2.32	1.54				
HEMBA1003637	2.15	0.95	0.99	3.26	5.54	3.57	1.75	2.71	1.99	*	+		
HEMBA1003640	2.27	1.59	2.11	4.99	4.15	5.22	3.36	5.53	2.27	**	+		
HEMBA1003645	1.63	0.53	1.13	3.97	2.86	2.71	2.66	3.44	1.36	*	+		
HEMBA1003646	0.89	0.8	1.19	3.33	3.36	4.74	1.35	3.89	1.8	**	+		
HEMBA1003647	0.79	0.36	0.72	3.69	2.19	3.35	1.03	2.87	1.04	**	+		
HEMBA1003656	3.32	1.76	1.62	4	4.27	4.72	3.61	3.92	2.65	*	+		
HEMBA1003662	2.77	1.1	0.73	3.91	3.34	1.69	3.38	3	3.35				

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Table 187

HEMBA1003666	1.38	1.05	0.83	1.72	1.7	1.06	0.87	1.13	0.89				
HEMBA1003667	14.71	11.01	9.94	14.75	22.82	18.78	15.24	10.59	14.49				
HEMBA1003670	0.91	0.22	0.29	1.11	1.61	1.82	0.56	1.43	0.85	*	+		
HEMBA1003674	26.03	18.94	18.61	21.67	28.7	30.08	14.76	19.25	20.49				
HEMBA1003677	3.73	1.52	2.36	7.63	8.16	6.96	10.74	10.88	8.28	**	+	**	+
HEMBA1003679	1.48	0.67	1.25	5.41	5.58	4.44	1.61	3.27	2.24	**	+		
HEMBA1003680	6.18	3.86	3.32	4.89	3.65	4.22	2.45	3.41	4.34				
HEMBA1003684	3.07	3.42	2.52	4.93	3.87	3.53	2.61	2.37	4.26				
HEMBA1003690	8.67	4.5	4.89	6.53	5.61	6.33	6.11	7.01	7.57				
HEMBA1003692	6.51	4.39	2.76	7.65	13.21	11.37	6.71	7.24	6.09	*	+		
HEMBA1003702	7.49	3.3	2.54	5.23	6.69	4.84	4.77	3.72	5.73				
HEMBA1003711	5.86	2.58	3.21	3.28	5.33	5.99	2.95	4.08	4.68				
HEMBA1003714	4.3	2.42	1.47	3.54	3.98	3.51	1.5	2.8	3.08				
HEMBA1003715	5.16	2.24	2.94	8.09	8.13	8	2.66	4.48	4.1	**	+		
HEMBA1003717	3.17	2.29	1.96	4.19	3.55	5.52	1.88	1.44	1.67	*	+		
HEMBA1003720	1.56	1.73	1.27	3.11	3.53	3.49	2.3	1.66	3.08	**	+		
HEMBA1003725	1.46	0.94	0.92	3.84	2.37	2.61	2.1	1.7	2.25	*	+	*	+
HEMBA1003728	6.2	3.24	4.06	5.16	6.27	6.67	5.85	4.48	3.55				
HEMBA1003729	3.99	1.42	2.32	6.36	5.84	4.38	3.64	4.72	3.3	*	+		
HEMBA1003732	1.63	1.1	1	3.52	2.12	1.25	0.95	1.54	1.47				
HEMBA1003733	2.5	4.71	1.16	4.86	6.33	5.47	2.99	3.73	3.5				
HEMBA1003742	6.12	2.9	4.2	5.24	4.87	5.32	2.62	6.27	5.03				
HEMBA1003743	2.64	1.63	1.2	2.32	2.37	3.69	2.34	1.46	1.92				
HEMBA1003758	5.8	2.98	4.74	10.06	11.45	11.44	7.34	3.52	6.11	**	+		
HEMBA1003760	5.32	2.29	2.62	4.55	3.7	4.58	3.57	4.5	4.37				
HEMBA1003764	5.57	1.67	3.47	5.12	2.71	2.62	3.98	3.91	4.87				
HEMBA1003769	11.09	7.81	6.22	7.38	7.99	10.09	8.32	6.25	8.19				
HEMBA1003773	4.06	2.15	2.74	3.4	2.78	2.89	3.34	3.66	3.74				
HEMBA1003783	5.9	5.63	5.15	7.21	10.97	7.92	4.02	5.97	4.35				
HEMBA1003784	1.56	0.55	0.26	1.01	1.64	1.14	0.84	1.59	1				
HEMBA1003794	22.02	14.74	15.29	16.32	23.57	18.51	19.15	20.16	23.83				
HEMBA1003799	3.18	0.83	0.69	1.6	1.44	2.62	1.76	1.29	1.44				
HEMBA1003803	5.18	3.99	2.9	7.41	7.07	8.96	7.06	6.07	5.89	*	+	*	+
HEMBA1003804	4.31	3.24	3.27	5.11	3.19	3.64	3.81	3.96	3.99				
HEMBA1003805	9.07	8.11	9.22	15.23	14.63	10.98	7.34	10.04	6.52	*	+		
HEMBA1003807	2.26	0.57	1.05	1.41	1.99	1.42	1.14	1.69	1.19				
HEMBA1003810	2.67	2.32	0.99	3.03	2.59	2.69	2.81	4.61	3.57				
HEMBA1003827	25.92	18.96	19.46	14.46	20.55	25.66	14.02	29.91	19.07				
HEMBA1003836	9.8	5.94	7.41	16.46	20.73	18.84	10.1	7.05	9.1	**	+		
HEMBA1003838	29.21	22.41	20.25	35.45	47.13	35.6	26.78	26.74	23.31	*	+		
HEMBA1003843	8.31	5.73	4.45	4.63	2.15	3.75	3.72	2.7	3.17				
HEMBA1003846	26.28	20.72	18.37	21.86	22.27	12.11	9.99	15.1	13.9			*	-
HEMBA1003856	3.23	2.48	1.56	1.62	2.7	2.03	1.6	2.63	2.09				
HEMBA1003857	5.6	3.94	4.15	8.14	11.16	11.16	4.4	7.01	4.61	**	+		
HEMBA1003864	4.85	1.81	2.77	3.23	4.07	4.12	3.31	3.39	2.74				
HEMBA1003866	1.42	0.62	1.37	1.22	1.21	1.69	0.7	1.76	0.89				
HEMBA1003868	13.28	7.75	6.42	9.42	7.15	9.18	5.91	7.86	7.2				
HEMBA1003879	2.14	1.42	1.52	4.08	4.35	3.36	3.08	2.74	2.28	**	+	*	+
HEMBA1003880	4.68	2.16	2.83	4.05	4.87	3.64	3.32	3.39	3.6				
HEMBA1003884	5.74	3.71	3.92	4	4.49	5.17	4.44	4.54	4.54				
HEMBA1003885	10.32	6.22	7.2	14.27	16.75	16.47	8.29	8.14	8.72	**	+		
HEMBA1003887	5.7	2.76	3.69	4.8	4.75	6.26	4.28	5.31	3.98				
HEMBA1003890	5.76	2.14	5.85	3.21	4.35	4.1	2.43	1.67	2.34				
HEMBA1003893	24.48	11.91	15.58	30.06	36.65	30.84	15.38	16.42	17.2	*	+		
HEMBA1003896	19.51	13.33	11.04	17.41	24	18.91	15.03	15.04	20.6				
HEMBA1003902	8.4	6.56	5.19	9.58	9.98	7.89	5.71	4.62	5.77				

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Table 188

HEMBA1003904	2.78	1.45	1.43	2.77	2.17	1.59	1.47	2.66	1.69				
HEMBA1003908	1.69	1.16	1.22	2.42	2.58	2.06	1.92	2.64	1.46	*	+		
HEMBA1003926	72.36	45.24	46.72	61.75	49.96	64.94	25.26	18.43	24.45			*	-
HEMBA1003937	3.1	1.85	1.98	6.12	8.5	7.61	2.66	5.69	3.16	**	+		
HEMBA1003939	1.28	1.62	1.87	1.85	4.47	4.22	0.72	2.97	2.45				
HEMBA1003940	2.82	0.88	1.71	2.17	3.19	2.37	0.51	2.52	1.7				
HEMBA1003941	4.35	2.77	1.79	1.96	4.65	3.03	2.55	3.88	2.82				
HEMBA1003942	2.44	1.82	1.09	3.64	3.65	2.58	2.38	2.63	2.03	*	+		
HEMBA1003945	9.46	3.83	5.74	8.44	8.96	9.42	7.88	6.57	7.46				
HEMBA1003949	2.14	1.99	0.59	2.89	3.58	3.78	1.92	2.25	1.36	*	+		
HEMBA1003950	1.45	1.52	0.64	1.83	1.87	1.76	1.11	1.8	1.56				
HEMBA1003953	1.96	0.44	1.34	3.08	3.28	3.34	1.95	3.21	1.37	*	+		
HEMBA1003958	6.98	4.78	4.74	10.87	13.86	10.68	4.23	6.52	6.23	**	+		
HEMBA1003959	2.84	3.02	3.46	6.74	9.97	6.27	2.64	3.74	2.94	*	+		
HEMBA1003960	7.33	2.27	2.98	3.59	5.1	3.92	2.8	3.92	3.79				
HEMBA1003966	4.91	3.07	2.16	3.5	4.6	3.28	2.1	2.93	3.48				
HEMBA1003967	5.85	3.63	2.68	3.94	3.8	3.19	1.89	3.17	2.35				
HEMBA1003968	3.76	2.02	2.13	4.21	6.16	3.59	4.13	4.11	3.84				
HEMBA1003974	41.47	29.67	25.73	95.3	104.1	103.5	100	82.53	110.2	**	+	**	+
HEMBA1003976	2.48	1.1	1.38	2.13	2.25	2.22	1.34	1.82	1.6				
HEMBA1003977	2.19	1.38	1.4	2.42	3.02	1.57	1.86	1.96	1.93				
HEMBA1003978	2.44	1.5	1.92	3.24	3.34	3.85	1.9	2.87	2.37	*	+		
HEMBA1003981	7.98	4.15	3.07	6.67	7.3	7.05	6.37	6.68	8.81				
HEMBA1003982	6.94	4.75	3.19	18.33	22.13	23.04	19.29	21.74	19.78	**	+	**	+
HEMBA1003985	2.27	1.26	0.95	3.01	1.91	1.85	1.02	2.35	1.03				
HEMBA1003987	3.79	1.42	2.2	4.67	5.44	5.59	3.67	4.19	3.44	*	+		
HEMBA1003989	2.32	1.65	1.59	4.16	4.13	5.73	3.24	3.75	3.69	**	+	**	+
HEMBA1004000	1.83	1.8	1.37	4.32	4.14	3.96	2.63	3.55	2.34	**	+	*	+
HEMBA1004006	1.37	0.24	1.22	2.13	0.94	1.32	1.17	2.2	0.95				
HEMBA1004007	6.04	2.39	4.27	10.96	12.86	11.45	4.4	6.87	6.82	**	+		
HEMBA1004010	2.94	1.19	1.2	2.7	3.56	3.85	6.4	6.08	6.71			**	+
HEMBA1004011	1.7	0.78	0.96	2.15	2.36	1.93	1.31	2.48	1.53	*	+		
HEMBA1004012	3.28	1.3	2.31	6.01	4.99	6.51	2.69	3.48	2.84	**	+		
HEMBA1004015	2.75	2.05	2.56	5.11	5.22	4.78	3.43	3.89	3.43	**	+	*	+
HEMBA1004024	5.55	4.27	3.76	12.33	16.73	14.13	7.3	6.98	6.78	**	+	*	+
HEMBA1004029	4.41	3.27	3.73	8.08	10.91	6.74	3.3	6.61	3.72	*	+		
HEMBA1004038	2.95	1.3	1.87	2.87	2.27	1.5	1.15	4.52	1.31				
HEMBA1004042	0.98	0.07	0.48	1.39	1.07	0.6	0.74	2.16	0.79				
HEMBA1004045	1.3	0.85	0.68	0.88	3.2	1.57	1.01	1.7	0.88				
HEMBA1004048	7.55	3.12	4.4	8.61	11.26	7.66	7.55	7.12	7.08				
HEMBA1004049	1.17	0.64	0.7	2.26	3.05	2.36	1.86	2.62	1.77	**	+	*	+
HEMBA1004051	4.38	1.98	1.73	3.51	4.36	4.02	9.79	8.74	8.15			**	+
HEMBA1004053	8.83	5.44	4.46	17.89	9.59	13.59	14.13	13.15	12.39			**	+
HEMBA1004055	2.65	0.36	1.81	2.57	2.89	2.7	1.3	3	1.6				
HEMBA1004056	7.5	3.93	5.65	20.02	18.97	17.23	8.27	9.56	8.48	**	+	*	+
HEMBA1004060	0.07	0.43	1.07	1.82	1.29	1.56	0.47	1.74	1.31	*	+		
HEMBA1004061	14.25	5.05	4.22	4.44	4.07	3.17	2.96	3.91	3.1				
HEMBA1004067	9.19	5.05	5.06	7.71	7.13	7.12	4.94	6.2	7.71				
HEMBA1004071	14.49	9.52	7.51	14.12	12.05	13.02	8.33	9.62	10.66				
HEMBA1004074	7.06	2.77	2.38	5.08	5.28	4.16	4.21	4.55	5.63				
HEMBA1004078	11.34	10.72	8	8.83	11.03	9.34	8.26	9.99	8.73				
HEMBA1004085	3.75	2.6	2.94	3.51	4.46	4.01	3.83	4.11	2.49				
HEMBA1004086	9.29	6.04	5.26	10.09	10	10.42	3.43	2.6	4.21				
HEMBA1004097	2.9	2.64	1.85	1.78	5.31	3.52	1.65	4.02	2.63				
HEMBA1004100	5.05	2.67	3.16	5.99	4.86	5.28	5.44	5.79	5.01				
HEMBA1004103	10.13	4.33	3.51	10.84	11.41	10.36	6.76	6.57	8.64				

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Table 189

HEMBA1004110	14.95	6.9	7.32	18.8	19.15	18.28	8.68	9.12	8.42	*	+		
HEMBA1004111	4.86	3.05	3.79	7.76	8.14	8.2	4.79	4.58	4.21	**	+		
HEMBA1004124	6.94	3.7	4.42	6.1	3.89	4.52	4.49	4.21	4.75				
HEMBA1004130	9.54	3.62	3.55	9.36	10.43	9.03	4.61	5.66	5.54				
HEMBA1004131	4.85	3.97	3.36	3.86	4.83	4.69	2.77	4.06	2.93				
HEMBA1004132	3.06	2.1	4.1	5.2	8.61	9.33	4.36	6.28	4.36	*	+		
HEMBA1004133	4.53	2.37	1.71	4.62	2.8	5.4	3.39	2.94	3.1				
HEMBA1004138	4.15	2.09	2.18	3.1	3.45	2.71	3.21	2.5	3.12				
HEMBA1004143	5.3	2.88	3.04	7.57	5.72	6.31	5.7	5.05	4.79	*	+		
HEMBA1004146	4.2	1.65	2.04	5.44	5.59	4.27	2.49	3.4	3.26				
HEMBA1004148	6.71	2.61	2.68	3.24	3.23	4.49	2.38	4.66	3.54				
HEMBA1004149	1.73	0.7	0.91	2.13	2.29	1.85	1.73	1.38	1.4	*	+		
HEMBA1004150	1.14	0.72	0.48	0.29	0.95	0.79	0.76	1.47	0.27				
HEMBA1004154	10.52	5.49	6.9	6.41	6.4	7.33	4.84	8.66	5.4				
HEMBA1004164	7.02	3.4	3.27	9.28	10.11	8.81	5.16	5.49	5.3	*	+		
HEMBA1004168	11.84	7.61	6.03	3.62	4.76	4.13	3.34	2.92	1.89			*	-
HEMBA1004199	0.92	0.62	0.74	1.67	1.3	1.87	1.47	1.95	1.4	*	+	*	+
HEMBA1004200	1.57	1.23	0.4	3.73	3.83	2.53	1.99	2.05	1.43	*	+		
HEMBA1004201	3.89	3.07	2.03	3.6	4.1	3.75	2.3	4.41	3.45				
HEMBA1004202	4.9	3.79	2.27	2.88	2.3	2.76	2.58	3.69	2.7				
HEMBA1004203	5.77	1.33	2.87	2.88	5.01	4.03	2.05	3.68	2.38				
HEMBA1004207	0.56	0.3	0.47	1.04	1.74	1.87	0.89	2.13	1.31	*	+		
HEMBA1004210	8.61	6.61	6.14	2.77	2.66	3.95	1.89	2.45	2.61	**	-	**	-
HEMBA1004225	5.03	3.74	3.98	8.75	9.84	8.6	5.26	5.3	4.25	**	+		
HEMBA1004227	3.79	2.62	4.1	4.2	4.62	3.31	3.12	4.12	2.59				
HEMBA1004235	7.02	4	4.13	5.38	8.95	5.38	4.38	6.22	4.55				
HEMBA1004237	3.9	2.42	2.47	3.59	4.2	5.86	2.12	3.58	2.89				
HEMBA1004238	6.25	1.89	3.24	4.96	7.33	6.03	3.76	4.17	3.98				
HEMBA1004241	0.67	0.27	0.46	0.34	1.31	1.04	0.22	1.55	0.61				
HEMBA1004242	32.46	19.09	20.5	23.42	40.5	41.44	12.31	21.44	17.84				
HEMBA1004243	13.89	7.41	6.2	5.78	8.65	6.42	6.33	5.94	4.6				
HEMBA1004246	2.25	1.26	2.23	4.03	4.82	3.81	2.36	4.78	2.1	**	+		
HEMBA1004247	5.45	2.79	1.32	2	4.11	3.23	3.04	3.5	3.55				
HEMBA1004248	1.69	0.88	1.09	3.22	4.63	3.53	2.79	3	3.44	**	+	**	+
HEMBA1004250	2.2	1.27	1.09	2.31	1.66	2.1	1.9	1.53	1.16				
HEMBA1004252	3.18	2.82	2.3	4.58	5.09	4.33	3.04	3.66	2.93	**	+		
HEMBA1004260	6.17	5.02	5.43	14.46	16.02	13.28	2.04	6.53	5.94	**	+		
HEMBA1004264	2.63	0.93	1.56	1.92	3.23	2.09	0.78	1.85	0.77				
HEMBA1004267	17.36	9.92	10.53	28.33	30.44	23.65	13.63	14.33	15.75	**	+		
HEMBA1004272	3.25	1.51	1.9	3.88	2.89	3.11	2.45	3.01	1.7				
HEMBA1004274	4.01	2.2	1.91	2.76	5.04	4.3	3.12	2.65	2.58				
HEMBA1004275	7.65	2.23	3.79	6.73	5.64	5.93	3.97	4.61	4.77				
HEMBA1004276	2.41	0.9	1.94	2.49	2.68	2.17	2.68	2.47	2.33				
HEMBA1004279	3.98	2.11	3.24	4.12	3.59	4.41	2.04	2.95	1.7				
HEMBA1004284	2.55	1.22	1.55	4.17	5.87	4.34	1.28	3.05	2.74	*	+		
HEMBA1004286	2.41	1.26	2.32	1.53	2.67	2.43	1.2	3	2.02				
HEMBA1004289	4.95	2.88	2.44	8.79	8.57	7.77	4.32	4.66	6.4	**	+		
HEMBA1004293	20.86	17.2	15.27	23.95	23.65	21.96	12.13	13.81	16.34	*	+		
HEMBA1004295	3.05	1.8	2.64	2.91	2.85	3.02	1.98	3.55	3.48				
HEMBA1004302	0.66	0.43	0.5	1.59	1.46	1.59	1.57	2.55	1.32	**	+	*	+
HEMBA1004306	15.93	11.78	11.41	15.21	18.98	13.88	13.95	14.44	16.14				
HEMBA1004312	2.81	2.1	2.08	6.27	6.34	5.38	1.96	3.12	2.81	**	+		
HEMBA1004314	2.53	1.33	1.74	4.02	5.28	5.79	1.6	3.72	2.38	**	+		
HEMBA1004321	6.87	2.68	4.89	6.41	11.51	10.55	3.56	5.85	5.02				
HEMBA1004323	6.15	3.8	3.34	8.44	11.8	9.65	4.55	5.84	5.92	*	+		
HEMBA1004327	4.25	2.43	2.21	4.5	3.91	4.05	2.91	3.47	3.95				

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Table 190

HEMBA1004329	6.64	4.05	3.69	10.1	11.36	10.31	6.59	6.39	7.21	**	+		
HEMBA1004330	3.08	1.92	1.4	2.71	3.14	3.34	2.64	3.02	3.26				
HEMBA1004334	3.9	1.95	1.91	3.91	3.51	4.57	2.69	2.68	1.57				
HEMBA1004335	4.91	2.24	2.81	7.41	9.8	7.49	5.19	6.78	5.7	*	+		
HEMBA1004341	6.84	4.27	5.5	4.53	6.2	5.05	5.02	6.83	6.93				
HEMBA1004344	17.75	13.13	14.74	15.95	19.67	19.67	18.23	19.51	24.66				
HEMBA1004347	4.63	3.35	2.01	5.16	6.48	5.36	2.73	3.19	3.71				
HEMBA1004349	8.89	2.46	3.99	12.23	16.69	10.37	7.71	6.98	8.61	*	+		
HEMBA1004352	5.41	3.1	3.3	7.91	8.12	10.45	4.93	5.52	5.36	*	+		
HEMBA1004353	8.35	7.6	6.31	15.51	16.38	15.96	6.75	8.35	9.31	**	+		
HEMBA1004354	4.38	1.54	2.32	5.25	5.81	6.37	3.27	4.92	3.61	*	+		
HEMBA1004356	2.81	2.85	3.03	5.06	4.66	5.46	5.28	5.77	4.17	**	+	*	+
HEMBA1004360	5.79	2.16	5.01	6.93	5.95	5.72	3.15	6.55	5.08				
HEMBA1004366	2.78	2.3	2.86	5.4	6.73	4.61	2.18	3.01	3.38	*	+		
HEMBA1004372	0.38	0.27	0.43	0.47	0.63	0.99	0.52	0.83	0.34				
HEMBA1004377	7.38	3.14	3.85	11.65	12.1	15.48	9.22	8.78	11.95	**	+	*	+
HEMBA1004389	18.67	11.71	10.38	8.69	8.39	17.15	9.23	8.15	7.38				
HEMBA1004391	2.93	2.48	2.45	7.42	5.09	7.12	3.62	4.64	3.41	**	+	*	+
HEMBA1004393	18.44	14.15	13.12	19.38	17.77	18.16	22.31	14.59	20.28				
HEMBA1004394	1.18	1.11	1.72	2.3	1.6	2.38	1.09	4.42	1.46				
HEMBA1004396	1.79	1.02	1.22	3.41	3.48	3.73	1.3	3.02	1.73	**	+		
HEMBA1004401	4.73	3.38	4.96	4.16	4.54	5.13	2.63	5.44	3.27				
HEMBA1004405	3.95	2.13	1.81	6.15	8.26	6.59	3.78	4.33	5.63	**	+		
HEMBA1004408	5.72	3.65	3.17	5.44	6.45	4.46	2.34	3.68	2.97				
HEMBA1004414	8.38	4.86	5.28	9.94	19.52	21.58	6.98	7.48	7.61	*	+		
HEMBA1004429	3.38	2.07	1.78	8.58	8.61	9.23	4.27	3.18	4.51	**	+		
HEMBA1004433	1.82	1.56	1.04	5.34	5.56	5.46	1.92	2.85	2.38	**	+		
HEMBA1004440	2.19	0.58	1.67	2.76	2.16	2.15	1.08	2.89	1.62				
HEMBA1004444	4.28	2	2.33	6.71	7.29	10.11	5.5	5.93	3.39	*	+		
HEMBA1004446	1.19	0.41	1.18	2.01	2.51	2.6	0.58	1.63	1.83	*	+		
HEMBA1004451	4.92	5.14	2.78	5.62	4.16	5.1	2.95	3.75	4.07				
HEMBA1004452	1.45	1.3	0.96	7.34	8.28	11.36	3.26	5.07	5.69	**	+	**	+
HEMBA1004454	2.75	3.17	2.58	3.68	3.73	5.7	3.62	3.63	3.66			*	+
HEMBA1004460	8.77	5.29	4.63	9.49	11.6	11.51	5.17	5.78	6.91	*	+		
HEMBA1004461	3.02	1.29	1.56	1.22	2.06	2.62	1.48	2	2.51				
HEMBA1004468	9.69	5.12	5.83	5.76	9.08	12.25	6.18	7.22	5.91				
HEMBA1004479	5.17	2.6	2.53	3.06	4.8	5.24	1.98	4.08	3.44				
HEMBA1004482	2.81	3.98	3.7	2.47	3.92	2.52	2.59	2.29	3.11				
HEMBA1004491	1.37	1	0.96	1.25	1.97	1.96	0.89	1.47	2.84				
HEMBA1004499	6.22	5.75	3.57	9.95	9.17	8.62	6.22	6.62	6.45	*	+		
HEMBA1004502	3.1	2.59	1.77	4.11	5.34	4.51	4.17	2.98	4.03	*	+		
HEMBA1004505	4.8	2.59	1.93	2.42	4.25	3.38	2.91	2.43	2.1				
HEMBA1004506	2.39	1.28	1.21	2.96	3.46	3.27	2.23	2.51	1.92	*	+		
HEMBA1004507	70.44	39.05	46.26	43.39	51.75	50.62	19.17	24.55	22.93			*	-
HEMBA1004509	5.46	3.62	4.71	3.53	4.82	5.37	2.96	3.83	2.3				
HEMBA1004523	1.41	0.75	0.59	1.16	1.53	1.37	1.32	1.24	1.24				
HEMBA1004528	3.19	1.97	1.1	3.38	4.01	3.33	4.31	3.09	4.88				
HEMBA1004534	6.12	2.73	4	6.77	8.18	7.93	6.04	5.56	6.21	*	+		
HEMBA1004536	4.76	3.38	3.05	3.55	4.6	4.52	2.5	2.23	2.99				
HEMBA1004538	21.21	15.5	13.77	31.9	33.44	32.76	19.4	20.15	17.02	**	+		
HEMBA1004542	2.99	2.19	1.59	3.03	3.58	3.02	3.51	3.43	2.25				
HEMBA1004552	7.56	6.12	5.53	7.59	13.46	14.87	4.88	6.44	7.28				
HEMBA1004554	2.07	2.28	0.95	2.8	2.16	2.43	2.95	3.09	3.26			*	+
HEMBA1004558	11.57	6.62	6.21	7.21	8.48	8.56	6.35	6.8	7.65				
HEMBA1004560	4.78	3.27	2.78	3.55	5.31	4.2	5.01	4.88	3.58				
HEMBA1004564	7.43	4.79	5.05	12.74	14.02	11.12	5.94	7.39	6.24	**	+		

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Table 191

HEMBA1004566	28.53	23.96	23.72	13.72	19.42	18.07	12.15	16.7	14.58	*	-	**	-
HEMBA1004573	2.19	1.72	1.51	3.93	5.22	5.71	3.32	3.47	1.99	**	+		
HEMBA1004576	2.94	1.45	1.92	18.03	33.01	34.57	7.81	8.41	10.12	**	+	**	+
HEMBA1004577	5	2.83	2.54	7.07	10.98	8.6	4.13	8.82	4.99	*	+		
HEMBA1004586	5.72	3.41	4.19	8.7	7.46	11.19	4.1	6.11	4.48	*	+		
HEMBA1004596	4.81	2.28	2.02	2.98	3.67	3.46	2.47	2.61	3				
HEMBA1004604	6.48	4.01	3.96	4.74	6.55	5.9	8.49	6.15	4.83				
HEMBA1004607	3.7	2.23	1.35	4.64	5.86	4.48	2.81	3.79	3.93	*	+		
HEMBA1004610	4.03	2.57	2.33	4.52	5.94	4.83	3.02	2.81	3	*	+		
HEMBA1004617	2.21	4.92	1	2.84	9.03	3.69	1.85	2.86	2.94				
HEMBA1004622	5.45	3.28	2.52	5.48	8.39	9.1	4.14	4.48	4.68				
HEMBA1004626	4.11	2.56	2.25	5.1	4.71	5.91	2.73	4.36	3.32	*	+		
HEMBA1004629	3.07	1.77	1.42	3.68	3.77	4.82	1.19	3.75	1.18	*	+		
HEMBA1004631	1.43	2.39	0.95	2.12	1.94	2.84	2.88	1.6	2.44				
HEMBA1004632	2.27	1.83	1.79	2.78	2.92	1.76	2.34	3.5	2				
HEMBA1004633	7.83	5.66	4.81	4.47	6.1	5.15	5.55	4.15	5.55				
HEMBA1004636	6.11	4.03	3.37	5.56	5.52	5.5	4.94	4.1	4.16				
HEMBA1004637	3.8	2.43	1.85	2.17	3.96	3.28	2.95	2.5	2				
HEMBA1004638	1.58	0.7	0.19	0.85	2.26	3.04	1.06	1.19	1.64				
HEMBA1004645	4.58	1.72	2.46	3.58	5.23	5.82	2.85	4.55	3.78				
HEMBA1004656	3.49	2.49	3.49	3.55	3.42	3.65	2.19	3.03	2				
HEMBA1004657	23.62	14.49	14.4	48.51	47.67	43.85	51.21	56.08	58.34	**	+	**	+
HEMBA1004666	1.8	1.42	1.03	2.78	2.47	2.72	1.97	2.35	2.06	**	+	*	+
HEMBA1004669	5.4	3.16	2.59	6.16	6.23	6.59	2.94	2.65	2.66	*	+		
HEMBA1004670	4.37	2.24	2	5.27	6.01	4.17	2.94	3.39	4.41				
HEMBA1004672	5.55	2.84	2.98	5.68	8.28	8.14	3.49	6.01	3.36	*	+		
HEMBA1004689	43.34	14.93	30.58	21.98	24.65	26.05	13.05	14.68	11.72				
HEMBA1004690	4.61	2.61	2.69	2.94	2.18	2.84	1.97	4.01	2.41				
HEMBA1004693	2.15	1.25	1.33	2.01	3.2	3.06	1.39	3.08	2				
HEMBA1004697	7.39	3.61	2.79	5.75	7.36	9.2	5.36	4.7	6.2				
HEMBA1004702	21.02	14.02	11.62	9.2	10.6	12.82	11.9	12.65	12.79				
HEMBA1004704	6.08	3.81	3.24	8.5	8.45	8.19	4.75	5.52	5.39	*	+		
HEMBA1004705	1.15	0.61	0.21	1.49	1.26	1.73	1.37	1.44	1.36				
HEMBA1004706	3.9	2.72	2.07	2.01	3.27	2.47	3.18	2.94	2.37				
HEMBA1004709	3.4	2.4	2.61	5.18	5.97	7.11	2.19	3.92	3.09	**	+		
HEMBA1004711	3.02	1.29	2.07	2.19	3.65	3.64	1.38	3.22	1.38				
HEMBA1004723	9.52	5.41	7.44	9.15	11.88	10.6	5.92	9.59	6.27				
HEMBA1004725	5.24	3.87	3.31	6.21	5.61	5.19	5.65	5.85	6.52			*	+
HEMBA1004730	1.7	2.99	1.13	11.04	3.71	3.48	1.14	4.24	1.15				
HEMBA1004733	1.86	1.11	1.27	1.93	2.88	2.54	1.38	2.89	2.03	*	+		
HEMBA1004734	2.06	1.99	1.5	2.15	2.83	2.85	2.1	2.82	2.29				
HEMBA1004736	3.46	3.3	2.73	5.69	8.26	7.15	2.94	3.83	4.08	**	+		
HEMBA1004748	4.24	1.57	1.93	4.83	6.28	6.83	2.64	4.21	2.49	*	+		
HEMBA1004749	7.35	4.59	5.33	5.23	6.38	10.26	4.24	7.9	6.41				
HEMBA1004751	3.74	2.05	2.99	5.29	6.07	7.15	2.9	5.44	3.62	*	+		
HEMBA1004752	5.63	3.05	2.11	4.83	5.66	7.24	4.55	3.43	5.1				
HEMBA1004753	85.27	60.35	45.13	73.61	76.67	82.04	35.88	33.51	34.18				
HEMBA1004755	12.21	10.42	8.56	18.13	22.58	19.53	19.43	13.65	17	**	+	*	+
HEMBA1004756	1.98	0.4	0.9	1.17	2.37	1.88	1.4	2.86	2.34				
HEMBA1004758	3.05	2.33	2.23	5.05	4.15	4.14	2.36	3.68	2.72	**	+		
HEMBA1004763	2.53	2.54	2.42	3.64	3.57	2.87	2.52	4.35	2.6	*	+		
HEMBA1004768	0.63	0.57	0.48	2.03	2.91	1.86	1.11	2.85	0.94	**	+		
HEMBA1004770	1.17	0.28	1.04	3.43	2.96	3.94	2.26	2.05	1.62	**	+	*	+
HEMBA1004771	3.01	1.5	1.36	3.25	3.04	3.46	2.2	2.12	2.05				
HEMBA1004775	6.8	4.62	3.7	7.13	8.07	9.04	7.62	7.16	8.82	*	+		
HEMBA1004776	3.71	2.57	1.18	9.61	3.42	2.31	3.1	3.48	4.38				

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Table 192

HEMBA1004778	4.28	3.09	3.12	5.87	7.81	8.46	5.37	4.86	3.66	*	+		
HEMBA1004784	1.55	1.14	0.87	1.97	2.67	2.4	1.81	2.87	1.66	*	+		
HEMBA1004785	2.2	0.85	1.41	2.94	2.11	2.82	2.94	3.76	2.42			*	+
HEMBA1004789	2.02	2.15	2.94	6	4.66	4.07	4.12	6.23	6.59	*	+	*	+
HEMBA1004795	1.94	0.91	1.99	4.74	2.62	2.39	1.99	2.85	2.46				
HEMBA1004797	3.34	1.51	1.57	3.19	4.14	4.19	3.42	2.94	4.14				
HEMBA1004803	1.73	1.53	0.52	3.19	3.28	3.24	3.3	2.11	2.68	**	+	*	+
HEMBA1004806	1.99	0.24	0.76	2.51	2.13	1.62	1.14	2.33	1.41				
HEMBA1004807	6.07	4.25	4.5	4.85	8.03	9.33	4.48	5.59	5.41				
HEMBA1004816	3.49	2.36	1.89	3.34	3.8	3.31	2.37	4.02	1.69				
HEMBA1004820	1.49	1.14	1.32	2.51	2.88	2.8	1.5	4.47	1.86	**	+		
HEMBA1004833	7.98	3.57	4.1	7.09	8.03	7.72	4.99	7.63	6.59				
HEMBA1004847	6.33	4.11	5.21	8.38	7.16	8.48	4.35	8.93	6.34	*	+		
HEMBA1004850	3.92	2.57	2.41	5.26	3.09	3.63	3.54	3.4	5.81				
HEMBA1004863	4.26	1.79	2.07	6.34	5.16	5.37	2.36	2.91	5.42	*	+		
HEMBA1004864	8.29	3.32	3.08	5.48	7.27	7.94	4.75	3.71	4.59				
HEMBA1004865	1.92	1.18	0.62	2.11	6.7	3.86	2.14	1.94	1.68				
HEMBA1004880	4.54	3.09	3.36	6.03	7.12	7.25	3.5	4.7	4.49	**	+		
HEMBA1004882	5.35	4.05	3.06	4.2	4.72	3.45	2.62	4.51	3.09				
HEMBA1004885	1.17	0.68	0.57	1.14	0.82	0.86	0.53	1	0.47				
HEMBA1004889	3.26	2.08	1.7	3.09	2.94	3.37	2.23	2.83	5.72				
HEMBA1004900	1.39	1.1	0.25	1.7	1.35	1.1	1.57	1.47	1.61				
HEMBA1004909	6.14	4.05	3.74	6.91	8	7.96	4.94	4.32	5.82	*	+		
HEMBA1004918	4.98	2.15	2.73	5.38	6.39	6.51	3.65	3	3.79	*	+		
HEMBA1004923	1.88	1.64	1.69	3.18	2.96	3.02	2.23	2.61	2.53	**	+	**	+
HEMBA1004929	2.42	1.04	1.11	2.68	2.08	2.3	2.43	1.05	1.27				
HEMBA1004930	5.54	5.02	5.16	8.04	11.27	11.38	5.24	6.2	5.58	*	+		
HEMBA1004933	2.24	1.54	1.06	2	2.4	2.08	1.19	1.47	2.06				
HEMBA1004934	0.55	0.77	0.07	1.15	0.99	1.58	1.85	2.74	1.58	*	+	*	+
HEMBA1004937	6.5	2.53	3.22	3.69	3.97	5.19	4.16	4.2	3.69				
HEMBA1004943	6.44	2.93	2.55	5.45	3.9	5.9	3.81	4.39	5.14				
HEMBA1004944	4.47	1.97	2.6	5.4	4.69	6.01	3.98	3.08	5.3	*	+		
HEMBA1004946	6.58	4.26	2.56	8.23	7.78	9.16	5.73	6.06	6.35	*	+		
HEMBA1004952	5.05	2.8	1.43	3.17	3.75	3.4	2.89	3.56	3.26				
HEMBA1004954	2.94	2.13	2.53	7.6	9.09	8.39	8.28	11.47	6.83	**	+	*	+
HEMBA1004956	1.7	0.98	0.85	2.16	2.35	1.65	2.19	1.65	0.68				
HEMBA1004960	4.22	1.35	1.83	3.33	4.35	3.89	3.18	2.33	2.62				
HEMBA1004971	2.85	2.08	2.33	3.11	3.19	2.48	4.48	3.31	3.12				
HEMBA1004972	7.97	3.44	5.28	7.05	7.91	7.94	4.91	4.41	4.71				
HEMBA1004973	4.05	2.96	1.6	4.3	3.46	4.03	3.1	2.58	3.76				
HEMBA1004977	14.24	10.04	6.48	10.74	14.23	17.72	5.8	5.62	5.43				
HEMBA1004978	3.63	3.21	1.82	4.34	4.05	5.53	3.79	4.18	2.53				
HEMBA1004980	2.51	2.43	1.78	4.29	5.14	5.81	2.73	3.03	2.97	**	+		
HEMBA1004982	1.4	0.95	0.55	1.1	1.4	2.11	0.94	2.12	0.81				
HEMBA1004983	1.7	1.5	1.07	1.2	1.85	1.29	1.7	1.13	1.37				
HEMBA1004995	4.75	4.53	4.44	5.51	5.64	4.6	3.99	3.69	4.53				
HEMBA1005004	4.11	3.34	2.48	4.8	3.41	3.91	3.87	2.23	2.59				
HEMBA1005008	5.55	2.4	3.38	3.53	5.55	4.97	3.01	4.08	3.22				
HEMBA1005009	10.15	9.95	7.66	7.94	11.36	8.06	4.21	5.06	5.68			**	-
HEMBA1005019	6.33	2.93	3.49	4.34	5.65	6.43	4.58	6.41	4.98				
HEMBA1005021	5.34	2.42	3.36	5.76	5.02	6.07	3.05	4.52	3.35				
HEMBA1005029	7.09	2.85	5.15	5.79	6.77	7.31	4.12	4.52	4.02				
HEMBA1005035	13.39	11.61	9.27	16.88	22.86	20.98	13.14	12.08	14.81	*	+		
HEMBA1005036	9.37	4.9	6.57	4.71	7.3	8.39	7.97	8.49	9.16				
HEMBA1005039	2.56	2.26	1.97	3.46	4.91	5.18	2.9	3.33	3.77	*	+	*	+
HEMBA1005047	3.73	2.69	2.58	2.7	3.22	4.69	3.19	3.28	3.52				

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Table 193

HEMBA1005050	8.01	4.69	4.35	6.4	8.24	6.75	4.64	5.95	4.47				
HEMBA1005062	2.24	3.49	0.58	2.31	2.34	1.56	1.28	2.55	1.35				
HEMBA1005066	1.59	0.53	1.22	1.43	2.19	2.08	0.94	1.37	2.12				
HEMBA1005067	10.97	5.24	5.8	11.93	6.24	15.81	3.48	6.87	4.63				
HEMBA1005070	54.34	32.66	23.12	7.48	7.23	9.46	4.96	6.22	5.67	*	-	*	-
HEMBA1005075	4.78	2.93	2.39	9.53	8.99	8.84	5.77	6.79	5.19	**	+	*	+
HEMBA1005078	9.58	7.81	5.77	9.39	9.72	10.05	5.01	5.86	6.72				
HEMBA1005079	12.04	7.57	6.48	19.42	17.72	15.43	8.5	9.75	11.45	*	+		
HEMBA1005083	2.66	1.46	0.66	1.94	3.02	2.07	1.27	2.07	1.73				
HEMBA1005084	7.91	6.72	4.77	5.71	7.85	8.74	5.49	4.34	5.97				
HEMBA1005088	2.86	1.68	1.86	2.41	5.46	5.18	1.67	3.51	1.49				
HEMBA1005089	5.98	4.14	4.5	9.36	10.56	9.53	2.93	5.59	4.57	**	+		
HEMBA1005090	33.54	22.43	17.55	44.06	43.43	42.47	20.48	22.61	17.3	*	+		
HEMBA1005096	5.76	3.96	4.37	6.03	5.87	6.22	4.23	3.3	6.27				
HEMBA1005101	5.71	2.76	3.85	3.75	5.23	3.72	2.48	3.36	3.77				
HEMBA1005107	4.5	1.82	2.91	2.69	3.89	3.12	3.06	3.74	2.52				
HEMBA1005113	1.43	0.81	0.45	8.23	11.09	10.71	5.43	5.23	6.51	**	+	**	+
HEMBA1005123	10.61	5.86	5.3	15.09	21.59	18.64	8.57	8.85	8.33	*	+		
HEMBA1005133	2.6	2.55	2.08	5.44	6.93	6.67	3.17	4.12	2.67	**	+		
HEMBA1005135	1.91	1.13	1.66	1.75	3.38	1.54	1.31	3.02	1.14				
HEMBA1005145	16.67	9.87	9.21	12.39	15.8	16.28	8.2	10.27	10.61				
HEMBA1005149	10.32	5.61	5.06	11.44	12.5	12.06	7.17	8.59	7.71	*	+		
HEMBA1005152	6.34	4.06	3.55	9.52	11.4	12.18	3.28	4.04	5.79	**	+		
HEMBA1005159	0.7	1.49	0.94	1.57	2.36	1.76	1.22	2.54	0.91				
HEMBA1005172	43.22	25.23	24.37	33.5	39.86	37.96	32.09	25.74	34.44				
HEMBA1005185	4.97	4.57	2.99	2.86	3.27	4.08	2.48	3.14	1.7				
HEMBA1005186	3.35	2.42	3.23	5.64	6.25	4.46	2.06	2.21	2.79	*	+		
HEMBA1005195	1.99	0.84	0.81	1.89	2.31	1.52	1.31	2.87	1.25				
HEMBA1005201	6.2	5.19	2.55	5.77	6.88	6.27	4.89	5.22	6.55				
HEMBA1005202	8.96	4.63	5.23	6.96	8.01	6.67	8.1	7.62	9.46				
HEMBA1005204	113.3	93.42	81.36	145.9	165	106.5	90.09	59.5	89.11				
HEMBA1005206	6.48	3.93	4.87	5.9	5.71	6.15	4.98	4.32	4.52				
HEMBA1005219	2.14	1.72	1.8	4.03	2.98	2.85	3.28	4.04	4.31	*	+	**	+
HEMBA1005223	3.02	2.16	2.78	4.29	3.41	4.21	2.9	3.66	3.28	*	+		
HEMBA1005229	0.71	0.07	0.59	1.25	1.02	0.47	0.51	2.08	0.98				
HEMBA1005230	4.24	4.62	2.37	7.34	7.76	6.64	2.52	4.81	4.22	*	+		
HEMBA1005232	0.15	0.54	0.47	1.05	1.44	1.37	1.1	0.73	0.86	**	+	*	+
HEMBA1005238	5.05	3.37	2.42	6.46	5.11	6.11	4.05	3.86	3.91				
HEMBA1005241	18.2	11.3	9.41	11.74	14.66	18	9.85	7.33	9.11				
HEMBA1005244	6.45	3.35	4.4	5.3	7.24	5.85	3.98	5	6.42				
HEMBA1005246	9.39	6.95	6.65	15.52	17.83	13.37	15.28	9.28	12.96	**	+		
HEMBA1005251	2.49	1.43	2.18	5.25	6.15	4.92	3.41	3.93	3.35	**	+	*	+
HEMBA1005252	3.83	2.63	3.03	3.56	4.92	3.46	2.88	4.5	4.38				
HEMBA1005267	1.63	0.84	1.67	10.27	7.55	7.28	1.17	3.13	1.81	**	+		
HEMBA1005274	1.18	0.71	0.61	1.46	2.14	1.62	1.18	1.08	1.02	*	+		
HEMBA1005275	1.9	0.81	0.85	2.82	4.11	3.4	1.92	2.54	1.27	*	+		
HEMBA1005288	3.5	1.84	2.36	6.6	8.72	6.93	3.45	3.43	3.32	**	+		
HEMBA1005293	1.91	2.03	0.55	4.54	1.95	1.33	0.58	2.15	1.2				
HEMBA1005296	401.9	314.1	296.6	377.8	403.7	432.4	228.1	207.4	230			*	-
HEMBA1005301	1.98	0.74	1.57	2.67	1.35	1.8	1.62	2.6	1.33				
HEMBA1005304	4.1	2.37	2.93	8.99	8.69	9.63	4.7	6.26	5.96	**	+	*	+
HEMBA1005305	2.8	1.25	1.81	4.03	4.81	4.66	2.57	4.35	2.78	**	+		
HEMBA1005311	2.04	1.03	1.55	2.81	2.74	3.45	0.88	2.3	2.36	*	+		
HEMBA1005313	6.91	3.99	3.19	6.31	4.42	4.78	4.14	4.74	6.56				
HEMBA1005314	0.55	0.27	0.2	1.02	1.14	0.89	1.2	0.4	1.03	**	+		
HEMBA1005315	4.12	1.27	1.36	3	4.13	3.44	3.48	2.53	3.28				

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Table 194

HEMBA1005317	1.33	0.36	0.19	4.23	3.8	4.6	1.25	1.46	1.92	**	+		
HEMBA1005318	1.08	0.85	0.59	0.97	1.89	1.29	1.43	1.82	1.13				
HEMBA1005324	3.04	2.4	1.83	6.59	7.62	7.75	5.26	6.51	7.55	**	+	**	+
HEMBA1005331	0.95	1.56	1.2	1.7	1.65	2.13	0.66	2.53	0.91				
HEMBA1005337	2.8	1.37	1.32	2.67	3.1	2.37	2.01	2.34	2.18				
HEMBA1005338	4.38	1.6	2.45	4.11	1.92	3.95	3.55	3.33	3.26				
HEMBA1005344	22.24	11.71	11.54	14.09	14.09	14.6	12.65	14.29	14.22				
HEMBA1005353	6.55	4.18	3.72	6.77	13.54	9.81	6.95	6.75	7.1				
HEMBA1005359	7.54	5.12	6.63	11.85	12.2	12.76	7.38	8.41	9.39	**	+		
HEMBA1005362	9.18	7.14	7.14	5.77	8.95	8.4	3.09	3.31	2.6			**	-
HEMBA1005364	0.89	1.26	0.41	1.96	2.44	1.02	1.19	1.6	1.68				
HEMBA1005367	3.22	2.29	1.05	4.88	6.98	6.68	5.63	8	6.43	*	+	**	+
HEMBA1005372	2.2	0.98	0.77	1.74	3.83	3.08	4.16	2.78	2.66			*	+
HEMBA1005374	6.99	3.71	3.35	12.54	10.52	8.75	6.1	6.58	7.22	*	+		
HEMBA1005379	1.84	1.63	1.2	1.2	1.49	2.65	1.75	1.09	1.97				
HEMBA1005382	7.86	4.67	5.2	10.89	7.83	8.14	5.58	6.98	6.52				
HEMBA1005384	4.42	2.21	2.13	6.74	6.14	5.84	4.87	4.21	4.01	*	+		
HEMBA1005386	6.04	3.65	3.38	6.45	5.92	6.1	5.2	4.67	5.78				
HEMBA1005389	5.36	3.94	2.77	5.75	6.88	6.02	2.6	5.56	3.66				
HEMBA1005394	6.27	3.67	3.58	3.93	4.59	4.22	2.21	4.81	3.15				
HEMBA1005403	11.32	8.45	6.9	16.3	23.03	11.57	16.03	13.06	13.2			*	+
HEMBA1005408	4.6	4.51	2.17	5.61	4.87	4.3	5.51	3.2	4.27				
HEMBA1005410	1.48	1.46	0.98	2.22	1.83	2.32	3.82	2.31	2.31	*	+	*	+
HEMBA1005411	3.32	2.25	1.72	8.56	7.19	8.45	4.84	3.85	4.74	**	+	*	+
HEMBA1005423	4.84	2.65	2.83	7.04	5.69	5.75	3.26	4.32	3.64	*	+		
HEMBA1005426	1.66	0.94	1.03	2.84	2.24	2.73	1.74	2.79	1.34	**	+		
HEMBA1005427	18.06	13.04	14.1	24.89	25.18	27.94	11.55	18.31	15.99	**	+		
HEMBA1005430	3.16	1.5	2.13	1.75	2.9	3.37	2.43	3.98	2.23				
HEMBA1005438	4.91	3.54	3.44	5.97	8.41	5.02	5.97	4.67	6.58				
HEMBA1005443	11.24	11.79	6.21	19.21	19.58	15.66	17.03	13.17	10.83	*	+		
HEMBA1005447	3.13	3.2	1.74	4.18	4.12	4.68	2.92	2.36	2.86	*	+		
HEMBA1005449	4.87	2.92	3.15	2.75	4.63	3.51	2.81	3.38	5.99				
HEMBA1005452	8.28	4.39	4.04	3.56	7.29	6.13	4.29	5.16	4.62				
HEMBA1005454	6.03	4.13	3.77	3.63	4.31	5.36	2.84	5.74	3.18				
HEMBA1005468	8.63	4.08	5.4	8.19	9.91	9.17	5.46	7.18	6.46				
HEMBA1005469	7.04	4.49	4.09	8.04	6.87	9.35	3.55	5.47	4.98				
HEMBA1005472	4.58	4.13	2.33	5.09	7.14	6.31	4.57	3.72	5.09				
HEMBA1005474	7.99	6.35	8.53	12.45	17.71	14.57	6.84	6.03	7.86	*	+		
HEMBA1005475	27.06	16.75	12.04	21.27	20.2	24.59	14.7	11.72	14.55				
HEMBA1005489	4.67	3.91	3.31	12.33	12.95	12.78	5.02	3.73	4.43	**	+		
HEMBA1005497	1.7	0.87	0.7	1.28	2.32	1.65	1.49	1.73	0.9				
HEMBA1005500	6.11	2.66	2.28	6.01	8.49	7.76	2.99	5.44	4.21				
HEMBA1005506	1.91	0.96	0.87	1.02	1.78	1.61	1.14	3.14	1.21				
HEMBA1005508	3	1.68	2.62	3.65	3.78	4.7	1.31	2.01	2	*	+		
HEMBA1005511	6.78	4.02	3.71	12.46	10.15	10.8	6.67	5.32	7.37	**	+		
HEMBA1005513	9.39	4.07	4.88	7.16	6.69	8.41	5.04	6.55	4.92				
HEMBA1005517	4.77	2.9	3.52	2.59	3.48	4.27	1.92	3.32	2.46				
HEMBA1005518	6.02	2.95	2.57	4.55	4.62	5.87	5.99	3.9	5.53				
HEMBA1005520	11.23	5.82	6.06	14.5	18.42	18.84	7.99	9.11	9.67	*	+		
HEMBA1005522	4.58	1.74	1.96	2.63	3.4	3.05	1.78	3.18	2.26				
HEMBA1005526	4	2.06	4.25	8.46	10.15	10.58	3.26	5.34	5.19	**	+		
HEMBA1005528	14.83	10.54	9.95	13.03	18.88	16.21	6.65	7.84	6.97			*	-
HEMBA1005530	5.44	2.29	3.17	4.84	6.25	8.18	4.67	4.21	3.84				
HEMBA1005538	4.71	2.93	2.46	83.2	102.3	97.16	227.3	162.3	210.6	**	+	**	+
HEMBA1005539	7.02	4.61	3.84	4.34	5.62	5.7	5.14	4.99	5.58				
HEMBA1005545	4.05	4.59	3.18	3.31	5.22	4.49	4.33	4.46	3.97				

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Table 195

HEMBA1005548	2.54	2.07	2.02	3.97	6.52	4.14	3.37	3.9	3.32	*	+	**	+
HEMBA1005552	9.98	4.38	5.49	14.16	16.16	16.24	6.88	9.1	7.91	**	+		
HEMBA1005558	5.62	4.78	4.01	4.12	4.94	4.94	2.89	4.54	2.98				
HEMBA1005568	4.56	2.35	2.64	4.41	6.84	7.67	2.66	3.77	3.75				
HEMBA1005570	22.81	14.72	12.89	3.4	5.87	4.67	2.86	3.28	4.18	*	-	*	-
HEMBA1005576	3.57	2.9	1.76	5.63	4.9	6.27	3.31	4.43	3.65	*	+		
HEMBA1005577	3.28	1.8	1.85	2.52	3.76	3.29	1.78	2.45	2.1				
HEMBA1005581	6.44	3.47	3.35	11.86	10.8	9.38	9.31	8.35	7.77	**	+	*	+
HEMBA1005582	3.79	2.19	1.67	4.94	4.83	5.37	3.11	3.69	2.69	*	+		
HEMBA1005583	2.18	2.16	1.54	2.99	3.77	4.66	2.3	2.75	1.62	*	+		
HEMBA1005588	3.6	2.49	3.31	8.28	7.89	9.86	3.63	5.17	4.67	**	+		
HEMBA1005593	3.44	3.2	2.65	4.18	6.03	3.87	2.97	3.28	2.95				
HEMBA1005595	2.58	2.31	1.83	3.46	4.98	5.89	3.2	2.15	3.87	*	+		
HEMBA1005597	13.38	9.58	8.44	10.53	12.2	11.02	8.53	9.47	8.93				
HEMBA1005606	12.27	7.53	6.44	5.89	7.11	6.3	8.22	8.78	11.95				
HEMBA1005609	5.25	3.66	3.27	10.52	11.83	10.56	4.85	5.36	5.71	**	+		
HEMBA1005616	5.15	3.24	2.69	6.77	7.27	7.69	4.76	5.32	4.74	*	+		
HEMBA1005621	5.71	4.59	4.34	4.48	5.05	3.45	2.83	4.75	2.83				
HEMBA1005627	4.83	2.61	2.82	6.51	8.02	6.48	3.29	4.97	4.83	*	+		
HEMBA1005628	5.64	3.83	3.44	12.81	11.82	14.97	10.64	9.94	13.34	**	+	**	+
HEMBA1005631	2.21	1.39	0.65	2.83	4.04	3.15	5.61	3.11	3.88	*	+	*	+
HEMBA1005632	11.01	3.49	3.42	8.83	9.02	7.82	5.06	4.35	5.44				
HEMBA1005634	6.35	2.76	2.05	5.36	8.63	6.5	4.98	5	6.87				
HEMBA1005662	1.07	1.53	1.02	2.26	2.43	2.33	2.04	1.73	1.38	**	+		
HEMBA1005666	4.52	3.82	4.32	9.91	8.09	7.3	6.48	6.28	5.06	**	+	*	+
HEMBA1005670	2.29	2.27	1.9	7.3	6.51	7	3.1	7.04	3.71	**	+		
HEMBA1005671	3.97	1.07	3.6	3.68	3.22	2.26	4.53	6.9	3.6				
HEMBA1005679	4.26	2.11	3.13	6.55	7.51	6.35	2.51	4.92	3.8	**	+		
HEMBA1005680	6.79	3.09	2.88	6.98	9.15	8.11	7.19	3.45	6.54				
HEMBA1005685	5.15	2.24	2.86	3.16	3.75	6.06	3.75	2.67	3.13				
HEMBA1005698	6.46	4.64	3.65	6.51	6.49	8.04	4.48	5.97	6.27				
HEMBA1005699	2.04	1.37	1.03	2.33	2.8	2.44	1.39	3.16	0.93	*	+		
HEMBA1005703	1.57	1.14	0.53	2.63	1.8	1.22	0.95	3.02	1.71				
HEMBA1005705	4.78	2.62	3.65	8.55	5.59	7.85	3.94	5.46	2.65	*	+		
HEMBA1005712	1.7	0.73	0.42	2.78	2.29	2.36	1.03	2.79	1.13	*	+		
HEMBA1005717	1.99	1.9	1.57	4.59	18.53	4.07	1.65	3.65	2.24				
HEMBA1005718	12.46	6.17	5.4	10.4	11.53	8.97	6.74	7.19	8.25				
HEMBA1005721	15.4	8.95	6.41	11.18	12.64	11.59	11.3	10.89	13.73				
HEMBA1005722	11.88	7.25	5.73	15.89	16.63	13.24	10.07	13.96	12.55	*	+		
HEMBA1005724	4.23	1.39	1.12	1.47	3.11	2.3	1.44	1.83	2.83				
HEMBA1005732	4.64	3.73	2.82	4.17	4.78	5.5	3.41	2.84	3.27				
HEMBA1005737	2.11	1.17	0.89	1.64	1.86	1.55	2.37	1.99	1.73				
HEMBA1005742	2.91	1.85	1.65	20.12	22.7	20.93	10.11	6.75	7.19	**	+	**	+
HEMBA1005746	3.55	2.22	2.55	2.88	5.21	3.91	2.28	2.67	1.49				
HEMBA1005747	6.73	2.98	3.61	4.2	6.34	4.06	4.88	4.78	5.21				
HEMBA1005749	16	15.05	7.61	16.72	17.56	14.78	13.73	10.17	19.02				
HEMBA1005755	1.55	1.38	0.58	2.76	3.45	1.74	2.11	2.82	2.29			*	+
HEMBA1005760	6.22	4.23	3.01	5.27	5.19	5.24	4.36	3.24	4.73				
HEMBA1005765	5.47	4.02	4.47	8.82	8.58	6.98	4.72	5.79	3.58	**	+		
HEMBA1005766	6.49	3.72	3.07	6.86	5.34	6.17	4.5	5.2	3.85				
HEMBA1005780	5.24	3.72	3.56	7.77	10.48	12.03	5.65	6.93	5.8	*	+	*	+
HEMBA1005795	2.44	2.1	2.01	3.69	3.63	2.88	1.69	3.18	1.68	*	+		
HEMBA1005809	23.36	22	11.6	14.58	20.18	18.5	16.89	18.97	9.81				
HEMBA1005813	3.44	3.32	2.49	3.52	4.47	4.04	2.83	4.45	3.63				
HEMBA1005815	6.13	3.52	2.7	5.29	7.35	4.96	4.74	5.46	7.01				
HEMBA1005822	4.2	1.96	2.92	8.67	7.02	9.4	4.99	3.69	6.16	**	+		

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Table 196

HEMBA1005829	7.71	4.11	4.16	9.68	9.82	10.65	5.68	6.05	6.18	*	+		
HEMBA1005833	5.58	4.05	3.69	5.07	5.16	5.6	4.09	4.46	5.21				
HEMBA1005834	6.55	4.34	5.21	12.06	12.18	15.25	4.16	7.19	5.66	**	+		
HEMBA1005844	55.19	32.63	42.62	52.31	50.88	44.4	13.71	22.39	16.54			*	-
HEMBA1005852	14.32	7.35	8.88	11.42	13.87	12.28	12.12	9.6	10.71				
HEMBA1005853	4.46	3.87	2.7	5.48	7.15	7.24	6.76	3.1	4.03	*	+		
HEMBA1005878	10.9	9.31	6.82	15.29	18.75	18.35	11.26	9.02	9.91	**	+		
HEMBA1005883	2.8	3.02	2.09	2.99	4.75	3.12	3.03	3.43	2.83				
HEMBA1005884	1.78	1.18	0.5	2.41	2.22	1.91	2.16	1.93	1.73				
HEMBA1005891	1.55	1.14	0.52	2.25	4.37	4.09	2.08	2.69	1.69	*	+		
HEMBA1005894	3.43	2.12	2.97	5.44	5.86	5.44	2.54	4.52	2.77	**	+		
HEMBA1005898	16.67	8.8	11.51	11.61	18.53	21.97	6.97	12.21	8.22				
HEMBA1005902	4.41	3.46	2.55	2.97	3.31	3.57	3.63	4.8	4.43				
HEMBA1005907	1.14	1	0.32	1.39	1.9	1.41	1.83	2.17	1.38			*	+
HEMBA1005909	0.96	0.99	0.06	0.74	1.52	0.83	1.8	0.82	0.95				
HEMBA1005911	5.56	3.24	3.54	5.59	8.12	8.18	4.97	3.97	5.62	*	+		
HEMBA1005912	6.61	6.28	5.64	8.63	10.33	8.51	7.27	7.15	4.9	*	+		
HEMBA1005913	3.32	1.87	2.67	4.85	5.83	5.39	4.23	6.09	5.19	**	+	*	+
HEMBA1005921	5.08	3.6	4.07	7.96	11.09	11.08	3.93	6.12	4.64	**	+		
HEMBA1005922	9.29	4.86	8.75	10.31	11.79	14.59	5.42	7.95	6.59				
HEMBA1005929	9.26	6.15	5.27	8.35	12.25	12.51	8.91	7.98	6.88				
HEMBA1005931	13.37	8.03	6.05	13.2	15.89	16.14	10.01	9.04	10.17				
HEMBA1005934	11.83	7.65	6.91	11.33	21.92	13.8	6.94	9.42	10.1				
HEMBA1005945	9.41	6.42	4.64	6.1	7.01	8.67	8.01	6.77	7.06				
HEMBA1005962	2.52	1.69	1.85	2.52	2.44	3.11	1.69	3.18	2.61				
HEMBA1005963	1.58	1.29	0.83	2.22	2.32	1.65	0.75	2.23	1.58				
HEMBA1005990	53.63	37.05	35.87	22.88	28.11	30.49	25.75	38.21	38.5				
HEMBA1005991	4.36	2.88	2.52	7.83	8.53	8.07	3.66	3.18	4.37	**	+		
HEMBA1005999	7.25	4.04	3.51	7.81	9.22	8.54	5.71	6.17	5.07	*	+		
HEMBA1006002	4.03	2.6	1.83	2.32	2.41	2.99	3.56	4.2	3.68				
HEMBA1006005	3.58	3.7	2.47	1.41	2.98	2.78	2.19	3.32	3.16				
HEMBA1006011	28.82	13.22	19.62	6.69	8.42	8.26	9.43	7.34	8.25	*	-		
HEMBA1006013	4.9	3.69	2.44	2.82	3.64	2.69	3.14	3.46	2.63				
HEMBA1006016	5.42	2.01	3.02	4.73	5.78	5.82	3.09	4.11	3.71				
HEMBA1006019	4.75	3.24	2.19	2.66	6.4	5.83	2.01	3.58	3.27				
HEMBA1006021	5.17	2.64	3.76	13.9	20.33	23.22	9.49	12.71	9.39	**	+	**	+
HEMBA1006022	6.7	7.43	3.24	7.5	7.39	6.93	5.83	6.01	8.3				
HEMBA1006031	4.39	5.2	2.1	3.55	7.12	4.25	2.82	4.39	3.34				
HEMBA1006035	3.57	1.83	2.1	2.68	3.31	3.32	3.52	3.36	3.1				
HEMBA1006036	11.47	5.72	5.91	13.84	22.61	19.36	7.96	7.38	10.66	*	+		
HEMBA1006042	5.24	3.69	2.84	6.48	8.01	7.56	4.36	7.77	4.18	*	+		
HEMBA1006044	1.69	0.79	0.7	2	1.1	1.58	0.9	2.05	1.25				
HEMBA1006045	4.3	3.06	2.36	5.33	6.87	5.75	4.69	7.34	3.91	*	+		
HEMBA1006048	5.42	3.01	4.33	5.37	6.23	4.19	3.1	3.81	2.5				
HEMBA1006053	5.79	4.06	2.48	4.5	6.49	3.55	3.66	3.74	4.34				
HEMBA1006055	1.82	1.84	1.28	1.8	2.36	2.19	1.75	2.52	2.48				
HEMBA1006058	4.72	2.18	2.21	2.56	3.95	3.04	3.54	3.28	3.39				
HEMBA1006063	15.52	11.99	10.03	16.08	16.03	13.94	13.46	9.12	10.83				
HEMBA1006067	1.98	1.55	1.25	1.72	2.65	1.7	2.65	2.72	2.71			**	+
HEMBA1006081	3.98	3.25	2.94	3.52	4.19	3.86	2.74	3.6	2.18				
HEMBA1006089	10.88	7.08	9.01	8.5	7.48	9.62	5.26	4.65	6.13			*	-
HEMBA1006090	2.72	1.74	2.31	2.48	4.09	2.53	1.71	3.25	2.66				
HEMBA1006091	8.41	4.97	5.38	6.67	13.08	9.53	6.54	5.82	7.45				
HEMBA1006093	4.66	3.46	1.8	4.22	4.68	5.91	4.02	4.39	5.59				
HEMBA1006099	8.2	2.83	3.57	7.25	7.27	6.62	8.7	6.8	7.75				
HEMBA1006100	4.94	3.58	3.48	6.75	7.94	7.84	5.43	4.52	4.63	**	+		

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Table 197

HEMBA1006108	5.03	2.45	2.82	5.62	4.96	3.72	3.28	3.95	3.28				
HEMBA1006114	5.25	4.63	5.08	7.3	10.42	7.17	4.76	5.44	5.87	*	+		
HEMBA1006121	6.32	2.33	4.31	5.84	6.44	7.33	4.17	6.55	4.7				
HEMBA1006124	3.12	2.28	2.5	3.33	4.9	2.3	1.89	3.9	2.53				
HEMBA1006125	10.14	8.44	4.52	7.52	17.2	16.18	9.52	10.87	14.31				
HEMBA1006130	2.62	2.68	2.39	2.72	3.08	4.43	3.7	4.3	4.1			**	+
HEMBA1006138	7.26	4.73	3.72	9.3	11.39	10.14	5.49	5.98	7.37	*	+		
HEMBA1006142	6.22	3.63	4.24	7.33	10.18	10.72	6.57	6.34	6.19	*	+		
HEMBA1006150	16.28	10.88	9.66	15.57	15.3	13.33	6.57	7.84	7.68				
HEMBA1006151	8.94	6.23	8.3	9.44	9.41	9.8	14.8	13.36	17.11			**	+
HEMBA1006155	4.31	2.12	3.11	2.99	2.19	2.62	2.75	4.44	3.92				
HEMBA1006158	1.99	2.23	1	5.52	2.28	1.62	0.79	3.02	2.04				
HEMBA1006164	7.82	6.93	4.48	10.95	14.83	12	6.46	6.96	7.98	*	+		
HEMBA1006171	3.78	1.96	1.78	2.93	3.7	4.2	6.07	5.07	5.46			*	+
HEMBA1006173	3.13	1.34	2.45	2.99	4.82	4.35	2.87	4.45	2.71				
HEMBA1006176	17.29	15.19	12.08	17.72	24.16	22.1	76.2	63.22	78.98			**	+
HEMBA1006182	2.42	1.06	1.52	2.8	3.22	2.43	1.16	3.5	1.94				
HEMBA1006197	6.41	5.46	4.82	12.32	9.66	9.7	4.32	5.89	5.15	**	+		
HEMBA1006198	9.58	7.2	6.52	9.4	9.55	10.32	5.65	8.56	6.79				
HEMBA1006213	2.56	0.9	1.99	3.02	4.19	4.18	1.76	2.58	3.01	*	+		
HEMBA1006217	23.81	12.95	14.09	28.71	29.21	22.65	54.8	57.77	74.75			**	+
HEMBA1006226	45.81	48.81	55.06	71.05	67.87	69.04	34.7	30.76	48.77	**	+		
HEMBA1006235	2.69	1.66	2.93	2.89	2.63	3.42	3.26	2	2.73				
HEMBA1006248	4.57	1.66	2.14	4.47	3.25	4.51	3.57	3.35	2.98				
HEMBA1006251	7.31	5.13	5.62	8.77	8.46	10.53	8.03	7.68	7.92	*	+	*	+
HEMBA1006252	2.83	2.65	0.76	1.86	2.33	3.7	2.51	1.94	2.08				
HEMBA1006253	5.52	3.08	3.71	4.06	4.47	4.75	2.99	2.68	1.89				
HEMBA1006259	4.17	1.88	2.86	4.37	4.88	6.45	2.66	2.31	3.49				
HEMBA1006261	6.4	3.95	3.39	6.02	5.83	6.2	5.45	3.63	10.61				
HEMBA1006268	3.66	2.08	1.88	4.46	4.9	5.18	2.58	2.36	4.27	*	+		
HEMBA1006271	7.71	2.93	4.51	11.62	12.09	12.3	7.07	5.33	10.91	**	+		
HEMBA1006272	2.81	1.63	1	2.86	2.92	3.49	2.16	1.96	2.4				
HEMBA1006273	5.39	2.09	3.07	4.81	3.79	4.4	5.32	3.06	3.91				
HEMBA1006276	2.93	1.9	3.24	3.4	4.55	3.76	2.55	1.66	2.29				
HEMBA1006278	1.93	1.63	1.33	4.06	4.19	3.8	2.43	1.58	2.09	**	+		
HEMBA1006283	7.35	3.25	3.5	4.82	5.8	5.93	4.92	3.12	4.11				
HEMBA1006284	3.83	2.26	2.04	5.58	2.8	4.34	3.15	2.33	3.82				
HEMBA1006291	4.96	1.36	1.34	4.1	2.68	4.41	3.86	3.13	3.18				
HEMBA1006292	2.77	2.02	1.73	2.32	2.22	1.89	2.26	1.67	2.38				
HEMBA1006293	3.02	0.92	0.7	1.9	1.76	2.36	1.54	1.85	1.56				
HEMBA1006299	3.49	2.22	1.51	13.99	12.93	16.92	7.99	7.28	10.15	**	+	**	+
HEMBA1006309	5.39	3.08	3.38	5.38	6.85	7.74	3.06	4.11	4.45				
HEMBA1006310	3.7	2.35	2.24	5.29	3.06	3.56	2.59	4.56	4.32				
HEMBA1006311	8.15	4.04	4.72	3.8	4.97	7.43	4.03	5.26	5.64				
HEMBA1006313	2.58	0.57	1	1.55	1.73	1.85	2.63	1.09	1.3				
HEMBA1006316	2.99	1.66	1.44	1.74	2.62	2.14	2.59	1.79	1.84				
HEMBA1006328	4.68	2.1	1.68	6.39	5.95	6.83	4.27	3.72	3.95	*	+		
HEMBA1006334	2.26	1.44	1.07	1.93	1.34	1.2	1.12	1.33	0.99				
HEMBA1006335	10.13	6.95	5.67	4.72	4.51	6.4	10.88	11.65	14.01			*	+
HEMBA1006344	4.43	2.82	4.27	9.97	8.14	7.72	4.65	6.26	4.98	**	+		
HEMBA1006347	5.25	2.13	2.64	4.75	3.92	6.02	3.02	3.83	3.69				
HEMBA1006349	6.07	2.73	2.89	4.44	4.96	6.67	4.94	4.8	4.22				
HEMBA1006352	3.21	2.07	2.2	4.23	3.53	3.79	3.57	2.77	2.87	*	+		
HEMBA1006357	9.36	4.79	5.03	14.77	13.42	14.23	7.21	5.46	6.81	**	+		
HEMBA1006358	4.06	2.27	1.93	3.39	4.53	4.11	2.56	2.11	2.8				
HEMBA1006359	11.9	9.22	8.59	18.27	21.46	21.84	9.68	5.92	7.59	**	+		

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Table 198

HEMBA1006360	7.98	4.95	5.62	5.47	3.56	4.4	1.94	2.36	2.5			*	-
HEMBA1006364	3.11	1.13	2.29	5.13	3.18	5.17	4.53	10.75	7.49			*	+
HEMBA1006377	9.83	4.08	4.81	9.68	6.73	11.12	5.12	6.15	6.04				
HEMBA1006380	8.33	2.76	3.16	7.63	7.47	9.64	4.68	4.63	5.81				
HEMBA1006381	27.84	15.11	15.63	23.73	22.47	28.24	18.48	12.8	18.34				
HEMBA1006385	9	3.81	3.21	10.12	10.82	10.06	5.78	6.06	7.86				
HEMBA1006390	10.59	5.3	6.11	5.74	8.16	9.4	6.45	5.63	5.84				
HEMBA1006391	5.9	2.52	2.93	4.19	2.98	3.66	3.7	3.39	4.92				
HEMBA1006398	1.24	0.85	0.78	1.46	2.48	2.33	1.32	1.57	1.25	*	+		
HEMBA1006405	6.46	2.31	3.39	3.97	5.97	7.86	4.98	4.43	6.01				
HEMBA1006410	10.66	4.34	6.26	48.24	9.18	6.95	5.67	6.99	5.47				
HEMBA1006416	7.58	3.75	4.83	11.17	11.6	10.4	5.86	5.53	5.52	**	+		
HEMBA1006418	4.85	2.81	2.36	4.42	4.54	5.46	2.95	3.19	4.26				
HEMBA1006419	8.31	4.08	4.44	13	13.16	12.95	7.56	6.59	6.8	**	+		
HEMBA1006421	2.57	1.36	2.21	4.58	3.93	3.93	2.69	2.86	2.95	**	+		
HEMBA1006424	1.92	1.1	0.54	1.6	1.43	2	1.13	1.24	1.46				
HEMBA1006426	6.91	3.24	3.97	14.78	13.77	12.89	6.5	5.72	7.38	**	+		
HEMBA1006430	4.14	1.54	1.15	3.22	4.8	4.46	2.25	2.55	3.21				
HEMBA1006438	3.24	1.25	2.86	4.15	5.58	5.24	2.63	2.65	2.43	*	+		
HEMBA1006445	5.47	3.56	1.09	4.34	6.2	5.79	5.24	5.14	9.95				
HEMBA1006446	2.47	0.4	0.6	1.78	0.97	2.17	2.61	1.77	0.98				
HEMBA1006456	9.3	7.18	5.88	27.97	39.53	36.06	25.26	23.55	25.96	**	+	**	+
HEMBA1006461	3.9	2.47	2.09	3.96	6.32	5.5	3.18	2.5	2.97				
HEMBA1006467	3.36	2.3	2.41	1.89	3.11	2.94	1.06	2.01	1.22			*	-
HEMBA1006470	3.32	2.6	1.74	4.73	4.89	6.17	2.71	2.99	2.35	*	+		
HEMBA1006471	2.77	2.01	2.5	2.54	4.17	4.09	1.83	2.8	1.93				
HEMBA1006474	3.4	0.88	1.69	1.95	2.26	1.5	0.73	1.98	1.64				
HEMBA1006476	7.63	2.81	3.49	7.03	6.55	10.28	5.71	6.01	8.9				
HEMBA1006482	53.61	36.99	43.8	47.46	64.27	63.44	24.67	21.43	26.34			*	-
HEMBA1006483	5.77	3.34	3.12	9.27	6.33	10.42	4.67	4.49	5.8	*	+		
HEMBA1006485	2.4	0.96	1.41	4.2	4.91	5.55	9.43	7.34	8.87	**	+	**	+
HEMBA1006486	22.07	14.47	14.17	13.5	21.65	20.32	9.55	5.18	8.79			*	-
HEMBA1006489	2.84	0.31	0.23	0.65	1.22	0.91	1.3	1.95	0.72				
HEMBA1006492	22.55	16.4	18.02	18.63	19.03	19.21	4.75	5.92	5.79			**	-
HEMBA1006494	1.6	0.13	1.42	1.49	1.22	1.56	0.94	0.97	0.8				
HEMBA1006497	4.42	2.46	1.3	2.7	3.38	4.13	3.19	2.22	2.93				
HEMBA1006501	6.77	2.17	3.41	4.37	3.72	6.05	2.94	2.94	4.13				
HEMBA1006502	14.3	11.26	8.46	15.96	17.52	16.95	15.96	11.43	17.31	*	+		
HEMBA1006507	3.4	0.73	1.23	5.85	4.08	5.84	2.92	3.88	4.16	*	+		
HEMBA1006517	4.63	2.62	2.31	5.72	6.14	5.82	3.68	4.27	4.71	*	+		
HEMBA1006521	3.02	1.72	1.98	2.24	2.27	2.97	3.41	3.45	2.36				
HEMBA1006529	6.54	5.38	7.96	6.72	7.42	7.81	5.9	6.56	6.87				
HEMBA1006530	1.54	0.77	2.01	2.93	1.8	2.4	1.35	1.69	1.44				
HEMBA1006535	2.61	2.15	0.64	3.13	3.63	3.67	2.05	1.48	2.17				
HEMBA1006536	5.93	3.85	4.16	6.52	8.47	8.22	4.62	4.48	4.48	*	+		
HEMBA1006540	4.27	2.17	1.9	4.22	2.42	3.65	2.42	2.05	2.05				
HEMBA1006544	1.52	0.67	1.46	2.15	3.36	3.6	2.21	2.99	2.6	*	+	*	+
HEMBA1006546	4.48	4.88	3.24	16.24	9.73	11.7	5.09	6.41	8.5	*	+		
HEMBA1006549	2.11	0.58	0.86	2.8	1.88	2.9	1.86	1.87	1.42				
HEMBA1006559	5.16	2.1	4.6	12.73	9.91	12.55	8.17	8.31	7.9	**	+	*	+
HEMBA1006562	2.22	0.76	1.85	3.22	2.69	2.84	1.63	3.25	2.16	*	+		
HEMBA1006566	1.5	1.62	0.13	0.8	1.28	0.97	1.14	1.33	0.88				
HEMBA1006569	4.26	2.46	1.96	4.02	5.76	5.28	3.58	2.64	3.6				
HEMBA1006572	1.59	0.24	0.54	0.56	0.89	1.09	1.05	1.04	1.21				
HEMBA1006579	2.51	1.31	1.43	2.63	2.93	3.26	6.37	6.01	6.92	*	+	**	+
HEMBA1006583	3.62	1.64	2.4	3.61	3.89	4.77	3.38	3.77	2.05				

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Table 199

HEMBA1006595	4.6	1.32	2.47	6.45	3.43	5.48	2.48	3.17	3.35				
HEMBA1006597	6.19	2.47	4	9.61	11.89	11.02	4.43	7.63	6.03	**	+		
HEMBA1006606	5.22	2.34	3.15	5.5	7.09	8.72	4.17	3.59	5.67	*	+		
HEMBA1006612	5.88	3.13	2.66	9.51	7.07	8.75	4.24	4.07	8.12	*	+		
HEMBA1006617	6.23	2.4	3.25	7.51	8.15	9.4	4.22	3.47	5.72	*	+		
HEMBA1006624	21.51	11.59	11.39	8.91	10.89	11.11	15.72	17.22	19.01				
HEMBA1006631	11.14	7.16	5.63	14.71	13.36	15.13	9.17	8.76	9.27	*	+		
HEMBA1006635	3.5	1.48	1.8	6.1	5.02	7.12	3.2	2.77	3.44	*	+		
HEMBA1006639	5.83	1.94	3.55	4.08	4.21	4.37	3.14	4	3.07				
HEMBA1006643	8.1	3.39	6.04	7.92	5.21	8.41	3.69	6.07	4.57				
HEMBA1006648	7.17	4.23	2.23	4.85	5.86	6.95	5.26	5.13	6.25				
HEMBA1006652	7.55	5.4	7.95	14.31	13.73	13.23	6.43	7.1	11.54	**	+		
HEMBA1006653	6.97	4.5	3.06	4.22	5.74	4.88	4.94	3.37	4.63				
HEMBA1006658	7.71	4.81	3.99	9.26	8.5	11.38	5.3	4.42	6.47	*	+		
HEMBA1006659	7.41	4.7	3.7	5.26	4.56	4.46	6.04	3.81	4.25				
HEMBA1006665	1.62	1.53	0.92	2.6	1.66	1.94	1.6	1.36	2.14				
HEMBA1006666	2.8	1.45	1.19	5.48	2.51	3.57	1.85	1.35	3.75				
HEMBA1006671	4.48	2.13	2.48	3.04	6.4	6.86	3.55	4.19	4.16				
HEMBA1006674	4.97	3.16	4.4	5.76	5.14	7.87	4.61	3.42	4.54				
HEMBA1006676	10.46	5.08	3.85	9.54	8.88	9.7	6.21	4.55	6.44				
HEMBA1006682	2.27	1.69	1.34	3.17	2.06	2.05	4.61	1.08	3.99				
HEMBA1006688	6.01	4.37	2.5	5.47	6.02	6.19	4.31	2.6	4.14				
HEMBA1006695	4.5	1.72	1.74	6.75	6.52	5.65	3.76	2.82	3.65	*	+		
HEMBA1006696	12.87	6.14	7.8	9.63	11.85	11.77	5.03	6.37	5.41				
HEMBA1006702	2.64	1.17	1.68	3.05	1.99	2.26	2.52	2.64	2.72				
HEMBA1006707	6.85	2.92	3.19	5.67	3.46	4.24	2.84	4.21	4.09				
HEMBA1006708	8.39	4.87	3.01	5.26	5	6.1	6.53	3.85	5.31				
HEMBA1006709	6.65	3.16	3.47	4.07	5.63	4.68	6.45	3.52	4.44				
HEMBA1006717	8.88	2.4	4.14	4.44	3.37	2.93	4.5	3.69	4.56				
HEMBA1006724	3.81	3.86	1.52	3.61	3.98	3.44	2.83	2.11	3.27				
HEMBA1006731	7.51	3.16	2.94	4.8	6.48	6.17	3.61	3.73	4.13				
HEMBA1006737	5.15	2.61	1.58	2.17	3.41	5.22	2.11	2.54	2.79				
HEMBA1006742	4.81	2.29	1.84	6.06	4.83	6.03	2.78	3.29	3.24				
HEMBA1006743	7.87	4.47	4.75	8.29	5.08	7.45	3.49	6.04	3.57				
HEMBA1006744	10.08	3.77	3.8	14.22	11.75	16.16	7.99	6.73	6.12	*	+		
HEMBA1006749	3.53	3.65	2.98	4.2	4.74	5.34	4.08	3.16	4.37	*	+		
HEMBA1006752	23.27	11.82	13.93	14.5	12.58	14.16	12.27	10.32	10.17				
HEMBA1006754	1.86	1.19	1.02	4.17	4.31	3.82	2.65	2.7	3.64	**	+	*	+
HEMBA1006758	8.94	5.63	3.63	4.07	5.41	4.85	3.57	4.16	2.9				
HEMBA1006767	3.06	1	1.61	2.61	3	3.72	1.69	2.22	2.41				
HEMBA1006770	13.78	5	6.03	7.89	10.06	11.16	4.74	6.16	6.66				
HEMBA1006779	10.4	3.74	5.54	13.72	14.85	14.12	6.44	8.3	7.48	*	+		
HEMBA1006780	7.08	3.47	3.59	13.82	10.5	10.84	7.75	5.05	6.84	*	+		
HEMBA1006789	4.72	5.04	4.21	3.76	5.14	4.99	3.13	3.89	4.1				
HEMBA1006795	8.9	4.61	4.5	12.12	13.21	10.55	5.76	4.72	5.99	*	+		
HEMBA1006796	7.65	2.94	3.34	4.85	4.95	4.32	4.94	2.99	4.97				
HEMBA1006805	6.94	4.11	2.79	6.38	6.88	9.56	5.8	4.23	4.32				
HEMBA1006807	41.87	16.77	24.31	34.14	30.28	35.28	17.64	15.46	18.76				
HEMBA1006813	2.76	1.69	0.75	4.56	3.37	2.07	1.6	1.54	1.68				
HEMBA1006819	5.85	2.89	4.93	3.44	4.06	3.24	2.46	2.97	2.69				
HEMBA1006821	4.19	2.43	1.27	6.45	6.7	7.35	2.91	3.28	3.89	**	+		
HEMBA1006824	6.62	2.68	2.84	7.05	7.56	7.49	5.6	3.8	3.89				
HEMBA1006832	34.7	31.52	23.59	34.4	30.12	38.56	20.42	16.73	24.06				
HEMBA1006834	23.99	11.25	13	13.06	14.6	15.62	11.33	8.76	11.95				
HEMBA1006835	4	1.43	1.9	3.69	3.2	3.36	2.22	2.96	1.96				
HEMBA1006843	103.5	33.5	66.05	133.5	136.8	126.1	52.72	23.1	39.64	*	+		

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Table 200

HEMBA1006849	7.06	2.5	3.59	4.52	8.98	7.67	3.87	4.24	3.66				
HEMBA1006850	3.68	2.41	3.49	4.12	5.88	5.61	3.45	4.3	5.71	*	+		
HEMBA1006861	27.48	13.2	13.78	18.39	17.49	22.76	27.79	29.56	33.72				
HEMBA1006865	7.81	4.59	4.59	10.66	9.55	9.31	6.64	6.59	6.33	*	+		
HEMBA1006867	3.05	3.03	2.02	5.38	6.39	7.32	3.39	3.7	4.23	**	+		
HEMBA1006873	3.17	1.82	1.33	4.27	2.94	4.49	4.02	3.19	3.84				
HEMBA1006877	6.27	2.4	2.17	3.46	3.06	5.26	2.31	2.13	2.61				
HEMBA1006878	4.34	4.51	3.67	4.81	4.9	5.52	4.18	3.51	3.8				
HEMBA1006879	17.53	11.84	12.53	14.59	8.5	17.01	9.97	13.17	14.21				
HEMBA1006884	6.78	4.78	7.19	7.57	8.09	8	6.14	4.53	8				
HEMBA1006885	14.47	10.91	10.29	11.14	13.59	13.12	8.92	9.99	11.51				
HEMBA1006886	9.88	9.1	5.85	13.2	13.5	12.51	7.07	6.68	7.13	*	+		
HEMBA1006889	6.59	4.3	4.26	4.32	5.23	5.84	3.48	4.25	4.38				
HEMBA1006896	16.57	11.14	9.96	13.58	12.6	17.46	13.28	8.89	13				
HEMBA1006900	11.28	4.72	4.94	6.26	7.37	10.33	5.94	4.33	6.61				
HEMBA1006902	2.57	1.63	2.97	3.06	2.5	3.31	2.84	4.11	2.62				
HEMBA1006912	9.86	3.49	5.48	8.69	10.41	10.91	5.79	6.47	5.76				
HEMBA1006914	14.14	7.94	10.37	14.19	14.05	16.96	6.19	5.9	9.72				
HEMBA1006916	9.91	7.1	4.15	7.61	7.72	7.02	3.84	3.67	4.33				
HEMBA1006921	5.33	2.22	1.77	2.75	3.09	2.98	2.63	2.52	3.45				
HEMBA1006926	4.69	3.93	4.04	8.12	6.37	6.61	5.19	4.08	4.59	**	+		
HEMBA1006927	2.56	1.45	1.11	4.26	3.27	5.93	2.47	2.76	2.3	*	+		
HEMBA1006929	3.54	1.38	2	3	2.51	2.71	2.05	2.99	1.84				
HEMBA1006936	6.81	2.92	3.95	7.43	7.48	8.89	3.83	5.74	3.63				
HEMBA1006938	1.33	0.26	0.47	5.31	1.59	1.56	1.54	1.69	0.91				
HEMBA1006941	16.53	11.05	11.6	12.22	7.8	9.63	10.28	8.93	11.52				
HEMBA1006942	8.19	4.07	6.53	8.73	9.65	14.5	10.35	7.57	10.44				
HEMBA1006945	25.04	16.05	14.06	21.51	28.59	29.47	11.94	11.2	11.54				
HEMBA1006949	2.9	1.1	0.96	1.63	1.82	4.13	0.8	1.36	1.9				
HEMBA1006952	3.78	1.55	1.57	2.91	2.65	3.54	2.84	4.46	4.01				
HEMBA1006960	10.85	6.07	5.14	11.23	9.86	8.27	10.08	9.22	8.03				
HEMBA1006973	3.3	3.69	3.3	7.1	4.93	5.77	3.56	4.84	3.61	*	+		
HEMBA1006974	5.62	2.6	4.96	7.66	9.22	8.05	3.96	5.98	3.51	*	+		
HEMBA1006976	2.71	1.15	1.73	3.59	2.62	4.04	2.12	3.56	2.05				
HEMBA1006989	0.83	0.32	0.23	0.34	1.18	1.21	0.38	0.32	1.18				
HEMBA1006993	7.77	3.49	2.52	13.12	7.8	8.64	3.93	4.49	6.13				
HEMBA1006996	1.18	0.27	0.63	0.83	0.78	0.99	0.66	1	0.65				
HEMBA1007001	5.49	3.33	4.13	8.5	12.04	10.88	5.67	5.2	5.4	**	+		
HEMBA1007002	5.81	2.2	3.66	4.91	3.97	4.41	3.34	3.47	2.91				
HEMBA1007013	3.72	1.85	2.69	3.52	4.62	4.75	3.38	4.47	2.43				
HEMBA1007016	3.01	1.36	1.4	2.83	2.49	3.86	1.86	2.87	2.52				
HEMBA1007017	0.36	0.56	0.46	1.7	1.63	2.47	0.33	1.63	0.45	**	+		
HEMBA1007018	9.21	6.01	5.67	4.76	4.66	5.23	4.98	4.73	5.19				
HEMBA1007044	9.95	5.07	6.68	9.58	7.21	9.83	7.74	6.77	8.84				
HEMBA1007045	2.71	0.74	1.32	2.37	2.16	3.02	2.18	2.14	3.63				
HEMBA1007051	4.5	1.5	2.49	3.07	5.64	4.56	4.1	1.96	3.57				
HEMBA1007052	2.79	1.47	1.81	2.94	3.23	3.76	2.14	1.66	1.93	*	+		
HEMBA1007053	2.08	1.3	1.15	3.49	2.13	3.23	2.17	2.69	2.75	*	+	*	+
HEMBA1007057	4.25	1.9	2.27	4.24	3.69	4.46	2.89	2.65	3.08				
HEMBA1007062	6.55	4.08	2.49	3.19	4.21	5.74	3.61	4.05	2.65				
HEMBA1007063	7.3	3.36	3.27	9.41	8.17	9.36	5.6	4.6	6.77	*	+		
HEMBA1007066	4.89	2.13	1.75	9.06	3.28	4.77	3.8	2.51	6.25				
HEMBA1007069	3.01	1.67	1.08	4.66	3.81	6.58	2.68	2.84	4.17	*	+		
HEMBA1007073	3.81	1.52	1.06	5.19	3.51	7.75	1.69	2.27	1.95				
HEMBA1007076	8.06	4.01	4.39	8.06	8.27	7.87	6.08	3.95	7.1				
HEMBA1007078	44.29	25.47	26.67	39.89	48.08	43.86	17.13	16.51	23.74				

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Table 201

HEMBA1007080	6.49	3.94	5.98	9.98	8.08	9.96	7.3	4.03	5.16	*	+		
HEMBA1007084	6.15	4.73	3.3	7.53	11.43	12.96	4.4	6.54	5.84	*	+		
HEMBA1007085	11.57	6.03	6.42	14.47	16.1	16.28	10.38	7.67	10.37	*	+		
HEMBA1007087	8.74	3.56	5.06	9.07	6.88	8.89	6.19	4.83	6.54				
HEMBA1007089	4	1.08	1.76	3.78	3.23	3.34	2.04	2.11	2.69				
HEMBA1007095	70.95	56.95	68.33	67.92	65.09	77.99	58.54	73.69	65.61				
HEMBA1007101	8.13	4.48	3.34	8.09	6.98	8.85	8.22	8.26	10.62				
HEMBA1007104	5.96	2.89	2.91	5.64	4.63	4.55	3.31	2.95	4.74				
HEMBA1007106	14.7	8.59	9.92	8.69	10.08	8.52	4.85	5.28	6.28			*	-
HEMBA1007112	2.54	1.7	2.5	2.24	3.01	4.69	1.68	1.95	2.11				
HEMBA1007113	6.43	3.26	3.02	9.57	10.18	12	5.01	4.74	6.51	**	+		
HEMBA1007121	15.29	6.28	8.37	20.01	26.55	24.61	14	11.02	13.68	*	+		
HEMBA1007129	4.97	2.15	2.01	4.97	3.24	4.17	3.35	2.12	2.39				
HEMBA1007147	5.38	3.65	3.3	8.42	7.76	8.81	5.26	3.94	5.49	**	+		
HEMBA1007149	4.94	2.77	3.26	6.72	8.54	6.33	4.3	4.3	4.5	*	+		
HEMBA1007151	8.13	3.85	3.81	6.44	7.95	11.22	3.61	4.33	3.79				
HEMBA1007172	7.56	3.48	4.13	7.44	5.05	7.28	4.12	5.13	4.04				
HEMBA1007174	5.89	2.49	3.67	3.93	3.83	5.88	2.72	4.89	2.91				
HEMBA1007176	9.03	5.34	6.92	9.78	8.83	9.47	8.52	8	9.63				
HEMBA1007178	32.55	18.88	15.14	19.06	21.65	17.59	9.08	8.47	7.89				
HEMBA1007185	10.22	4.41	3.64	8.36	9.55	9.52	7.01	9.23	10.25				
HEMBA1007186	5.79	5.42	2.99	5.38	6.38	4.34	5.55	4.63	4.28				
HEMBA1007194	10.77	5.25	6.27	6.05	8.58	8.52	4.54	4.6	4.86				
HEMBA1007200	4.17	3	2.87	3.85	3.81	6.07	2.25	5.2	3.91				
HEMBA1007203	7.33	3.38	4.4	6.6	5.9	7.76	3.26	5.38	5.31				
HEMBA1007206	5.36	1.62	4.58	8.87	7.23	9.37	4.17	4.51	4.13	*	+		
HEMBA1007224	4.31	3.41	3.02	7.21	8.94	7.9	5.84	2.98	5.52	**	+		
HEMBA1007226	8.11	2.53	3.92	5.1	4.65	5.56	3.57	3.89	3.99				
HEMBA1007240	8.19	3.25	3.14	6.63	3.95	5.13	4.82	3.47	3.83				
HEMBA1007241	2.29	1.82	2.1	4.38	3.16	4.31	2.93	3.05	2.77	*	+	**	+
HEMBA1007242	3.53	1.89	1.63	1.79	3.06	2.59	1.23	2.17	2.42				
HEMBA1007243	5.49	1.9	2.36	5.15	4.7	4.56	2.5	2.45	3.07				
HEMBA1007251	3.85	1.52	2.26	3.21	2.8	3.04	1.54	2.44	1.83				
HEMBA1007256	2.11	1.7	2.58	4.85	3.63	4.4	1.15	2.23	2.07	**	+		
HEMBA1007267	8.06	2.62	3.26	10.13	10.25	11.99	6.27	4.97	6.51	*	+		
HEMBA1007273	2.76	1.75	1.08	1.92	1.89	2.71	1.52	1.78	1.02				
HEMBA1007279	2.55	1.22	1.16	1.3	3.65	2.92	1.5	1.89	2.13				
HEMBA1007281	2.07	1.07	0.43	1.29	1.21	1.04	1.02	1.25	1.12				
HEMBA1007283	6.62	2.63	3.23	3.75	3.81	4.38	2.75	2.29	3.75				
HEMBA1007288	3.75	1.29	2.66	5.75	6.28	6.21	1.78	2.89	4.17	**	+		
HEMBA1007291	3.22	0.96	1.72	2.4	3.14	3.81	1.55	2.4	4.26				
HEMBA1007299	23.93	13.7	15.73	10.56	22.18	16.89	17.86	19.6	16.71				
HEMBA1007300	6.22	3.89	1.52	4.87	4.49	5.57	2.96	3.67	3.54				
HEMBA1007301	4.77	2.47	2.12	3.91	6.06	4.53	5.31	3.92	4.11				
HEMBA1007319	5.04	2.71	2.66	4.51	4.51	4.65	2.4	2.58	1.88				
HEMBA1007320	3.5	1.62	1.5	3	2.95	3.58	2.72	2.88	2.98				
HEMBA1007322	28.33	24.69	28.25	30.89	47.79	40.83	20.16	16.66	16.95			**	-
HEMBA1007323	6.68	1.59	2.78	3.35	2.99	4.54	1.69	2.27	2.61				
HEMBA1007326	16.87	9.35	13.09	29.82	36.45	31.07	12.34	13.22	15.57	**	+		
HEMBA1007327	6.34	3.6	4.38	10.61	13.22	12.6	4.55	6.34	5.25	**	+		
HEMBA1007332	13.26	4.92	5.19	6.74	8.15	8.34	6.2	5.28	6.24				
HEMBA1007341	3.07	1.51	1.92	5.68	4.8	6.45	2.94	3.15	3.13	**	+		
HEMBA1007342	3.54	1.8	1.84	3.52	2.33	2.69	2.06	2.55	1.53				
HEMBA1007347	6.86	4.49	4.81	9.76	12.67	13.86	6.9	5.92	8.38	**	+		
HEMBA1007353	2.54	1.91	1.06	2.5	3.01	2.77	1.29	2.06	1.66				
HEMBB1000005	5.95	3.76	2.97	7.43	7.91	9.69	2.81	4.53	3.98	*	+		

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Table 202

HEMBB1000008	6.33	3.99	3.55	9.32	9.9	11.83	4.69	4.68	5.58	**	+		
HEMBB1000018	9.18	4.31	7.12	14.89	18.9	20.93	7.15	7.95	8.65	**	+		
HEMBB1000024	8.61	5.93	3.83	12.18	15.58	14.42	6.22	5.32	8.3	**	+		
HEMBB1000025	7.18	1.68	2.62	5.76	5.35	5.09	4.63	4.5	5.11				
HEMBB1000030	5.99	4.74	5.88	11.95	12.01	10.44	5.68	5.83	6.43	**	+		
HEMBB1000036	5.65	4.09	3.36	4.79	4.59	7.69	4.76	4.78	5.5				
HEMBB1000037	6.62	4.31	5.17	7.83	6.16	9.26	6.18	5.41	5.32				
HEMBB1000039	3.3	1.35	2.08	5.56	6.46	6.46	3.88	3.39	2.84	**	+		
HEMBB1000044	8.31	2.86	3	8.94	8.97	9.22	3.67	5.53	3.74				
HEMBB1000048	4.16	1.72	3.61	5.69	6.15	8.14	3.51	4.43	3.25	*	+		
HEMBB1000050	5.5	1.49	1.55	3.76	8.59	5.41	2.51	2.18	3.82				
HEMBB1000054	5.55	2	2.53	9.07	6.03	8.7	7.15	3.88	5.66	*	+		
HEMBB1000055	24.4	16.2	17.8	18.24	19.34	22.83	9.69	8.54	9.54			*	-
HEMBB1000059	8.8	6.35	7.84	16.75	19.27	21.09	9.69	10.78	9.65	**	+	*	+
HEMBB1000072	9.51	4.64	5.32	12.83	10.68	11.19	7.97	7.6	5.64	*	+		
HEMBB1000081	3.87	1.35	1.85	5.08	5.24	4.46	3.77	3.99	4.68	*	+		
HEMBB1000083	4.74	2.08	3.56	8.88	6	6.36	3.2	5.07	6.07	*	+		
HEMBB1000089	3.6	2.1	3.13	10.31	7.12	8.77	3.62	4.07	4.02	**	+		
HEMBB1000094	10.03	4.21	5.44	7.27	9.1	10.43	5.68	3.83	7.07				
HEMBB1000097	2.21	1.8	1.66	3.6	3.78	2.43	2.31	1.65	1.94	*	+		
HEMBB1000099	6	2.44	5.07	9.23	13.61	11.37	6.57	5.71	7.13	*	+		
HEMBB1000103	11.08	5.29	6.37	9.34	10.14	10.72	4.69	6.24	4.67				
HEMBB1000106	6.42	4	5.39	8.37	6.27	6.82	6.5	5.47	4.71				
HEMBB1000113	2.17	2	1.61	3.56	3.45	3.36	1.25	3.37	2.9	**	+		
HEMBB1000119	4.55	2.45	4.15	5.3	3.89	4.98	2.17	5.09	5.65				
HEMBB1000133	36.74	19.87	32.19	17.43	2.43	25.47	18.03	19.17	26.05				
HEMBB1000134	8.1	5.02	4.94	5.99	6.85	11.63	3.4	5.64	6.33				
HEMBB1000136	4.52	2.17	1.45	2.82	2.31	2.54	3.01	2.62	4.93				
HEMBB1000141	5.34	2.26	2.68	7.34	8.23	8.82	4.82	3.93	6.2	*	+		
HEMBB1000144	4.28	3	3.58	12.18	6.95	9.35	4.11	4.95	6.86	*	+		
HEMBB1000147	3	2.36	0.48	3.68	2.83	3.66	1.75	1.4	2.8				
HEMBB1000152	4.26	2.59	2.98	3.85	2.52	3.5	2.62	3.23	3.16				
HEMBB1000154	3.63	1.65	1.97	5.05	4.98	5.15	2.28	3.46	4.23	*	+		
HEMBB1000155	3.1	2.14	2.06	3.13	4.38	4.5	2.17	2.09	2.04	*	+		
HEMBB1000173	11.42	5.05	6.29	19.61	16.74	17.56	10.24	8.45	9.62	**	+		
HEMBB1000175	3.73	1.02	1.8	5.42	5.67	6.02	2.9	2.66	4.4	*	+		
HEMBB1000176	5.82	2.57	3.52	6.79	7.3	6.93	5.44	4.12	6.38	*	+		
HEMBB1000198	2.93	1.33	0.9	2.24	0.81	1.87	1.77	0.77	1.87				
HEMBB1000208	3.02	2.41	1.68	3.5	2.31	3.21	2.28	1.81	1.61				
HEMBB1000209	4.47	2.11	2.26	5.05	5.4	5.79	2.1	3.16	2.24	*	+		
HEMBB1000212	4.74	2.38	2.45	3.32	2.97	6.08	1.78	3.81	2.18				
HEMBB1000215	12.22	6.74	7.81	16.21	19.51	21.21	10.04	11.3	10.31	*	+		
HEMBB1000217	18.97	9.31	7.7	15.35	13.44	12.33	8.45	8.5	11.37				
HEMBB1000218	7.88	3.65	4.15	11.14	12.99	13.65	6.32	5.71	6.71	**	+		
HEMBB1000226	9.75	5.82	3.67	9.36	7.18	7.09	5.55	5.63	5.67				
HEMBB1000230	2.5	1.54	1.56	3.16	2.41	2.47	1.66	1.86	2.28				
HEMBB1000240	2.54	1.04	1.59	2.21	2.34	2.83	1.25	2.23	1.86				
HEMBB1000244	3.34	2.45	3.05	3.32	3.23	3.4	1.54	2.3	1.85			*	-
HEMBB1000250	1.92	1.49	1.19	1.79	2.36	1.56	0.91	1.67	0.72				
HEMBB1000258	8.84	4.21	4.45	9.29	10.64	11.84	4.49	4.85	5.22	*	+		
HEMBB1000264	11.16	4.23	7.12	14.33	14.62	15.26	8.98	6.17	8.91	*	+		
HEMBB1000266	7.49	4.1	3.58	5.54	5.59	6.27	4.11	3.08	5.07				
HEMBB1000272	2.85	3.68	1.74	6.38	5.8	6.11	4.03	3.45	3.01	**	+		
HEMBB1000274	2.69	2.43	1.42	2.28	4.59	4.22	4.06	2.32	2.95				
HEMBB1000276	2.16	0.94	0.86	1.1	3.12	1.78	0.56	0.79	1.49				
HEMBB1000284	1.6	1.41	0.82	1.43	1.65	1.76	0.92	1.04	2.24				

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Table 203

HEMBB1000307	4.53	1.84	2.11	5.17	5.68	6.34	1.82	4.17	2.46	*	+		
HEMBB1000309	4.37	1.32	2.88	3.56	4.27	5.98	1.82	3.44	1.73				
HEMBB1000312	1.28	2.42	1.55	2.15	2.18	2.23	2	1.79	3.52				
HEMBB1000317	3.2	2.61	1.78	3.01	2.88	2.59	3.81	2.77	1.93				
HEMBB1000318	4.73	1.3	2.1	5.96	5.69	5.2	3.19	2.91	3.3				
HEMBB1000332	1.76	1.25	0.79	0.91	1.05	1.63	1.26	1.46	1.31				
HEMBB1000335	2.8	1.5	1.13	1.18	3.42	3.3	2.66	1.47	1.27				
HEMBB1000336	4.55	1.96	1.92	2.95	2.84	3.92	3.25	2.93	2.41				
HEMBB1000337	14.36	7.11	10.05	9.07	12	11.79	6.71	8.68	8.74				
HEMBB1000338	4.54	3.23	3.69	5.82	6.25	7.43	2.29	3.11	3.62	*	+		
HEMBB1000339	6.86	3.25	2.73	8.08	11.02	9.45	5.52	5.3	4.99	*	+		
HEMBB1000341	6.67	3.9	3.27	5.51	6.05	5.75	4.88	3.76	5.53				
HEMBB1000343	5.14	3.78	3.56	8.73	11.85	8.26	4.26	5.37	4.59	*	+		
HEMBB1000354	5.87	3.91	3.47	10.81	11.74	10.84	4.26	5.4	6.59	**	+		
HEMBB1000358	6.98	3.62	4.09	5.18	4.64	6.14	4.86	3.92	4.34				
HEMBB1000369	3.23	1.7	2.29	3.08	3.51	3.68	1.39	2.56	1.97				
HEMBB1000373	11.86	5.42	7.78	12.45	14.15	14.43	4.75	5.77	6.52				
HEMBB1000374	8.03	4.3	5.09	13.94	16.47	17.13	5.55	9.31	7.38	**	+		
HEMBB1000376	11.27	4.35	3.91	16.2	18.49	19.55	9.94	8.36	10.29	*	+		
HEMBB1000383	4.6	2.17	1.96	4.57	3.4	3.45	10.39	7.52	9.9			**	+
HEMBB1000391	6.84	4.23	4.83	6	8.02	7.16	4.22	5.21	3.67				
HEMBB1000399	5.23	1.96	3.15	3.41	3.17	3.69	3.69	3.13	1.81				
HEMBB1000402	2.6	1.48	0.94	2.16	3.1	1.88	0.98	2.21	2.08				
HEMBB1000404	1.75	0.76	1.14	1.48	2.07	2.27	1.05	1.58	1.14				
HEMBB1000407	1.46	1.26	1.6	1.67	2.46	3.55	0.54	2.33	2.09				
HEMBB1000420	6.02	3.01	5.42	7.53	9.7	10.11	3.76	5.07	4.73	*	+		
HEMBB1000430	59.23	34.65	23.06	49.23	46.08	51.49	46.72	34.37	41.23				
HEMBB1000434	18.16	8.94	9.74	22.34	23.72	31.12	11.49	11.35	12.88	*	+		
HEMBB1000438	2.81	0.97	1.46	1.87	3.06	1.59	2.06	2.06	1.78				
HEMBB1000441	5.61	4.55	3.22	9.46	9.64	11.7	6.15	5.84	7.17	**	+		
HEMBB1000447	6.8	2.32	3.46	10.82	16.06	18.31	25.43	26.28	30.87	*	+	**	+
HEMBB1000449	1.31	0.73	0.5	2.05	2.12	2.41	1.36	2.6	1.7	**	+		
HEMBB1000453	8.09	6.85	8.91	11.38	10.07	15.36	7.99	10.3	12.98				
HEMBB1000455	2.98	3.4	2.03	3.63	4.91	3.97	1.67	3.24	1.52				
HEMBB1000472	7.59	4.06	3.3	4.71	4.91	6.8	5.17	4.42	5.06				
HEMBB1000480	9.8	3.69	3.57	8.18	11.17	10.77	5.35	5.7	6.17				
HEMBB1000486	7.07	2.27	3.48	8.16	9.71	10.13	5.36	5.39	6.03	*	+		
HEMBB1000487	2.41	1.44	1.32	2.02	2.24	3.56	1.77	2.52	2.72				
HEMBB1000490	9.25	6.82	8.08	12.41	16.92	19.33	9.89	8.92	10.33	*	+		
HEMBB1000491	6.31	3.37	4.57	9.52	7.65	10.48	5.02	4.69	3.79	*	+		
HEMBB1000492	2.22	0.64	1.44	4.93	5.13	7.41	2.99	2.91	3.63	**	+	*	+
HEMBB1000493	4.06	2.22	4.19	4.24	6.19	6.18	1.66	2.72	2.91				
HEMBB1000510	6.41	3.47	4.28	6.87	9.13	11.79	5.4	4.78	5.74				
HEMBB1000516	4.76	2.42	3.32	9.01	5.12	5.56	4.9	3.1	6.78				
HEMBB1000518	1.77	0.89	0.96	2.32	1.98	1.84	1.86	2.02	1.38				
HEMBB1000523	5.6	4.26	4.37	10.14	11.92	12.71	5.32	6.89	8.07	**	+		
HEMBB1000530	2.95	1.4	1.93	9.88	7.75	9.87	4.5	4.51	2.86	**	+		
HEMBB1000542	8.28	5.69	6.91	10.8	11.2	12.53	8.2	7.18	7.39	**	+		
HEMBB1000550	1.32	0.8	1.53	2.82	2.53	3.26	1.75	3.01	2.05	**	+		
HEMBB1000554	7.82	3.63	5.16	11.58	14.79	21.33	5.25	6.34	9.2	*	+		
HEMBB1000556	7.65	3.11	3.74	5.66	6.17	8.22	5.32	4.21	5.38				
HEMBB1000564	4.88	2.2	2.92	4.79	4.84	5.7	5.46	2.87	3.44				
HEMBB1000567	11.63	5.99	6.65	15.29	18.3	19.22	9.27	9.36	9.27	*	+		
HEMBB1000569	5.23	1.99	2.42	5.2	5.06	5.8	7.16	8.5	8.18			*	+
HEMBB1000573	7.84	3.79	4.94	12.01	13.33	13.4	9.04	8.26	7.72	**	+		
HEMBB1000575	5.33	4.35	4.85	8.19	11.22	12.98	7.01	6.31	6.36	*	+	**	+

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Table 204

HEMBB1000579	1	0.63	1.23	1.94	1.94	1.61	0.75	2.27	0.83	*	+		
HEMBB1000585	1.32	0.9	1.33	2.89	2.66	2.35	1.39	2.41	1.82	**	+		
HEMBB1000586	5.03	2.33	2.86	4.93	10.49	10.9	3.19	3.33	3.66				
HEMBB1000589	4.34	3.31	2.32	4.73	9.62	7.86	4.05	4.47	4.07				
HEMBB1000591	6.2	2.47	3.35	5.53	10.43	9.55	5.26	4.88	5.68				
HEMBB1000592	3.62	1.12	1.49	3.68	3.48	4.83	5.06	2.83	3.4				
HEMBB1000593	5.63	3.16	4.14	7.95	8.98	9.6	4.23	4.57	4.71	**	+		
HEMBB1000595	9.73	4.88	6.49	11.51	8.83	10.26	5.12	4.65	3.54				
HEMBB1000598	3.08	2.45	2	3.88	5.18	4.28	2.89	4.3	2.68	*	+		
HEMBB1000611	1.33	0.64	1.43	2.46	1.17	1.82	0.83	1.24	1.6				
HEMBB1000617	12.12	5.56	4.61	11.59	16.06	19.06	7.94	6.34	10.85				
HEMBB1000623	7.8	2.76	2.97	7.01	3.89	6.02	4.57	2.94	6.61				
HEMBB1000630	2.59	1.28	1.39	2.17	2.39	2.78	2.69	2.13	3.79				
HEMBB1000631	10.27	4.76	4.53	6.2	6.77	8.48	8.04	7.46	8.07				
HEMBB1000632	6.25	2.1	3.02	6.63	6.59	8.13	4.84	4.67	4.51				
HEMBB1000636	13.35	4.72	8.11	7.29	10	13.28	8.71	9.3	9.58				
HEMBB1000637	26.51	17.46	16.75	28.37	43.24	52.91	24.53	21.76	22.76				
HEMBB1000638	1.76	0.67	1.19	2.95	4.12	4.45	1.31	0.92	1.68	**	+		
HEMBB1000642	10.59	4.41	5.99	11.15	12.92	13.73	6.73	6.84	9.2	*	+		
HEMBB1000643	1.65	1.83	1.24	2.38	2.51	3.19	2.28	0.92	1.97	*	+		
HEMBB1000649	3.91	2.47	2.78	5.9	5.23	6.96	3.56	3.95	5.15	*	+		
HEMBB1000652	6.02	2.91	2.8	5.46	7.5	7.04	3.21	3.43	4.33				
HEMBB1000655	12.28	6.34	8.07	9.28	11.26	11.56	6.56	3.92	6.25				
HEMBB1000665	1.52	0.76	1.22	2.5	1.48	1.81	2.25	0.85	1.56				
HEMBB1000668	2.21	0.39	1.35	5.91	7.44	6.43	4.09	4.69	4.22	**	+	**	+
HEMBB1000671	9.73	3.87	4.11	15	14.71	15.82	8.84	8.17	8.33	**	+		
HEMBB1000673	2	0.92	2.42	2.06	2.03	2.24	2.77	0.96	1.66				
HEMBB1000679	1.96	1.55	2.94	3.03	1.89	3.47	3.49	2.72	4.24				
HEMBB1000684	10.32	4.72	6.06	13.49	17.19	16.84	8.71	6	9.32	*	+		
HEMBB1000692	2.42	1.11	1.48	1.94	1.06	1.01	1.68	1.28	1.89				
HEMBB1000693	6.65	3.11	3.35	5.7	3.46	5.14	5.27	4.98	4.93				
HEMBB1000705	4.28	2.03	1.45	4.17	5.14	4.6	2.08	2.85	2.66				
HEMBB1000706	2.4	0.82	1.33	4.76	1.91	1.69	2.35	1.33	2.24				
HEMBB1000709	5.9	4.56	2.82	9.88	15.43	11.7	9.92	8.98	12.92	*	+	*	+
HEMBB1000714	4.07	1.84	2.28	3.51	2.48	3.46	4.34	1.56	2.5				
HEMBB1000725	3.83	2.12	2.8	3.51	3.57	2.91	4.38	2.17	3.5				
HEMBB1000726	6.74	3.26	3.37	8.38	10.66	11.11	5.09	6.26	5.9	*	+		
HEMBB1000729	5.92	3.12	3.67	3.82	5.2	5.28	2.93	3.03	3.74				
HEMBB1000738	6.27	2.98	4.84	7.01	7	9.14	5.8	4.68	8.01				
HEMBB1000749	6.38	4.5	8.03	10.82	12.38	19.82	6.87	7.43	9.13				
HEMBB1000763	4.28	1.52	4.69	3.87	3.73	4.04	3.58	5.24	3.54				
HEMBB1000770	2.56	1.54	1.45	4.69	5.02	5.12	3.94	2.82	2.01	**	+		
HEMBB1000774	4.01	2.16	2.61	6.02	5.76	6.03	4.48	3.56	3.59	**	+		
HEMBB1000777	16.82	8.94	10.71	11.64	9.96	10.04	11.16	9.95	10.48				
HEMBB1000781	4.68	2.51	2.03	4.83	6.62	5.74	2.82	4.66	5.27				
HEMBB1000788	1.26	1.09	0.22	0.77	1.4	0.96	0.82	1.05	1.38				
HEMBB1000789	3.3	1.16	1.77	2.42	1.9	2.76	1.89	2.74	1.95				
HEMBB1000790	4.72	2.05	3.39	5.79	6.37	7.78	3.19	2.91	4.28	*	+		
HEMBB1000794	0.97	0.54	1.08	1.04	2.04	2.15	0.72	1.24	1.02				
HEMBB1000807	7.3	3.23	3.76	7.53	4.81	6.34	3.19	2.77	3.98				
HEMBB1000809	10.2	3.24	6.13	7.78	12.54	11.13	7.52	8.8	9.69				
HEMBB1000810	6.83	2.64	2.68	4.19	3.73	4.74	4.18	2.82	5.16				
HEMBB1000821	3.04	1.01	1.43	1	1.91	2.05	1.27	2.15	1.75				
HEMBB1000822	1.16	1.15	0.89	1.14	1.34	1	1.68	1.67	1.68			**	+
HEMBB1000826	3.27	2.25	2.9	2.37	8.91	8.1	2.85	5.14	2.76				
HEMBB1000827	4.04	1.85	2.66	4.07	6.2	5.58	3.55	3.41	2.85				

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Table 205

HEMBB1000831	5.58	1.72	2.71	4.5	3.81	4.21	2.23	2.64	2.11				
HEMBB1000835	4	1.57	1.01	4.73	4.53	5.6	3.04	2.52	2.85	*	+		
HEMBB1000840	6.38	3.54	3.15	8.28	10.6	8.97	6.91	4.2	4.08	*	+		
HEMBB1000848	4.7	2.4	2.04	8.23	8.85	8.6	7.06	5.5	6.33	**	+	*	+
HEMBB1000852	0.54	0.28	0.27	0.52	0.36	0.24	1.16	0.97	0.61			*	+
HEMBB1000857	7.91	6.39	3.23	5.68	6.47	7.09	4.42	3.6	4.37				
HEMBB1000858	5.33	2.35	2.78	9.3	8.37	8.17	3.94	3.82	2.97	**	+		
HEMBB1000867	5.01	2.6	3.3	9.23	10.12	8.69	3.49	5.17	4.45	**	+		
HEMBB1000870	4.43	1.73	2.81	6.64	6.44	7.5	2.8	3.34	3.99	*	+		
HEMBB1000876	2.52	1.01	1.78	2.03	2.41	3.32	1.17	1.96	2.6				
HEMBB1000881	4.52	2.25	2.68	3.85	3.48	4.21	3.8	3.6	3.52				
HEMBB1000883	1.07	0.87	0.48	2.38	2.52	2.42	1.86	2.24	1.15	**	+		
HEMBB1000887	16.17	10.38	8.54	18.39	28.8	26.71	14.31	15.73	15.23	*	+		
HEMBB1000888	1.52	0.47	0.72	0.71	0.87	1.25	1.08	2.54	2.95				
HEMBB1000890	4.2	1.91	2.82	6.2	6.22	11.04	3.56	3.57	3.05	*	+		
HEMBB1000893	3.13	1.95	2.57	3.14	8.44	5.73	3.88	3.35	2.73				
HEMBB1000900	2.72	1.85	1.78	2.31	2.75	4	1.77	1.83	1.88				
HEMBB1000905	7.13	4.79	4.05	6.15	5.33	7.36	6.49	7.74	6.04				
HEMBB1000908	3.42	1.78	2.53	3.45	3.15	4.99	2.18	3.31	2.95				
HEMBB1000910	3.27	1.5	0.99	3.5	4.25	4.18	2.64	2.6	2.61	*	+		
HEMBB1000913	1.53	1.02	1.16	2.35	1.71	3.01	2.43	2.82	3.12			**	+
HEMBB1000915	125.5	96.58	90.74	52.7	70.12	78.2	138.4	94.57	151.2	*	-		
HEMBB1000917	5.94	3.71	3	10.02	9.8	10.14	6.41	5.43	5.2	**	+		
HEMBB1000927	3.9	2.3	4.04	2.93	2.18	2.45	3.26	2.61	3.09				
HEMBB1000932	1.41	0.52	1.78	2.08	2.21	2.86	1.55	1.9	0.46				
HEMBB1000933	63.34	47.44	31.38	44.11	52.4	49.52	46.54	37.21	45.55				
HEMBB1000936	7.16	3.79	4.04	4.95	3.87	5.38	3.06	2.19	2.36				
HEMBB1000939	9.8	5.4	5.5	8.13	8.11	6.88	7.11	4.16	5.78				
HEMBB1000941	1.26	1.52	1.91	2.33	1.33	3.43	1.03	2.28	3				
HEMBB1000947	3.84	2.12	3.17	3.27	3.95	6.16	2.65	3.42	5				
HEMBB1000954	2.09	0.96	1.77	3.22	2.47	2.01	1.52	2.5	2.09				
HEMBB1000959	1.47	0.69	1.99	4.15	4.21	5.2	2.08	3.64	2.15	**	+		
HEMBB1000973	0.93	0.22	1.08	1.36	1.53	1.02	0.58	1.34	0.88				
HEMBB1000975	6.35	2.45	2.52	2.87	4.55	4.7	3.97	3.56	3.46				
HEMBB1000981	1.55	0.65	1.17	2.92	1.74	2.12	1.91	1.15	1.6				
HEMBB1000985	4.16	2.16	3.38	6.79	6.53	7.43	6.9	5.56	5.46	**	+	*	+
HEMBB1000991	2.4	0.94	2.24	1.58	2.01	2.39	1.83	3.86	2.04				
HEMBB1000996	6.16	2.86	5.71	15.05	12.65	14.03	9.39	6.89	7.92	**	+		
HEMBB1001000	0.81	0.42	1.96	2.31	1.45	2	2.11	2.4	1.74				
HEMBB1001004	0.63	0.42	0.74	2.36	1.33	1.9	1.27	2.5	0.58	*	+		
HEMBB1001008	0.9	0.72	1.22	1.95	1.11	0.92	0.7	1.72	0.82				
HEMBB1001011	4.86	1.41	1.32	2.52	2.1	3.78	2.71	1.63	2.77				
HEMBB1001014	5.41	3.41	2.83	4.86	8.33	8.51	5.54	2.65	5.28				
HEMBB1001020	3.52	1.22	3.22	5.91	7.22	5.47	4.21	2.46	3.29	*	+		
HEMBB1001024	3.88	2.55	2.6	4.94	7.97	7.2	4.48	3.54	3.57	*	+		
HEMBB1001026	4.57	3.08	2.54	5.25	5.33	6.61	2.93	3.4	3.78	*	+		
HEMBB1001037	2.04	0.83	2.17	4.63	4.48	3.78	3.41	3.94	2.4	**	+		
HEMBB1001042	2.63	0.37	1.26	3.42	3.22	3.69	2.16	3.39	1.69	*	+		
HEMBB1001046	3.55	2.14	2.26	3.89	3.63	3.68	3.15	4.56	3.14				
HEMBB1001047	5	1.57	1.46	5.39	4.72	4.88	2.39	1.51	4.62				
HEMBB1001048	8.53	3.68	3.67	9.65	6.39	8.39	5.59	5.14	7.15				
HEMBB1001051	1.18	0.9	0.65	0.91	1.6	1.29	0.9	1.3	2.48				
HEMBB1001056	4.02	2.51	1.82	4.56	3.43	4.23	3.26	2.37	3.48				
HEMBB1001058	4.62	1.41	2.29	4.81	4.08	5.54	4.01	2.62	3.49				
HEMBB1001060	1.13	0.14	0.28	1.95	1.91	2.6	0.75	1.53	1.56	*	+		
HEMBB1001063	4.1	1.41	1.69	3.82	4.69	5.11	3.01	2.79	2.86				

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Table 206

HEMBB1001068	7.81	3.48	2.43	5.74	4.82	6.22	5.55	5.34	6.4				
HEMBB1001082	5.14	1.53	2.93	10.11	5.98	8.43	4.89	3.46	4.79	*	+		
HEMBB1001095	14.6	9.13	9.13	9.72	6.9	9.06	5.98	7.72	8.46				
HEMBB1001096	3.56	1.37	1.54	4.69	5.52	4.24	2.24	1.72	3.53	*	+		
HEMBB1001101	21.47	17.94	10.93	10.99	11.87	12.38	8.8	9.1	8.37				
HEMBB1001102	2.77	1.29	0.76	2.93	2.4	3.87	2.39	1.32	2.26				
HEMBB1001104	5.43	2.94	3.94	9.11	5.73	9.85	5.68	2.83	4.42	*	+		
HEMBB1001105	3.73	2.54	3.47	3.95	6.18	9.09	3.39	3.81	3.94				
HEMBB1001112	8.37	6.64	4.97	5.94	6.55	6.82	6.29	6.97	5.99				
HEMBB1001113	7.58	3.55	4.62	10.53	11.56	12	7.39	5.47	7.82	**	+		
HEMBB1001114	7.84	3.54	5.33	11.15	12.39	11.97	6.57	3.79	5.55	**	+		
HEMBB1001115	12.69	6.52	6.38	8.41	6.32	7.74	8.1	3.98	5.13				
HEMBB1001117	1.26	0.59	1.14	3.99	3.99	7.09	4.39	3.19	2.89	*	+	**	+
HEMBB1001119	2.73	0.69	1.36	3.27	2.76	3.17	1.69	1.82	2.33				
HEMBB1001126	17.3	8.41	6.34	12.51	13.52	16.39	9.04	9.96	8.26				
HEMBB1001133	7.22	2.46	6.43	7.94	11.25	15.48	5.58	5.96	7.46				
HEMBB1001137	4.69	1.94	2.48	3.07	2.31	3.24	4.3	2.74	3.49				
HEMBB1001142	10.97	4.26	5.7	14.69	16.82	16.36	7.91	5.78	10.87	*	+		
HEMBB1001145	8.34	3.24	4.81	10.74	10.95	12.08	5.82	4.69	6.65	*	+		
HEMBB1001151	8.95	6.02	5.47	5.12	6.22	5.78	8.53	8.19	8.82				
HEMBB1001153	5.68	3.55	3.85	6.9	7.36	7.26	5.29	4.07	4.12	*	+		
HEMBB1001158	5.25	4.46	4.73	8.21	9.2	10.97	4.6	4.37	5.83	**	+		
HEMBB1001169	5.93	2.46	2.66	6.12	6.91	7.13	3.71	3.73	4.71				
HEMBB1001170	2.28	0.23	1.68	2.09	1.33	2.33	1.48	1.17	1.14				
HEMBB1001175	4.7	2.5	2.14	5.28	3.05	6.25	4.06	3.09	3.56				
HEMBB1001177	11.32	4.92	7.58	14.33	14.36	15.14	8.51	7.62	8	*	+		
HEMBB1001182	7.1	3.3	3.03	8.51	7.41	6.84	6.75	4.9	5.74				
HEMBB1001192	4.01	1.43	2.59	3.22	2.9	2.65	3.81	3.22	2.43				
HEMBB1001199	1.24	0.85	1.37	0.51	1.77	3.72	1.58	1.98	1.27				
HEMBB1001200	0.7	0.28	0.37	0.41	0.29	1.06	0.14	0.69	0.72				
HEMBB1001208	6.24	1.58	2.41	2.54	3.62	5	2.67	3.31	3.15				
HEMBB1001209	8.96	2.6	4.27	8.47	9.46	10.64	6.12	3.72	4.78				
HEMBB1001210	3.39	3.6	6.25	13.57	15.06	13.24	8.2	7.86	10.28	**	+	*	+
HEMBB1001215	56.1	31.37	29.04	36.73	42.52	41.17	25.87	19.36	26.75				
HEMBB1001217	4.33	2.5	3.14	2.96	3.91	4.21	4.42	3.57	4.01				
HEMBB1001218	4.39	2.08	2.28	6.07	7.97	8.92	4.93	4.87	4.51	*	+		
HEMBB1001221	1.61	1.15	0.66	1.21	1.16	1.19	2.11	1.68	0.87				
HEMBB1001224	2.88	1.37	1.83	3.46	3.87	4.78	1.63	2.85	1.71	*	+		
HEMBB1001230	3.6	1.44	3.39	4.28	5.22	5.68	2.22	3.15	2.2	*	+		
HEMBB1001234	9.13	2.44	8.29	5.98	6.49	5.96	5.83	7.02	6.04				
HEMBB1001235	5.5	2.57	3.09	3.97	3.82	5.68	4.42	5.01	5.46				
HEMBB1001237	11.86	5.88	6.73	9.88	9.37	10.19	7.04	5.53	6.3				
HEMBB1001242	3.75	2.48	2.08	4.97	4.37	4.59	4.13	4.47	3.96	*	+		
HEMBB1001244	1.32	1.13	0.4	0.82	0.94	1.53	1.73	1.61	1.2				
HEMBB1001249	3.12	1.54	0.34	2.25	4.83	2.55	2.05	1.99	2.11				
HEMBB1001253	6.29	1.42	2.97	13.67	4.84	8.24	2.79	2.84	4.65				
HEMBB1001254	2.47	0.84	1.05	1.37	2.56	1.79	1.57	2.54	1.52				
HEMBB1001266	1.23	0.44	1.59	2.72	2.03	1.62	2.12	1.69	5.16				
HEMBB1001267	7.87	4.02	4.63	13.5	11.84	13.24	5.84	7.38	7.93	**	+		
HEMBB1001271	4.61	1.62	1.38	4.06	3.96	5.87	2.53	2.67	2.49				
HEMBB1001282	6.27	3.11	3.61	3.44	3.72	3.72	3.96	3.68	3.39				
HEMBB1001287	13.66	7.12	7.62	9.05	8.08	10.38	11.92	6.12	11.75				
HEMBB1001288	3.65	1.71	2.11	2.38	2.54	2.69	2.09	2.39	1.58				
HEMBB1001289	10.93	6.03	8.57	15.81	16.55	18.1	8.4	7.7	5.92	**	+		
HEMBB1001290	3.6	2.6	2.26	3.2	3.1	5.19	4.49	3.29	2.53				
HEMBB1001294	2.74	1.82	3.02	1.97	1.99	2.92	2.55	2.49	2.42				

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Table 207

HEMBB1001299	11.58	8.15	6.05	9.03	8.73	7.82	6.87	6.29	8.87				
HEMBB1001302	6.82	4.33	3.28	5.31	5.44	7.1	4.47	4.4	7.2				
HEMBB1001304	1.87	0.87	0.83	1.3	1.76	2.94	1.91	2.12	1.37				
HEMBB1001314	2.52	0.38	1.35	1.89	2.07	2.7	1	1.94	1.9				
HEMBB1001315	2.2	0.42	0.99	1.6	0.99	1.5	2.82	1.66	1.14				
HEMBB1001317	5.5	2.93	3.71	6	6.29	9.01	6.12	6.25	7.04			*	+
HEMBB1001326	1.44	0.28	0.42	1.14	1.37	0.97	0.93	1.85	0.56				
HEMBB1001331	3.49	1.15	3.33	3.16	5.21	4.92	2.94	2.32	3.4				
HEMBB1001335	2.13	0.58	1.32	2.09	1.33	1.73	1.47	0.84	0.69				
HEMBB1001337	4.69	2.11	3.26	4.29	6.51	6.35	3.43	4.14	3.13				
HEMBB1001339	3.42	1.11	1.36	2.82	1.69	2.07	1.52	2.17	1.96				
HEMBB1001344	2.99	1.77	1.84	2.4	2.3	3.56	2.28	2.27	2.05				
HEMBB1001346	3.15	2.58	2.53	3.75	3.57	4.79	2.76	4.39	3.22	*	+		
HEMBB1001348	1.96	1.25	1.97	4.3	3.56	4.57	1.75	3.51	2.64	**	+		
HEMBB1001350	2.69	1.8	2.82	11.17	12.83	10.95	7.44	8.11	8.86	**	+	**	+
HEMBB1001356	1.82	0.34	1.21	2	1.23	1.35	0.99	1.53	1.63				
HEMBB1001364	1.29	0.93	0.89	1.8	2.27	2.41	2.29	1.24	1.25	**	+		
HEMBB1001366	3.41	1.36	1.76	6.29	5.97	7.89	2.97	3.23	3.76	**	+		
HEMBB1001367	5.44	2.63	4.67	5.82	13.11	9.17	6.34	5.62	5.1				
HEMBB1001369	1.88	0.36	0.91	2.5	3.44	2.87	2.19	3.7	2.34	*	+		
HEMBB1001380	3.65	2.5	3.07	8.69	9.13	10.12	4.6	7.63	4.24	**	+		
HEMBB1001381	7.54	3.35	4.95	9.78	7.21	8.91	5.88	6.12	6.67				
HEMBB1001384	2.77	2.23	5.27	4.04	4.7	5.21	2.99	5.46	4				
HEMBB1001387	1.33	0.72	1.19	2.84	1.92	3.26	0.78	2.08	0.69	*	+		
HEMBB1001394	2.01	1.22	0.71	4.71	4.19	4.99	2.39	2.44	2.66	**	+	*	+
HEMBB1001407	3.37	1.49	0.8	2.53	3.21	2.87	4.47	1.2	2				
HEMBB1001410	1.19	0.14	0.37	0.55	0.79	0.77	0.44	1.14	0.17				
HEMBB1001413	2.53	1.15	2.11	4.01	6.2	3.82	2.17	2.18	2.56	*	+		
HEMBB1001419	3.82	1.67	2	5.53	5.54	4.76	5.16	3.44	3.45	*	+		
HEMBB1001421	1.55	0.78	1.24	9.94	7.28	9.56	5.74	5.75	4.91	**	+	**	+
HEMBB1001424	0.54	0	0.28	0.9	0.45	0.6	0.84	1.22	0.47				
HEMBB1001426	2.45	0.64	1.42	3.9	4.18	3.95	2.09	3.09	1.9	**	+		
HEMBB1001429	10.12	5.99	4.62	6.28	4.44	8.1	5.21	7.29	9.1				
HEMBB1001436	11.8	4.02	6.29	22.88	14.63	21.79	9.57	8.07	10.97	*	+		
HEMBB1001443	1.46	1.5	1.3	2.55	2.11	3.84	5.74	4.67	5.74			**	+
HEMBB1001449	4.24	1.68	1.33	4.21	5.76	5.46	2.38	1.89	2.76				
HEMBB1001454	4.2	2.22	2.85	4.88	5.14	6.3	1.94	2.02	3.61	*	+		
HEMBB1001458	4.34	4.36	3.05	7.92	4.69	4.55	3.87	3.06	3.94				
HEMBB1001461	2.41	1.63	1.39	3.76	3.78	6.76	3.87	1.93	2.34	*	+		
HEMBB1001463	4.41	1.84	3.33	6.77	8.03	7.56	3.07	2.66	3.3	**	+		
HEMBB1001464	1.53	1.48	0.96	1.16	0.81	1	0.81	0.25	1.04				
HEMBB1001466	1.71	1.2	0.87	3.03	2.72	4.34	2.85	2.09	4.25	*	+		
HEMBB1001482	3.03	1.42	1.06	1.64	2.18	1.42	2.97	1.16	2.1				
HEMBB1001500	2.17	1.05	0.9	2.57	2.02	2.37	1.04	1.45	1.55				
HEMBB1001505	8.22	5.06	7.49	13.32	13.9	13.27	5.5	6.16	7.01	**	+		
HEMBB1001521	2.58	1.03	1.95	4.68	3.52	3.79	2.8	2.46	2.3	*	+		
HEMBB1001527	14.66	7.32	7.32	12.93	16.36	15.19	7.53	11.09	12.62				
HEMBB1001530	7.24	3.1	6.46	5.19	6.93	5.94	6.69	5.92	5.53				
HEMBB1001531	5.66	2.3	2.38	5.05	4.74	5.69	3.58	2.66	2.99				
HEMBB1001532	2.05	0.38	0.82	1.99	0.87	2.3	1.76	1.25	1.24				
HEMBB1001535	3.86	2.42	2.26	4.62	4.93	5.74	3.17	2.1	4.36	*	+		
HEMBB1001536	5.02	2.43	2.77	5.57	4.42	5.08	2.95	2.46	3.39				
HEMBB1001537	3.43	1.79	1.93	5.9	3.91	6.35	3.35	2.86	3.81	*	+		
HEMBB1001542	10.24	4.77	6.29	8.68	10.49	11.37	4.75	4.74	4.61				
HEMBB1001543	4.42	2	4.45	6.17	7.07	7.41	4.96	3.35	2.51	*	+		
HEMBB1001547	1.69	0.68	1.1	3.41	2.74	1.36	1.07	2.16	2.08				

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Table 208

HEMBB1001548	11.61	4.55	5.07	6.22	6.23	8.02	13.1	5.3	6.57				
HEMBB1001551	2.02	1.27	1.35	2.89	1.88	2.65	2.33	1.18	2				
HEMBB1001555	3.38	2.36	2.27	4.34	5.15	4.75	3.71	2.88	3.52	**	+		
HEMBB1001562	6.73	3.72	2.72	6.03	4.98	4.88	4.48	4.21	3.29				
HEMBB1001564	143.7	103.7	84.35	117.1	130.5	149.5	73.73	78.89	81.45				
HEMBB1001565	4.34	2.01	6.14	5.35	4.71	6.93	2.17	3.81	2.88				
HEMBB1001569	3.35	1.85	2.92	2.44	1.48	3	2.68	1.66	2.47				
HEMBB1001573	4.11	1.78	1.25	2.55	2.8	4.22	1.76	2.85	2.7				
HEMBB1001585	5.19	3.43	2.13	7.14	9.58	10.48	5.06	4.35	4.95	*	+		
HEMBB1001586	2.45	1.89	1.57	2.45	2.59	4.79	2.08	2.01	1.8				
HEMBB1001588	9.91	4.02	1.68	7.84	12.44	10.86	6.94	6.15	5.93				
HEMBB1001595	2.38	2.13	1.24	3.04	4.7	3.31	4.54	3.91	4.77	*	+	**	+
HEMBB1001596	7.58	3.68	4.12	10.26	11.71	11.73	8.26	5.8	7.17	**	+		
HEMBB1001599	1.66	1.47	1.01	2.08	1.72	2.54	1.43	2.23	1.83				
HEMBB1001603	1.5	0.25	0.77	1.78	2.38	2.95	1.47	2.06	1.36	*	+		
HEMBB1001606	0.98	0.3	0.79	0.72	0.7	0.98	0.73	0.96	0.76				
HEMBB1001612	7.29	5.01	5.69	10.05	12.84	11.6	6.84	5.75	5.35	**	+		
HEMBB1001618	2.21	1.9	1	2.28	2.95	2.82	2.58	3.52	1.79				
HEMBB1001619	2.74	2.34	1.59	5	7.12	6.26	2.86	3.86	3.26	**	+		
HEMBB1001623	3.47	2.37	1.26	9.12	1.21	1.26	2.81	2.15	1.28				
HEMBB1001625	0.39	0.5	0.61	1.56	1.46	2.32	2.13	1.91	2.02	*	+	**	+
HEMBB1001630	2.05	0.69	1.57	1.73	2.03	1.92	0.69	0.97	1.11				
HEMBB1001635	2.2	0.75	1.17	3.5	2.23	1.77	1.56	1.05	1.51				
HEMBB1001637	3.51	1.4	2.57	3.58	4.43	4.86	2.1	2.95	2.6				
HEMBB1001641	1.95	0.54	0.63	1.54	1.04	1.19	1.35	0.64	1.26				
HEMBB1001653	5.49	2.4	2.56	5.29	5.68	6.05	3.35	3.68	4.27				
HEMBB1001665	1.36	1.13	0.8	0.24	0.85	0.87	0.48	0.61	0.56			*	-
HEMBB1001666	2.05	1.95	2.11	3.16	2.96	2.94	3.08	3.78	1.71	**	+		
HEMBB1001667	2.49	2.15	1.55	5.36	1.62	4.96	1.46	1.39	2.66				
HEMBB1001668	1.24	0.08	2.02	7.77	6.22	7.71	3.16	4.06	4.45	**	+	*	+
HEMBB1001669	1.14	0.56	0.64	1.01	1.36	1.96	0.82	0.73	1.12				
HEMBB1001670	4.9	1.43	3.88	3.76	6.22	5.35	4.26	5.99	6.05				
HEMBB1001673	9.43	4.46	3.65	7.18	5.87	10.36	4.73	4.98	5.54				
HEMBB1001675	4.45	1.52	2.55	2.96	2.17	2.25	2.39	2.98	2.34				
HEMBB1001679	3.43	1.92	1.36	3.15	2.26	1.5	2.37	3.04	2.3				
HEMBB1001684	3.34	2.15	1.93	2.33	2.97	3.86	3.7	4.19	3.07				
HEMBB1001685	0.43	0.79	0.82	2.14	2.22	2.08	1.31	1.84	3.11	**	+		
HEMBB1001695	0.91	0	0.49	2.21	2.23	2.38	1.38	2.34	1.74	**	+	*	+
HEMBB1001703	8.08	2.9	6.21	6.72	7.83	9.08	5.46	5.54	6.16				
HEMBB1001704	4.34	1.92	3.68	6.91	10.28	8.29	3.81	4.11	3.01	*	+		
HEMBB1001706	5.33	4.91	1.92	7.82	8.35	10.07	3.64	3.58	4.65	*	+		
HEMBB1001707	5.79	3.89	4.11	6.65	6.58	7.83	3.81	4.55	4.31	*	+		
HEMBB1001717	2.9	1.19	1.54	2.56	2.78	3.16	1.54	2.73	1.87				
HEMBB1001731	36.41	33.52	31.32	28.11	26.74	25.14	22.32	14.43	19.67	*	-	**	-
HEMBB1001734	3.1	2.92	2.47	4.7	5.73	6.77	4.4	3.15	4.26	**	+		
HEMBB1001735	2.54	0.66	2.3	5.4	4.73	5.13	2.48	3.07	2.77	**	+		
HEMBB1001736	5.75	4.06	4.43	6.69	5.77	10.19	4.22	3.36	4.39				
HEMBB1001747	2.44	0.77	1.23	3.44	4.21	3.48	1.4	1.37	2.22	*	+		
HEMBB1001749	8.77	3.39	4.72	11.21	15.68	17.47	7.58	5.43	7.33	*	+		
HEMBB1001753	7.34	3.22	3.36	7.29	7.53	8.22	6.29	5.11	5.25				
HEMBB1001756	3.12	1.84	2.45	2.82	2.94	4.26	3.19	1.55	3.2				
HEMBB1001757	0.84	0.19	0.52	0.79	1.64	1.25	0.88	2.16	1.24				
HEMBB1001760	1.15	0.71	0.71	1.53	1.28	1.9	0.58	2.3	0.49	*	+		
HEMBB1001762	2.92	1.03	2.15	2.66	1.94	2.8	2.3	3.2	2.05				
HEMBB1001780	11.82	11.49	14.29	11.74	11.14	12.3	6.31	7.75	11.3				
HEMBB1001785	0.42	0.01	1.19	1.62	1.09	1.43	0.08	1.04	1.6				

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Table 209

HEMBB1001788	5.11	2.85	2.49	8.04	8.23	9.77	5.27	5.14	5.83	**	+		
HEMBB1001793	13.59	3.52	4.92	5.61	7.12	5.14	6.71	5.28	5.84				
HEMBB1001797	0.88	0.62	1.95	0.94	0.65	0.97	1.07	1.81	1.9				
HEMBB1001802	6.5	3.72	4.06	7.5	8.03	6.58	5.93	6.91	6.06				
HEMBB1001812	5.74	3.61	5.29	9.39	12.73	12.64	5.58	6.99	9.37	**	+		
HEMBB1001815	20.05	9	15.52	27.98	23.86	26.02	37.42	29.06	44.83	*	+	*	+
HEMBB1001816	5.07	2.26	3.92	9.09	8.62	9.45	5.29	4.77	4.9	**	+		
HEMBB1001831	1.2	0.45	0.53	1.8	1.74	1.99	0.55	2.73	1.28	*	+		
HEMBB1001834	19.83	12.47	10.64	12.5	19.26	19.83	14.74	13.9	15.71				
HEMBB1001836	4.06	3.15	2.68	7.01	7.21	7.9	3.1	3.18	4.01	**	+		
HEMBB1001839	1.83	0.36	0.78	1.33	1.05	1.21	1.58	1.39	1.02				
HEMBB1001841	4.21	3.05	4.61	6.62	7.34	6.85	8.41	7.68	5.57	**	+	*	+
HEMBB1001844	4.31	2.59	2.19	5.78	3.8	4.04	2.62	4.06	3				
HEMBB1001847	11.75	7.16	10.2	21.65	17.41	24.55	7.68	9.92	9.98	**	+		
HEMBB1001848	2.73	1.25	1.47	4.72	2.91	3.06	15.56	19.7	16.79			**	+
HEMBB1001850	7.3	4.6	5.92	9.74	8.83	8.43	10.59	7.86	13.13	*	+		
HEMBB1001859	6.4	9.16	9.93	12.13	14.98	16.02	18.07	14.33	23.47	*	+	*	+
HEMBB1001863	6.66	2.82	3.58	9.9	10.12	11.35	6.68	3.16	7.05	**	+		
HEMBB1001867	1.21	1.36	0.82	2.34	2.45	3.53	2.08	1.31	1.98	*	+		
HEMBB1001868	3.28	1.27	0.26	2.34	1.83	1.98	2.3	1.36	2				
HEMBB1001869	4.99	3.41	2.47	4.55	8.08	7.57	3.34	3.94	4.05				
HEMBB1001872	3.4	4.06	0.84	4.75	2.37	1.57	2.65	1.38	2.04				
HEMBB1001874	2.47	1.57	1.58	3.42	1.79	3.58	3.5	1.76	2.08				
HEMBB1001875	1.3	0.4	3.1	2.27	2.57	2.84	2.23	0.73	0.98				
HEMBB1001880	9.6	4.1	4.24	11.57	10.59	10.4	5.78	4.19	6.8				
HEMBB1001899	2.12	0.58	0.29	1.53	1.49	1.79	2.01	0.55	1.92				
HEMBB1001903	4.86	1.84	3.46	4.45	3.55	4.47	5.08	3.38	4.99				
HEMBB1001905	6.94	3.72	4.24	3.83	3.28	4.45	3.35	1.95	3.04				
HEMBB1001906	3.51	0.89	1.09	3.56	2.45	3.39	2.27	3.05	2.44				
HEMBB1001908	1.61	2.17	1.92	5.17	4.2	3.43	1.41	2.29	3.44	*	+		
HEMBB1001910	2.88	1.38	0.82	4.07	3.93	6.71	2.4	1.88	3.55	*	+		
HEMBB1001911	6.98	2.87	4.02	9.07	10.54	12.95	3.98	4.78	7.22	*	+		
HEMBB1001915	4.25	1.76	1.83	6.42	5.24	7.19	5.74	2.92	4.49	*	+		
HEMBB1001921	5.38	3.56	4.5	10.21	11.3	11	5.97	4.64	6.62	**	+		
HEMBB1001922	3.83	1.35	3.8	5.95	3.77	3.39	3.48	2.3	3.67				
HEMBB1001925	3.73	2.29	2.11	4.2	3.69	3.62	2.81	2.27	3.72				
HEMBB1001930	0.59	0.63	0.42	2.23	1.25	1.36	0.41	1.35	1.01	*	+		
HEMBB1001944	3.88	3.55	3.94	5.26	8.37	10.06	2.98	4.95	4.6	*	+		
HEMBB1001945	5.17	3.58	5.47	3.15	4.34	6.51	3.41	6.48	6.46				
HEMBB1001947	6.49	1.48	5.58	2.11	3.59	4.92	2.72	2.7	2.62				
HEMBB1001950	6.47	3.08	4.75	4.98	5.8	5.65	5.08	4.12	4.55				
HEMBB1001952	4.62	1.75	2.38	5.87	7.63	6.22	3.88	3.07	2.9	*	+		
HEMBB1001953	3.33	1.23	1.69	3.8	4.29	3.6	2.72	2.28	2.79				
HEMBB1001957	3.22	1.56	1.85	3.38	4.52	4.53	3.81	1.96	3.18	*	+		
HEMBB1001959	7.02	7.17	6.24	7.94	4.73	8.54	5.15	5.79	4.06			*	-
HEMBB1001962	4.04	1.76	3.14	4.32	4.25	6.26	2	2.46	5.87				
HEMBB1001967	11.44	5.2	6.57	12.83	15.13	16.73	7.11	8.82	7.6	*	+		
HEMBB1001973	5.08	2.32	4.1	4.86	6.84	9.36	3.18	5.36	3.55				
HEMBB1001978	7.53	3.35	6.01	7.28	6.5	6.97	5.55	5.59	5.54				
HEMBB1001983	20.88	11.32	14	10.33	15.1	15.82	11.27	9.2	12.69				
HEMBB1001987	1.67	0.99	0.76	2.21	2.1	2.79	2.2	1.61	1.87	*	+		
HEMBB1001988	1.86	1.73	2.04	2.83	3.58	3.43	2.01	2.02	1.85	**	+		
HEMBB1001990	4.65	2.51	4.22	4.26	6.45	6.12	4.77	3.77	5.16				
HEMBB1001996	2.64	1.19	1.29	1.17	1.43	2.67	1.72	2.23	1.63				
HEMBB1001997	4.3	2.22	2.71	5.89	6.32	7.41	2.43	4.16	2.74	*	+		
HEMBB1001999	15.97	11.41	12.12	8.02	17.07	19.1	5.81	7.78	7.71			*	-

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Table 210

HEMBB1002002	0.83	0.59	1.4	1.42	1.71	2.28	1.59	0.62	1.07				
HEMBB1002005	8.43	2.74	4.65	11.77	11.48	12.25	6.14	5.42	7.41	*	+		
HEMBB1002009	0.77	2.18	1.38	1.25	1.38	2.16	0.85	1.5	0.79				
HEMBB1002013	2.33	1.35	1.79	1.62	1.81	3.45	1.55	1.11	1.73				
HEMBB1002015	7.48	4.38	3.67	9.87	8.21	13.87	7.92	7.55	9.97				
HEMBB1002024	12.18	6.96	6.46	7.22	8.12	8.32	6.32	9.38	7.79				
HEMBB1002035	3.12	1.84	1.81	4.86	5.45	3.22	1.97	2.8	1.44	*	+		
HEMBB1002039	3.05	1.27	3	3.79	6.93	5.61	2.49	3.6	2.96				
HEMBB1002041	7.09	2.89	3.99	5.42	7.13	7.97	5.81	4.83	6.2				
HEMBB1002042	7.43	3.78	4.66	7.93	11.47	10.08	5.53	6.71	6.67	*	+		
HEMBB1002043	4.31	1.3	3	5.84	8.07	8.67	4.27	3.64	4.54	*	+		
HEMBB1002044	1.54	1.29	1.16	1.41	1.89	1.39	1.48	2.04	1.41				
HEMBB1002045	13.56	9.28	9.85	18.7	19.69	19.62	11.33	11.49	14.07	**	+		
HEMBB1002049	0.94	0.9	1.48	2.03	3.05	3.51	1.86	1.85	1.5	*	+	*	+
HEMBB1002050	2.63	0.87	2.41	2.24	3.31	3.77	1.82	2.42	2.29				
HEMBB1002051	2.77	1.42	2.72	3.76	4.08	3.57	1	2.97	1.66	*	+		
HEMBB1002068	11.05	4.29	3.65	7.71	6.55	7.57	7.7	4.29	6.63				
HEMBB1002069	13.1	6.94	8.01	16.77	20.06	18.1	11.13	9.92	13.2	*	+		
HEMBB1002075	2.31	1.12	2.72	4.01	5.39	4.96	2.61	2.52	2.47	*	+		
HEMBB1002079	3.29	1.28	2.08	2.22	2.42	2.23	2.53	2.39	1.66				
HEMBB1002080	1.83	2.55	0.96	2.15	2.98	4.39	1.68	2.81	2.3				
HEMBB1002082	2.22	1.44	1.38	1.35	2.4	2.6	1.2	1.53	2.07				
HEMBB1002084	1.85	1.72	1.75	2.73	3.83	5.21	2.72	3.71	3.91	*	+	*	+
HEMBB1002088	11.64	8.26	10.3	14.66	19.71	16.32	16.11	15.05	19.56	*	+	*	+
HEMBB1002092	8.42	4.12	3.19	8.1	10.6	9.29	6.67	5.28	5.88				
HEMBB1002094	8.51	6.18	7.26	14.48	15.44	15.77	7.48	6.89	8.09	**	+		
HEMBB1002103	13.1	13.5	12.83	61.49	68.55	57.48	66.63	34.04	51.6	**	+	*	+
HEMBB1002109	6.77	3.65	4.41	10.27	12.78	11.5	7.97	4.24	7.06	**	+		
HEMBB1002115	44.63	28.15	32.39	41.8	53.57	63.47	24.84	22.28	27.42				
HEMBB1002120	2.22	0.77	1.3	3.55	2.83	2.5	1.74	2.54	1.48	*	+		
HEMBB1002121	1.32	0.72	1.59	2.14	1.84	1.52	1.15	1.56	1.25				
HEMBB1002134	29.98	14.03	18.39	22.56	28.18	29.08	20.1	20.18	26.29				
HEMBB1002136	5.67	2.48	3.78	3.62	3.43	4.97	3.89	4.13	4.88				
HEMBB1002138	3.55	2.31	2.47	7.41	6.73	5.61	7.6	5.28	8.06	**	+	*	+
HEMBB1002139	3.56	2.49	3.1	6.05	5.07	6.19	3.34	5.1	3.14	**	+		
HEMBB1002141	5.57	2.73	5.33	5.02	6.05	7.64	4.99	5.45	6.15				
HEMBB1002142	4.26	2.17	2.9	5.21	4.83	7.21	3.06	3.4	2.29				
HEMBB1002145	2.66	1.68	2.79	4.87	2.84	2.91	1.83	3.33	2.18				
HEMBB1002152	2.89	1.29	3.31	6.08	5.5	7.8	2.66	3.88	3.38	*	+		
HEMBB1002162	4.47	2.09	2.74	4.63	5.63	4.42	2.84	4.52	4.28				
HEMBB1002173	2.01	1.5	1.53	4.12	5.2	7.12	2.21	2.47	3.85	*	+		
HEMBB1002189	5.63	4.01	3.4	9.38	12.87	12.35	5.18	5.01	5.41	**	+		
HEMBB1002190	4.01	6.72	3.24	8.35	6.45	9.57	5.06	3.62	5.05				
HEMBB1002193	4.3	2.37	3.54	3.79	4.24	4.57	3.11	3.84	2.85				
HEMBB1002217	8.31	4.18	4.51	10.88	11.96	11.17	4.63	6.35	5.39	*	+		
HEMBB1002218	21.17	7.63	13.71	19.12	24.55	22.92	14.78	13.7	19.7				
HEMBB1002228	4.29	2.39	3.53	7.69	9.04	7.22	3.92	7.05	4.8	**	+		
HEMBB1002232	2.54	0.96	2.12	5.44	4.77	4.87	2	4.33	3.46	**	+		
HEMBB1002245	2.24	0.69	1.25	1.7	1.97	1.97	1.7	1.11	1.6				
HEMBB1002247	2.78	1.52	2.56	1.84	2.86	2.26	3.27	2.52	2.93				
HEMBB1002249	8.45	3.73	4.77	12.48	12.32	13.64	6.18	5.35	5.42	**	+		
HEMBB1002254	2.12	1.02	1.52	4.72	4.67	7.07	3.96	3.27	2.9	**	+	*	+
HEMBB1002255	0.31	0.16	1.07	0.59	0.84	2.46	0.5	0.92	0.27				
HEMBB1002266	1.03	0.51	0.66	4.13	2.54	2.5	1.25	1.72	1.36	*	+	*	+
HEMBB1002271	56.56	35.65	38.07	20.53	29.91	28.83	14.93	16.36	14.09			*	-
HEMBB1002280	1.89	0.47	1.28	2.71	3.38	2.75	1.12	1.95	1.11	*	+		

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Table 211

HEMBB1002296	19.39	12.59	10.1	13.85	9.77	11.58	17.38	19.09	20.6				
HEMBB1002300	5.98	2.27	2.27	4.97	4.83	5.06	3.39	2.79	3.87				
HEMBB1002302	4.79	2.37	2.24	3.34	4.96	4.22	3.13	3.11	2.5				
HEMBB1002306	2.53	0.59	1.19	2.95	4.01	3.53	2.16	2.15	1.9	*	+		
HEMBB1002316	1.37	0.21	1.01	1.05	1.85	1.65	1.5	1.08	0.63				
HEMBB1002326	9.34	4.41	4.08	6.83	11.8	13.52	5.14	6.95	5.58				
HEMBB1002327	3.74	1.52	2.2	3.25	6.69	8.05	1.41	2.57	2.14				
HEMBB1002329	6.65	2.85	3.03	3.55	3.52	4.81	3.39	4	4.24				
HEMBB1002340	2.45	1.14	0.8	2.72	7.22	1.38	1.47	2.32	1.56				
HEMBB1002342	18.78	10.67	11.1	11.48	10.39	11.81	11.37	10.6	12.37				
HEMBB1002358	8.06	4.65	5.88	8.32	11.43	13.39	7.12	5.37	8.32				
HEMBB1002359	4.65	2.7	3.21	2.57	3.59	5.52	2.05	3.08	3.75				
HEMBB1002364	3.68	2.01	1.94	4.35	5.19	5.12	3.24	2.77	3.18	*	+		
HEMBB1002366	26.64	15.48	15.83	13.61	16.98	21.16	15.49	15.91	17.68				
HEMBB1002371	2.23	1.84	1.61	9.83	11.88	12.5	6.86	8.63	8.95	**	+	**	+
HEMBB1002381	6.41	3.55	2.93	4.03	6.29	6.16	5.19	4.39	5.77				
HEMBB1002383	10.2	4.93	4.09	9.89	9.52	10.26	9.31	9.32	10.54				
HEMBB1002387	11.72	4.82	7.2	7.69	8.97	9.71	6.05	7.95	7.6				
HEMBB1002409	4.35	2.96	2.55	5.95	6.17	9.26	3.8	3.76	3.86	*	+		
HEMBB1002413	10.96	4.94	5.84	12.47	15.22	15.46	7.04	7.35	7.5	*	+		
HEMBB1002415	2.9	1.63	1.04	2.46	1.99	2.7	2.07	2.58	1.35				
HEMBB1002424	2.41	2.37	3.44	2.94	2.65	5.7	0.8	2.25	2.17				
HEMBB1002425	6.05	3.85	3.42	8.18	9.21	12.24	4.22	6.67	5.02	*	+		
HEMBB1002427	8.18	4.1	4.67	3.14	4.27	5.26	6.03	4.48	3.96				
HEMBB1002442	12.17	4.35	6.23	11.86	16.23	14.17	10.19	3.68	8.32				
HEMBB1002447	8.82	3.51	5.23	10.28	11.65	12.71	5.54	5.46	6.69	*	+		
HEMBB1002453	10.1	3.7	4.44	12.2	12.96	16.06	5.85	7.3	7.02	*	+		
HEMBB1002457	8.34	2.86	3.7	8.87	9.3	9.53	4.63	5.01	4.51				
HEMBB1002458	1.84	0.2	0.83	2.21	1.65	2.32	1.18	4.23	1.59				
HEMBB1002463	13.99	7.17	7.29	17.97	18.05	22.29	8.48	10.09	10.66	*	+		
HEMBB1002465	3.55	1.09	2.46	1.87	2.68	3.41	1.36	3	1.53				
HEMBB1002477	3.8	1.74	1.62	2.44	2.7	2.39	2.93	1.14	1.8				
HEMBB1002479	1.35	1.53	2.03	10.77	11.28	12.82	19.91	17.51	11.35	**	+	**	+
HEMBB1002489	8.63	4.67	4.63	7.48	7.18	7.8	5.28	6.57	5.43				
HEMBB1002492	2.72	1.93	0.73	4.55	5.38	4.56	3.26	3.14	4.65	**	+		
HEMBB1002495	5.34	4.27	3.39	5.35	7.91	6.17	5.79	5.24	4.34				
HEMBB1002502	0.83	0.8	0.28	1.27	3.14	4.39	2.38	2.95	1.77			*	+
HEMBB1002509	0.76	0.61	0.36	0.32	0.93	0.91	0.52	1.26	0.72				
HEMBB1002510	2.29	0.9	0.49	1.25	0.69	0.67	0.59	1.16	0.95				
HEMBB1002520	10.96	4.42	7.37	13.08	19.28	16.87	8.43	9.05	9.26	*	+		
HEMBB1002522	2.46	1.73	4.71	2.71	2.15	2.36	2.66	2.31	4.74				
HEMBB1002527	9.87	7.21	7.79	8.36	11.1	10.55	7.47	6.16	5.86				
HEMBB1002530	7.03	2.68	3.29	3.79	4.83	3.48	4.44	3.46	4.55				
HEMBB1002531	2.36	2.37	1.2	1.94	1.74	2.82	1.39	2.3	1.35				
HEMBB1002534	4.63	2.48	3.25	4.66	8.41	8.39	2.99	3.62	3.89				
HEMBB1002536	2.96	1.03	1.7	1.05	3.49	2.9	1.99	2.14	1.93				
HEMBB1002544	3.87	12.89	3.66	4.05	4.44	5.77	1.79	5.33	2.36				
HEMBB1002545	6.5	3.17	3.97	5.87	8.72	7.62	5.47	5.22	6.78				
HEMBB1002550	3.53	1.59	2.38	1.73	2.12	4.1	3.45	2.4	2.04				
HEMBB1002556	8.37	2.84	4.27	10.84	11.6	10.64	5.58	6.3	7.41	*	+		
HEMBB1002571	11.52	7.77	9.15	11.56	13.65	12.93	12.05	12.33	11.31				
HEMBB1002579	9.78	5.85	5.85	7.97	13.11	12.32	6.51	5.4	6.55				
HEMBB1002582	7.48	3.22	3.33	10.72	9.33	10.11	3.01	4.39	4.41	*	+		
HEMBB1002584	5.81	3.4	4.16	3.75	2.97	2.76	1.46	2.06	1.93			*	
HEMBB1002587	12.23	4.61	5.2	12.45	17.92	18.78	8.13	9.27	7.5	*	+		
HEMBB1002590	5.23	2.47	3.26	5.42	7.78	6.92	3.77	4.99	5.06	*	+		

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Table 212

HEMBB1002596	11.09	4.04	5.16	6.59	10.3	10.29	7.09	7.57	6.28				
HEMBB1002600	3.89	1.64	1.46	3.06	2.9	2.86	2.13	3.4	3.88				
HEMBB1002601	4.5	1.39	1.18	5.04	4.66	4.04	3.46	3.02	3.12				
HEMBB1002603	4.45	2.06	2.73	4.75	4.46	7.27	5.07	4.62	4.32				
HEMBB1002607	3.19	2.05	1.88	4.13	5.39	8.14	1.36	2.63	2.56	*	+		
HEMBB1002610	1.6	0.63	1.12	0.91	2.52	2.41	0.43	2.1	1.33				
HEMBB1002613	5.8	3.36	3.29	5.19	8.86	7.2	3.09	3.91	3.13				
HEMBB1002614	1.91	1.05	1.32	2.97	5.34	5.46	7.36	8.1	8.6	*	+	**	+
HEMBB1002615	6.52	2.3	1.68	3.51	2.94	3.31	2.18	2.84	3.84				
HEMBB1002617	2.28	1.5	2.31	5.27	5.83	5.57	3.83	2.69	3.29	**	+	*	+
HEMBB1002623	5.51	3.51	3.7	8.51	8.93	10.54	4.79	3.06	5.59	**	+		
HEMBB1002624	8.23	4.59	5.1	6.42	9.16	10.04	4.11	4.54	4.4				
HEMBB1002631	1.08	1.05	0.85	1.12	1.79	1.91	1.08	2.01	0.67				
HEMBB1002635	2.64	1.42	1.61	2.73	3.71	3.6	1.53	2.71	1.37	*	+		
HEMBB1002644	8.49	6.36	7.31	6.79	8.07	10.17	5.35	5.79	6.57				
HEMBB1002654	5.54	2.29	1.98	4.78	6.75	4.59	5.18	4.74	4.09				
HEMBB1002661	7.71	3.01	2.12	14.08	5.44	5.88	4.41	4.24	3.58				
HEMBB1002663	6.55	2.14	3.41	6.43	8.16	7.85	4.77	5.41	5.8				
HEMBB1002664	6.6	3.98	5.84	6.11	8.43	8.44	6.92	5.8	5.93				
HEMBB1002677	0.49	0.35	0.24	0.79	1.17	0.86	0.54	1.89	0.92	*	+		
HEMBB1002683	4.48	3.9	3.87	8.9	10.99	11.79	5.35	4.88	6.92	**	+		
HEMBB1002684	1.16	0.65	1	2.27	2.67	2.14	1.24	1.93	1.3	**	+		
HEMBB1002686	2.67	1.11	1.21	1.17	1.78	1.98	0.85	2.28	1.79				
HEMBB1002692	1.09	0.83	0.68	1.18	2.26	3.02	1.37	1.16	1.64			*	+
HEMBB1002693	15.96	10.15	10.49	21.46	23.57	25.74	17.35	13.97	17.93	**	+		
HEMBB1002697	2.36	2.43	3.54	11.69	11.93	8.98	4.98	6.73	4.87	**	+	*	+
HEMBB1002699	13.26	6.7	7.9	16.74	17.15	20.25	11.78	11.33	10.9	*	+		
HEMBB1002702	1.17	1.29	1.36	2.27	1.04	3.55	1.45	4.46	2.44				
HEMBB1002705	6.1	3.71	4.11	7.64	8.16	7.66	4.07	5.33	4.38	*	+		
HEMBB1002712	1.15	0.19	1.21	2.36	1.07	1.65	1.32	2.34	0.92				
IMR321000028	14.59	7.8	9.64	7.27	7.89	8.64	3.38	5.26	3.94			*	-
IMR321000031	3.67	1.78	1.78	4.24	3.4	4.34	3.69	3.39	3.59				
IMR321000034	24.92	15.48	15.01	18.47	24.81	26.67	19.77	14.09	22.91				
IMR321000039	17.93	8.99	10.18	11.47	11.22	20.12	13.91	11.79	14.04				
IMR321000044	0.32	0.19	0.19	0.47	1.02	1.05	0.71	2.7	0.69	*	+		
IMR321000063	54.36	30.23	33.89	54.62	56.68	67.83	34.49	32.64	37.87				
IMR321000085	21.71	12.85	13.46	11.07	12.01	16.43	14.38	12.89	14.05				
IMR321000089	3.32	1.43	2.9	5.84	3.39	4.37	2.16	3.41	3.89				
IMR321000091	5.29	4.33	6.45	10.44	10.54	14.12	6.4	9.24	7.99	**	+		
LIVER1000004	3.29	1.11	1.67	1.51	1.5	1.97	2.55	2.25	2.71				
LIVER1000008	3.19	0.85	0.9	1.97	1.35	1.87	1.63	1.58	2.33				
LIVER1000011	7.48	3.96	4.16	3.89	4.34	5.74	4.62	4.33	4.73				
LIVER1000022	18.53	8.45	9.73	12.74	12.74	14.58	13.3	11.15	13.79				
LIVER1000025	7.77	2.12	4.44	3.72	7.23	8.2	3.81	4.34	4.79				
LIVER1000030	4.56	1.88	1.59	2.3	3.48	3.86	1.46	2.61	2.79				
LIVER1000045	2.68	1.73	3.56	1.99	4.14	2.47	1.85	3.55	1.86				
LIVER1000046	6.12	3.21	3.54	3.3	3.9	5.04	5.21	3.87	9.2				
LIVER1000072	2.92	1.19	0.82	1.98	3.04	1.6	2.51	2.14	2.54				
LIVER1000077	4.63	3.26	3.43	3.77	4.63	3.6	5.23	4.42	4.9				
LIVER1000080	2	1.34	1.23	2.91	3.37	3.99	2.78	3.35	3.42	**	+	**	+
LIVER1000086	4.56	1.24	1.67	1.64	5.31	2.33	4.25	3.53	3.07				
LIVER1000092	2.68	1.43	1.4	3.38	2.77	3.26	2.88	3.19	2.12	*	+		
LIVER1000095	4.08	1.45	1.83	2.66	3.55	3.63	2.08	3.97	1.97				
LIVER1000097	2.68	0.88	1.06	2.99	2.32	2.56	2.6	1.48	1.37				
LIVER1000098	2.82	0.74	1.66	1.13	2.25	2.13	2.82	1.76	2.99				
LIVER1000100	8.61	3.08	3.61	4.27	5.23	7.01	4.06	5.3	6.22				

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Table 213

LIVER1000101	3.81	2.12	1.66	2.9	3.56	2.76	4.13	3.57	3.85					
LIVER1000106	3.32	1.56	1.67	3.52	2.18	3.06	2.2	1.66	2.75					
LIVER1000108	2.84	1.54	1.24	2.99	3.68	3.4	2.48	3.48	3.39	*	+			
LIVER1000115	2.61	1.46	1.12	3.02	3.28	3.44	1.96	2.92	2.86	*	+			
LIVER1000120	5.02	2.94	2.41	3.82	3	3.25	3.35	2.12	2.66					
LIVER1000138	4.91	0.99	2.36	1.52	2.93	3.2	2.89	4.4	2.68					
LIVER1000146	11.83	5.09	5.8	8.13	11.73	11.21	7.01	6.1	7.3					
LIVER1000148	11.43	4.5	7.19	7.38	7.37	7.45	6.46	5.27	6.13					
LIVER1000157	33.53	16.69	18.55	25.58	33.97	31.92	16.84	15.36	18.47					
LIVER1000161	7.22	4.95	3.61	5.26	5.68	6.24	4.45	3.94	6.08					
LIVER1000167	4.56	2.13	2.81	3.19	3.07	3.13	1.51	2.38	2.42					
LIVER1000174	3.84	1.31	1.5	1.69	2.19	2.47	1.08	2.69	2.65					
LIVER1000185	6.12	3.35	4.22	3.51	3.56	3.98	2.75	3.21	2.98					
LIVER1000187	3.26	1.56	0.93	1	1.39	1.74	0.82	3.36	0.61					
LIVER1000190	1.95	1.11	1.59	1.96	1.59	2.03	2.89	1.41	1.66					
LIVER1000192	10.65	6.24	5.2	5.75	5.77	6.49	6.06	5.8	6.02					
MAMMA1000009	5.3	2.68	2.46	6.62	5.77	8.83	4.6	3.23	5.23	*	+			
MAMMA1000015	5.84	1.77	1.87	1.64	2.88	3.59	3.38	2.5	2.77					
MAMMA1000019	5.66	2.6	2.84	4.89	9.82	8.95	3.81	3.64	4.85					
MAMMA1000020	3.8	3.44	4.09	3.56	8.72	8.06	4.37	4.09	4.16					
MAMMA1000024	2.87	0.82	0.95	1.1	1.88	2.53	1.55	2.13	2.01					
MAMMA1000025	4.87	2.19	2.6	4.8	5.71	6.47	3.27	3.34	4.13					
MAMMA1000043	10.51	5.09	5.02	14.31	20.26	13.23	7.72	9.62	9.43	*	+			
MAMMA1000045	1.69	0.97	1.62	2.91	3.36	3.57	3.47	1.81	1.55	**	+			
MAMMA1000046	6.47	2.08	3.57	6.03	7.6	8.45	5.17	3.75	4.66					
MAMMA1000055	6	3.15	3.53	2.8	3.48	4.97	5.81	4.07	2.35					
MAMMA1000057	12.48	5.52	7.03	12.15	20.3	15.59	7.03	7.1	8.26					
MAMMA1000060	14.43	7.18	9.91	16.29	13.21	18.23	10.59	9.1	11.91					
MAMMA1000069	7.73	3.61	4.66	6.69	8.82	10.74	4.08	5.81	4.8					
MAMMA1000084	9.73	3.57	5.05	11.91	14.34	16.88	5.45	7.65	6.73	*	+			
MAMMA1000085	3.47	1.96	1.87	2.74	2.35	3.06	1.99	2.32	2.6					
MAMMA1000092	5.41	2.13	2.26	4.85	6.6	6.02	2.97	4.24	4.71					
MAMMA1000096	3.78	3.03	1.78	3.72	4.8	6.47	4.17	3.9	6.06					
MAMMA1000097	4.13	2.95	3.91	5.52	4.24	6.86	3.6	3.62	3.89					
MAMMA1000102	5.12	2.21	2.7	5.22	5.81	5.02	2.56	4.65	3.65					
MAMMA1000103	3.31	1.56	2.28	4.58	6.05	6.54	2.94	4.29	3.37	*	+			
MAMMA1000106	2.7	1.79	2.13	3.04	5.09	5.41	1.36	3.69	2.27	*	+			
MAMMA1000117	2.72	1.52	1.22	1.31	2.51	2.71	0.5	1.62	1.27					
MAMMA1000118	8.14	2.71	2.77	3.78	7.64	6.37	5.72	5.22	4.29					
MAMMA1000129	4.52	1.62	2.67	3.35	3.9	5.18	1.94	2.89	2.82					
MAMMA1000133	4.27	1.92	2.22	2.89	3.17	3.71	2.86	2.72	3.28					
MAMMA1000134	3.24	1.82	3.24	6.48	6.88	8.35	3.29	3.76	4.59	**	+			
MAMMA1000139	3.29	2.4	1.31	3.92	4.25	4.14	3.22	2.8	2.68	*	+			
MAMMA1000141	3.46	1.27	2.24	4.07	4.79	6.79	1.97	2.52	1.91	*	+			
MAMMA1000143	2.16	0.91	1.71	2.99	2.74	3.39	1.31	2.55	1.46	*	+			
MAMMA1000150	10.88	7.04	8	8.79	14.06	12.33	3.84	10.55	5.74					
MAMMA1000155	10.85	5.54	5.47	9.19	13.85	13.81	7.6	7.75	9.58					
MAMMA1000163	5.58	3.38	2.67	5.07	6.46	5	2.15	2.84	6.5					
MAMMA1000171	7.29	4.5	4.08	8.95	12.01	14.93	6.64	7.02	7.82	*	+			
MAMMA1000173	6.86	4.32	5.72	5.71	7.66	7.6	5.97	5.63	5.95					
MAMMA1000175	4.12	1.18	0.23	1.4	1.36	1.53	1.51	3.3	1.81					
MAMMA1000183	7	6.5	5.17	8.02	15.13	12.18	4.61	6.16	5.98					
MAMMA1000191	6.82	3.67	4.83	4.54	6	5.86	3.61	5.7	4.78					
MAMMA1000192	13.21	7.3	7.84	8.79	11.31	9.83	5.1	9.07	11.26					
MAMMA1000193	6.03	2.64	1.36	3.73	3.78	4.43	3.35	3.38	4.25					
MAMMA1000198	11.19	3.7	4.24	11.67	15.53	12.34	7.74	5.71	7.75					

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Table 214

MAMMA1000204	7.62	4.53	5.82	9.51	6.8	8.54	5.56	4.69	5.2				
MAMMA1000207	6.14	2.58	4.15	4.25	4.43	7.49	4.2	4.63	3.58				
MAMMA1000214	3.73	2.36	3.5	6.05	6.43	8.36	3.87	5.19	4.02	*	+		
MAMMA1000220	3.64	2.49	2.27	4.02	3.64	4.91	4.36	4.51	3.83			*	+
MAMMA1000221	4.11	1.84	1.12	2.33	12.39	3.34	2.86	3.69	1.65				
MAMMA1000226	3.4	1.09	2.76	2.96	2.31	2.84	1.92	4.54	2.53				
MAMMA1000227	5.88	3.58	3.47	4.08	7.55	8.07	3.93	3.56	5.9				
MAMMA1000230	6.36	3.63	3.36	3.79	7.14	7.18	4.32	4.39	3.89				
MAMMA1000241	5.23	2.78	2.92	6.17	10.99	9.16	5.63	6.94	5.92	*	+	*	+
MAMMA1000245	71.79	48.41	41.99	49.62	55.47	70.51	36.86	32.29	42.56				
MAMMA1000248	10.75	5.11	8.19	10.32	13.93	13.73	8.64	7.83	9.87				
MAMMA1000251	4.47	3.42	3.86	6.07	8.71	10	3.62	6.05	5.41	*	+		
MAMMA1000254	2.89	1.15	1.35	4.06	5.79	5.07	1.95	5.72	2.71	*	+		
MAMMA1000257	7.12	4.26	6.71	11.96	14.47	16.44	5.81	9.74	10.27	**	+		
MAMMA1000262	12.13	6.11	6.35	9.28	17.3	14.89	11.45	12.94	13.68				
MAMMA1000264	1.54	1.94	1.06	2.96	5.16	6.26	1.9	2.25	1.92	*	+		
MAMMA1000266	1.41	0.76	1.44	2.49	3.39	2.45	2.4	2.54	1.43	*	+		
MAMMA1000270	8.33	3.85	6.34	9.35	14.72	13.36	5.23	6.67	8.24	*	+		
MAMMA1000271	3.79	2.55	1.83	6.46	5.81	4.43	3.8	4.01	4.5	*	+		
MAMMA1000277	2.17	1.07	1.86	2.66	2.04	3.91	1.48	2.33	1.37				
MAMMA1000278	2.46	1.53	1.53	2.26	1.74	1.78	1.61	3.39	1.57				
MAMMA1000279	4.53	3.12	3.68	7.71	9.92	13.85	2.86	4.21	4.62	*	+		
MAMMA1000283	2.8	0.74	1.34	2.2	3.06	3.24	2.27	2.64	2.53				
MAMMA1000284	7.09	3.1	3.89	5.31	5.61	7.3	4.33	4.12	6.21				
MAMMA1000287	3.34	1.37	2.39	5.26	5.17	6.99	4.97	3.06	4.33	*	+		
MAMMA1000294	18.13	8.47	8.55	15.55	11.48	16.82	12.33	10.64	11.59				
MAMMA1000298	1.54	0.71	0.82	0.74	1.91	1.79	1.37	1.29	1.02				
MAMMA1000302	5.12	2.71	2.69	5.15	5.37	6.89	4.36	4.77	2.99				
MAMMA1000303	4	2.05	1.59	2.54	3.44	3.95	1.95	2.67	2.43				
MAMMA1000305	1.38	0.71	0.71	1.7	2.67	3.22	1.16	1.69	1.13	*	+		
MAMMA1000307	12.76	5.57	7.52	10.78	17.15	13.46	11.84	12.09	11.6				
MAMMA1000309	0.76	0.89	1.4	1.06	1.34	1.72	1.77	0.93	1.2				
MAMMA1000312	1.8	1.04	0.87	1.28	0.56	1.1	1.25	1.47	0.9				
MAMMA1000313	2.67	3.77	1.89	3.1	6.23	5.66	3.12	2.28	2.98				
MAMMA1000331	4.12	2.28	1.93	3.93	3.97	5.29	3.56	3.45	3.82				
MAMMA1000335	6.16	2.7	3.37	3.54	3.79	3.88	3.68	2.45	3.73				
MAMMA1000339	3.25	1.33	2.61	3.01	4.9	3.33	2.91	2.77	1.92				
MAMMA1000340	2.6	1.63	1.41	3.96	4.43	4.29	1.81	3.28	2.22	**	+		
MAMMA1000348	3.33	1.48	2.34	6.45	6.9	6.21	5.1	3.51	6.66	**	+		
MAMMA1000356	8.13	2.7	3.74	9.76	8.55	10.65	5.97	5.34	5.67				
MAMMA1000358	4.37	2.17	1.44	5.1	4.35	4.38	3.5	3.09	3.71				
MAMMA1000360	7.72	3.05	2.69	11.41	9.78	10.42	6.57	4.42	6.39	*	+		
MAMMA1000361	7.91	2.97	4.89	10.45	10.37	13.01	6.44	5.43	7.13	*	+		
MAMMA1000363	5.44	2.67	2.71	3.44	2.89	4.74	2.99	2.83	3.16				
MAMMA1000370	8.4	6.64	6.2	6.19	7.25	6.56	6.68	7.49	4.91				
MAMMA1000371	6.81	4.41	6.08	4.39	3.58	5.6	4.96	6.77	5.24				
MAMMA1000372	11.86	4.03	5.98	15.22	16.38	16.77	7.36	6	7.47	*	+		
MAMMA1000385	4.62	2.3	2.77	5.18	7.04	8.05	4.85	4.48	5	*	+		
MAMMA1000388	6.44	2.83	3.67	5.65	4.46	4.85	4.91	3.34	5.06				
MAMMA1000395	5.17	2.17	2.95	3.65	4.16	4.78	3.21	2.41	3.84				
MAMMA1000402	7.68	3.41	2.88	9.51	10.11	10.62	5.46	6.68	5.96	*	+		
MAMMA1000403	6.72	2.73	3.78	6.04	7.7	8.56	4.71	5.83	4.03				
MAMMA1000410	4.02	2.21	1.56	4.09	5.7	5.12	2.32	3.4	1.98				
MAMMA1000413	1.97	0.9	1.1	2.1	2.16	1.61	0.81	1.47	1.21				
MAMMA1000414	3.35	1.71	2.96	4.73	3.34	2.27	4.52	4.04	1.89				
MAMMA1000416	14.38	8.87	8.86	11.04	19.59	15.46	12.54	10.99	12.32				

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Table 215

MAMMA1000421	7.88	5.58	3.16	7.31	11.57	11.97	5.34	5.28	5.81				
MAMMA1000422	4.93	2.9	1.84	2.34	3.07	4.44	2.35	2.99	4.14				
MAMMA1000423	3.67	2.88	1.35	2.17	3.71	4.12	2.5	2.73	2.24				
MAMMA1000424	0.47	0.75	0.45	1.27	1.37	1.76	1.14	1.64	1.04	**	+	*	+
MAMMA1000429	32.94	14.89	22.85	23.37	29.25	34.16	20.87	25.24	25.81				
MAMMA1000431	7.98	3.3	4.81	7.45	10.34	14.08	4.8	6.35	5.12				
MAMMA1000432	4.6	2.09	3.06	2.28	3.64	3.72	3.43	4.61	3.15				
MAMMA1000437	6.14	5.61	6.7	6.37	13.88	6.85	9.07	7.74	6.38				
MAMMA1000444	10.06	5.02	5.92	12.4	21.04	12.87	7.66	9.16	10.21				
MAMMA1000446	5.86	2.32	2.37	3.48	5.41	5.04	2.92	3.11	3.2				
MAMMA1000449	5.06	1.88	4.07	4.87	7.02	6.19	3.35	3.99	3.47				
MAMMA1000457	3.42	1.31	1.57	3.54	3.24	3.66	3.14	3.48	3.29				
MAMMA1000458	3.87	1.25	2.08	2.19	3.1	2.93	2.24	2.82	1.85				
MAMMA1000468	1.49	0.06	0.79	0.79	1.06	1.13	0.34	1.08	0.62				
MAMMA1000472	11.38	4.74	6.91	9.55	12.61	11.92	6.13	7.53	8.61				
MAMMA1000473	5.96	3.57	3.53	12.63	7.19	13.81	5.26	5.18	5.28	*	+		
MAMMA1000477	5.82	2.74	2.51	5.72	8.15	7.58	3.74	4.02	3.75				
MAMMA1000478	9	4.17	4.73	12.94	18.52	17.59	8.49	7.88	8.95	*	+		
MAMMA1000483	14.86	5.67	8.42	11.14	12.83	12.05	7.76	6.25	5.28				
MAMMA1000490	3.41	1.2	1.17	3.21	2.92	3.1	1.71	2.32	2.64				
MAMMA1000496	2.46	1.87	1.02	2.44	3.29	2.49	1.44	3.16	1.85				
MAMMA1000500	1.56	0.84	0.9	2.28	2.75	1.98	1.08	1.9	1.36	*	+		
MAMMA1000501	11.66	5.38	5.27	11.85	14.49	13.05	6.88	6.5	10.43				
MAMMA1000503	1.33	0.54	0.92	1.59	1.74	1.27	1.8	2.54	1.09				
MAMMA1000506	12.82	9.48	10.39	12.58	12.2	12.4	9.73	8.88	12.24				
MAMMA1000510	7.01	5.28	6.34	4.55	7.48	6.55	5.31	5.02	4.6				
MAMMA1000515	7.48	2.78	3.25	5.65	6.45	7.72	3.13	3.76	3.48				
MAMMA1000516	5.84	1.9	2.82	5.98	7.85	7.2	2.82	3.57	3.21				
MAMMA1000522	2.27	1.18	1.41	3.64	3.92	3.54	1.42	3.62	1.52	**	+		
MAMMA1000524	7.63	2.43	4.92	8.34	11.81	13.33	5.04	5.34	4.54	*	+		
MAMMA1000528	1.85	0.58	1.07	2.05	2.46	2.53	1.6	1.39	1.82	*	+		
MAMMA1000534	2.5	1.5	1.3	2.79	2.83	2.9	2.6	2.21	1.6	*	+		
MAMMA1000541	10.98	5.23	5.03	6.32	9.31	8.45	6.48	6.33	7.6				
MAMMA1000550	4.4	3.04	2.74	4.35	5.4	3.92	4.73	3.37	2.94				
MAMMA1000556	1.48	1.03	1.14	1.83	2.63	2.37	0.93	2.78	1.93	*	+		
MAMMA1000559	4.37	1.96	1.73	4.8	7.23	5.02	4.99	3.84	3.11				
MAMMA1000565	4.72	1.49	2.86	6.83	6.65	5.82	4.27	3.68	2.63	*	+		
MAMMA1000567	3.83	3.37	3.67	5.22	7.17	6.61	3.18	4.82	3.63	*	+		
MAMMA1000576	15.99	9.01	6.07	17.4	30.24	29.01	12.9	10.14	12.06	*	+		
MAMMA1000582	5.54	2.74	3.08	4.19	5.56	6.62	5.53	3.7	3.87				
MAMMA1000583	4.38	2.28	1.5	5.07	4.75	6.13	4.1	3.32	3.54				
MAMMA1000585	3.99	1.32	2.85	5.97	7.85	8.52	3.94	4.82	4.06	*	+		
MAMMA1000587	3.21	2.47	2	4.38	5.07	2.06	5.51	4.86	2.27				
MAMMA1000591	3.28	1.11	2.12	2.42	2.51	3.46	1.69	4.06	3.09				
MAMMA1000594	6.52	3.99	5.77	13.18	11.99	15.24	6.18	7.35	5.58	**	+		
MAMMA1000597	21.18	8.64	13.27	24.68	32.8	31.71	15.42	19.85	17.87	*	+		
MAMMA1000605	15	7.83	7.51	16.1	27.17	27.84	15.98	12.24	13.96	*	+		
MAMMA1000612	7.9	2.22	3.52	4.29	4.53	4.73	3.74	1.84	4.78				
MAMMA1000614	21.9	15.16	16.51	11.47	18.81	18.51	16.91	14.24	15.41				
MAMMA1000616	0.69	0.1	0.08	2.78	1.16	2.29	1.88	2.45	1.31	*	+	*	+
MAMMA1000621	3.29	2.06	2.49	3.22	4.74	3.92	2.54	4.56	2.58				
MAMMA1000623	3.66	0.62	3.18	3.6	1.78	3.6	1.68	2.93	1.92				
MAMMA1000625	21.85	13.69	19.79	20.91	20.47	21.13	14.29	16.77	23.93				
MAMMA1000635	0.42	0.29	0.29	1.14	0.49	1.07	0.07	1.98	0.45				
MAMMA1000643	3.78	2.57	1.76	4.32	6.22	6.75	3.82	3.69	4.44	*	+		
MAMMA1000646	10.28	5.04	4.34	5.25	6.7	11.98	4.93	10.71	4.89				

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Table 216

MAMMA1000652	8.47	3.81	5.01	8.32	13.85	13.05	5.34	6.27	6.14				
MAMMA1000657	5.07	3.94	3.85	6.77	10.59	9.73	5.63	6.14	5.11	*	+		
MAMMA1000664	2.69	1.1	1.96	4.49	4.5	4.2	2.58	4.29	2.35	**	+		
MAMMA1000667	4.79	1.98	2.15	4.21	4.93	5.76	3.08	4.06	3.71				
MAMMA1000668	2.4	1.13	1.67	3.73	2.97	3.09	0.95	4.13	2.08	*	+		
MAMMA1000669	1.17	0.4	0.79	2.08	2.59	2.37	1.24	0.92	0.96	**	+		
MAMMA1000670	7.56	4.44	3.7	4.32	4.44	6.75	2.59	5.1	5.48				
MAMMA1000672	7.79	2.99	3.4	4.22	3.53	5.63	3.72	4.19	6.43				
MAMMA1000681	4.68	1.14	3.03	2.41	2.85	4.06	2.7	2.22	3.58				
MAMMA1000684	35.85	22.61	24.91	21.42	31.5	29.68	12.4	13.65	15.36			*	-
MAMMA1000696	6.4	3.52	4.51	7.83	11.25	15.25	8.55	6.27	7.54	*	+		
MAMMA1000702	8.51	4.05	5.46	6.26	5.22	7.23	5.02	5.02	4.55				
MAMMA1000706	3.68	1.19	1.86	2.9	2.36	3.42	2.81	1.88	2.14				
MAMMA1000707	3.62	1.77	1.28	1.62	3.45	1.98	2.41	2.52	2.5				
MAMMA1000713	5.4	2.54	3.24	5.36	5.73	6.33	4.52	4.76	4.87				
MAMMA1000714	7.46	4.12	5.15	8.57	7.81	8.68	8.73	7.85	8.07				
MAMMA1000718	3.29	2.59	1.62	6.31	6.72	5.21	3.55	3.17	4.84	**	+		
MAMMA1000720	11.1	3.49	5.25	10.45	13.49	12.85	6.43	5.97	7.74				
MAMMA1000723	2.28	1.69	2.12	4.14	3.59	4.23	2.79	2.97	1.93	**	+		
MAMMA1000731	1.86	0.62	0.69	2.69	3.19	3.37	2.54	2.31	2.78	*	+	*	+
MAMMA1000732	4.46	2.1	1.55	3.27	6.08	6	3.73	4.07	3.22				
MAMMA1000733	2	0.47	0.64	1.76	2.5	2.33	0.99	1.71	0.41				
MAMMA1000734	19.84	13.3	8.71	14.98	15.8	18.61	13.99	14.24	10.98				
MAMMA1000736	12.43	4.93	6.22	7.65	6.62	9.44	6.16	4.05	8.82				
MAMMA1000738	9.86	3.76	4.66	5.29	7.95	8.71	4.04	5.76	4.24				
MAMMA1000744	6.53	4.63	4.71	11	10.23	11.31	6.26	6.39	7.29	**	+		
MAMMA1000746	1.48	2.11	1.07	4.85	6.59	5.04	2.55	4.44	6.76	**	+		
MAMMA1000748	9.39	7.13	8.61	8.38	10.56	16.11	5.63	9.36	9.45				
MAMMA1000751	19.32	15.21	15.9	12.13	17.33	24.65	8.32	12.47	10.06			*	-
MAMMA1000752	4.99	3.06	2.62	6.31	5.93	7.52	3.57	3.3	3.21	*	+		
MAMMA1000757	16.42	7.46	8.63	15.03	20.13	20.42	10.82	9.38	12.45				
MAMMA1000760	13.83	4.85	6.07	16.93	20.12	21.36	9.26	10.09	9.12	*	+		
MAMMA1000761	7	5.05	5.28	10.4	11.63	13.03	5.86	6.75	6.32	**	+		
MAMMA1000775	4.08	1.66	2.88	3.15	4.48	7.4	3.92	4.45	3.2				
MAMMA1000776	6.7	4.59	3.36	9.35	9.08	9.79	6.68	5.65	5.84	*	+		
MAMMA1000778	5.98	3.45	2.59	7.46	6.58	10.39	4.17	4.75	3.98				
MAMMA1000781	5.48	3.83	3.81	4.84	4.93	5.96	2.78	5.06	3.06				
MAMMA1000782	15.43	7.59	9.38	7	8.75	12.93	6.89	10.66	10.04				
MAMMA1000784	6.69	3.02	3.41	4.23	8.26	6.49	8.78	3.6	3.47				
MAMMA1000788	18.64	7.23	10.16	10.95	9.2	11.24	9.78	6.25	8.61				
MAMMA1000798	2.84	1.31	1.28	2.57	6.45	2.47	2.42	2.49	2.05				
MAMMA1000802	10.19	4.79	5.55	11.64	14.85	12.54	8.45	6.23	7.37	*	+		
MAMMA1000810	10.4	4.83	5.83	11.45	14.19	14.79	8.3	8.84	9.48	*	+		
MAMMA1000813	3.06	1.41	1.3	0.97	1.08	1.47	1.17	2.87	1.61				
MAMMA1000814	11.43	4.36	6.48	10.9	13.12	14.78	6.64	8.56	8.44				
MAMMA1000824	4.94	1.4	2.5	6.51	8.16	10.38	6.57	7.55	6.92	*	+	*	+
MAMMA1000827	5.81	3.08	3.37	6.5	5.83	6.58	3.91	3.77	4.74				
MAMMA1000831	3.49	2.19	2.43	2.04	2.83	2.54	2.49	2.54	3.51				
MAMMA1000838	7.72	7.34	6.75	10.55	7.02	15.37	8.46	6.62	9.4				
MAMMA1000839	9.86	5.11	5.3	13.32	14.94	15.98	11.39	9.61	11.68	**	+		
MAMMA1000841	2.16	2.22	2.46	2.34	3.62	2.61	2.07	3.51	3.1				
MAMMA1000842	9.7	5.15	5.18	5.26	8.56	8.54	4.59	6.92	6.8				
MAMMA1000843	1.45	0.52	0.63	1.44	1.42	1.66	1.24	1.97	1.12				
MAMMA1000845	2.99	0.85	1.74	2.17	3.73	3.02	1.45	3.21	2.14				
MAMMA1000851	12.84	5.8	5.26	10.17	14.4	13.52	7.61	8.15	8.58				
MAMMA1000854	5.64	2.1	2.3	6.34	4.33	5.81	6.81	5.87	6.68				

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Table 217

MAMMA1000855	1.7	1.63	1.03	1.59	2.99	3.96	1.06	2.13	1.04					
MAMMA1000856	6.3	3.91	3.68	6.66	6.53	6.39	5.69	5.47	5.67					
MAMMA1000859	30.54	14.5	21.77	15.43	16.32	21.44	10.77	8.93	11.82					
MAMMA1000862	3.63	1.84	2.53	2.21	2.9	4.05	1.42	1.82	1.19					
MAMMA1000863	6.2	3.01	3.04	4.59	9.69	8.1	4.1	6.66	5.5					
MAMMA1000865	0.8	0.11	0.15	0.67	1.37	0.92	0.2	1.71	0.5					
MAMMA1000867	4.15	2.15	1.95	2.19	5.49	3.51	1.75	2.5	2.37					
MAMMA1000875	9.92	4.24	6.11	6.91	11.92	12.78	4.67	4.48	7					
MAMMA1000876	4.63	2.26	3.14	3.33	5.28	6.68	4.51	3.48	5.36					
MAMMA1000877	9.58	4.24	6.31	9.18	13.08	15.47	7.32	6.45	8.51					
MAMMA1000878	8.16	4.46	5.1	7.91	13.1	10.3	5.72	5.68	6.98					
MAMMA1000880	4.25	2.2	2.38	4.84	4.93	5.5	2.27	3.49	2.89	*	+			
MAMMA1000881	4.86	3.39	4.01	5.58	9.07	9.97	3.7	4.59	4.69	*	+			
MAMMA1000883	4.1	2.09	3.9	3.29	3.78	3.16	2.41	3.12	3.57					
MAMMA1000897	0.87	0.78	1.52	1.35	2.84	1.6	1.61	1.81	0.9					
MAMMA1000898	14.3	5.37	5.9	6.61	8.53	8.2	8.24	7.58	9.2					
MAMMA1000905	6.32	4.16	3.03	7.58	8.06	10.95	4.06	4.04	6.22	*	+			
MAMMA1000906	4.24	2.45	3	4.3	3.89	5.72	2.87	4.2	3.18					
MAMMA1000908	1.27	0.39	0.86	1.42	2.93	1.74	2.49	2.77	1.87			*	+	
MAMMA1000911	0.41	1.25	0.84	1.86	2.28	2.63	8.08	5.76	7.77	*	+	**	+	
MAMMA1000914	5.03	2.41	2.68	4.67	4.17	3.32	1.99	2.14	2.33					
MAMMA1000920	3.12	1.17	2.51	3.63	3.17	3.45	2.05	3.06	3.19					
MAMMA1000921	3.37	3.29	3.26	3.61	9.57	6.95	3.48	3.25	3.54					
MAMMA1000931	8.02	4.92	5.62	10.56	14.6	15.07	6.35	6.66	5.94	*	+			
MAMMA1000940	6.43	3.57	4.1	8.17	7.42	11.2	5.43	7.24	5.59	*	+			
MAMMA1000941	8.08	4.42	5.26	11.96	15.08	14.97	7.8	6.29	7.57	**	+			
MAMMA1000942	16.28	7.28	9.32	16.51	16.66	17.99	9.16	10.49	11.15					
MAMMA1000943	8.02	5.62	7.75	12.59	16.34	17.28	9.76	9.93	7.72	**	+			
MAMMA1000952	8.49	4.92	6.82	13.66	13.4	12.11	7.68	8.43	10.02	**	+			
MAMMA1000956	1.29	1.15	1.49	1.35	3.18	2.29	2.16	3.08	2.19			*	+	
MAMMA1000957	6.37	3.36	2.47	7.39	11.27	10.47	4.72	6	5.03	*	+			
MAMMA1000962	14.04	6.88	6.94	17.04	23.21	26.2	11.63	8.86	12.79	*	+			
MAMMA1000966	7.34	3.73	4.5	10.84	15.74	12.34	4.66	6.62	6.12	*	+			
MAMMA1000968	7.71	3.48	2.83	8.85	11.98	9.01	6.3	7.27	5.97	*	+			
MAMMA1000972	1.58	1.55	1.15	4.38	2.9	3.02	2.22	4.51	2.3	*	+			
MAMMA1000973	3.5	1.69	1.59	3.69	3.21	4.33	2.55	2.9	1.2					
MAMMA1000975	2.22	2.8	2.6	2.48	6.62	3.03	2.24	4.33	2.06					
MAMMA1000976	7.5	4.17	5.75	10.05	14.48	15.04	6.28	7.31	7.44	*	+			
MAMMA1000979	6.1	3.13	2.84	6.83	11.15	7.34	4.03	3.36	5.99					
MAMMA1000986	8.92	4.73	5.33	9.12	17.71	11.66	6.36	10.27	8.03					
MAMMA1000987	4.61	3.28	2.96	7.53	9.04	9.57	3.67	3.25	4.14	**	+			
MAMMA1000988	6.9	4.02	3.13	9.98	9.41	10.85	6.42	4.87	6.36	*	+			
MAMMA1000994	3.37	2.44	3.14	3.15	4.33	4.9	3.61	4.21	3.97			*	+	
MAMMA1000998	3.52	2.26	2.81	4.12	6.42	7.42	3.48	4.56	3.6	*	+			
MAMMA1001003	1.84	1.4	1.47	5.67	6.98	6.89	2.14	3.71	2.23	**	+			
MAMMA1001007	0.12	0.01	0.3	0.22	0.03	0.58	0.25	0.21	0.73					
MAMMA1001008	6.4	6.37	4.3	6.99	5.97	6.01	5.02	5.89	7.81					
MAMMA1001013	6.8	3.38	4.83	15.25	11.23	8.98	5.96	5.39	9.13	*	+			
MAMMA1001014	7.76	3.67	2.44	4.42	6.29	6.7	2.43	2.82	2.35					
MAMMA1001021	7.09	2.52	2.8	7.68	6.46	6.9	4.64	3.79	3.74					
MAMMA1001024	8.72	3.44	3.61	8.02	10.11	9.19	4.3	6.16	5.88					
MAMMA1001025	1.98	1.65	0.42	0.75	1.1	1.07	0.62	0.65	0.73					
MAMMA1001028	3.61	3.77	2.41	1.41	2.09	2.3	1.65	2.01	1.32			-	-	
MAMMA1001030	3.45	1.67	2.14	3.47	2.37	4.44	2.07	2.57	2.47					
MAMMA1001035	13.14	8.77	7.89	19	23.71	18.79	11.21	8.37	14.57	**	+			
MAMMA1001036	11.51	6.94	5.48	11.14	14.27	13.18	7.47	5.06	7.52					

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Table 218

MAMMA1001037	9.85	4.28	3.71	10.53	13.73	9.2	7.98	5.87	7.42				
MAMMA1001038	3.03	1.45	2.07	4.49	7.26	6.95	4.49	3.88	6.41	*	+	*	+
MAMMA1001041	6.12	4.31	3.78	4.26	5.32	5.37	5.37	4.53	3.75				
MAMMA1001043	9.46	4.63	3.66	5.68	7.75	7.15	4.92	3.72	4.88				
MAMMA1001050	6.35	5.89	3.9	5.29	10.15	10.16	5.02	6.56	5.49				
MAMMA1001054	5.51	4.13	3	8.5	8.45	8.15	5.21	3.63	4.46	**	+		
MAMMA1001059	15.39	8.08	6.23	9.1	11.74	11.86	8.44	7.77	9.49				
MAMMA1001066	16.43	8.7	9.35	16.38	15.95	15.31	10.1	8.21	12.62				
MAMMA1001067	3.67	2.44	1.56	5.04	5.4	5.91	3.35	3.05	4.31	*	+		
MAMMA1001072	11.88	5.32	6.63	6.72	4.61	6.46	5.54	4.86	5.86				
MAMMA1001073	5.21	2.94	1.75	2.04	3.72	2.45	1.94	3.03	2.39				
MAMMA1001074	3.99	4.38	2.27	4.13	9.96	13.79	3.27	3.81	5.24				
MAMMA1001075	5.54	2.96	3.2	3.06	7.9	7.5	2.62	3.18	3.18				
MAMMA1001078	7.94	4.65	4.05	9.11	13.65	11.41	7.34	5.68	7.64	*	+		
MAMMA1001080	22.36	9.18	10.44	11.87	12.56	12.61	9.96	10.5	13.83				
MAMMA1001082	4.52	3.3	1.66	3.03	5.82	3.36	3.3	2.6	2.45				
MAMMA1001091	0.73	0.99	0.34	1.07	1.55	1.04	1.3	1.37	1.5			*	+
MAMMA1001092	3.38	1.71	1.14	4.68	5.06	3.84	2.72	2.57	3.2	*	+		
MAMMA1001094	23.07	10.75	8.74	19.47	15.51	11.95	11.1	12.09	9.06				
MAMMA1001105	8.97	7.82	3.9	7.84	13.25	10.97	5.27	6.89	7.2				
MAMMA1001110	1.34	0.28	1.07	0.83	1.4	1.91	0.64	1.83	0.87				
MAMMA1001126	11.76	5.19	6.22	18.27	20.42	20.62	10.8	7.93	10.63	**	+		
MAMMA1001133	13.96	7.98	6.29	17.52	21.82	18.6	12.41	9.09	11.57	*	+		
MAMMA1001139	16	10.86	8	75.48	52.51	90.41	4.72	2.94	4.09	**	+	*	-
MAMMA1001141	3.54	2.73	2.73	3.35	3.24	4.02	3.37	4.28	4.25				
MAMMA1001143	9.1	5.11	2.81	6.09	8.1	8.79	3.94	3.97	7.09				
MAMMA1001145	8.33	4.95	3.62	3.46	6.81	6.75	3.46	5.11	7.05				
MAMMA1001150	8.4	3.25	2.79	2.57	3.1	4.61	3.41	4.01	4.33				
MAMMA1001154	10.09	4.99	5.59	11.85	11.71	18.3	6.93	7.19	6.3				
MAMMA1001159	9.34	6.32	4.92	5.06	4.86	4.07	3.31	2.7	4.01				
MAMMA1001161	14.59	7.23	8.28	17.47	24.12	19.35	11.34	7.11	8.84	*	+		
MAMMA1001162	8.3	3.74	4.22	6.24	6.6	5.21	4.88	5.43	5.84				
MAMMA1001181	5.83	2.22	1.87	4.38	4.79	3.53	3.65	3.3	3.3				
MAMMA1001186	7.43	2.73	2.8	9.55	11.46	10.04	5.94	5.12	6.23	*	+		
MAMMA1001189	5.2	2.45	3.28	2.21	6.23	8.54	2.7	3.48	4.97				
MAMMA1001191	7.35	3.89	3.31	3.72	5.24	6.78	3.27	4.86	5.76				
MAMMA1001198	420.1	187.9	245.8	305.4	416.1	499.3	169.9	159.8	188.3				
MAMMA1001202	22.54	12.72	10.05	25.35	28.4	25.81	14.74	13.68	16.11	*	+		
MAMMA1001203	10.49	4.64	4.15	9.25	14.44	10.45	6.11	7.56	8.28				
MAMMA1001206	4.15	2.67	2.33	5.52	7.44	5.57	3.53	2.86	3.88	*	+		
MAMMA1001208	6.57	2.81	3.7	5.42	5.59	5.39	4.2	3.8	4.35				
MAMMA1001215	10.79	5.58	5.27	10.75	14.22	15.01	5.67	7.42	7.48				
MAMMA1001220	9.93	5.68	4.3	14.65	18.62	17.06	7.53	7.5	9.1	**	+		
MAMMA1001222	1.59	0.92	0.2	0.96	1.98	1.96	-0.04	1.13	0.9				
MAMMA1001223	4.89	1.72	1.83	2.87	4.51	4.18	2.3	4.01	2.37				
MAMMA1001232	8.78	2.9	3.18	7.54	10.45	9.18	4.93	4.96	6.51				
MAMMA1001234	7.4	4.59	2.41	6.32	6.84	8.88	3.78	3.73	6				
MAMMA1001237	2.49	1.76	1.72	1.22	2.15	2.66	1.99	1.8	2.56				
MAMMA1001243	2.36	1.9	1.62	4.41	7.15	5.33	4.22	3.46	4.95	*	+	**	+
MAMMA1001244	2.4	1.42	0.68	1.53	3.03	2.44	2.05	2.71	3.6				
MAMMA1001249	5.06	0.96	1.74	3.77	9.25	4.93	2.44	3.57	4.08				
MAMMA1001256	2.41	7.77	2.44	2.13	6.99	6.49	2.44	2.38	3.83				
MAMMA1001259	5.56	2.92	3.02	4.36	6.71	5.33	2.23	3.39	5.03				
MAMMA1001260	13.79	6.11	6.31	13.52	13.26	12.23	7.61	6.68	10.66				
MAMMA1001262	9.64	6.71	5.97	8.72	6.36	5.96	5.41	6.02	8.33				
MAMMA1001268	4.72	2.75	3.01	9.39	6.71	7.53	3.74	4.95	5.14	*	+		

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Table 219

MAMMA1001271	18.48	7.38	8.91	10.48	14.14	10.31	9.58	8.4	12.04				
MAMMA1001274	4.43	3.8	2.81	4.94	7.96	7.95	4.24	5.07	5.33	*	+		
MAMMA1001280	1.75	0.68	1.07	1.62	2.08	1.61	1.59	2.67	1.12				
MAMMA1001283	7.51	3.83	5.22	4.97	9.33	8.85	4.6	3.72	6.27				
MAMMA1001284	9.53	6.17	5.52	8.14	10.72	8.86	5.52	7.53	9.35				
MAMMA1001286	24.45	16.7	10.97	12.09	12.45	13	5.97	6.39	7.92				
MAMMA1001289	8.47	4.9	3.19	5.53	5.66	7.55	4.68	4.32	5.33				
MAMMA1001292	6.67	3.9	2.86	4.2	6.48	5.22	3.23	4.27	4.41				
MAMMA1001296	7	4.06	4.91	10.25	16.18	16.77	6.43	5.53	5.34	*	+		
MAMMA1001298	4.11	3.91	3.07	8.57	9.18	8.84	4.16	3.98	4.76	**	+		
MAMMA1001305	5.35	2.58	3.48	7.15	5.55	7.22	4.85	4.29	6.18	*	+		
MAMMA1001309	1.7	1.52	0.97	5.04	3.61	5.38	2.09	2.69	2.33	**	+	*	+
MAMMA1001310	10.44	4.9	7.15	8.11	11.15	12.2	4.69	5.11	6.27				
MAMMA1001322	2.58	0.43	0.4	1.79	2.43	1.77	1.08	1.1	1.59				
MAMMA1001324	4.35	2.2	1.73	3.98	4.2	3.7	1.97	2.42	3.42				
MAMMA1001330	13.9	7.33	5.29	11.99	11.29	12.32	6.89	5.13	7.87				
MAMMA1001333	10.64	5.27	5.22	12.45	17.04	13.72	7.27	8.49	8.86	*	+		
MAMMA1001334	19.83	12.61	11.33	16.84	18.12	18.43	11.85	9.39	18.95				
MAMMA1001337	6.8	2.68	3.43	4.92	5.69	6.15	4.3	5.31	5.13				
MAMMA1001341	3.94	2.12	2.51	4.82	3.58	4.32	2.93	4.08	4.66				
MAMMA1001343	4.64	4.02	3.95	10.45	11.27	11.13	3.36	5.55	6.66	**	+		
MAMMA1001344	3.2	1.52	0.8	2.99	5.13	4.05	4.81	3.84	5.02			*	+
MAMMA1001346	3.61	1.95	1.75	2.88	2.78	3.94	2.71	2.77	4.61				
MAMMA1001383	13.98	5.18	5.89	17.88	22.89	19.58	10.5	8.81	9.31	*	+		
MAMMA1001388	6.8	2.8	3.94	7.53	10.07	7.51	5.93	5.82	6.51				
MAMMA1001396	11.03	6.21	4.6	12.55	13.22	12.6	7.14	6.44	7.15	*	+		
MAMMA1001397	8.15	4.45	6.77	11.06	10.6	9.93	5.76	7.2	5.97	*	+		
MAMMA1001401	12.38	7.29	6.74	14.61	13.5	16.44	10.3	14.7	12.59	*	+		
MAMMA1001408	3.01	1.06	1.25	3.39	2.85	2.94	2.29	2.63	3.03				
MAMMA1001411	13.87	6.35	6.18	6.44	8.45	4.19	7.07	7.42	10.12				
MAMMA1001414	8.9	4.02	3.1	8.97	5.29	6.61	6.05	4.52	6.79				
MAMMA1001415	10.6	3.71	5.04	5.41	5.06	7.32	4.77	5.68	6.24				
MAMMA1001418	5.7	2.73	2.09	6.08	5.21	5.62	4.02	2.75	3.87				
MAMMA1001419	4.73	2.65	2.23	4.77	8	8.11	4.53	3.83	4.07	*	+		
MAMMA1001420	3.1	2.15	1.27	3.76	5.4	5.17	2.79	4.4	3.79	*	+		
MAMMA1001426	18.02	14.05	10.52	23.03	29.5	27.85	14.93	16.81	15.67	*	+		
MAMMA1001428	19.49	9.42	10.79	23.13	21.75	19.76	15.67	13.18	13.4				
MAMMA1001432	11.31	4.42	3.74	13.45	13.13	13.68	6.17	5.31	10.64	*	+		
MAMMA1001435	5.17	2.46	1.9	6.79	5.64	6.54	4.02	2.35	4.67	*	+		
MAMMA1001442	5.06	2.93	3.93	6.1	7.84	8.67	6.15	4.58	6.02	*	+		
MAMMA1001446	12.46	5.86	4.49	8.24	8.89	13.91	4.69	4.66	5.57				
MAMMA1001450	4.63	2.5	2.67	4.93	4	5.12	3.59	2.97	3.49				
MAMMA1001452	6.13	3.91	3.22	5.79	9.5	8.17	5.22	5.47	4.79				
MAMMA1001465	26.46	18.98	20.83	12.75	32.75	41.93	22.64	25.99	25.3				
MAMMA1001476	5.04	2.17	1.67	4.15	3.25	3.38	3.37	3.42	3.65				
MAMMA1001478	8.65	3.83	3.78	10.05	11.02	9.81	4.96	6.35	7.03	*	+		
MAMMA1001479	12.55	5.38	4.01	10.03	11.12	10.85	9.53	8.55	11.85				
MAMMA1001487	3.39	1.73	3.53	4.32	4.6	4.59	2.05	2.41	4.9				
MAMMA1001498	9.96	8.14	3.99	14.3	13.63	9.71	5.08	12.98	6.54				
MAMMA1001501	10.61	5.97	4.92	6.54	6.18	6.58	4.88	5.96	6.07				
MAMMA1001502	8.18	4.06	3.9	5.74	5.38	7.37	5.92	4.78	5.08				
MAMMA1001510	2.96	0.75	0.46	1.67	1.4	1.25	0.55	1.62	1.38				
MAMMA1001522	5.03	2.4	1.29	4.2	3.19	3.32	3.17	2.13	2.87				
MAMMA1001529	6.71	2.99	3.35	4.53	4.35	5.16	2.95	3.56	4.27				
MAMMA1001532	9.52	5.54	4.9	8.06	8.4	11.77	6.31	5.77	5.73				
MAMMA1001533	5.96	3.56	2.76	3.85	3.07	5.41	3.42	3.85	4.91				

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Table 220

MAMMA1001534	1.04	1	0.48	0.51	0.82	0.82	0.58	0.71	1.3				
MAMMA1001535	4.92	2.88	1.16	1.88	3.67	4.55	1.49	2.38	2.87				
MAMMA1001547	6.61	3.6	2.98	6.07	6.82	8.95	4.29	5.11	5.04				
MAMMA1001551	6.07	3.86	3.57	4.63	5.65	6.3	4.24	3.97	4.09				
MAMMA1001569	3.5	1.48	2.2	2.86	2.79	2.47	2.33	2.98	1.96				
MAMMA1001575	8.12	4.85	4.3	5.13	5.29	4	4.97	4.91	5.14				
MAMMA1001576	20.26	7.19	9.68	8.21	9.38	6.87	9.09	8.98	9.31				
MAMMA1001584	4.62	2.36	1.31	4.08	5.15	3.32	1.55	1.67	4.4				
MAMMA1001586	1.88	3.47	0.76	1.07	3.5	1.99	1.25	2.13	3.7				
MAMMA1001590	12.7	4.74	4.76	9.14	12.67	13.3	5.6	5.77	7.89				
MAMMA1001599	4.33	1.21	1.88	2.45	2.99	4.36	2.56	2.76	2.04				
MAMMA1001600	5.33	1.77	2.89	2.89	5.09	5.36	2.48	3.86	2.92				
MAMMA1001604	7.87	5.11	1.45	4.32	5.42	5.07	3.4	3.25	5.07				
MAMMA1001606	9.46	4.93	4.75	9.09	8.64	10.49	4.91	6.03	6.85				
MAMMA1001609	2.95	1.2	1.3	2.12	2.38	3.64	2.68	2.56	2.15				
MAMMA1001614	4.39	2.53	1.88	2.49	3.22	3.59	2.48	3.41	3.61				
MAMMA1001615	6.67	1.9	1.82	2.35	2.21	3.65	2.11	2.71	3.83				
MAMMA1001619	19.31	10.08	12.63	10.87	10.6	14.3	14.55	8.6	14.72				
MAMMA1001620	8.92	3.44	4.44	6.63	10.03	12.83	4.85	6.18	5.9				
MAMMA1001623	3.58	4.58	2.08	1.56	2.91	2.34	1.28	2.13	2.52				
MAMMA1001626	2.57	1.13	1.2	1.48	2.12	1.89	1.75	2.77	3.1				
MAMMA1001627	2.24	1.39	0.54	2.13	3.22	2.88	2.13	2.52	2.05				
MAMMA1001630	3.02	5.98	2.09	4.38	4.01	5.45	2.54	3.3	3.8				
MAMMA1001633	6.31	4.02	1.66	8.75	9.37	5.34	5.49	3.61	5.08				
MAMMA1001634	8.31	4.18	4.46	11.22	16.21	13.47	7.21	6.09	6.17	*	+		
MAMMA1001635	8.83	4.02	2.32	12.04	8.31	8.32	5.06	3.5	2.52				
MAMMA1001649	4.06	1.62	1.65	3.2	3.67	3.34	1.61	2.68	2.21				
MAMMA1001654	7.5	5.7	4.13	5.16	7.53	6.42	3.33	5.51	3.69				
MAMMA1001660	28.42	20.01	15.26	32.5	33.59	28.79	16.52	14.53	17.32				
MAMMA1001663	16.19	8.13	7.37	24.06	22.04	19.25	11.83	9.81	14.91	*	+		
MAMMA1001670	6.04	4.74	3.32	6.72	7.02	6.98	4.35	4.11	5.69	*	+		
MAMMA1001671	3.01	0.89	1.27	2.72	3.99	2.13	1.77	2.54	1.32				
MAMMA1001679	4.8	3.29	3	3.03	4.77	2.84	4.71	2.51	4.64				
MAMMA1001683	6.21	3.81	4.22	11.62	10.92	14.02	7.47	6.25	5.71	**	+		
MAMMA1001686	1.2	1.06	0.86	1.34	1.65	3.46	1.07	2.23	3.61				
MAMMA1001688	27.08	14.53	17.18	23.31	26.84	30.3	37.53	34.87	43.95			*	+
MAMMA1001689	10.7	4.3	2.46	5.85	12.72	6.26	3.96	2.83	5.24				
MAMMA1001692	5.97	3.39	4.03	11.66	13.26	13.23	4.66	4.11	3.69	**	+		
MAMMA1001711	7.12	3.2	3.17	7.6	8.99	7.95	4.59	5.62	7.5				
MAMMA1001715	5.07	1.86	2.28	7.77	5.67	4.34	3.14	3.85	3.95				
MAMMA1001730	5.56	2.96	1.32	1.82	2.04	2.43	2.03	3.01	2.56				
MAMMA1001735	17.93	11.2	11.92	16.49	13.17	19.36	14.97	10.91	15.84				
MAMMA1001740	2.62	1.39	2.19	3.94	5.07	3.81	2.69	2.45	2.08	*	+		
MAMMA1001743	63.77	35.5	45.41	34.01	34.01	44	19.91	22.06	23.3			*	-
MAMMA1001744	1.18	0.45	0.11	1.34	1.3	0.81	0.46	0.4	0.67				
MAMMA1001745	12.45	7.1	4.31	14.99	16.74	16.98	8.77	5.37	11.73	*	+		
MAMMA1001751	5.01	2.42	3.03	4.8	5.52	7.04	3.9	3.22	3.1				
MAMMA1001752	15.56	8.33	10.02	13.09	14.3	13.11	10.96	9.67	11.14				
MAMMA1001754	5.78	4.59	3.53	9.06	6.92	8.14	9.82	5.67	8.59	*	+		
MAMMA1001757	1.64	0.65	0.62	1.81	1.16	1.05	0.91	2.59	1.38				
MAMMA1001760	15.19	8.82	7.01	15.51	12.28	21.03	9.85	11.53	17.24				
MAMMA1001764	2.52	1.27	1.35	2.11	2.1	2.28	1.29	2.52	2.02				
MAMMA1001767	3.67	2.6	1.45	4.72	4.48	6.08	3.4	1.82	3.79	*	+		
MAMMA1001768	3.4	1.95	1.15	4.85	4.7	4.24	2.45	3.01	3.52	*	+		
MAMMA1001769	10.2	4.54	6.07	16.86	18.38	16.58	8.55	6.27	9.46	**	+		
MAMMA1001771	7.06	9.36	4.23	3.92	5.03	5.23	5.55	6.69	8.65				

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Table 221

MAMMA1001773	6.61	3.09	3.86	5.22	5.33	3.63	5.11	4.68	6.54				
MAMMA1001778	4.17	2.72	2.42	4.48	7.37	5.12	3.01	4.78	4.22				
MAMMA1001783	6.42	4.36	3.89	10.62	14.19	14.31	4.67	8.23	6.82	**	+		
MAMMA1001785	8.22	2.97	5.14	14.68	12.34	15.26	7.67	8.51	8.54	**	+		
MAMMA1001788	2	0.87	0.27	0.81	1.38	1.73	1.53	0.58	0.8				
MAMMA1001790	5.36	3.86	1.92	6.66	16.36	9.58	3.91	3.27	3.37				
MAMMA1001800	3.52	2.19	1.41	1.85	4.05	2.73	1.44	1.76	1.56				
MAMMA1001804	6.25	3.82	2.87	4.53	3.88	4.64	4.42	4.04	3.96				
MAMMA1001806	3.43	3.08	1.93	7.24	8.78	6.25	3.11	4.51	5.23	**	+		
MAMMA1001812	2.22	1.53	1.51	2.28	2.36	2.64	1.38	2.87	1.34				
MAMMA1001815	1.3	0.41	0.62	2.99	1.2	2.47	2.3	2.24	1.48			*	+
MAMMA1001817	1.37	3.74	1.14	2.04	2.4	3.09	1.01	1.65	1.29				
MAMMA1001818	2.76	5.34	1.53	1.82	5.05	3.5	2.09	2.95	4.34				
MAMMA1001819	5.52	3.47	3.12	6.33	7.32	6.74	3.51	2.89	5.62	*	+		
MAMMA1001820	2.45	1.25	0.82	2.09	2.1	3.98	4.93	5.44	3.89			**	+
MAMMA1001824	6.23	3.21	3.26	6.85	6.39	6.61	3.99	4.27	4.97				
MAMMA1001832	3.67	1.55	1.58	4.4	5.34	6.5	1.89	2.88	2.54	*	+		
MAMMA1001836	7.21	6.9	2.37	8.79	8	7.74	7.22	5.59	4.27				
MAMMA1001837	8.71	5.61	5.12	7.73	9.45	10.52	4.01	4.19	6.46				
MAMMA1001848	3.49	1.69	1.44	2.63	4.08	4.52	1.91	2.78	1.99				
MAMMA1001850	20.05	8.18	11.43	18.79	13.27	17.94	12.58	9.7	17.74				
MAMMA1001851	6.25	2.81	2.47	7.34	6.62	10.7	4.31	3.59	5.68				
MAMMA1001852	7.89	5.2	4.18	14.68	10.33	12.24	6.74	5.9	7.65	*	+		
MAMMA1001854	8.11	3.75	3.83	5.47	8.12	7.92	4.25	4.74	5.11				
MAMMA1001858	5.29	6.33	3.33	4.8	9.86	6.77	4.43	4.52	4.66				
MAMMA1001864	6.57	3.87	3.53	5.26	5.92	6.2	4.84	4.25	4.74				
MAMMA1001868	7.13	2.35	1.77	6.07	8.46	12.04	4.49	2.72	4.43				
MAMMA1001874	2.56	0.8	0.99	1.13	2.27	2.32	0.71	0.85	1.82				
MAMMA1001878	14.71	6.24	5.55	12.93	17.25	13.98	8.14	7.86	10.4				
MAMMA1001880	8.73	3.97	3.36	7.33	11.41	9.31	6.98	4.88	7.07				
MAMMA1001885	8.89	4.03	4.1	9.41	9.07	9.64	3.45	4.7	8.89				
MAMMA1001890	10.42	4.8	4.27	13.94	12.16	12.45	5.05	4.52	6.53	*	+		
MAMMA1001893	8.64	3.63	4.1	6.16	5.52	7.2	5.63	4.73	6.76				
MAMMA1001901	3.39	1.13	2.13	3.15	3.75	4.39	2.43	2.45	3.16				
MAMMA1001907	12.12	8.44	5.76	15.43	12.7	15.66	5.86	7.16	6.54	*	+		
MAMMA1001908	16.6	10.48	11.12	10.97	16.32	14.93	6.4	9.69	8.54				
MAMMA1001919	1.82	0.17	0.6	0.94	1.34	0.71	1.26	0.88	0.98				
MAMMA1001931	3.36	2.44	1.38	2.23	3.72	3.2	2.14	2.05	2.86				
MAMMA1001937	5.76	3.91	4.17	7.43	4.75	5.56	4.86	3.34	6.3				
MAMMA1001951	9.42	4.25	4.02	11.76	11.79	12.88	6.81	5.98	6.3	*	+		
MAMMA1001956	12.62	6.26	4.43	11.46	11.33	13.51	7.86	7.63	5				
MAMMA1001957	7.69	6.91	2.97	9.44	10.13	11	3.86	6.71	4.82	*	+		
MAMMA1001960	8.09	4.17	5.2	8.83	7.29	10.11	4.77	4.56	4.66				
MAMMA1001963	1.4	0.45	0.94	0.59	0.92	1.24	0.53	1.56	0.54				
MAMMA1001969	14.58	7.72	8.73	21.99	28.29	25.27	9.69	8.49	9.83	**	+		
MAMMA1001970	13.52	3.54	5.52	13.53	17.34	15.88	8.28	8.88	8.45				
MAMMA1001978	1.45	1.06	0.2	0.2	0.85	0.8	1.52	1.12	0.55				
MAMMA1001992	10.84	5.7	4.65	11.47	10.31	11.31	7.27	6.07	8.17				
MAMMA1001994	10	5.97	3.81	5.9	10.24	11.51	7.66	6.84	4.2				
MAMMA1002008	4.32	3.45	1.54	2.22	2.63	3.21	2.43	4.92	3.14				
MAMMA1002009	6.14	4.06	3.61	6.87	8.92	11.78	3.75	4.94	3.85	*	+		
MAMMA1002011	7.71	3.01	4.35	2.88	2.54	4.06	2.17	2.53	2.34				
MAMMA1002022	5.37	5.17	1.74	4.7	10.07	6.42	3.41	3.09	3.25				
MAMMA1002024	16.93	11.72	9.52	17.19	15.15	15.52	13.59	12.95	15.19				
MAMMA1002032	11.99	7.54	5.7	14.48	16.59	16.42	8.97	9.05	9.69	*	+		
MAMMA1002033	7.72	10.65	3.5	9.82	12.49	7.85	5.26	4.36	7.58				

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Table 222

MAMMA1002041	2.83	1.69	0.23	3.14	3.37	3.59	1.39	2.49	3.1				
MAMMA1002042	5.88	3.59	2.24	4.97	5.99	7.54	2.94	3.98	4.72				
MAMMA1002045	2.41	1.74	1.47	5.35	8.87	6.75	3	4.53	2.32	**	+		
MAMMA1002047	5.33	2.17	2.02	3.83	6.17	6.04	1.68	3.55	2.24				
MAMMA1002056	12.39	6.58	4.37	20.56	18.36	19.17	8.24	9.27	8.66	**	+		
MAMMA1002058	6.27	2.84	3.39	8	8.2	9.71	5.08	4.13	6.51	*	+		
MAMMA1002060	1.5	3.41	0.94	1.36	1.83	1.14	1.54	1.23	1.52				
MAMMA1002065	9.08	4.91	4.66	8.35	11.05	9.12	3.27	5.48	5.84				
MAMMA1002068	6.34	2.81	1.47	4.59	6.64	9.1	3.39	3.22	5.73				
MAMMA1002070	4.29	2.1	1.76	2.92	4.72	3.16	2.15	3.57	3.06				
MAMMA1002078	5.04	2.14	3.64	3.66	4.1	4.18	2.08	3.2	5.45				
MAMMA1002080	6.83	3.54	2.1	2.95	4.44	2.95	2.06	5.27	3.19				
MAMMA1002082	8.06	4.39	2.39	7.44	9	7.6	3.58	5.19	3.55				
MAMMA1002084	5.52	4.28	3.59	5.1	6.35	5.81	3.08	4.41	3.89				
MAMMA1002087	2.38	2.18	1.81	1.76	3.43	2.93	2.59	2.65	3.27				
MAMMA1002091	5.42	7.29	2.65	4	6.91	4.49	4.2	3.64	5.26				
MAMMA1002093	1.93	2	0.58	5.96	1.9	2.8	1.65	1.71	2.83				
MAMMA1002095	5.4	2.74	3.59	3.25	4.43	4.61	2.69	3.88	4.12				
MAMMA1002108	5.49	3.13	2.43	2.96	4.71	4.19	2.48	1.84	3.62				
MAMMA1002112	2.09	1.02	0.93	2.26	2.09	1.19	0.86	2.05	1.87				
MAMMA1002118	4.48	1.67	0.26	1.23	3.74	1.59	0.63	2.22	1.71				
MAMMA1002119	8.58	4.34	2.71	5.72	6.62	5.85	3.59	5.08	6.24				
MAMMA1002125	9.57	5.01	5.66	13.06	12.09	12.55	6.22	5.68	8.12	*	+		
MAMMA1002126	13.46	5.9	6.29	18.17	24.01	20.42	8.52	7.83	10.14	*	+		
MAMMA1002128	5.36	2.96	2.77	3.71	5.08	4.6	3.95	3.22	4.97				
MAMMA1002132	10.12	4.97	5.63	12.89	10.87	14.39	10.04	6.43	10.71	*	+		
MAMMA1002140	1.72	1.95	1.35	4.11	5.59	3.44	1.38	1.98	2.23	*	+		
MAMMA1002142	6.23	4.13	6.33	4.88	8.41	5.57	2.7	5.34	6.44				
MAMMA1002143	7.91	3.86	1.2	4	8.63	6.78	4.54	4.01	8.01				
MAMMA1002145	12.14	5.89	4.12	12.19	9.19	9.27	7.73	5.23	7.12				
MAMMA1002147	4.21	2.54	2.46	6.44	4.91	6.18	4.06	3.93	4.81	*	+		
MAMMA1002153	5.55	2.41	3.01	3.35	4.54	5.5	3.13	4.08	5.58				
MAMMA1002155	9.29	6.93	5.81	15.05	16.47	13.36	7.79	8.57	9.36	**	+		
MAMMA1002156	0.5	0.43	0.34	1.18	0.77	0.53	0.87	1.99	2.58				
MAMMA1002158	3.36	2.26	1.87	4.83	4.63	4.78	2.02	3.6	3.09	**	+		
MAMMA1002164	4.2	5.9	2.06	5.48	5	6.18	2.35	2.71	6.87				
MAMMA1002165	9.16	4.19	3.07	5.86	7.65	9.97	4.78	4.68	8.08				
MAMMA1002170	2.61	1.94	1.29	2.52	2.68	1.48	2.55	4.49	2.09				
MAMMA1002174	4.84	4.21	3.36	9.26	11.06	9.43	3.61	5.85	5.69	**	+		
MAMMA1002175	3.66	3.08	1.47	4.24	3.36	3.13	3.56	5.23	4.15				
MAMMA1002180	9.95	5.24	8.36	6.25	12	9.82	8.31	11.32	10.45				
MAMMA1002198	7.77	3.94	4.6	11.59	10.97	8.42	5.79	8.09	5.83	*	+		
MAMMA1002205	6.94	2.43	4.08	12.68	10.23	10.6	4.99	6.19	5.86	*	+		
MAMMA1002206	4.97	3.21	3.83	3.93	5.39	5.02	3.15	4.77	5.02				
MAMMA1002209	5.93	1.39	2.1	5.8	6.14	5.58	2.65	3.01	4.62				
MAMMA1002215	25.36	13.93	13.82	17.32	25.36	18.76	19.04	14.22	18.26				
MAMMA1002219	6.6	5.08	3.39	6.83	8.53	7.54	5.44	5.14	6.2				
MAMMA1002224	8.1	9.24	5.62	14.79	19.7	17.59	7.17	10.07	8.16	**	+		
MAMMA1002229	3.07	2.57	2.61	4.9	4.15	4.71	3.87	4.96	3.11	**	+		
MAMMA1002230	5.84	5.63	4.35	11.67	10.96	14.46	5.06	7.28	7.47	**	+		
MAMMA1002233	5.99	1.67	2.56	4.66	5.13	4.71	1.73	5.03	4.75				
MAMMA1002234	2.42	2.28	2.06	6.51	4.38	3.03	2.11	2.84	3.32				
MAMMA1002236	9.04	9.45	4.47	5.41	11.26	4.51	4.88	5.38	10.34				
MAMMA1002243	5.3	1.99	1.09	3.09	2.98	3.83	2.89	2.41	4				
MAMMA1002250	6.06	6.45	2.48	6.45	6.62	8.63	6.12	5.22	8.76				
MAMMA1002253	25.92	17.49	11.68	17.95	18.93	21.68	17.92	18.81	17.12				

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Table 223

MAMMA1002267	5.13	1.56	2.1	4.1	8	6.58	5.59	7.23	7.33			*	+
MAMMA1002268	4.34	3.93	2.18	3.97	3.15	4.33	1.93	3.77	3.06				
MAMMA1002269	3.53	2.77	0.37	2.27	1.57	2.25	1.64	1.13	1.9				
MAMMA1002282	3.17	4.02	1.28	2.38	4.52	4.47	2.52	2.77	2.84				
MAMMA1002292	8	3.86	4.57	6.11	4.23	6.12	4.47	3.55	4.28				
MAMMA1002293	13.94	6.19	6.42	18.8	17.8	21.12	10.21	8.07	15.59	*	+		
MAMMA1002294	6.97	4.11	3.04	6.45	7.32	6.27	5.03	5.25	5.73				
MAMMA1002297	5.17	2.14	2.44	5.18	5.03	6.05	4.2	2.91	4.33				
MAMMA1002298	5.95	2.63	2	5.32	4.87	5.66	3.33	3.41	4.16				
MAMMA1002299	3.71	2.19	2.17	3.02	3.23	3.18	3.21	2.61	2.25				
MAMMA1002308	4.09	3.82	1.96	6.63	7.73	3.7	2.44	2.99	3.59				
MAMMA1002310	24.32	15.32	19.7	26.21	29.99	31.31	20.38	19.58	18.88	*	+		
MAMMA1002311	10.38	6.89	2.86	14.02	13.82	13.05	10.49	6.04	10.98	*	+		
MAMMA1002312	7.11	4.07	0.96	3.66	5.77	5.39	2.87	2.07	3.97				
MAMMA1002317	5.37	4.98	2.41	6.38	13.31	8.87	4.49	3.92	7.76				
MAMMA1002319	8.07	2.35	5.23	7.19	7.92	8.72	5.3	5.48	6.56				
MAMMA1002322	6.31	4.11	5.15	10.22	11.41	12.06	4.9	7.5	6	**	+		
MAMMA1002329	4.15	2.37	1.67	2.9	3.82	5.04	2.2	3.87	3.47				
MAMMA1002332	4.13	2.74	1.9	3.61	6.19	6.87	2.13	3.26	3.02				
MAMMA1002333	7.26	4	2.1	6.05	5.74	3.04	3.25	4.13	4.42				
MAMMA1002335	10.93	3.6	4.03	10.38	8	8.37	5.57	5.29	6.32				
MAMMA1002339	7.73	3.96	3.73	8.81	10.04	9.53	3.71	3.46	7.48	*	+		
MAMMA1002347	6.93	4.17	2.03	4.83	7.45	7.07	4.3	4.21	4.94				
MAMMA1002351	3.84	5.05	2.4	3.45	5.38	4.65	4.23	5.29	5.91				
MAMMA1002352	5.21	4	2.14	4.04	3.97	4.72	2.11	1.72	2.04				
MAMMA1002353	9.22	7.52	2.31	5.95	8.94	7.55	4.37	4.54	4.03				
MAMMA1002355	5.34	3.25	2.3	4.76	5.27	7.77	2.43	4.79	2.85				
MAMMA1002356	3.57	2.35	1.19	3.19	4.03	4.8	2.05	2.5	2.26				
MAMMA1002359	13.77	9.98	8.17	18.6	20.01	21.01	10.51	7.95	8.5	**	+		
MAMMA1002360	4.19	2.61	1.63	3.14	2.98	2.4	3	1.64	2.41				
MAMMA1002361	6.53	2.69	2.54	6.26	7.25	5.96	4.09	4.49	5.12				
MAMMA1002362	3.93	2.21	1.89	3.56	5.61	4.11	4.72	2.96	3.12				
MAMMA1002367	6.65	2.94	3.45	4.37	4.72	4.67	3.85	4.3	4.84				
MAMMA1002371	7.21	3.57	4.06	7.96	12.17	10.93	5.47	3.81	6.44	*	+		
MAMMA1002380	6.65	2.95	5.07	7.2	8.08	10.65	3.09	4.7	4.45				
MAMMA1002384	4	1.78	2.02	5.31	7.82	7.61	2.14	4.39	2.73	*	+		
MAMMA1002385	1.81	2.58	0.88	2.71	5.37	2.61	2.77	1.86	3.22				
MAMMA1002390	7.22	4.09	4.3	4.23	4.19	5.43	8.27	6.12	7.86				
MAMMA1002392	6.65	3.55	1.7	3.98	7.13	4.08	2.98	3.25	3.05				
MAMMA1002396	10.94	5.98	7.24	14.33	18.89	22.98	6.91	9.41	11.76	*	+		
MAMMA1002399	6.9	2.88	1.85	8.11	6.41	8.49	4.7	4.28	4.05				
MAMMA1002400	1.74	0.88	0.89	1.88	3.53	2.38	2.6	2.64	0.96				
MAMMA1002409	4.98	2.45	2.94	3.65	3.94	4.37	3.81	6.25	5				
MAMMA1002411	5.54	2.15	1.5	3.44	5.65	4.97	2.26	3.08	1.74				
MAMMA1002413	12.21	5.64	2.48	9.88	11.9	8.93	6.13	5.59	4.64				
MAMMA1002417	3.93	2.05	1.27	4.37	4.53	3.05	1.96	4.22	3.47				
MAMMA1002427	6.03	2.26	2.41	5.84	9.22	5	5.51	3.52	6.07				
MAMMA1002428	3.76	1.67	1.82	4.3	5.95	5.66	4.02	3.17	2.93	*	+		
MAMMA1002433	8.04	2.9	2.73	4.67	5.92	6.23	3.94	2.95	5.38				
MAMMA1002434	8.11	3.72	2.87	9.52	10.57	9.58	3.29	5.17	4	*	+		
MAMMA1002446	3.79	2.83	2.72	3.64	5.3	4.09	2.21	3.52	3.36				
MAMMA1002447	6.44	2.97	3.54	5.33	7.97	7.41	2.58	4.01	4.02				
MAMMA1002454	19.95	10.05	7.32	23.49	19.29	16.59	13.96	10.08	15.17				
MAMMA1002461	12.83	8.73	5.05	6.25	10.29	8.7	5.37	6.47	8.29				
MAMMA1002463	8.41	6.54	4.81	4.6	7.71	7.29	6.73	4.8	6.72				
MAMMA1002464	7.42	5.06	2.53	4.57	5.16	4.31	6.56	4.89	5.9				

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Table 224

MAMMA1002466	7.61	3.8	3.03	7.05	8.64	7.32	9.99	8.37	11.38			*	+
MAMMA1002470	5.61	2.03	2.45	2.62	3.83	4.24	2.19	2.79	3.07				
MAMMA1002475	2.73	2.58	1.69	4.8	5.81	4.75	1.5	3.35	3.39	**	+		
MAMMA1002480	1.82	0.76	1.1	1.61	2.6	1.72	0.67	1.56	1.72				
MAMMA1002485	11.15	6.59	4.25	5.55	8.76	7.85	6.2	6.28	8.64				
MAMMA1002494	6.22	5.16	3	7.41	9.6	7.67	4.89	3.44	6.03	*	+		
MAMMA1002498	5.71	3.03	1.34	3.92	2.98	3.69	2.66	2.39	3.29				
MAMMA1002524	7.17	3.31	2.26	5.6	4.65	6.85	3.63	4.86	5.05				
MAMMA1002530	5.79	3.23	2.55	4.12	8.81	3.19	5.21	4.47	5.09				
MAMMA1002538	4.01	3.96	2.85	3.37	4.2	2.1	2.88	2.7	3.45				
MAMMA1002545	8.19	4.19	5.05	10.66	9.93	10.97	4.47	4.9	6.19	*	+		
MAMMA1002554	4	1.52	3.49	3.57	3.68	3.97	1.82	2.91	3.1				
MAMMA1002556	9.93	4.82	2.86	7.06	11.34	10.05	5.76	5.07	5.23				
MAMMA1002561	10.06	3.9	4.44	12.05	12.4	15.05	9.97	6.01	8.09	*	+		
MAMMA1002565	4.89	4.2	3.26	4.07	7.56	4.55	3.68	2.91	4.58				
MAMMA1002566	4	2.15	0.94	5.93	2.4	2.55	2.16	2.54	3.99				
MAMMA1002571	7.22	3.36	3.15	5.32	6.04	4.33	4.11	4.2	3.94				
MAMMA1002573	11.2	4.78	6.52	15.53	15.17	13.55	7.02	8.07	9.44	*	+		
MAMMA1002576	6.01	1.71	4.22	10.04	10.33	6.3	4	6.04	6.94				
MAMMA1002584	11.01	7.77	8.72	19.33	19.85	20.62	8.27	12.03	12.19	**	+		
MAMMA1002585	7.85	4.99	2.28	4.43	8.97	3.79	4.59	2.67	4.69				
MAMMA1002586	4.6	2.19	2.47	3.71	4.21	5.32	2.84	2.51	4.3				
MAMMA1002589	4.94	2.94	1.69	6.3	6.89	4.51	3.93	3.36	4.69				
MAMMA1002590	10.71	5.82	7.42	10.33	15.26	8.36	9.91	9.3	15.5				
MAMMA1002593	7.21	1.7	2.9	10.38	6.09	7.62	3.83	4.23	4.78				
MAMMA1002597	5.27	4.72	2.89	5.79	7.99	6.52	3.32	4.98	3.89				
MAMMA1002598	28.18	14.66	17.3	23.76	26.47	26.12	9.35	11.37	10.26				
MAMMA1002603	3.82	2.48	2.87	6.45	7.78	6.16	3.06	4.45	5.16	**	+		
MAMMA1002612	18.88	8.49	7.35	14.76	23.79	19.09	13.04	8.06	15.93				
MAMMA1002617	20.5	11.92	10.78	21.62	26.8	21.46	18.22	10.24	15.46				
MAMMA1002618	8.07	5.37	4.36	5.18	5.81	5.01	3.29	4.53	3.87				
MAMMA1002619	2.75	1.98	1.32	3.42	3.69	3.38	3.52	2.56	2.73	*	+		
MAMMA1002622	4.65	2.19	2.57	6.98	7.16	7	3.88	4.47	5.21	**	+		
MAMMA1002623	3.7	4.09	2.66	8.45	8.43	10.17	4.49	5.06	6.96	**	+		
MAMMA1002625	1.31	0.77	1.1	4.74	4.02	3.9	1.84	3.63	1.92	**	+		
MAMMA1002627	0.15	0.77	0.52	0.63	0.61	1.31	0.61	0.89	0.31				
MAMMA1002629	5	1.49	4.04	8.25	13.1	6.87	3.59	5.41	7.41				
MAMMA1002631	3.02	0.94	0.62	3.54	2.28	2	1.53	1.32	2.73				
MAMMA1002633	8.62	2.1	5.7	4.72	6.74	7.92	3.72	4.69	4.2				
MAMMA1002636	3.59	1.19	1.71	4.59	3.63	5.19	2.99	3.81	3.18				
MAMMA1002637	1.74	1.17	1.01	2.51	1.67	1.58	1.65	2.79	2.2				
MAMMA1002646	5.71	2.6	2.44	4.61	4.24	4.68	2.72	3.67	2.73				
MAMMA1002648	9.62	6.84	5.82	8.64	14.71	12.83	6.98	7.83	7.07				
MAMMA1002650	0.72	0.4	0.49	1.46	0.42	1.02	0.69	0.35	0.84				
MAMMA1002652	6.32	1.69	4.33	6.84	5.22	9.05	3.61	3.81	5.06				
MAMMA1002655	6.13	2.3	1.98	3.61	1.81	5.05	3.34	3.19	3.44				
MAMMA1002662	5.15	2.31	2.11	6.95	6.87	5.4	4.01	4.49	5.25	*	+		
MAMMA1002665	11.8	6.1	10.13	10.87	17.41	15.49	7.23	8.06	7.62				
MAMMA1002671	7.41	2.14	3.42	5.62	4.48	5.33	3.61	3.41	3.76				
MAMMA1002673	7.4	3.46	4.23	7.31	8.7	9.27	5.9	6.54	4.84				
MAMMA1002684	9.53	3.22	5.59	4.24	7.51	8.57	6.73	6.88	7.64				
MAMMA1002685	3.8	1.88	0.7	2.75	4.35	3.69	1.82	1.26	1				
MAMMA1002692	7.2	4.36	3.76	8	7.57	6.47	4.09	3.19	4.9				
MAMMA1002693	8.11	3.16	4.22	9.2	3.75	8.99	4.65	5.78	5.13				
MAMMA1002698	5.29	1.74	2.15	6.64	6.43	7.76	3.35	3.54	3.9	*	+		
MAMMA1002699	2.23	0.61	0.97	1.33	2.22	1.52	1.64	1.71	1.92				

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Table 225

MAMMA1002701	5.66	2.9	4.33	9.27	7.16	8.59	4.61	5.08	5.08	*	+		
MAMMA1002708	7.94	5.73	7.17	9.47	9.6	11.7	5.3	7.78	6.06	*	+		
MAMMA1002711	5.14	1.55	3.02	5.08	5.35	9.25	4.88	5.17	3.67				
MAMMA1002712	8.23	3.4	3.83	5.92	5.37	4.49	4.33	4.65	3.86				
MAMMA1002716	3.03	1.15	1.75	3.45	3.66	6.18	3.63	4.99	6.27			*	+
MAMMA1002721	5.09	3.43	2.39	8.57	10.12	9.06	4.73	4.05	4.78	**	+		
MAMMA1002723	3.9	1.75	1.64	3.74	4.55	4.64	2.71	2.75	3.13				
MAMMA1002727	1.94	0.37	0.28	1.65	1.68	1.6	1.31	1.6	1.09				
MAMMA1002728	18.85	12.15	13.58	19.57	15.85	19.98	10.65	11.63	8.96				
MAMMA1002742	24.64	11.73	11.42	17.86	18.78	18.95	12.46	17.75	16.29				
MAMMA1002743	3.32	1.38	1.48	2.64	3.77	2.84	1.3	3.55	2.08				
MAMMA1002744	5	2.18	1.83	8.37	6.2	7.98	3.63	3.32	2.37	*	+		
MAMMA1002746	2.51	0.63	0.79	1.49	2.16	1.83	2.14	1.51	0.81				
MAMMA1002748	3.99	1.96	1.48	3.96	2.53	5.35	2.11	2.64	2.6				
MAMMA1002754	3.27	1.38	1.23	3.72	4.67	3.51	3.5	2.37	3.36				
MAMMA1002758	1.75	1.23	0.68	1.23	1.77	1.88	1.75	1.78	0.81				
MAMMA1002762	15.53	11.07	16.89	14.23	17.23	16.31	8.35	12.66	9.99				
MAMMA1002764	6.2	2.6	2.93	8.75	9.77	8.81	4.73	4.74	4.79	*	+		
MAMMA1002765	4.28	1.57	1.43	2.94	4.93	4.38	2.62	3.87	2.62				
MAMMA1002769	1.56	0.46	0.63	2.76	2.64	1.76	3.07	2.6	2.53	*	+	**	+
MAMMA1002771	7.14	1.91	2.56	3.71	2.39	3.56	2.38	4.39	2.84				
MAMMA1002775	8.17	3.51	3.32	3.63	6.17	5.65	3.96	3.51	3				
MAMMA1002780	4.25	0.67	1.1	3.25	4.36	3.86	1.61	2.45	1.84				
MAMMA1002782	3.73	1.77	1.35	3.47	4.14	4.44	2.59	3.58	3.12				
MAMMA1002795	1.54	0.63	0.41	1.27	1.55	2.07	1.2	2.31	1.82				
MAMMA1002796	5.26	2.04	2.88	2.31	3.68	4.71	3.08	4.01	2.78				
MAMMA1002805	1.95	1.42	2.03	2.66	2.54	2.92	1.33	2.31	1.29	*	+		
MAMMA1002806	7.18	3.13	2.76	7.9	8.06	6.82	4.84	4.21	4.71				
MAMMA1002807	5.28	1.74	0.98	3.68	4.66	5.86	3.42	3.27	3.02				
MAMMA1002814	3.87	2.51	3.12	7.45	7.16	7.74	4.16	4.93	4.92	**	+	*	+
MAMMA1002817	1.7	0.51	0.6	1.42	1.13	1.4	0.99	1.61	0.6				
MAMMA1002820	1.34	1.92	0.86	2.57	2.4	3.83	1.38	1.74	1.69	*	+		
MAMMA1002830	27.11	10.85	16.25	30.04	35.58	32.67	18.44	20.75	20.74	*	+		
MAMMA1002833	6.78	4.02	4.05	10.31	9.78	13.03	4.43	6.24	5.25	*	+		
MAMMA1002835	3.11	0.73	1.29	2.37	4.3	3.68	1.9	2.74	1.11				
MAMMA1002838	5.08	1.94	1.5	7.62	5.02	5.3	2.99	3.7	3.52				
MAMMA1002842	6.45	2.71	2.75	6.39	9.1	5.17	5.25	5.53	5.55				
MAMMA1002843	4.18	1.22	2.78	4.36	3.92	4.27	2.84	3.41	2.54				
MAMMA1002844	15.29	8.97	10.98	13.02	14.25	13.61	12.26	13.86	18.37				
MAMMA1002845	0.94	0.26	0.38	2.62	1.75	2.18	15.33	12.73	11.67	**	+	**	+
MAMMA1002857	92.97	61.45	71.01	93.18	91.48	102.4	49.65	49.13	49.57				
MAMMA1002858	270.3	178.2	193.7	198.5	285	325.3	136.6	154.1	144.4				
MAMMA1002863	6.79	3.17	3.17	4.69	5.56	4.89	3.85	6.3	4.27				
MAMMA1002868	5.34	2.46	2.35	7.72	6.47	7.85	3.3	3.69	4.4	*	+		
MAMMA1002869	6.13	2.1	3.45	4.16	4.01	5.84	3.15	3.68	3.35				
MAMMA1002871	0.97	0.66	0.13	2.7	2.82	2.55	1.36	2.18	2.35	**	+	*	+
MAMMA1002875	4.77	2.06	2.53	6.78	7.19	6.9	3.55	3.8	4.77	*	+		
MAMMA1002879	3.84	2.9	2.39	3.98	5.13	4.33	4.2	4.17	4.62			*	+
MAMMA1002880	3.28	1.24	0.99	2.01	1.85	1.9	3.12	3.06	1.4				
MAMMA1002881	5.17	2.92	2.09	6.15	9.22	4.65	3.67	4.57	4.68				
MAMMA1002885	5.25	2.85	2.52	4.49	4.87	6.69	2.72	4.39	2.98				
MAMMA1002886	6.24	3.43	2.66	5.52	4.58	6.71	3.64	3.49	2.72				
MAMMA1002887	3.89	0.95	1	1.97	1.75	1.77	2.34	1.93	1.82				
MAMMA1002890	5.13	2.67	3.05	8.31	4.7	8.72	5.27	5.4	5.01				
MAMMA1002892	5.88	3.48	2.47	7.32	8.24	6.42	4.17	5.23	4.57	*	+		
MAMMA1002893	8.86	9.67	8.59	8.18	9.34	9.39	5.69	3.91	5.29			**	-

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Table 226

MAMMA1002895	1.52	1.02	0.66	3.67	2.82	2.63	1.68	3.27	1.67	**	+		
MAMMA1002898	5.3	1.67	2.43	5.04	3.66	3.54	3.19	4.2	4.28				
MAMMA1002905	7.3	4.24	4.9	4.36	3.31	5.5	4.49	4.07	7.6				
MAMMA1002906	7.09	3.55	2.11	4.13	4.15	4.17	3.6	4.08	4.37				
MAMMA1002908	5.1	3.63	2.55	7.12	10.01	7.24	3.97	3.94	6.08	*	+		
MAMMA1002909	11.19	2.36	4.9	18.65	20.5	19.49	11.96	9.14	7.19	**	+		
MAMMA1002918	8.8	4.28	4.36	7.71	4.97	6.64	4.29	3.86	3.85				
MAMMA1002925	3.35	2.63	1.48	9.46	7.99	8.84	13.12	8.46	14.83	**	+	**	+
MAMMA1002926	7.82	4.53	3.55	10.54	8.94	10.54	4.02	3.98	2.94	*	+		
MAMMA1002930	4.28	1.73	3.17	5.74	5.95	7.07	4.01	5.04	2.57	*	+		
MAMMA1002937	5.96	2.45	3.44	4.74	4.53	5.73	3.19	3.43	4.76				
MAMMA1002938	3.7	2.19	0.47	2.73	4.56	4.15	4.37	4.59	4.01				
MAMMA1002941	1.15	1.12	0.39	3.44	2.75	4.14	1.85	1.74	2.91	**	+	*	+
MAMMA1002947	6.2	1.75	2	3.69	4.63	4.41	4	2.74	2.53				
MAMMA1002964	3.13	0.8	1.6	3.89	5.54	5.2	2.56	3.32	2.95	*	+		
MAMMA1002967	2.77	0.81	0.72	2.65	3.25	3.1	2.15	2.36	2				
MAMMA1002970	10.68	5	6.77	15.62	18.38	19.77	9.12	10.6	10.22	**	+		
MAMMA1002971	5.36	1.91	2.72	5.34	4.3	4.54	3.53	5.4	3.71				
MAMMA1002972	3.58	1.23	1.8	5.51	3.48	3.8	2.78	4.51	3.78				
MAMMA1002973	3.05	2.45	2.19	5.84	7.86	5.49	3.04	3.4	3.84	**	+		
MAMMA1002979	49.45	21.28	20.21	54.78	50.04	57.56	26.52	29.51	38.14				
MAMMA1002982	1.17	0.84	0.21	1.07	1.04	1.44	0.75	0.85	2.52				
MAMMA1002987	2.51	2.1	1.94	4.65	4.24	4.32	2.66	3.22	2.69	**	+		
MAMMA1003003	6.44	2.24	3.39	6.63	8.14	8.81	3.38	3.94	4.55				
MAMMA1003004	2.44	1.12	1.78	4.34	4.64	5.27	2.45	2.33	3.36	**	+		
MAMMA1003007	3	0.97	0.37	1.72	3.13	2.66	1.67	2.02	2.34				
MAMMA1003011	6.89	3.86	2.58	10.11	6.23	6.02	5.56	4.68	6.89				
MAMMA1003013	4.71	2.5	3.6	5.96	2.57	4.98	4.47	2.47	4.04				
MAMMA1003015	3.11	1.7	0.83	3.85	3.23	4.39	2.92	3.35	3.6				
MAMMA1003019	1.94	0.48	0.77	1.44	1.99	1	1.47	1.37	1.39				
MAMMA1003020	4.98	3.11	2.83	4.85	4.06	4.94	3.36	4.67	2.34				
MAMMA1003026	2.22	1.04	1.33	2.17	1.21	1.23	1.15	1.94	1.66				
MAMMA1003031	10.83	4.3	5.89	8.39	13.69	12.78	6.3	8.07	8.55				
MAMMA1003033	4.26	3.18	1.65	3.05	5.95	7.17	2.79	4.73	3.1				
MAMMA1003035	9.17	3.04	2.57	6.09	5.43	4.4	3.27	3.33	2.99				
MAMMA1003039	2.73	0.66	0.77	3.23	4.07	2.57	2.03	1.92	2.63				
MAMMA1003040	5.92	4.5	4.4	12.47	14.15	15.98	6	7.82	5.59	**	+		
MAMMA1003044	5.54	1.89	2.06	8.57	6.1	5.51	3.66	3.75	3.73				
MAMMA1003047	24.49	9.27	14.52	16.47	16.89	16.3	13.85	12.65	14.22				
MAMMA1003049	1.66	0.7	0.16	1.59	1.6	1.36	1.06	0.97	1.99				
MAMMA1003055	3.44	1.83	1.31	3.88	3.78	5.3	1.65	3.16	2.91				
MAMMA1003056	3.11	0.29	1.13	1.54	2.14	2.78	1.67	3.29	1.4				
MAMMA1003057	4.22	3.06	2.41	5.23	4.85	4.4	3.28	3.47	3.84				
MAMMA1003066	4.41	2.68	2.13	7.59	8.47	7.26	3.45	3.84	3.94	**	+		
MAMMA1003075	2.52	1.24	0.49	2.49	1.99	2.02	1.98	1.74	1.75				
MAMMA1003089	3.39	2.37	1.55	7.01	9.09	5.24	3.86	3.79	4.04	*	+		
MAMMA1003092	2.28	2.1	0.75	1.76	2.8	2.59	1.29	2.14	0.99				
MAMMA1003095	3.31	3.21	2.49	5.68	6.41	6.17	3.79	3.05	2.04	**	+		
MAMMA1003099	4.62	1.71	1.38	5.27	3.36	5.17	3.64	4.12	3.25				
MAMMA1003102	4.98	1.87	1.62	3.02	1.85	3.96	2.26	3.51	2.66				
MAMMA1003104	3.42	0.58	0.51	3.71	2.62	2.21	2	1.93	0.79				
MAMMA1003113	7.31	2.8	2.6	2.96	4.59	4.44	3.67	4.2	3.98				
MAMMA1003126	5.27	3.19	2.59	5.46	4.59	6.5	4.92	4.89	5.03				
MAMMA1003127	3.2	0.92	0.9	2.49	3.46	2.32	2.81	3.43	2.3				
MAMMA1003131	14.8	5.77	8.64	6.66	11.84	10.58	7.76	9.54	7.3				
MAMMA1003135	2.29	0.95	1.03	2.13	1.48	2.22	0.96	2.28	1.38				

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Table 227

MAMMA1003140	1.69	0.85	0.6	1.74	1.79	2.62	1.07	1.84	1.32				
MAMMA1003146	3.17	0.64	1.39	1.41	2.11	2.74	2.14	2.47	2.39				
MAMMA1003150	14.6	5.76	6.23	12.63	11.24	8.45	5.72	10.32	7.8				
MAMMA1003154	8.12	5.17	3.61	5.99	6.38	3.91	3.93	4.78	3.8				
MAMMA1003155	3.73	2.43	2.74	2.68	3.2	4.47	4.25	3.56	2.96				
MAMMA1003157	3.72	2.17	1.5	8.43	9.53	5.52	5.81	5.42	4.11	*	+	*	+
MAMMA1003163	3.24	2.63	2.53	2.86	3.42	4.51	2.32	3.21	3.84				
MAMMA1003164	4.04	1.62	1.78	2.36	3.89	3.12	1.98	3.3	1.9				
MAMMA1003166	2.64	0.97	1.34	1.14	2.03	2.6	0.94	1.46	0.67				
NB9N31000010	14.76	5.71	8.03	2.59	3.65	2.88	2.38	3.3	2.11				
NB9N31000016	7.03	5.06	4.31	4.14	3.19	3.67	2.48	3.3	3.54				
NB9N31000043	6.43	3.37	2.66	3.6	4.63	3.3	4.03	4.8	3.85				
NB9N31000045	19.15	14.02	9.92	7.25	11.2	10.47	9.72	9.74	10.85				
NB9N31000054	6.46	2.26	2.68	6.57	6.74	6.4	6.39	5.01	4.4				
NB9N31000076	2.64	1.86	1.23	4.27	5.28	5.06	3.51	3.29	3.06	**	+	*	+
NB9N31000086	3.3	1.41	1.24	4.91	5.73	5.78	4.03	3.25	4.37	**	+		
NT2RM1000001	3.65	2.34	1.78	2.42	3.06	4.27	1.46	2.56	2.65				
NT2RM1000018	18.02	4.88	9.18	11.8	18.97	15.96	10.32	8.58	7.34				
NT2RM1000032	2.53	0.99	1.56	3.18	2.12	2.58	1.32	2.6	2.8				
NT2RM1000035	11.4	5.02	6.42	9.17	9.42	10.51	8.5	7.07	7.86				
NT2RM1000037	13.15	8.99	9.27	10.68	10.22	12.08	8.43	7.97	9.91				
NT2RM1000039	11.18	9.88	11.7	14.16	13.27	16.95	11.97	10.55	15.86	*	+		
NT2RM1000042	80.13	61.43	48.95	80.07	94.16	101.1	34.69	35.38	37.43			*	-
NT2RM1000055	1.63	0.44	0.19	1.9	1.2	1.06	0.56	1.65	0.56				
NT2RM1000059	10.72	6.4	6.93	10.31	13.85	13	8.96	10.38	10.03				
NT2RM1000062	2	0.27	0.62	1.05	1.09	1.16	1.09	1.18	1.04				
NT2RM1000065	113.3	91.26	69.94	64.48	58.5	52.5	34.11	33.99	50.67			*	-
NT2RM1000066	35.22	18.22	21.68	21.61	23.29	23.48	22.94	24.27	17.75				
NT2RM1000071	63.91	66.46	45.7	62.4	99.26	85.6	34.56	28.87	36.37			*	-
NT2RM1000080	3.9	1.47	1.12	2.18	2.14	2.55	1.54	2.09	2.44				
NT2RM1000086	19.75	10.02	12.84	15.85	21.11	21.57	16.5	12.7	16.82				
NT2RM1000092	3.84	1.47	1.22	4.35	3.45	3.58	5.38	4.65	2.8				
NT2RM1000118	0.16	0.1	0.44	0.44	0.48	0.43	0.45	1.71	0.2				
NT2RM1000119	1.47	0.16	1.14	1.49	1.8	1.27	0.45	3.87	1.63				
NT2RM1000121	3.95	2.18	1.02	2.75	2.63	2.42	2.12	2.47	2.71				
NT2RM1000122	20.69	10.42	10.67	11.66	9.11	15.06	12.71	8.89	10.81				
NT2RM1000127	3.09	0.8	1.57	1.55	1.35	2.79	1.74	2.29	1.61				
NT2RM1000131	1.39	0.57	0.54	0.93	0.82	1.7	1.32	1.99	1.76				
NT2RM1000132	3.41	2.17	2.19	3.36	2.6	3.36	3.07	3.21	1.8				
NT2RM1000153	2.4	1.2	1	2.3	1.9	1.72	2.33	2.75	1.99				
NT2RM1000184	12.46	9.34	11.07	12.61	11.31	13.35	27.02	24.07	25.86			**	+
NT2RM1000186	0.96	0.05	1.17	1.92	0.66	0.6	1.01	1.84	0.71				
NT2RM1000187	7.97	7.07	3.88	7.69	10.3	6.3	4.37	5.12	5.93				
NT2RM1000199	2.43	1.17	0.94	2.23	1.56	2.06	2.22	2.21	0.97				
NT2RM1000213	4.77	2.05	1.72	5.31	3.68	5.55	3.01	2.88	2.04				
NT2RM1000215	22.27	12.67	13.12	16.61	13.19	18.25	21.54	17.2	19.32				
NT2RM1000218	4.96	1.49	2.25	6.26	5.56	5.79	6.91	7.15	6.31			*	+
NT2RM1000224	14.47	7.85	6.71	14.79	9.45	14.6	5.58	5.7	6.61				
NT2RM1000236	11.3	7.18	4.01	4.18	3.11	5.39	11.74	17.39	13.83				
NT2RM1000242	-0.07	0.1	-0.14	0.21	0.11	0.96	0.08	1.21	-0.15				
NT2RM1000244	3.77	1.77	0.73	1.27	1.58	1.27	0.95	0.89	0.64				
NT2RM1000252	31.79	17.18	15.85	26.05	28.99	28.97	19.44	15.24	17.84				
NT2RM1000256	20.24	12.26	8.91	9.14	16.96	11.49	13.69	10.22	13.24				
NT2RM1000257	16.34	9.13	9.74	4.83	6.53	7.09	5.1	3.9	3.96			*	-
NT2RM1000260	32.33	14.76	16.72	33.82	31.04	33.35	23.69	23.35	23.61				
NT2RM1000269	12.22	8.71	9.44	5.25	3.16	4.72	1.74	2.23	1.16	**	-	**	-

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Table 228

NT2RM1000271	0.75	0.2	0.04	1.21	0.35	0.58	0.94	0.84	0.49				
NT2RM1000272	54.56	36.55	40.59	39.42	48.05	51.89	35.16	41.56	36.18				
NT2RM1000273	25.51	11.38	15.12	14.18	12.87	14.49	8.99	9.27	12				
NT2RM1000274	58.21	39.03	46.94	45.24	44.74	49.05	21.9	22.39	26.39			*	-
NT2RM1000280	3.79	2.05	1.14	3.65	3.57	2.6	4.36	3.9	4.03				
NT2RM1000295	1.04	0.33	0.49	1.43	1.42	1.12	1.49	1.59	1.89	*	+	*	+
NT2RM1000300	3.37	1.19	1.93	2.35	3.27	3.66	2.84	2	3				
NT2RM1000304	119.7	75.04	105.1	129.6	102.4	124.9	50.36	59.48	58.8			*	-
NT2RM1000314	14.79	10.41	9.09	12.21	10.45	12.98	11.38	9.76	12.93				
NT2RM1000318	24.15	19.1	20.62	18.95	25.93	22.36	13.38	12.74	12.13			**	-
NT2RM1000335	2.7	1.54	1.86	2.64	0.98	2.51	2.11	1.75	0.87				
NT2RM1000341	1.86	1.47	0.19	1.35	0.97	1.03	1.64	1.09	1.69				
NT2RM1000350	12.53	6.61	5.41	9.68	8.63	6.11	10.39	8.69	12.6				
NT2RM1000354	1.42	1.08	1.09	1.11	0.94	2.05	1.14	0.93	0.85				
NT2RM1000355	24.12	12.19	10.53	22.94	22.89	22.53	40.93	26.81	41.82			*	+
NT2RM1000361	3.67	1.47	2.35	2.55	2.08	2.7	1.88	1.68	2.1				
NT2RM1000365	1.06	0.28	0.15	0.8	0.83	1.19	0.3	0.84	1.1				
NT2RM1000372	20.32	11.77	14.09	12.5	15.42	19.07	11.35	13.11	12.12				
NT2RM1000377	4.71	2.13	0.97	3.33	3.33	3.84	3.13	2.47	2.45				
NT2RM1000388	4.08	1.38	1.89	2.94	1.24	2.04	2.06	1.76	3.15				
NT2RM1000394	1.97	0.69	0.13	1.46	1.54	2.03	0.91	0.83	1.86				
NT2RM1000399	1.06	0.34	0.04	1.59	1.17	1.07	1.01	1.52	1.09				
NT2RM1000407	3.28	1.69	1.8	2.92	2.58	2.42	3.74	2.39	2.69				
NT2RM1000421	1.21	0.17	0.31	0.84	0.59	1.24	0.64	0.87	1.2				
NT2RM1000422	184.9	121.2	142.5	178.6	203	174.3	67.17	77.47	67.99			*	-
NT2RM1000430	2.25	0.23	1.58	0.73	1.22	1.54	1.8	1.12	1.6				
NT2RM1000462	11.14	6.84	5.58	14.5	17.82	8.39	4.89	8.25	6.36				
NT2RM1000499	5.37	2.3	2.51	3.94	5.62	7.36	4.89	3.83	3.47				
NT2RM1000512	22.47	26.43	20.07	26.5	33.66	27.9	17.58	19.86	18.1				
NT2RM1000519	29.78	19.56	14.02	7.45	11.19	11.75	14.89	14.37	13.43				
NT2RM1000527	18.16	11.14	6.22	5.88	7.16	7	1.98	1.37	2.55			*	-
NT2RM1000539	12.49	8.93	7.21	6.18	6.43	8.69	2.33	4.94	2.74			*	-
NT2RM1000542	5.88	1.72	2.37	3.23	3.3	5.23	2.07	2.93	2.21				
NT2RM1000553	3.65	0.83	1.64	1.16	1.39	3.69	1.46	2.07	1.37				
NT2RM1000555	54.21	28.45	27.23	49.44	36.73	39.14	24.87	25.09	25.78				
NT2RM1000558	5.67	1.77	2.83	4.02	2.67	3.58	2.91	2.6	1.85				
NT2RM1000563	5.22	2.56	1.89	2.43	2.32	3.96	2.78	2.56	3.17				
NT2RM1000566	7.28	3.71	3.24	1.61	1.5	1.27	1.81	1.72	3.16				
NT2RM1000570	26.49	17.4	16.59	16.76	14.37	17.79	32.95	44.77	33.54			*	+
NT2RM1000571	6.81	1.94	3.76	2.38	2.48	3.22	3.14	4.7	3.91				
NT2RM1000574	1.29	0.74	0.74	1.47	2.46	0.57	1.31	2.11	1.66				
NT2RM1000580	1.69	0.26	0.99	1.9	0.77	2.4	1.57	1.93	1.37				
NT2RM1000620	10.67	5.15	5.67	13.49	19.91	14.9	8.69	7.05	7.31	*	+		
NT2RM1000623	1.16	0.68	-0.02	1.17	0.81	0.94	0.79	1.05	0.97				
NT2RM1000630	2.05	1.24	0.77	1.67	2.19	1.83	1.87	1.47	1.67				
NT2RM1000633	27.41	17.8	20.59	31.5	32.02	35.16	25.03	10.45	15.13	*	+		
NT2RM1000634	2.52	1	0.44	1.48	1.48	2.34	1.07	2.17	0.81				
NT2RM1000642	6.47	2.65	3.78	2.95	2.59	5.44	3.92	6.2	4.71				
NT2RM1000647	37.58	16.74	23.8	20.92	20.8	27.77	21.56	20.3	24.27				
NT2RM1000648	2.04	0.41	0.84	1.58	1.79	2.24	1.08	2.71	1.07				
NT2RM1000650	3.85	1.26	1.26	3.06	2.28	2.37	2.52	2.44	1.64				
NT2RM1000661	6.75	4.13	3.51	3.45	3.05	3.31	3.37	4.05	2.46				
NT2RM1000666	25.38	12.8	15.49	0.79	0.92	0.69	0.89	0.98	0.83	*	-	*	-
NT2RM1000669	3.69	1.54	2.15	2.54	2.09	3.44	2.17	1.76	1.75				
NT2RM1000672	18.91	9.34	13.85	40.77	46.8	48.09	11.37	11.65	12.71	**	+		
NT2RM1000681	7.08	2.25	3.13	16.21	18.15	17.39	29.47	23.33	30.9	**	+	**	+

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Table 229

NT2RM1000691	1.49	0.33	0.72	2.19	3.8	4.38	1.16	2.44	1.23	*	+		
NT2RM1000698	9.46	4.02	2.95	1.73	2.75	2.69	1.76	3.25	2.56				
NT2RM1000699	5.92	1.52	1.15	3.89	3.52	2.89	2.18	3.43	1.91				
NT2RM1000702	6.62	2.57	3.45	4.5	3.42	3.78	4.09	2.32	3.62				
NT2RM1000703	17.1	15.01	10.3	10.55	11.96	11.61	8.87	8.94	9.74				
NT2RM1000704	65.68	42.42	42.04	15.75	17.49	15.71	13.71	12.1	16.78	*	-	*	-
NT2RM1000725	2.89	1.28	2.86	8.31	19.48	14.98	22.1	28.8	20.7	*	+	**	+
NT2RM1000726	2.12	1.3	1.96	2.34	2.21	3.46	1.65	2.75	1.67				
NT2RM1000731	5.27	2.15	2.93	3.31	4.19	2.99	4.88	3.29	2.95				
NT2RM1000741	1.93	0.67	1.46	0.89	1.2	1.46	1.17	1.5	1.29				
NT2RM1000742	23.68	12.81	12.51	8.34	8.53	8.89	7.58	8.47	7.71				
NT2RM1000744	6.58	2.57	2.31	5.25	4.4	4.66	2.69	3.48	4.72				
NT2RM1000746	6.6	3.69	2.39	2.21	4.12	4.39	2.87	3.97	3.11				
NT2RM1000747	7.04	3.26	3.4	5.08	4.8	5.81	8.95	8.11	9.87			*	+
NT2RM1000752	2.53	0.89	1.4	2.34	2.42	2.14	1.42	2.26	1.37				
NT2RM1000767	7.61	2.5	4.43	7.29	7.21	8.59	10.72	8.37	9.7			*	+
NT2RM1000770	5.9	2.04	3.1	5.61	2.94	6.75	3.14	3.37	3.76				
NT2RM1000772	2.24	0.1	0.45	1.66	1.02	0.57	0.12	1.61	0.68				
NT2RM1000779	21.92	14.11	10.14	21.3	25.71	21.61	29.07	21.85	26.85				
NT2RM1000780	3.49	1.84	0.6	4.74	3.37	4.7	3.33	3.29	1.67				
NT2RM1000781	0.57	0.24	0.41	1.11	0.76	1.25	0.94	2.16	0.86	*	+		
NT2RM1000789	3.24	2.46	2.34	3.02	3.98	4.62	2.09	4.84	3.17				
NT2RM1000800	7.44	3.44	7.11	8.01	9.85	8.74	6.51	5.53	7.87				
NT2RM1000802	9.35	5.25	6.84	5.12	5.47	5.85	9.59	9.36	9.75				
NT2RM1000811	0.9	0.16	0.89	1.36	1.11	1.28	0.91	1.35	0.23				
NT2RM1000826	26.11	13.59	16.15	23.62	25.62	25.75	12.43	12.08	10.27				
NT2RM1000829	4.42	3.56	2.62	8.2	6.8	9.18	6.67	6.07	6.37	**	+	**	+
NT2RM1000831	96.56	76.65	61.3	78.41	75.7	87	48.08	33.56	47.08			*	-
NT2RM1000833	6.27	2.21	1.64	3.09	3.54	4.73	6.47	7.68	4.1				
NT2RM1000834	4.84	2.51	2.09	5.62	3.9	3.49	3.8	5.68	4.28				
NT2RM1000841	32.04	19.08	20.07	17.66	18.86	19.57	17.83	9.4	13.52				
NT2RM1000848	22.37	12.31	11.25	14.54	11.17	13.09	8.36	10.63	15.1				
NT2RM1000850	1.25	0.36	0.94	1.01	0.67	1.33	1.5	1.94	1.75			*	+
NT2RM1000852	3.74	0.76	1.24	2.68	2.43	2.34	2.39	3.1	1.87				
NT2RM1000853	1.46	0.57	0.14	1.6	2.87	1.74	1.25	0.52	1.87				
NT2RM1000855	19.04	8.47	10.06	15.32	18.2	15.69	26.5	18.76	20.5				
NT2RM1000857	20.9	10.06	10.76	20.92	27.84	24.62	16.83	13.46	17.36				
NT2RM1000858	22.68	8.04	9.94	22.93	26.24	26.47	20.88	15.02	18.54				
NT2RM1000867	15.69	9.11	9.26	15.56	10.14	14.92	15.07	11.26	10.73				
NT2RM1000874	9.77	5.6	5.03	6.49	6.79	8.79	8.74	7.92	8.94				
NT2RM1000882	4.01	2.76	2.65	5.69	5.23	6.94	2.13	4.39	2.7	*	+		
NT2RM1000883	17.32	10.68	13.68	15.2	15.74	17.32	14.61	9.93	20.96				
NT2RM1000885	31.05	13.08	10.39	19.2	20.71	27.92	20.23	18.36	23.03				
NT2RM1000893	3.73	1.65	2.82	3.47	1.63	2.22	4.97	4.49	6.3			*	+
NT2RM1000894	14.4	9.62	11.92	7.88	9.3	10.29	9.51	9.36	13.18				
NT2RM1000898	2.53	0.85	1.96	3.01	2.71	4.11	3.76	3.77	6.2			*	+
NT2RM1000899	1.45	0.26	1.26	1.48	1.2	1.14	1.07	1.69	0.72				
NT2RM1000905	55.04	22.33	30.63	36.24	41.24	41.41	17.87	22.74	23.3				
NT2RM1000910	7.05	2.93	6.34	6.29	7.41	5.83	7.31	6.05	5.79				
NT2RM1000914	8.32	4.94	2.32	6.53	12.83	8.37	4.34	8.86	6.23				
NT2RM1000919	4.65	2.11	2.49	5.45	3.02	4.5	2.58	2.81	4.74				
NT2RM1000921	2.3	0.73	0.47	1.57	1	2.01	1.98	1.39	1.88				
NT2RM1000922	7.7	4.51	3.3	6.07	5.41	6.35	3.4	3.21	3.38				
NT2RM1000924	3.33	1.7	1.15	2.35	2.35	2.87	1.24	2.25	1.77				
NT2RM1000927	3.83	1.15	1.76	5.16	2.77	6.27	2.3	3.24	2.14				
NT2RM1000951	8.45	4.91	4.93	9.07	6.69	6.96	5.29	7.06	3.5				

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Table 230

NT2RM1000956	16.88	9.05	9.11	8.8	11.37	15.79	15.38	17.86	10.86				
NT2RM1000960	13.57	6.62	8.78	22.97	30.24	31.63	21.49	20.35	17.47	**	+	*	+
NT2RM1000961	4.69	3.03	1.81	5.01	3.8	5.09	4.95	2.93	3.68				
NT2RM1000962	10.02	5.16	7.78	8.82	8.11	7.03	6.17	4.67	6.47				
NT2RM1000973	24.68	15.4	13.27	17.56	15.99	16.81	11.83	13.98	10.68				
NT2RM1000978	0.62	0.04	-0.01	0.17	0.58	0.51	0.69	0.66	1.52				
NT2RM1000982	2.39	1.7	1.71	1.03	0.94	2.7	1.35	1.92	1.56				
NT2RM1000991	4.41	2.48	1.07	2.93	3.33	3.07	1.23	1.71	2.43				
NT2RM1000994	8.78	4.48	6.65	3.77	4.2	8.32	4.28	3.9	4.29				
NT2RM1001002	11.56	5.39	7.09	9.93	9.4	9.55	4.65	6.66	4.14				
NT2RM1001003	9.4	5.64	4.27	5.67	5.91	6.46	6.24	6.75	4.66				
NT2RM1001008	1.85	1.09	0.94	1.76	1.19	2.21	0.79	1.95	1.36				
NT2RM1001011	8.02	5.18	3.04	5.49	6.15	5.88	8.36	7.88	8.53				
NT2RM1001013	2.47	1.58	1.45	1.29	3.7	3.05	2.27	3.51	2.54				
NT2RM1001017	2.77	1.58	1.89	1.79	2.82	2.34	1.35	1.86	1.5				
NT2RM1001018	31.03	16.64	15.26	25.69	26.32	22.96	12.01	17.57	15.08				
NT2RM1001026	5.92	2.62	3.94	6.27	6.63	8.85	2.75	5.72	4.3				
NT2RM1001028	3.4	0.93	2.15	2.01	2.78	3.77	1.36	3.31	2.13				
NT2RM1001043	15.05	7.93	6.39	4.61	4.5	5.16	5.79	4.43	5.13				
NT2RM1001044	4.89	2.09	2.59	3.97	3.59	4.24	2.42	2.42	2.72				
NT2RM1001059	2.09	0.86	1.15	1.37	1.59	1.67	1.46	1.35	0.96				
NT2RM1001063	2.45	1.26	1.65	1.46	2.05	1.8	2.13	2.29	2.06				
NT2RM1001066	1.88	0.18	0.47	1.26	1.05	1.21	0.72	1.03	1.71				
NT2RM1001072	1.32	0.2	0.66	1.3	1.67	2.06	1.25	1.37	0.66				
NT2RM1001074	3.05	0.93	1.31	1.69	2.05	3.12	1.02	1.75	1.85				
NT2RM1001076	1.54	0.37	0.75	0.28	0.39	1.03	0.31	0.72	0.38				
NT2RM1001082	6.04	3.83	2.77	7.68	5.09	7.64	2.86	4.04	3.38				
NT2RM1001085	2.68	0.85	0.53	1.55	1.52	1.92	1.8	2.19	0.8				
NT2RM1001092	7.52	3.6	5.96	8.95	10.4	8.32	6.31	3.61	6.43				
NT2RM1001102	3.26	0.53	1.68	1.38	1.75	2.72	1.2	2.01	1.94				
NT2RM1001103	0.88	0.73	0.28	3.91	4.58	4.4	2.72	2.34	1.98	**	+	**	+
NT2RM1001105	1	0.24	0.43	1.87	1.39	1.31	0.88	1.29	1.26	*	+		
NT2RM1001112	2.67	1.09	1.84	2.3	1.58	2.94	0.99	2.93	1.7				
NT2RM1001115	4.95	1.32	1.99	4.02	5.02	6.62	3.14	4.83	3.48				
NT2RM1001122	8.5	4.16	3.4	8.68	4.04	8.48	4.45	3.73	3.94				
NT2RM1001136	4.05	1.12	0.91	2.5	2.13	2.13	2.47	2.49	2.41				
NT2RM1001139	6.27	3.92	2.62	3.53	3.94	4.14	5.81	5.51	4.63				
NT2RM2000003	2.91	3.18	0.75	4.84	2.4	1.79	5.06	2.26	0.96				
NT2RM2000006	5.44	1.69	3.43	6.16	4.98	7.47	3.88	4.21	4.64				
NT2RM2000010	9.71	5.56	5.39	7.07	8.33	10.49	7.05	5.99	5.68				
NT2RM2000013	2.55	2.71	2.44	3.49	3.87	4.31	1.27	2.57	2.16	**	+		
NT2RM2000030	4.2	1.71	3.04	3.74	3.15	4.87	1.68	3.63	1.98				
NT2RM2000032	14.54	8.15	3.59	5.5	2.42	5.43	3.03	2.67	4.06				
NT2RM2000039	7.04	3.95	5.72	5.91	6.33	6.41	4.47	6.78	5.88				
NT2RM2000042	1.29	2.29	1.74	1.36	3.51	3.21	7.29	2.12	2.85				
NT2RM2000092	8.22	4.26	4.76	1.43	1.14	1.72	2.08	1.91	0.73	*	-	*	-
NT2RM2000093	5.44	2.68	4.48	6.31	4.11	9.84	5.21	4.37	5				
NT2RM2000101	5.58	2.71	2.34	4.26	5.98	6.15	4.54	4.36	4.29				
NT2RM2000104	4.75	4.44	4.18	5.66	3.53	4.65	2.85	2.72	1.51			*	-
NT2RM2000124	3.3	1.98	1.26	2.86	2.54	1.84	2.16	2.28	2.14				
NT2RM2000155	2.24	1.76	1.1	2.45	4.74	4	2.88	2.71	3.03			*	+
NT2RM2000191	16.4	9.01	10.98	10.77	15.67	11.6	7.34	7.57	8.37				
NT2RM2000192	3.67	3.12	2.39	2.43	2.62	2.15	1.03	2.04	1.36			*	-
NT2RM2000239	6.19	3.2	3.93	5.19	4.97	5.78	6.05	5.06	6.76				
NT2RM2000240	21.06	15.5	8.47	21.89	29.21	21.68	13.11	14.37	17.25				
NT2RM2000241	6.65	3.31	3.03	7.38	6.29	6.04	4.13	7.91	5.35				

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Table 231

NT2RM2000250	6.85	2.87	3.45	6.74	6.95	8.42	4.64	4.72	5.57				
NT2RM2000259	9.6	4.08	4.77	6.02	9.47	7.13	5.19	6.42	6.9				
NT2RM2000260	9.93	9.2	6.51	4.88	7.9	8.73	11.23	8.04	9.57				
NT2RM2000265	2.4	1.14	0.66	1.28	0.86	1.86	1.3	1.27	1.08				
NT2RM2000287	10.73	4.68	6.12	10.38	10.35	12.59	6.93	10.27	8.06				
NT2RM2000306	16.48	15.91	13.02	16.75	16.33	10.75	17.88	8.38	16.11				
NT2RM2000312	57.19	46.28	42.21	59.66	41.08	60.14	43.74	21.02	32.47				
NT2RM2000322	6.45	2.73	3.3	5.49	4.98	2.77	3.63	4.55	3.78				
NT2RM2000343	5.35	4.3	5.69	10.01	10.47	9.81	6.04	4.74	6.91	**	+		
NT2RM2000359	5.94	2.73	3.95	5.3	4.77	4.66	3.08	3.35	2.77				
NT2RM2000362	15.37	16.06	11.14	15.03	19.07	17.41	12.3	11.08	9.04				
NT2RM2000363	2.27	1.12	1.53	3.15	1.57	1.39	1.27	1.95	1.06				
NT2RM2000368	20.14	10.44	9.67	11.84	14.77	11.87	10.3	9.5	10.03				
NT2RM2000371	111	74.6	73.79	116.3	62.15	121.3	50.3	42.75	56.01			*	-
NT2RM2000374	4.78	2.52	1.94	6.65	5.32	5.42	4.66	3.93	3.68	*	+		
NT2RM2000387	11.91	6.37	5.79	20.24	13.27	20.63	9.51	12.58	11.14	*	+		
NT2RM2000393	3.45	1.01	1.83	2.71	1.61	3.18	1.81	3.53	1.53				
NT2RM2000395	1.44	0.49	0.91	2.24	0.76	1.26	1.08	2.52	0.72				
NT2RM2000402	7.26	1.87	2.95	6.33	6.77	7.71	5.51	6.64	5.38				
NT2RM2000405	5.34	2.42	2.76	3.26	3.78	4.88	2.25	2.56	2.19				
NT2RM2000407	19.34	9.57	10.6	5.59	9.51	9.38	8.65	7.51	10.04				
NT2RM2000410	3.06	1.14	0.97	2.09	2.96	2.28	2.57	1.94	2.16				
NT2RM2000420	4.52	1.56	1.71	6.72	7.81	5.85	4.96	3.72	3.6	*	+		
NT2RM2000422	14.32	4.96	7.79	15.68	12.45	9.99	14.38	10.45	10.29				
NT2RM2000423	3.93	2.29	3.18	9.3	10.31	11.58	4.01	3.67	2.37	**	+		
NT2RM2000452	4.1	1.67	3.69	10.71	9.43	9.18	6.96	4.45	5.45	**	+		
NT2RM2000469	1.22	0.59	0.27	2.22	1.54	1.32	1.52	1.06	1.82				
NT2RM2000490	4.98	2.59	1.93	4.39	4.04	3.10	5.95	3.52	4.92				
NT2RM2000497	2.77	1.77	1.58	7.44	5.74	5.87	2.86	3.26	4.3	**	+		
NT2RM2000502	4.18	2.99	2.68	7.32	4.36	3.54	3.69	2.68	5.35				
NT2RM2000504	2.49	1.56	2.01	5.06	3.93	4.92	5.83	4.60	4.88	**	+	**	+
NT2RM2000514	5.60	3.19	3.45	8.34	7.66	5.47	4.66	4.70	6.69				
NT2RM2000522	0.63	0.58	0.61	1.36	0.80	1.01	0.53	0.67	1.87				
NT2RM2000540	5.03	4.07	2.80	5.25	6.86	2.78	4.31	3.32	4.3				
NT2RM2000556	0.38	0.75	0.50	1.40	1.96	0.69	3.19	0.77	0.73				
NT2RM2000565	4.89	2.53	3.37	4.40	4.50	4.25	5.66	3.06	4.57				
NT2RM2000566	5.85	4.38	3.46	8.37	5.27	4.67	4.65	4.38	5.92				
NT2RM2000567	4.29	3.05	2.89	4.78	3.00	1.68	3.19	2.38	4.64				
NT2RM2000569	6.50	3.15	2.85	8.65	8.54	6.48	4.57	3.91	4.43				
NT2RM2000577	11.83	4.68	6.45	6.50	8.99	3.96	4.84	6.67	8.79				
NT2RM2000581	6.47	3.33	5.21	7.46	8.40	4.99	4.74	5.34	7.76				
NT2RM2000582	5.88	3.81	3.49	9.44	7.98	6.09	7.69	6.61	8.15	*	+	*	+
NT2RM2000588	22.92	13.30	11.99	23.97	16.17	19.54	16.8	11.46	18.28				
NT2RM2000589	11.18	6.26	6.74	9.54	8.57	7.04	5.39	6.22	7.18				
NT2RM2000594	11.31	9.59	11.31	3.91	4.21	3.25	3.27	3.48	2.37	**	-	**	-
NT2RM2000599	22.01	15.12	17.66	19.78	24.09	21.66	15.2	13.93	15.24				
NT2RM2000609	2.49	1.70	2.43	4.47	3.94	3.24	1.96	3.24	2.3	*	+		
NT2RM2000612	3.82	2.55	2.84	4.46	7.55	3.95	4.78	3.73	4.27				
NT2RM2000622	8.85	7.06	10.37	13.55	16.80	10.42	7.83	8.92	10.48				
NT2RM2000623	23.78	13.14	15.60	19.91	22.53	23.26	22.22	15.23	19.45				
NT2RM2000624	16.48	10.64	4.76	11.37	17.12	10.30	8.76	8.23	137.7				
NT2RM2000632	5.44	2.83	2.35	3.85	3.76	2.79	2.22	2.21	7.42				
NT2RM2000635	2.91	2.32	2.35	7.82	9.57	5.76	5	4.36	4.83	**	+	**	+
NT2RM2000636	3.87	2.82	3.19	5.69	5.77	3.68	4.63	3.86	4.55				
NT2RM2000639	4.56	3.86	3.29	4.47	7.45	4.02	3.6	6.93	4.67				
NT2RM2000649	4.09	4.81	3.74	4.86	8.90	5.64	4.74	5.82	6.57				

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Table 232

NT2RM2000658	7.80	7.19	11.39	10.12	9.62	7.80	6.87	5.57	7.23				
NT2RM2000660	27.64	11.87	13.50	20.31	25.06	18.91	13.54	13.65	15.55				
NT2RM2000669	7.79	4.71	4.17	9.97	13.43	8.55	3.67	4.50	6.66				
NT2RM2000689	29.82	30.60	28.82	42.51	72.34	55.67	22.11	19.71	38.62	*	+		
NT2RM2000691	4.67	3.54	3.74	5.23	6.41	4.14	4.29	3.98	4.19				
NT2RM2000714	13.27	8.60	10.19	9.82	10.81	9.42	13.37	9.65	17.53				
NT2RM2000718	1.36	1.54	1.09	3.28	7.10	3.02	2.42	2.48	2.19			**	+
NT2RM2000732	6.10	4.20	5.69	12.72	15.74	11.49	5.7	6.42	7.79	**	+		
NT2RM2000735	24.38	15.21	20.46	56.19	49.62	47.05	16.37	24.66	27.14	**	+		
NT2RM2000740	6.48	2.95	2.62	6.53	5.49	3.44	3.93	3.46	2.74				
NT2RM2000743	21.35	12.67	14.35	10.73	9.73	9.68	2.24	1.81	2.16			**	-
NT2RM2000772	11.89	7.81	9.52	17.15	14.77	14.45	6.23	7.95	10.31	*	+		
NT2RM2000773	11.75	6.40	6.69	9.73	11.32	9.29	9.82	8.51	8.01				
NT2RM2000776	12.66	6.48	11.36	17.08	19.56	14.42	12.22	8.19	11.56	*	+		
NT2RM2000784	11.22	7.09	6.83	7.88	10.63	6.42	6.22	6.90	7.64				
NT2RM2000795	9.52	5.29	6.34	17.74	18.61	15.80	6.53	8.43	10.09	**	+		
NT2RM2000796	27.57	17.52	26.46	2.02	2.40	3.17	1.82	2.65	1.66	**	-	**	-
NT2RM2000798	14.84	8.16	10.91	45.29	27.47	24.14	26.69	20.97	28.82	*	+	**	+
NT2RM2000801	37.70	23.20	28.38	26.35	37.85	28.51	31.37	32.22	38.5				
NT2RM2000821	3.67	2.04	2.27	8.85	6.90	6.15	5.86	5.63	5.4	**	+	**	+
NT2RM2000829	36.66	22.85	41.47	29.93	25.94	16.17	15.48	17.92	19.23			*	-
NT2RM2000837	5.77	3.15	3.99	6.12	6.76	5.46	5.15	4.55	4.39				
NT2RM2000924	6.69	5.13	4.70	12.18	14.72	8.21	5.5	6.80	8.89	*	+		
NT2RM2000930	14.27	7.36	9.58	15.72	15.41	13.15	7.93	7.73	11.49				
NT2RM2000937	2.93	2.09	3.52	5.00	4.64	3.14	1.89	3.58	2.8				
NT2RM2000939	6.56	3.88	4.32	5.94	7.25	6.23	4.34	5.73	5.56				
NT2RM2000942	141.00	79.29	113.17	107.50	122.19	108.41	73.07	66.91	67.18				
NT2RM2000951	4.09	2.69	2.78	3.88	3.40	4.39	3.48	3.83	3.33				
NT2RM2000952	5.14	3.58	3.50	6.02	4.82	4.48	3.55	3.67	3.9				
NT2RM2000966	11.75	10.12	10.87	9.00	11.41	11.06	9.18	10.30	5.82				
NT2RM2000973	22.49	16.16	17.58	24.24	28.57	21.97	14.32	17.17	15.94				
NT2RM2000983	10.51	6.87	10.06	15.15	16.05	11.81	9.62	13.40	12.47	*	+		
NT2RM2000984	3.34	2.49	1.94	4.17	6.33	3.91	3.14	3.09	3.89				
NT2RM2000994	17.72	5.91	15.58	25.00	22.32	16.64	8.13	8.32	6.15				
NT2RM2001004	6.95	4.49	3.43	6.09	8.10	5.86	5.16	4.92	6.83				
NT2RM2001022	113.50	66.21	87.63	148.44	181.02	157.90	78.72	73.28	91.6	*	+		
NT2RM2001035	10.78	6.86	10.47	14.95	15.69	13.90	7.29	8.73	9.42	*	+		
NT2RM2001038	4.09	2.22	2.89	6.55	5.43	6.97	3.62	3.51	3.32	*	+		
NT2RM2001043	2.10	1.71	2.70	4.88	5.53	4.13	3.52	4.59	4.54	**	+	*	+
NT2RM2001050	8.66	4.61	6.50	7.54	9.45	9.85	5.61	5.16	6.52				
NT2RM2001055	4.62	4.14	3.41	6.16	5.15	5.46	4.13	4.67	4.8	*	+		
NT2RM2001065	6.07	2.63	3.08	8.01	7.85	5.22	3.46	3.40	2.98				
NT2RM2001075	101.53	60.27	56.87	59.75	60.87	48.63	40.45	36.79	33.7				
NT2RM2001083	13.68	8.75	8.30	8.28	9.63	7.55	10.14	7.92	7.18				
NT2RM2001100	8.62	6.13	5.38	7.77	11.80	7.92	8.12	5.53	6.12				
NT2RM2001105	18.36	12.31	11.09	26.95	28.47	25.34	13.8	13.76	12.91	**	+		
NT2RM2001109	5.91	3.28	4.91	5.36	6.02	5.10	4.49	5.78	4.86				
NT2RM2001110	9.13	5.14	5.81	7.93	9.23	8.95	5.5	5.40	7.45				
NT2RM2001126	4.23	4.04	4.69	10.78	10.09	7.28	4.72	4.73	5.55	**	+		
NT2RM2001131	9.35	4.34	5.26	6.74	7.12	6.44	4.76	4.21	3.9				
NT2RM2001141	9.27	7.43	7.38	17.22	17.01	12.50	8.53	7.69	8.62	*	+		
NT2RM2001152	3.64	1.47	1.46	2.09	3.47	2.45	1.42	1.89	2.81				
NT2RM2001177	8.38	4.92	5.00	10.70	11.58	8.68	5.53	6.90	6.04	*	+		
NT2RM2001194	10.76	6.38	8.60	11.33	15.08	9.90	8.38	9.20	9.42				
NT2RM2001195	3.62	3.00	3.18	4.85	7.13	3.67	3.45	3.91	3.64				
NT2RM2001196	7.18	4.57	6.50	10.22	17.76	12.85	4.98	6.12	9.71	*	+		

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Table 233

NT2RM2001201	13.08	8.55	9.63	10.72	11.46	9.31	8.37	10.02	9.79				
NT2RM2001221	6.92	2.79	3.15	5.91	7.22	4.72	4.61	5.13	3.98				
NT2RM2001238	2.81	1.05	1.43	3.40	2.72	2.10	1.81	2.65	3.37				
NT2RM2001243	6.98	4.99	5.16	9.29	9.00	6.32	4.34	5.08	4.64				
NT2RM2001244	4.98	5.59	4.41	14.49	19.11	7.34	5.11	6.41	7.87				
NT2RM2001247	15.41	9.79	11.87	12.82	15.98	10.20	6.66	8.32	9.67				
NT2RM2001256	2.93	2.70	3.12	2.39	2.54	2.02	2.24	3.49	2.22	*	-		
NT2RM2001269	1.76	1.73	1.47	3.07	6.49	3.10	1.39	5.05	2.29				
NT2RM2001278	7.64	6.14	6.38	12.27	11.97	10.88	6.39	7.92	7.27	**	+		
NT2RM2001291	4.14	2.35	1.90	4.62	4.03	2.79	3.65	2.48	3.16				
NT2RM2001294	10.67	6.20	5.16	12.58	9.68	9.06	8.36	5.49	6.33				
NT2RM2001295	4.70	3.78	3.23	5.43	4.66	4.21	4.46	4.14	4.92				
NT2RM2001302	5.63	4.69	4.19	1.74	2.61	0.97	2.97	3.64	4.24	**	-		
NT2RM2001306	2.52	1.56	1.39	3.47	5.32	4.74	2.64	2.44	2.72	*	+		
NT2RM2001312	1.22	1.12	0.35	2.84	2.71	1.41	1.03	2.09	1.77				
NT2RM2001319	5.09	3.21	4.08	5.71	5.46	5.01	3.84	5.43	5.66				
NT2RM2001324	8.85	3.42	3.83	7.05	8.29	8.06	5.36	6.31	4.89				
NT2RM2001345	12.36	6.03	4.96	4.58	10.06	7.26	10.14	5.50	8.05				
NT2RM2001360	9.69	4.48	4.35	8.36	5.80	5.82	6.45	4.63	6.16				
NT2RM2001370	1.53	1.04	0.81	1.70	1.86	1.18	1.6	2.44	2.47			*	+
NT2RM2001391	1.02	1.38	1.05	3.81	3.30	1.71	1.72	1.73	1.75	*	+	**	+
NT2RM2001393	6.61	4.78	7.01	5.53	6.68	4.32	4.86	4.39	4.92				
NT2RM2001420	2.35	0.95	1.41	3.00	4.15	1.59	1.98	2.45	1.71				
NT2RM2001423	11.93	5.27	6.94	5.59	7.80	3.34	2.15	4.14	4.71				
NT2RM2001424	18.20	9.15	9.42	11.35	10.96	8.30	11.11	9.35	12.67				
NT2RM2001482	15.21	7.55	7.78	14.57	12.13	9.92	11.31	8.31	11.15				
NT2RM2001499	16.92	9.02	7.05	8.26	6.45	6.32	5.19	4.43	7.42				
NT2RM2001504	3.91	2.51	1.97	4.23	4.34	3.86	4.03	2.84	4.42				
NT2RM2001524	2.28	1.47	1.87	2.95	3.08	2.80	2.63	3.34	2.29	*	+		
NT2RM2001530	0.78	0.43	0.54	2.16	2.44	1.43	1.65	1.93	1.93	*	+	**	+
NT2RM2001533	5.77	3.13	3.08	6.59	7.98	5.62	5.57	5.84	5.16				
NT2RM2001540	29.91	19.29	20.03	25.11	24.66	12.51	8.93	9.56	11.82			*	-
NT2RM2001544	5.22	2.70	2.16	5.77	5.72	5.39	4.13	3.93	3.57				
NT2RM2001547	10.18	3.47	3.29	5.82	9.93	4.61	8.42	7.52	11.22				
NT2RM2001558	4.96	2.25	2.36	3.07	3.85	4.04	4.67	2.71	4.49				
NT2RM2001575	4.76	2.31	3.04	7.85	7.43	4.47	3.66	3.23	5.49				
NT2RM2001582	3.25	3.39	2.40	5.42	5.69	4.66	5.53	3.88	4.63	**	+	*	+
NT2RM2001588	2.97	1.41	1.47	4.20	4.38	3.50	3.05	3.37	3.85	*	+		
NT2RM2001592	1.95	2.06	1.67	3.66	3.58	2.66	2.98	2.38	2.72	*	+	*	+
NT2RM2001603	7.68	4.12	5.42	8.07	9.92	5.79	4.3	6.45	7.62				
NT2RM2001605	6.36	3.57	2.87	8.10	9.32	7.63	6.11	4.82	7.04	*	+		
NT2RM2001611	4.43	2.58	2.01	5.92	8.58	4.85	5.15	3.69	4.23				
NT2RM2001613	5.87	2.94	3.70	6.48	9.87	7.29	8.01	9.10	11.64			*	+
NT2RM2001626	11.27	5.06	6.34	7.63	9.90	5.32	10.52	8.42	10.76				
NT2RM2001632	8.60	4.62	8.41	12.48	14.32	11.43	11.18	11.01	12.96	*	+	*	+
NT2RM2001633	1.62	1.36	1.29	4.23	3.15	3.36	2.92	3.34	2.97	**	+	**	+
NT2RM2001635	6.76	5.69	4.97	6.78	9.41	8.26	7.11	8.37	8.13			*	+
NT2RM2001636	4.43	3.06	3.83	4.52	5.10	3.16	3.81	3.42	3.49				
NT2RM2001637	2.79	1.78	2.31	4.20	4.67	2.96	3.03	3.93	2.28	*	+		
NT2RM2001639	4.58	2.65	2.19	3.05	3.54	3.49	2.88	2.16	3.34				
NT2RM2001641	3.30	2.69	1.81	2.72	3.01	1.92	1.93	2.95	2.91				
NT2RM2001643	3.00	1.41	2.34	4.92	3.73	2.89	3.15	3.35	3.43				
NT2RM2001648	3.60	1.94	2.50	5.96	6.92	4.37	6.52	6.11	8.21	*	+	**	+
NT2RM2001652	4.13	2.45	1.80	4.68	5.72	3.86	2.23	2.96	4.29				
NT2RM2001659	1.81	1.41	1.26	2.31	1.88	1.34	2.02	2.75	2.32			*	+
NT2RM2001660	2.12	1.41	1.99	2.87	4.60	2.23	2.13	3.03	3.35				

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Table 234

NT2RM2001664	5.67	1.74	2.53	4.44	5.25	4.88	2.57	2.77	3.63				
NT2RM2001668	7.83	4.11	5.80	12.91	11.03	10.32	6.9	5.64	6.89	*	+		
NT2RM2001670	5.07	2.93	3.57	4.21	4.81	3.14	3.67	3.52	4.76				
NT2RM2001671	2.26	2.13	2.75	6.03	4.05	5.74	4.08	5.29	5.9	*	+	**	+
NT2RM2001675	0.53	0.71	0.81	1.96	1.15	1.66	0.84	1.96	0.76	*	+		
NT2RM2001681	1.11	1.22	1.01	3.34	4.29	2.27	1.69	3.16	1.72	*	+		
NT2RM2001685	3.03	2.26	1.29	2.06	2.47	1.90	1.92	3.02	2.65				
NT2RM2001688	2.78	1.66	2.54	4.45	4.23	2.30	3.29	2.37	2.72				
NT2RM2001695	7.30	3.32	3.64	20.95	20.35	18.16	12.07	10.51	12.36	**	+	**	+
NT2RM2001696	13.28	6.12	3.86	8.81	10.82	9.78	6.65	6.44	6.65				
NT2RM2001698	8.16	4.37	3.88	5.88	6.34	6.37	6.66	7.84	5.32				
NT2RM2001699	2.40	2.32	1.42	3.33	3.59	3.21	1.64	3.47	3.24	*	+		
NT2RM2001700	2.41	1.38	1.03	2.93	2.03	1.36	1.5	2.70	2.35				
NT2RM2001704	6.94	4.34	5.63	17.99	22.84	16.16	12.13	13.06	13.82	**	+	**	+
NT2RM2001706	5.19	2.60	4.07	6.98	8.64	6.26	3.29	5.55	5.04	*	+		
NT2RM2001714	1.72	1.75	2.15	3.05	3.64	2.23	1.71	2.86	4.84				
NT2RM2001716	16.89	6.66	8.99	10.52	14.37	8.33	10.03	10.20	4.62				
NT2RM2001718	13.66	7.01	6.41	14.04	11.83	11.25	5.12	7.15	10.53				
NT2RM2001723	6.13	3.06	3.78	9.65	9.89	7.73	4.12	5.35	3.42	*	+		
NT2RM2001727	5.93	4.01	4.52	4.87	5.62	5.99	5.45	6.14	6.96				
NT2RM2001730	3.02	1.57	1.66	3.08	3.68	4.44	2.79	3.79	2.6				
NT2RM2001738	6.78	3.40	5.60	4.93	5.41	3.52	4.55	4.50	4.55				
NT2RM2001743	4.12	2.65	1.97	3.64	5.10	2.62	3.21	3.25	2.82				
NT2RM2001753	4.87	2.89	3.87	7.06	7.68	7.46	4.96	5.77	5.73	**	+		
NT2RM2001755	11.15	5.43	7.63	8.83	12.50	9.88	7.94	7.72	5.34				
NT2RM2001760	6.52	3.36	4.22	8.42	9.37	6.40	10.28	9.84	11.76			**	+
NT2RM2001765	2.13	1.98	1.79	3.23	3.97	3.48	2.65	2.41	2.82	**	+	*	+
NT2RM2001767	12.87	8.82	9.72	11.08	15.03	8.12	9.19	9.22	14.64				
NT2RM2001768	3.41	2.58	3.68	3.47	6.28	4.04	2.49	2.74	3.01				
NT2RM2001771	4.11	3.62	4.50	11.05	14.86	9.39	5.06	5.82	8.71	**	+		
NT2RM2001778	1.70	1.61	1.19	3.14	4.69	2.67	2.01	2.74	1.97	*	+		
NT2RM2001782	3.37	2.78	3.39	3.01	4.59	4.13	3.83	4.97	5.07			*	+
NT2RM2001784	3.64	1.97	1.45	2.55	4.38	1.85	2.15	2.16	2.26				
NT2RM2001785	11.40	5.25	4.67	8.49	7.03	6.72	4.99	4.72	4.92				
NT2RM2001792	5.79	3.39	4.17	6.69	5.40	4.24	3.59	5.22	5.39				
NT2RM2001795	9.85	4.56	3.32	7.91	9.48	5.77	7.27	6.25	5.93				
NT2RM2001797	5.04	2.64	2.13	7.82	15.93	10.34	3.54	4.95	3.54	*	+		
NT2RM2001800	3.26	2.51	2.46	4.20	4.38	3.21	2.99	3.72	2.42				
NT2RM2001803	3.60	2.31	2.65	4.14	6.89	5.00	2.04	3.10	3.17				
NT2RM2001805	1.03	0.92	2.17	2.21	3.99	1.67	0.87	3.16	1.79				
NT2RM2001806	5.77	1.94	1.66	4.46	3.73	2.85	3.42	3.44	3.44				
NT2RM2001813	3.38	1.75	1.74	2.55	3.99	2.42	1.83	1.59	3.71				
NT2RM2001814	3.09	1.71	2.83	3.06	4.28	2.96	1.96	3.02	3.47				
NT2RM2001818	2.38	1.33	1.54	3.40	2.50	2.32	1.89	3.32	1.89				
NT2RM2001823	1.26	1.12	0.39	0.95	1.88	0.91	0.96	2.06	1.08				
NT2RM2001825	10.44	6.78	7.32	10.86	11.22	8.43	10.54	16.17	16.27			*	+
NT2RM2001832	4.52	2.18	1.93	4.11	5.31	3.71	1.98	4.92	3.68				
NT2RM2001839	16.50	9.01	12.64	20.38	24.01	12.42	26.45	40.89	49.99			*	+
NT2RM2001840	7.75	3.07	2.83	17.33	13.18	10.65	7.84	6.84	7.97	*	+		
NT2RM2001851	7.34	4.30	5.43	12.87	13.61	10.39	7.97	4.60	6.49	**	+		
NT2RM2001855	5.55	3.48	2.68	4.96	5.56	4.20	7.12	5.33	6.29				
NT2RM2001867	3.35	3.93	2.06	5.68	4.49	3.19	3.59	2.29	4.09				
NT2RM2001869	28.84	23.52	26.51	34.13	35.79	25.24	15.38	12.75	18.43			**	-
NT2RM2001879	0.65	1.04	0.48	2.26	1.68	1.53	1.35	1.12	1.72	*	+	*	+
NT2RM2001883	3.25	3.47	2.90	9.89	19.82	12.52	5.43	4.02	7.24	*	+		
NT2RM2001886	2.86	1.25	2.11	3.84	5.06	2.09	1.79	1.91	1.93				

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Table 235

NT2RM2001887	4.05	2.53	2.07	3.94	3.93	2.72	2.74	2.00	2.87				
NT2RM2001896	968.51	557.14	625.69	446.49	419.99	290.65	817.5	613.90	955.7				
NT2RM2001902	1.32	1.09	1.03	2.63	3.33	2.08	2.5	1.84	1.37	*	+		
NT2RM2001903	10.52	8.17	6.65	10.52	9.78	8.75	7	6.78	10.05				
NT2RM2001930	5.61	3.44	3.21	5.48	6.96	3.46	4.44	4.85	6				
NT2RM2001935	3.82	1.91	1.54	3.50	4.79	3.97	2.7	3.75	4.62				
NT2RM2001936	5.82	4.45	4.35	6.11	7.15	5.56	4.64	4.90	5.38				
NT2RM2001939	8.71	5.44	6.44	8.93	8.81	3.78	2.77	3.30	4.35			*	-
NT2RM2001941	6.75	2.80	2.92	6.78	5.32	3.44	5.9	3.69	5.46				
NT2RM2001950	7.11	3.51	4.45	5.50	5.26	4.20	5.45	4.64	5.47				
NT2RM2001952	2.47	1.60	2.55	2.69	4.21	2.27	1.88	1.01	2.57				
NT2RM2001976	28.42	15.82	19.71	28.96	35.93	24.29	16.42	13.99	23.68				
NT2RM2001982	4.42	1.68	2.40	3.83	3.46	2.37	2.4	2.21	2.73				
NT2RM2001983	2.90	2.45	2.37	3.29	3.84	2.68	3.58	3.72	3.62			**	+
NT2RM2001984	9.80	5.19	8.10	8.76	9.27	5.57	9.18	6.75	8.16				
NT2RM2001989	11.11	6.20	6.87	11.27	9.42	7.93	6.29	5.35	7.09				
NT2RM2001996	14.80	9.47	8.75	13.23	9.98	7.81	6.58	6.93	7.66				
NT2RM2001997	6.28	4.07	2.81	7.04	8.03	5.28	7.41	5.47	7.79				
NT2RM2001998	4.75	3.45	3.00	4.75	6.36	4.13	5.37	3.71	5.85				
NT2RM2001999	10.41	5.56	7.08	6.38	11.36	7.48	5.73	5.79	10.27				
NT2RM2002003	10.66	5.49	8.27	9.09	11.29	8.39	10.04	6.40	24.73				
NT2RM2002004	1.63	1.64	2.11	1.09	1.63	1.85	1.23	1.86	1.25				
NT2RM2002009	4.47	4.69	3.31	8.66	11.16	6.73	5.88	6.79	8.4	*	+	*	+
NT2RM2002014	2.01	1.63	2.37	3.01	3.07	2.13	1.7	1.98	2.36				
NT2RM2002019	24.72	12.04	19.38	13.08	13.17	13.22	11.49	8.63	11.15				
NT2RM2002029	6.40	7.22	6.06	8.84	11.57	6.10	8.68	6.47	10.53				
NT2RM2002030	5.25	5.14	4.68	5.36	8.72	3.88	5.86	5.43	6.29				
NT2RM2002034	8.15	6.62	4.89	14.77	20.00	13.04	13.54	8.03	15.03	*	+		
NT2RM2002049	3.95	2.79	2.89	4.72	8.26	6.22	5.53	3.64	6.92	*	+		
NT2RM2002055	0.27	0.82	0.37	0.80	1.13	1.85	1.04	1.68	0.63				
NT2RM2002072	15.43	11.44	16.71	17.13	17.10	21.32	19.05	15.56	22.41				
NT2RM2002088	7.49	4.56	5.69	7.90	6.52	5.70	5.75	6.67	7.06				
NT2RM2002091	15.11	10.25	9.22	22.42	19.93	19.66	8.6	12.53	10.62	*	+		
NT2RM2002100	4.63	3.56	2.83	7.24	10.07	3.66	3.27	4.23	5.16				
NT2RM2002109	5.17	3.65	3.18	8.12	10.78	4.99	4.99	4.26	6.51				
NT2RM2002126	17.67	11.99	12.06	15.99	24.43	15.73	17.49	13.92	19.27				
NT2RM2002128	3.48	2.83	1.99	3.84	5.46	3.66	3.24	2.92	3.02				
NT2RM2002129	4.13	2.91	3.80	6.20	6.87	4.06	5.78	4.67	7.21				
NT2RM2002142	9.10	5.41	12.04	10.00	15.48	9.23	8.42	6.45	11.18				
NT2RM2002144	3.36	3.30	2.97	3.37	3.35	3.00	3.79	3.97	3.53			*	+
NT2RM2002145	6.78	4.33	5.19	6.26	8.85	5.46	5.35	5.34	6.65				
NT2RM2002153	23.74	16.73	21.12	12.42	16.25	18.91	6.63	5.66	6.16			**	-
NT2RM2002163	3.16	2.77	2.30	3.73	2.93	2.52	3.34	5.43	2.91				
NT2RM2002170	3.33	3.09	3.14	5.55	7.02	5.69	2.89	3.62	2.63	**	+		
NT2RM2002178	5.79	2.91	3.21	5.77	6.57	4.62	3.87	4.53	5.9				
NT2RM2002179	2.75	2.13	3.45	13.46	15.53	10.86	9.37	9.17	14.68	**	+	*	+
NT2RM2002270	6.01	3.32	3.61	5.54	5.51	3.68	4.91	5.60	3.82				
NT2RM2002326	3.03	1.98	3.43	11.14	9.52	7.64	7.73	8.34	6.08	**	+	**	+
NT2RM2002337	4.10	3.34	2.03	4.41	8.58	3.20	3.05	2.79	3.57				
NT2RM2002339	7.43	4.86	4.58	4.19	4.70	6.27	6.54	7.31	8.68				
NT2RM2002345	4.47	3.51	3.00	6.85	4.79	5.38	4.35	5.79	4.74				
NT2RM2002368	4.40	3.36	3.81	8.23	7.04	7.08	3.82	5.20	3.26	**	+		
NT2RM2002381	1.63	1.57	2.71	2.99	3.95	2.46	1.73	3.26	3.15				
NT2RM2002424	6.30	4.83	5.88	15.99	15.30	14.85	6.59	9.16	9.11	**	+		
NT2RM2002450	4.28	2.58	3.43	4.26	4.94	3.98	2.13	3.11	1.67				
NT2RM2002482	3.24	2.34	3.46	4.41	2.79	3.35	3.25	3.29	2.2				

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Table 236

NT2RM2002492	21.46	13.29	16.96	23.80	28.37	23.64	14.79	12.77	15.74	*	+		
NT2RM2002575	14.83	8.83	9.60	12.39	15.50	9.64	5.47	4.77	4.26			*	-
NT2RM2002580	10.54	5.71	6.88	9.66	15.19	13.67	6.89	8.73	8.24				
NT2RM2002592	21.59	13.02	21.47	22.05	25.36	18.29	13.81	13.13	16.44				
NT2RM2002608	14.51	10.47	15.10	11.85	17.10	10.74	12.25	12.95	16.2				
NT2RM2002615	7.16	4.68	6.11	4.32	3.11	3.23	2.34	3.30	2.9	*	-	*	-
NT2RM2002622	7.42	4.82	9.06	37.13	40.07	28.33	10.87	12.05	11.06	**	+	*	+
NT2RM2002630	7.98	5.03	5.96	13.25	13.42	12.82	6.17	6.79	6.95	**	+		
NT2RM2002634	5.03	2.59	3.78	7.49	9.33	4.95	4.93	3.29	2.99				
NT2RM2002645	23.59	12.83	21.14	22.24	21.50	17.33	18.84	24.20	13.44				
NT2RM2002646	14.00	9.34	10.97	13.76	16.22	12.07	10.73	9.69	15.13				
NT2RM2002647	20.09	9.61	14.48	15.78	21.02	13.76	11.26	13.21	13.26				
NT2RM2002652	5.04	3.66	3.21	6.10	6.51	3.39	2.65	3.93	4.06				
NT2RM2002692	7.77	5.58	7.47	11.71	20.77	13.98	11.29	13.53	12.54	*	+	**	+
NT2RM2002721	24.72	15.21	18.70	28.40	46.33	25.49	20.79	20.54	32.86				
NT2RM2002748	79.54	53.04	79.10	79.94	75.77	78.90	26.04	31.33	37.42			*	-
NT2RM2002764	5.43	3.03	2.52	10.76	7.77	4.58	3.86	3.77	3.77				
NT2RM2002772	11.93	7.88	8.81	11.61	12.84	7.73	4.61	5.99	7.99				
NT2RM2002811	9.63	5.90	5.86	8.67	8.08	6.76	5.99	5.21	6.14				
NT2RM2002818	6.94	3.95	3.88	7.36	7.54	5.33	2.65	4.06	4.31				
NT2RM2002879	2.57	1.77	2.32	2.29	3.75	1.84	3.18	4.11	4.37			*	+
NT2RM2002979	11.80	7.84	8.67	10.47	13.00	9.87	8.38	6.63	6.92				
NT2RM2002981	4.75	2.96	3.25	4.20	5.55	4.27	4.3	5.20	4.19				
NT2RM2002995	3.40	2.64	2.64	3.84	3.50	4.10	2.62	3.34	2.85	*	+		
NT2RM2003031	3.92	1.02	1.63	4.33	4.68	2.72	3.7	2.74	3.72				
NT2RM2003042	21.41	10.74	8.21	17.59	19.62	15.87	7.89	8.90	9.64				
NT2RM2003044	3.74	2.06	1.81	3.99	6.41	3.64	2.33	3.97	3.12				
NT2RM2003090	4.60	2.18	1.89	2.49	4.89	3.16	3.07	3.31	2.92				
NT2RM2003095	3.67	1.54	1.20	3.30	4.47	3.32	3.18	3.65	3.25				
NT2RM2003116	5.36	5.13	6.83	5.86	7.80	6.25	3.24	6.72	6.31				
NT2RM2003222	2.53	2.08	1.54	2.39	2.31	1.74	0.73	3.10	1.35				
NT2RM2003224	15.53	10.87	13.94	24.44	25.63	15.64	6.09	8.22	11.35				
NT2RM2003250	14.48	5.65	5.15	9.14	10.21	4.29	3.99	3.24	3.21				
NT2RM2003258	2.29	2.33	1.33	2.70	2.97	1.92	4.64	2.60	3.37				
NT2RM2003262	12.60	10.45	8.76	10.06	13.00	11.50	9.36	7.15	7.82				
NT2RM4000023	1.99	1.44	1.54	4.90	4.52	3.88	4.13	2.29	4.66	**	+		
NT2RM4000024	2.91	2.48	1.20	3.30	4.50	2.17	2.67	1.90	2.29				
NT2RM4000027	8.53	4.07	5.06	2.82	3.04	1.62	1.79	2.08	2.61				
NT2RM4000030	5.84	5.94	5.16	8.87	6.03	4.15	5.42	5.51	5.41				
NT2RM4000033	1.51	1.27	1.03	2.93	3.16	1.42	1.59	1.08	1.27				
NT2RM4000034	2.39	1.22	1.22	3.53	2.94	1.45	2.28	1.04	1.5				
NT2RM4000046	2.68	1.77	1.53	3.42	3.11	1.75	3.04	1.82	3.01				
NT2RM4000052	4.15	1.71	1.72	3.48	3.49	2.40	3.28	1.71	3.37				
NT2RM4000054	26.80	19.29	17.31	21.55	22.04	23.11	25.09	20.51	27.5				
NT2RM4000061	2.10	1.10	0.99	1.68	1.71	1.22	2.51	1.77	1.98				
NT2RM4000074	9.55	7.34	6.67	13.37	15.17	7.83	6.11	5.94	7.27				
NT2RM4000085	2.96	0.88	2.51	4.65	4.96	3.33	2.05	2.94	4.07				
NT2RM4000086	5.73	3.89	4.54	5.27	5.35	3.12	1.65	3.66	5.45				
NT2RM4000100	5.36	2.82	2.66	5.25	5.01	3.76	5.82	4.53	4.32				
NT2RM4000101	3.85	2.50	2.70	3.14	2.31	2.97	4.25	3.04	4.67				
NT2RM4000102	36.64	21.10	21.71	40.33	40.26	40.80	33.11	25.16	36.34				
NT2RM4000104	1.41	0.89	0.77	2.16	1.98	1.38	2.39	2.42	1.99			**	+
NT2RM4000115	1.25	1.28	1.23	1.59	2.32	1.33	1.87	1.24	1.33				
NT2RM4000129	2.55	2.06	1.92	3.48	3.51	3.33	3.04	3.19	2.54	**	+		
NT2RM4000139	2.48	1.32	1.75	2.52	1.95	2.96	1.63	2.77	2.58				
NT2RM4000149	1.92	1.98	1.88	3.18	3.67	2.07	1.43	1.95	2.57				

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Table 237

NT2RM4000155	8.41	4.25	5.85	5.71	7.89	3.63	6.31	2.89	10.88				
NT2RM4000156	4.06	2.82	3.12	3.91	5.14	3.25	4.15	3.34	7.54				
NT2RM4000167	2.76	1.86	2.44	3.27	3.78	2.46	1.7	2.54	2.08				
NT2RM4000169	19.79	11.82	12.59	15.78	28.83	16.15	10.62	8.62	22.74				
NT2RM4000191	5.46	2.93	3.98	7.00	12.87	3.95	5.75	4.22	5				
NT2RM4000197	6.21	3.61	5.57	1.78	3.32	3.20	2.07	2.72	3.62				
NT2RM4000198	6.32	5.24	5.02	9.16	10.86	8.33	6.38	7.74	6.83	**	+		
NT2RM4000199	3.97	1.83	1.79	3.99	4.05	3.81	2.77	3.05	3.55				
NT2RM4000200	3.35	2.42	1.54	4.45	2.14	1.95	1.94	2.20	2.16				
NT2RM4000202	3.63	1.09	1.43	2.56	2.87	2.44	2.2	2.07	1.78				
NT2RM4000210	4.14	2.52	2.72	3.86	8.22	3.80	3.01	2.97	3.68				
NT2RM4000215	5.18	3.07	5.47	7.27	8.45	5.15	4.83	4.89	4.29				
NT2RM4000220	2.94	2.54	2.79	4.64	4.57	3.49	4.1	4.60	5.77	*	+	*	+
NT2RM4000229	5.01	3.09	3.00	5.45	4.41	4.69	4.07	4.71	4.56				
NT2RM4000231	4.55	4.22	5.24	5.48	9.85	6.48	5.25	5.36	6.29				
NT2RM4000233	15.69	9.94	12.92	10.36	8.30	6.63	11.95	12.79	13.03				
NT2RM4000244	3.55	2.12	1.68	2.06	1.74	1.35	2.28	2.40	1.4				
NT2RM4000251	3.33	1.28	1.28	2.48	6.47	3.24	2.39	3.65	3.7				
NT2RM4000255	2.86	2.35	2.55	3.65	4.00	4.45	3.46	3.56	4.05	**	+	**	+
NT2RM4000265	4.79	2.78	4.25	9.35	12.26	8.62	3.89	4.46	7.5	**	+		
NT2RM4000283	70.67	47.66	58.69	22.90	27.64	23.33	20.04	20.53	29.33	**	-	**	-
NT2RM4000284	3.79	2.43	3.13	4.73	5.37	4.18	3.75	4.06	5.01	*	+		
NT2RM4000290	3.63	2.15	2.31	4.25	6.01	4.45	4.22	4.40	5.11	*	+	*	+
NT2RM4000295	2.18	1.74	1.84	1.64	1.85	1.54	2.16	2.51	2.05				
NT2RM4000306	9.76	5.69	5.53	3.29	5.79	3.80	4.99	4.91	4.19				
NT2RM4000307	1.99	1.95	1.34	6.27	6.75	5.25	9.66	12.35	13.1	**	+	**	+
NT2RM4000309	4.39	2.45	3.20	3.45	3.57	3.25	2.21	2.77	3.12				
NT2RM4000313	4.53	2.93	3.37	6.76	7.38	6.57	4.37	4.56	4.95	**	+		
NT2RM4000318	3.24	1.42	3.10	6.35	5.08	6.14	3.2	4.49	3.95	**	+		
NT2RM4000324	3.33	2.91	2.72	5.10	4.10	4.09	3.41	4.13	3.13	*	+		
NT2RM4000326	2.66	2.08	2.02	2.52	2.48	2.90	1.91	4.16	2.37				
NT2RM4000327	5.98	3.83	5.87	11.13	9.36	9.04	5.82	4.08	6.84	**	+		
NT2RM4000344	18.32	6.89	6.35	13.95	16.21	14.72	10.48	11.38	12.84				
NT2RM4000349	6.58	3.84	3.66	6.40	5.99	6.38	4.94	4.61	4.8				
NT2RM4000354	5.00	2.70	3.37	3.28	2.86	2.19	2.4	2.57	3.45				
NT2RM4000356	4.16	1.61	1.73	2.39	4.18	5.03	2.81	3.86	2.82				
NT2RM4000366	51.05	23.81	40.37	61.56	72.80	50.45	36.85	39.74	37.86				
NT2RM4000368	4.89	2.95	4.56	12.45	6.89	8.75	3.93	5.00	5.04	*	+		
NT2RM4000373	3.91	2.54	3.44	5.84	6.63	5.55	3.15	4.00	4.07	**	+		
NT2RM4000386	2.58	1.67	2.32	2.56	2.07	2.16	1.54	2.11	1.77				
NT2RM4000395	7.43	3.02	3.38	5.38	8.33	4.62	3.75	3.62	2.41				
NT2RM4000414	8.01	4.62	4.45	4.72	6.23	4.47	6.27	6.74	7.44				
NT2RM4000417	3.81	2.15	2.35	2.45	4.44	3.37	1.96	2.94	5.43				
NT2RM4000421	4.32	3.14	3.21	5.52	5.35	4.92	3.28	3.80	2.75	*	+		
NT2RM4000425	5.83	3.82	4.77	12.15	12.72	12.65	6.8	7.68	8.72	**	+	*	+
NT2RM4000433	3.24	1.87	2.39	3.27	3.60	3.54	5.12	3.76	4.32			*	+
NT2RM4000436	5.20	2.98	5.09	4.80	5.70	3.50	3.27	3.38	2.58				
NT2RM4000444	2.77	3.48	2.67	4.83	3.05	2.47	3.64	2.66	2.6				
NT2RM4000457	15.74	6.60	7.42	19.58	21.46	13.99	7.15	6.46	8.49				
NT2RM4000471	2.61	2.36	2.45	4.93	5.40	4.25	2.75	2.88	3.1	**	+	*	+
NT2RM4000472	18.08	9.02	12.03	39.03	47.24	22.44	10.92	7.97	22.46	*	+		
NT2RM4000486	3.65	3.27	2.92	5.46	7.04	5.93	3.74	4.42	3.79	**	+		
NT2RM4000490	4.88	4.19	2.87	2.63	4.80	4.02	3.72	6.17	4.86				
NT2RM4000496	4.08	3.13	4.22	2.96	3.44	3.46	3.56	4.42	3.51				
NT2RM4000505	13.63	8.59	11.63	16.76	17.74	14.63	12.93	15.48	13.33	*	+		
NT2RM4000511	58.96	34.63	49.12	52.44	54.53	48.10	20.11	21.96	24.23			*	-

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Table 238

NT2RM4000514	5.53	2.38	2.75	8.23	11.94	5.81	3.95	5.11	3.73					
NT2RM4000515	16.72	6.51	7.89	17.68	19.19	15.60	8.65	8.97	10.58					
NT2RM4000517	52.07	29.36	32.93	47.60	48.78	40.92	19.63	19.22	17.95					
NT2RM4000520	2.37	1.45	1.44	1.17	1.70	1.58	0.83	2.01	2.17					
NT2RM4000531	1.99	2.27	1.67	2.66	3.68	3.90	3.09	4.12	3.6	*	+	**	+	
NT2RM4000532	1.32	0.65	0.82	1.96	2.81	1.58	1.14	2.83	2.21	*	+			
NT2RM4000533	3.05	2.29	3.20	1.70	2.71	1.77	1.32	2.54	1.44					
NT2RM4000534	1.94	0.89	1.21	1.63	2.79	1.54	1.47	2.29	1.5					
NT2RM4000563	8.72	3.55	3.49	6.44	4.79	3.51	5.01	4.09	5.24					
NT2RM4000566	4.57	2.22	2.28	4.38	4.92	2.84	2.28	2.65	3.1					
NT2RM4000568	3.97	2.58	1.85	3.65	4.45	3.11	2.68	3.32	5.31					
NT2RM4000585	4.60	2.16	1.71	2.71	3.64	3.29	2.11	2.49	3.12					
NT2RM4000587	2.44	1.07	2.17	2.90	3.56	2.74	2.55	3.03	3.48					
NT2RM4000590	2.10	1.53	1.91	1.79	3.35	2.47	1.66	3.17	1.73					
NT2RM4000593	7.87	4.39	5.71	12.59	12.23	10.68	4.27	7.40	6.4	**	+			
NT2RM4000595	2.17	1.55	2.08	3.28	3.82	2.26	2.16	3.13	4.82					
NT2RM4000603	12.55	6.66	8.52	9.64	5.73	7.27	4.44	2.74	3.84					
NT2RM4000611	4.28	4.40	1.85	3.49	3.25	3.20	4.67	2.74	3.19					
NT2RM4000616	3.34	2.92	1.37	4.32	4.33	3.69	3.56	2.86	2.97					
NT2RM4000621	16.48	12.72	9.94	21.48	22.15	19.49	9.4	8.56	8.57	*	+			
NT2RM4000648	2.01	1.43	1.11	2.32	1.95	1.99	1.76	2.62	1.65					
NT2RM4000649	5.47	3.71	4.22	6.21	6.35	6.84	6.07	5.86	5.42	*	+			
NT2RM4000658	8.60	4.07	5.16	8.70	7.92	4.74	5.84	5.98	5.36					
NT2RM4000661	10.99	4.92	5.69	11.11	10.38	8.21	15.64	14.68	17.57			*	+	
NT2RM4000673	9.96	5.23	4.31	6.63	5.66	5.28	8.2	4.95	5.83					
NT2RM4000674	5.01	2.88	2.93	4.58	4.03	4.02	5.28	3.25	4.19					
NT2RM4000689	6.44	3.20	3.50	4.50	6.19	4.47	3.52	4.05	3.79					
NT2RM4000698	35.87	22.93	21.16	15.46	17.90	22.28	17.5	16.82	14.8					
NT2RM4000700	3.46	2.08	2.83	3.85	2.02	2.52	2.49	2.37	1.32					
NT2RM4000701	9.78	5.90	5.74	10.46	14.71	8.86	7.95	6.35	8.32					
NT2RM4000712	2.69	1.64	2.42	4.68	4.33	3.64	2.57	3.33	2.41	*	+			
NT2RM4000717	12.02	5.07	6.36	11.87	8.62	8.11	7.27	6.28	7.15					
NT2RM4000733	8.98	3.57	6.27	6.72	6.26	7.78	7.76	4.90	6					
NT2RM4000734	9.72	3.11	3.90	7.75	4.13	5.58	5.8	4.00	5.07					
NT2RM4000741	4.49	2.29	3.56	3.14	3.42	3.32	3.44	4.03	2.18					
NT2RM4000744	3.69	2.68	2.61	2.80	6.32	4.46	2.85	3.92	3					
NT2RM4000749	11.40	7.45	11.83	11.62	13.08	12.36	13.08	12.48	13.4					
NT2RM4000751	6.54	4.81	4.52	15.28	14.53	10.59	6.43	6.81	9.13	**	+			
NT2RM4000752	4.53	2.37	3.48	4.41	5.68	4.78	3.23	4.75	8.68					
NT2RM4000760	4.53	2.84	2.99	5.14	6.37	2.91	5.41	3.73	5.34					
NT2RM4000761	996.52	787.70	799.46	925.45	928.88	688.98	521.4	1076.26	1043					
NT2RM4000764	27.63	19.80	15.48	20.84	20.29	16.92	30.21	26.08	33.56					
NT2RM4000768	14.67	8.26	9.77	8.91	9.00	6.52	3.2	6.21	5.06			*	-	
NT2RM4000778	4.92	2.41	4.01	2.84	3.65	2.97	1.85	2.67	2.07					
NT2RM4000779	8.60	6.98	9.29	9.01	13.32	14.40	9.71	7.63	14.65					
NT2RM4000787	4.24	2.50	3.69	7.64	7.50	6.95	5.13	4.57	3.51	**	+			
NT2RM4000790	3.29	2.32	3.49	4.70	4.95	5.71	2.8	3.89	2.61	*	+			
NT2RM4000795	17.99	8.62	8.95	7.60	7.29	5.12	10.59	11.21	13.05					
NT2RM4000796	9.52	5.97	4.89	6.98	7.91	6.65	7.34	5.94	6.5					
NT2RM4000798	4.86	3.32	1.92	4.08	3.21	6.07	3.4	3.16	3.56					
NT2RM4000800	25.53	16.14	15.27	24.04	32.78	23.66	18.49	15.32	20.57					
NT2RM4000813	9.68	4.14	5.79	3.70	5.76	3.65	5.28	6.71	6.8					
NT2RM4000820	6.65	4.53	5.35	8.29	7.69	8.43	5.66	5.99	4.55	*	+			
NT2RM4000827	7.32	3.89	5.09	8.78	8.63	9.18	6.29	5.93	5.97	*	+			
NT2RM4000830	6.10	3.43	4.84	5.47	6.76	7.08	5.66	6.54	4.35					
NT2RM4000833	7.52	4.61	4.22	4.98	5.08	4.81	5.7	5.33	4.23					

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Table 239

NT2RM4000841	5.06	3.39	2.43	4.05	5.93	4.27	4.63	4.44	4.32				
NT2RM4000846	9.09	5.94	7.28	12.84	12.70	15.11	9.96	10.78	11.36	**	+	*	+
NT2RM4000848	7.88	5.40	5.25	6.98	11.06	5.33	7.53	6.82	8.25				
NT2RM4000852	6.75	4.64	5.34	13.69	17.70	14.08	11.97	13.34	10.93	**	+	**	+
NT2RM4000855	4.73	2.86	4.28	6.84	5.05	6.75	4.95	4.71	3.45	*	+		
NT2RM4000859	13.33	7.63	8.66	12.33	11.71	13.85	10.92	13.05	13.48				
NT2RM4000868	3.39	2.48	3.24	2.56	3.27	2.72	2.54	2.52	2.34				
NT2RM4000870	7.43	4.59	4.58	4.56	7.18	4.83	5.21	5.55	10.16				
NT2RM4000879	5.36	4.71	2.54	2.94	5.60	3.69	4.73	3.05	8.38				
NT2RM4000882	13.28	7.67	8.34	13.87	16.02	12.84	11.37	9.53	8.64				
NT2RM4000887	7.73	5.89	6.66	6.98	5.77	6.42	10.56	10.15	7.39				
NT2RM4000895	5.73	3.47	4.08	7.64	7.37	6.94	4.46	6.14	5.95	*	+		
NT2RM4000897	7.53	4.28	4.64	9.70	11.04	6.20	7.51	8.32	7.28				
NT2RM4000901	2.04	1.85	1.79	2.60	2.63	3.31	2.13	2.92	1.47	*	+		
NT2RM4000950	0.56	0.78	1.17	2.14	1.27	1.24	1.41	2.19	1.17				
NT2RM4000965	9.86	4.20	4.55	3.73	5.50	4.12	5.03	3.46	4.87				
NT2RM4000971	5.30	5.00	2.48	7.54	6.04	2.89	3.53	4.64	7.17				
NT2RM4000979	4.99	2.53	1.69	2.02	3.14	2.85	2.38	2.83	3.27				
NT2RM4000987	2.44	1.53	2.68	3.20	3.68	2.75	2.62	4.83	3.64				
NT2RM4000989	4.94	3.38	3.37	4.04	2.94	2.51	3.27	4.13	3.58				
NT2RM4000991	0.93	1.02	1.31	2.15	2.31	2.55	2.33	4.87	2.11	**	+		
NT2RM4000992	11.24	7.63	10.16	7.25	5.43	5.90	4.54	4.54	4.18	*	-	**	-
NT2RM4000996	4.06	2.34	3.75	9.54	9.91	8.12	3.46	4.48	3.87	**	+		
NT2RM4000997	9.49	3.35	2.92	6.90	7.64	7.96	5.25	6.12	5.29				
NT2RM4001001	22.10	15.26	10.21	12.02	9.69	11.49	22.6	17.92	9.97				
NT2RM4001002	5.24	3.19	3.25	8.21	8.99	8.70	5.14	6.05	8.69	**	+		
NT2RM4001016	4.56	3.14	3.04	3.93	5.46	2.92	3.16	3.93	3.9				
NT2RM4001025	115.98	53.32	70.45	58.33	60.27	42.54	40.15	40.87	41.74				
NT2RM4001027	0.14	0.43	0.68	0.22	0.31	0.94	0.68	1.67	1.36				
NT2RM4001032	1.80	1.46	0.81	3.10	2.87	2.32	1.9	2.71	1.77	*	+		
NT2RM4001047	1.37	0.95	0.95	2.05	2.61	2.62	1.72	2.11	1.51	**	+	*	+
NT2RM4001049	10.71	3.63	3.82	6.40	6.54	4.49	5.52	5.09	5.26				
NT2RM4001051	6.70	3.93	4.20	7.11	12.15	4.54	5.61	4.11	11.9				
NT2RM4001052	8.14	4.27	4.08	6.07	7.39	5.45	8.57	7.89	6.02				
NT2RM4001053	27.19	14.20	21.35	17.33	19.31	15.07	12.02	9.63	10.5				
NT2RM4001054	3.61	1.72	2.96	2.73	3.57	4.09	2.66	3.55	3.62				
NT2RM4001059	7.61	4.52	5.00	8.40	9.15	6.24	6.45	6.67	8.15				
NT2RM4001071	4.06	2.69	2.57	4.40	6.02	4.14	3.25	5.00	2.66				
NT2RM4001084	4.94	2.76	3.04	3.73	6.30	5.46	4.17	4.56	4.31				
NT2RM4001092	7.29	2.48	2.72	5.06	4.22	4.55	3.22	2.32	2.04				
NT2RM4001100	12.18	6.64	7.67	10.87	11.09	10.86	6.95	8.94	8.4				
NT2RM4001116	1.86	1.58	1.69	2.27	2.62	2.03	2.58	1.98	1.6	*	+		
NT2RM4001119	4.12	2.84	2.77	3.79	5.02	3.34	2.23	3.61	4.07				
NT2RM4001140	16.77	10.70	11.39	11.80	11.74	11.76	7	6.89	6.74			*	-
NT2RM4001148	13.85	6.50	6.41	8.02	8.87	5.20	9.72	12.16	8.38				
NT2RM4001151	3.04	2.82	2.68	3.38	3.91	4.17	3.34	5.07	4.04	*	+		
NT2RM4001155	3.85	1.95	2.51	2.48	2.96	3.06	2.88	3.51	1.43				
NT2RM4001157	4.58	2.01	1.48	3.42	3.84	2.43	3.68	3.71	2.97				
NT2RM4001160	6.16	2.57	2.15	5.06	4.60	3.14	2.68	2.65	4.39				
NT2RM4001163	28.46	18.93	15.30	35.95	37.53	27.65	20.27	18.39	15.85				
NT2RM4001187	5.15	3.42	2.71	6.56	6.27	4.41	3.87	4.84	4.54				
NT2RM4001191	4.08	1.58	2.81	4.80	3.69	3.67	1.67	2.71	2.13				
NT2RM4001200	5.87	3.23	4.14	11.90	10.51	10.62	3.7	6.92	6.13	**	+		
NT2RM4001203	5.49	3.54	4.23	5.75	6.16	5.89	3.38	6.37	4.68				
NT2RM4001204	1.21	0.66	1.10	1.28	1.38	1.01	0.49	2.21	0.81				
NT2RM4001217	2.79	2.05	1.40	2.03	2.19	2.27	3.13	2.64	2.28				

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Table 240

NT2RM4001245	8.44	3.64	3.02	4.82	4.98	4.20	6.1	4.52	4.33				
NT2RM4001247	3.08	1.77	1.70	4.91	4.46	4.61	4.28	3.78	3.75	**	+	*	+
NT2RM4001256	2.68	1.97	1.44	2.55	3.37	2.58	2.83	3.46	2.47				
NT2RM4001258	3.01	1.08	1.34	2.58	2.80	3.08	2.91	3.65	2.07				
NT2RM4001267	3.85	1.81	3.09	2.74	2.85	2.20	1.95	2.54	1.48				
NT2RM4001273	4.22	3.00	2.18	5.27	4.13	4.07	4.07	4.58	3.5				
NT2RM4001281	4.83	2.17	2.72	3.21	3.18	3.70	4.92	3.04	3.76				
NT2RM4001286	200.90	135.14	135.42	284.75	209.56	246.97	164.2	134.29	151.3	*	+		
NT2RM4001290	9.86	4.80	5.69	5.57	5.18	5.39	8.08	8.05	9.32				
NT2RM4001309	4.86	3.06	2.25	4.98	6.28	4.18	3.55	4.91	3.92				
NT2RM4001313	5.02	3.13	3.38	10.23	11.21	8.30	5.64	5.09	6.07	**	+		
NT2RM4001316	3.10	1.87	1.63	4.90	3.32	2.72	2.34	3.07	2.48				
NT2RM4001320	3.57	1.99	1.80	4.35	3.95	2.99	2.67	3.38	1.95				
NT2RM4001321	2.36	1.76	2.19	4.88	3.23	3.63	2.96	3.26	2.18	*	+		
NT2RM4001325	4.26	2.86	2.43	3.61	4.06	3.37	3.66	2.87	3.97				
NT2RM4001333	9.63	4.30	7.26	19.73	18.36	12.94	10.99	11.48	14.86	*	+		
NT2RM4001340	15.08	7.81	6.58	8.67	7.96	8.93	6.1	7.09	9.47				
NT2RM4001344	5.69	1.98	2.69	4.58	3.47	5.21	3.57	4.25	3.42				
NT2RM4001347	2.27	2.16	1.78	2.66	5.15	3.34	3.4	3.43	2.43			*	+
NT2RM4001357	6.92	4.15	5.35	6.32	6.10	5.55	4.34	5.12	6.64				
NT2RM4001360	5.77	3.29	3.38	4.26	4.44	4.12	4.69	3.72	3.64				
NT2RM4001371	4.54	2.79	3.83	7.15	6.45	5.83	3.62	4.03	2.04	*	+		
NT2RM4001377	10.12	5.47	3.83	5.72	6.90	5.90	6.53	6.36	7.54				
NT2RM4001382	27.64	18.16	15.30	26.18	25.29	24.42	17.41	14.13	18.42				
NT2RM4001384	2.18	1.75	1.21	2.08	4.07	2.57	1.73	1.84	2.63				
NT2RM4001400	1.97	1.68	1.05	5.11	4.43	3.04	4.16	3.64	2.67	*	+	*	+
NT2RM4001409	2.47	2.29	2.32	4.11	6.40	4.45	3.11	3.39	3.96	*	+	*	+
NT2RM4001410	3.95	1.97	3.57	4.82	7.04	5.31	4.02	3.43	5.37	*	+		
NT2RM4001411	0.83	0.77	0.89	2.84	2.80	2.65	2.26	2.50	1.14	**	+		
NT2RM4001412	3.72	2.65	2.59	3.20	3.12	4.78	3.05	4.81	2.12				
NT2RM4001414	4.96	2.76	1.91	3.88	3.24	3.95	8.58	4.11	4.61				
NT2RM4001436	10.71	5.74	4.93	8.68	8.18	5.45	5.99	5.69	6.31				
NT2RM4001437	3.31	2.10	1.69	4.84	3.86	4.25	2.81	3.12	5.09	*	+		
NT2RM4001444	17.08	11.93	9.02	14.24	23.31	17.28	9.91	10.57	15.43				
NT2RM4001454	1.52	1.27	0.92	2.66	2.43	3.18	2.53	2.75	3.91	**	+	*	+
NT2RM4001455	1.97	1.35	0.94	1.41	2.43	2.26	1.92	2.49	2.53				
NT2RM4001483	8.15	6.48	6.83	17.59	20.73	16.59	7.89	9.09	9.1	**	+		
NT2RM4001489	2.71	2.11	2.58	4.94	4.32	3.30	3.82	3.97	2.42	*	+		
NT2RM4001495	18.14	8.14	7.60	6.61	8.27	8.97	13.02	9.27	7.52				
NT2RM4001499	12.77	8.16	6.92	3.39	3.00	2.48	3.08	3.42	2.67	*	-	*	-
NT2RM4001515	3.27	1.91	1.68	2.35	4.06	1.83	1.52	2.44	1.37				
NT2RM4001519	5.12	2.84	4.04	2.41	3.33	2.32	2.38	4.57	1.4				
NT2RM4001522	6.04	4.16	3.86	10.17	8.78	6.98	5.57	5.11	4.64	*	+		
NT2RM4001523	2.87	2.23	1.80	2.40	4.75	2.55	2.53	3.39	1.48				
NT2RM4001550	9.31	4.21	5.82	7.65	10.18	9.65	4.79	5.78	4.65				
NT2RM4001553	13.10	6.91	9.72	15.17	15.42	12.48	9.84	10.30	8.03				
NT2RM4001554	6.26	1.91	2.23	3.10	3.46	2.19	2.03	3.40	3.47				
NT2RM4001557	1.82	1.50	1.72	2.44	4.16	3.37	2.15	2.77	2.22	*	+	*	+
NT2RM4001565	4.45	2.55	3.09	4.16	3.19	4.16	3.34	4.45	3.44				
NT2RM4001566	8.15	6.36	5.54	21.07	22.32	19.38	14.82	13.59	12.47	**	+	**	+
NT2RM4001569	1.07	2.72	1.12	1.58	1.44	1.53	1.39	2.06	0.92				
NT2RM4001579	2.12	1.63	1.82	2.74	2.69	2.72	4.53	3.33	2.15	**	+		
NT2RM4001582	2.62	2.33	2.55	3.71	4.48	4.20	3.06	3.87	3.26	**	+	*	+
NT2RM4001589	8.35	5.09	6.66	12.13	12.37	10.11	11.51	12.65	14.42	*	+	**	+
NT2RM4001592	3.41	2.19	1.04	2.79	0.97	1.51	1.07	1.30	2.99				
NT2RM4001594	6.13	3.39	4.24	4.38	6.50	3.46	3.95	3.79	5.84				

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Table 241

NT2RM4001597	9.12	5.34	5.09	9.11	10.92	8.47	7.88	8.77	8.89				
NT2RM4001605	2.56	1.50	0.61	1.85	2.19	2.01	1.99	3.21	1.69				
NT2RM4001609	89.25	51.45	54.24	71.13	77.23	52.58	39.95	36.11	41.37				
NT2RM4001610	12.00	8.23	7.07	12.20	9.44	8.76	11.99	11.53	14.72				
NT2RM4001611	2.42	1.85	2.60	3.39	3.10	2.31	2.05	3.53	1.91				
NT2RM4001618	9.99	6.27	7.80	11.85	10.16	11.99	7.45	6.31	7.61				
NT2RM4001622	26.67	8.64	17.82	10.07	12.08	11.47	11.1	11.92	5.45				
NT2RM4001624	6.68	3.27	2.64	4.78	7.08	4.67	4.35	3.33	5.32				
NT2RM4001625	6.46	4.15	3.63	6.09	6.98	6.57	5.81	6.49	4.68				
NT2RM4001629	3.08	1.43	1.44	3.13	3.87	3.98	3.34	3.46	2.65				
NT2RM4001632	29.86	24.78	26.14	43.08	46.42	34.45	16.71	16.75	13.76	*	+	**	-
NT2RM4001642	2.85	2.24	1.81	3.57	2.70	1.88	1.79	3.45	2.28				
NT2RM4001647	17.28	7.78	9.99	11.15	12.30	10.77	8	8.01	6.38				
NT2RM4001650	0.99	1.51	1.38	2.58	3.80	3.02	1.93	2.32	1.3	**	+		
NT2RM4001662	7.87	3.75	2.87	5.79	6.00	4.16	5.7	4.40	5.34				
NT2RM4001666	5.31	2.73	1.99	5.11	5.72	2.91	2.77	3.37	5				
NT2RM4001670	11.64	5.63	4.93	10.66	7.77	4.83	7.89	5.98	5.85				
NT2RM4001682	7.63	4.69	7.88	11.61	13.13	10.67	7.98	7.62	9.49	*	+		
NT2RM4001710	3.51	1.93	3.14	2.89	2.81	2.52	2.94	3.14	3.23				
NT2RM4001712	4.09	1.48	2.36	6.28	6.47	3.67	3.14	2.79	2.86				
NT2RM4001714	9.74	6.27	6.28	8.33	6.94	5.10	4.33	4.54	3.78				
NT2RM4001715	9.70	6.79	8.58	10.69	5.46	8.50	6.49	7.88	6.36				
NT2RM4001727	9.24	3.95	4.64	8.67	8.28	6.42	5.55	4.51	4.54				
NT2RM4001731	13.05	6.04	4.43	9.34	11.19	3.94	6.46	7.94	7.44				
NT2RM4001735	10.60	7.33	6.23	6.67	8.99	10.11	4.77	6.71	9.86				
NT2RM4001739	4.78	4.21	5.14	4.57	4.78	3.04	2.46	4.65	3.94				
NT2RM4001741	9.97	6.74	4.99	10.67	11.48	8.89	9.93	7.28	7.04				
NT2RM4001746	4.40	2.92	3.08	6.46	6.23	6.82	4.23	5.87	3.98	**	+		
NT2RM4001754	5.88	4.22	4.77	3.77	2.85	3.40	2.26	3.95	2.51	*	-	*	-
NT2RM4001757	3.98	2.34	2.64	6.30	5.38	5.11	4.27	5.17	3.56	*	+		
NT2RM4001758	4.03	1.40	1.41	2.95	3.14	0.90	2.11	1.49	2.63				
NT2RM4001768	9.33	3.18	2.78	8.73	9.23	6.03	4.74	5.46	7.46				
NT2RM4001775	1.60	0.85	0.48	1.68	1.19	1.13	0.51	1.89	2.16				
NT2RM4001776	1.24	0.67	0.70	2.08	1.65	1.01	0.84	1.95	1.26				
NT2RM4001783	3.30	1.81	1.77	3.52	4.08	2.55	1.62	3.51	1.6				
NT2RM4001793	5.58	4.64	4.50	8.16	8.15	6.01	4.19	4.76	4.23	*	+		
NT2RM4001810	3.48	2.21	2.29	3.20	3.69	2.65	2.04	3.39	2.03				
NT2RM4001813	3.11	0.62	1.16	2.31	2.18	1.56	2	3.91	2.71				
NT2RM4001818	3.22	2.40	2.49	5.46	4.70	3.11	4.89	3.44	5.14			*	+
NT2RM4001819	11.19	5.78	6.63	9.55	9.42	7.47	10.81	7.51	7.34				
NT2RM4001823	3.13	1.86	1.29	2.61	3.40	2.11	3.37	1.94	1.66				
NT2RM4001828	8.26	6.14	6.03	15.07	18.35	11.62	9.17	6.53	11.85	*	+		
NT2RM4001835	3.34	2.52	2.50	5.07	6.41	5.16	6.93	7.44	8.93	**	+	**	+
NT2RM4001836	3.42	2.60	1.50	3.55	5.57	1.89	3.02	2.62	2.83				
NT2RM4001841	7.03	4.07	5.20	3.69	3.84	5.28	4.46	6.00	6.72				
NT2RM4001842	2.54	1.03	0.84	4.40	5.14	3.61	2.15	3.10	2.2	*	+		
NT2RM4001843	7.33	3.08	3.29	4.61	4.36	4.19	6.63	4.29	4.74				
NT2RM4001856	7.28	3.36	2.92	6.92	6.61	6.34	6.76	4.92	39.96				
NT2RM4001858	4.41	2.01	2.89	4.19	5.25	3.77	3.99	3.14	3.55				
NT2RM4001861	15.16	9.14	7.90	8.10	8.14	9.12	7.69	7.66	6.31				
NT2RM4001863	5.18	5.03	4.89	5.35	5.57	4.84	4.1	2.95	4.25			*	-
NT2RM4001865	4.40	1.50	1.71	4.54	5.77	6.01	3.87	4.69	4.27	*	+		
NT2RM4001869	6.80	4.12	4.66	5.90	4.78	4.71	3.79	3.46	3.8				
NT2RM4001873	9.91	7.88	7.75	6.45	7.32	6.28	5.39	4.87	5.18			**	-
NT2RM4001876	20.13	9.94	9.70	9.48	8.26	10.48	13.84	12.07	14.41				
NT2RM4001880	6.36	4.04	3.70	6.23	5.32	5.66	5.53	4.83	6.28				

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Table 242

NT2RM4001885	12.23	5.39	5.31	15.89	14.89	14.46	9.96	8.97	11.11	*	+		
NT2RM4001889	17.90	10.90	9.56	25.74	24.82	26.44	14.72	12.91	12.79	**	+		
NT2RM4001894	3.99	3.32	3.07	4.15	4.34	4.16	5.09	3.83	3.49				
NT2RM4001897	4.68	3.36	3.66	5.57	7.84	6.03	9.17	7.60	6.62	*	+	**	+
NT2RM4001899	4.37	2.59	2.66	5.10	4.85	5.00	3.8	4.79	3.2	*	+		
NT2RM4001905	14.13	19.47	18.60	6.62	5.76	7.88	4.18	4.49	4.16	**	-	**	-
NT2RM4001922	4.57	2.06	2.67	5.98	6.27	5.24	3.2	3.09	2.6	*	+		
NT2RM4001930	7.89	5.36	5.01	6.12	7.65	5.79	3.76	3.60	3.88				
NT2RM4001938	3.35	3.03	2.31	4.03	4.25	3.01	4.12	3.88	3.78			*	+
NT2RM4001940	8.88	7.21	7.25	7.65	9.61	6.94	5.41	5.68	5.3			*	-
NT2RM4001942	48.53	24.69	36.35	81.10	98.59	62.39	57.57	65.30	79.98	*	+	*	+
NT2RM4001953	4.86	4.02	3.80	11.16	10.73	8.47	5.44	7.13	6.71	**	+	*	+
NT2RM4001965	3.95	3.09	2.78	3.89	4.20	5.02	3.08	4.34	1.87				
NT2RM4001966	4.92	2.59	2.69	5.18	4.42	3.96	3.32	4.68	3.49				
NT2RM4001969	4.52	3.56	2.88	4.01	4.54	3.26	3.65	2.05	3.76				
NT2RM4001974	3.18	2.93	2.68	3.45	3.46	4.29	4	3.93	2.9				
NT2RM4001979	7.10	5.28	4.65	8.51	9.51	9.19	5.57	5.12	5.65	*	+		
NT2RM4001980	8.43	6.53	5.48	9.14	11.80	9.30	5.72	6.09	7.18				
NT2RM4001984	0.37	0.36	2.68	1.04	2.24	1.27	3.83	2.41	1.54				
NT2RM4001987	5.43	3.22	4.46	5.44	5.41	4.74	6.11	4.65	5.13				
NT2RM4002013	4.01	2.99	3.04	5.45	6.17	4.31	4.16	6.39	4.96	*	+		
NT2RM4002018	1.35	1.30	1.91	4.17	2.80	1.86	2.66	3.82	2.52			*	+
NT2RM4002033	5.95	4.44	3.94	8.70	9.58	8.70	6.99	4.97	5.08	**	+		
NT2RM4002034	10.16	6.70	5.00	9.69	8.87	7.70	7.22	5.62	6.43				
NT2RM4002044	17.29	9.91	9.34	16.54	14.23	14.16	9.93	9.20	9.33				
NT2RM4002047	4.89	3.52	4.39	7.70	9.18	8.38	5.94	5.42	6.2	**	+	*	+
NT2RM4002054	5.22	3.24	3.62	4.72	4.27	3.95	3.64	4.57	3.02				
NT2RM4002055	4.93	3.27	3.62	3.58	4.71	3.15	4.05	4.74	4.4				
NT2RM4002059	10.05	6.75	9.67	10.16	11.99	13.43	18.25	24.17	33.19			*	+
NT2RM4002061	3.42	2.42	3.12	3.99	4.28	3.66	2.26	2.93	1.81	*	+		
NT2RM4002062	6.37	2.90	3.38	2.10	2.75	3.44	2.98	2.78	3.12				
NT2RM4002063	8.92	6.28	4.96	9.35	7.20	6.28	7.35	7.35	6.46				
NT2RM4002066	5.12	2.57	2.72	3.13	3.43	2.84	3.67	3.65	2.97				
NT2RM4002067	1.89	1.36	1.11	3.88	3.13	3.49	1.44	3.55	1.91	**	+		
NT2RM4002073	3.81	3.18	2.17	3.78	3.91	3.14	2.82	4.59	3.46				
NT2RM4002074	3.75	3.15	4.02	2.89	4.67	3.46	2.89	2.92	2.59			*	-
NT2RM4002075	1.30	1.13	1.76	2.76	2.64	2.94	1.69	2.40	1.5	**	+		
NT2RM4002076	4.00	1.21	3.46	2.32	2.53	2.49	2.84	3.24	1.6				
NT2RM4002078	12.66	8.15	5.73	7.75	7.44	9.12	8.77	7.66	8.72				
NT2RM4002081	5.48	5.00	3.54	7.62	9.31	8.00	5.52	7.35	6.24	**	+		
NT2RM4002082	4.26	2.31	2.02	3.34	2.38	2.66	2.89	2.98	2.86				
NT2RM4002093	3.89	2.69	2.12	7.05	6.79	4.47	2.74	4.50	3.5	*	+		
NT2RM4002109	5.34	3.93	2.60	5.27	7.18	5.20	3.25	3.84	4.24				
NT2RM4002115	3.73	2.51	2.56	3.60	4.16	3.32	2.9	3.99	2.74				
NT2RM4002118	2.39	1.49	2.46	3.46	6.34	3.85	3.47	4.78	5.61			*	+
NT2RM4002128	1.76	1.98	1.98	2.53	2.32	2.56	1.95	1.96	1.45	**	+		
NT2RM4002137	5.40	3.31	3.77	3.32	5.16	4.10	4.08	2.63	2.49				
NT2RM4002139	6.38	4.93	5.07	14.74	15.06	13.57	6.58	7.18	6.59	**	+		
NT2RM4002140	7.07	3.90	5.01	9.78	11.72	9.95	6.8	5.99	6.18	**	+		
NT2RM4002145	5.69	2.65	3.96	6.30	6.51	4.16	4.2	6.86	5.05				
NT2RM4002146	12.58	8.18	8.37	8.91	7.31	8.60	4.94	6.93	3.9				
NT2RM4002161	1.51	1.71	1.05	2.14	2.32	1.65	1.38	2.18	1.6				
NT2RM4002174	2.04	1.62	2.29	4.40	6.82	5.43	2.41	4.19	3.45	**	+		
NT2RM4002178	4.27	1.80	4.02	7.72	6.53	7.07	4.59	6.24	4.61	*	+		
NT2RM4002180	14.71	6.92	6.30	9.50	9.96	6.78	4.56	4.83	5.69				
NT2RM4002185	5.31	3.85	4.04	4.39	4.78	3.75	5.7	4.91	5.17				

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Table 243

NT2RM4002189	27.09	13.74	15.74	14.48	15.82	14.29	21.97	17.24	13.45				
NT2RM4002194	14.06	6.46	6.54	8.20	8.96	5.67	5.24	4.78	7.73				
NT2RM4002198	9.72	5.05	4.64	9.60	7.14	7.42	3.99	6.05	4.24				
NT2RM4002205	6.04	2.24	4.01	10.17	8.07	7.85	3.89	6.45	5.48	*	+		
NT2RM4002213	8.85	5.39	4.89	8.71	11.13	8.58	6.75	7.49	6.59				
NT2RM4002216	13.98	11.40	13.83	9.67	12.26	12.25	5.51	6.10	8.64			**	-
NT2RM4002226	11.71	3.35	5.45	7.00	6.75	5.32	2.56	2.81	2.06				
NT2RM4002237	12.13	5.23	4.66	6.69	6.79	4.62	5.28	4.25	5.13				
NT2RM4002240	3.83	1.22	1.76	2.57	3.67	3.49	1.94	2.86	3.13				
NT2RM4002251	4.23	2.41	3.59	5.58	5.63	2.99	3.14	4.22	3.57				
NT2RM4002256	9.61	4.69	5.30	9.65	8.00	8.72	6.39	6.24	6.69				
NT2RM4002262	2.51	1.66	3.08	3.94	4.02	2.93	2.54	4.64	4.87				
NT2RM4002266	3.81	3.04	1.77	5.13	5.13	3.56	1.74	3.97	3				
NT2RM4002276	6.07	4.19	4.53	7.03	5.98	6.29	6.42	7.40	4.56				
NT2RM4002278	5.55	3.50	2.06	5.22	5.68	3.41	2.26	1.92	4.58				
NT2RM4002281	10.82	3.97	3.78	8.02	12.45	5.87	8.47	7.73	8.03				
NT2RM4002287	4.73	2.14	2.11	4.48	2.86	2.45	3.19	4.14	1.9				
NT2RM4002294	3.56	2.28	1.67	6.99	5.40	3.49	3.08	4.20	3.5				
NT2RM4002298	4.25	1.83	2.68	5.32	3.86	5.10	6.58	7.80	6.73			**	+
NT2RM4002301	2.19	2.10	1.85	3.43	4.22	3.48	1.84	3.94	2.05	**	+		
NT2RM4002306	4.28	2.89	2.26	4.38	4.65	4.86	3.01	4.34	2.42				
NT2RM4002323	4.07	3.11	3.95	9.92	6.06	6.87	4.61	4.01	2.32	*	+		
NT2RM4002334	48.90	21.85	22.81	35.78	25.59	28.97	30.63	31.70	22.58				
NT2RM4002339	2.06	1.58	1.46	1.24	1.64	1.38	3.19	1.21	1.93				
NT2RM4002344	3.34	2.36	2.32	3.06	3.36	3.28	1.98	2.28	1.57				
NT2RM4002345	3.14	4.48	1.33	2.81	6.18	3.52	3.97	3.81	7.59				
NT2RM4002352	2.56	1.55	1.37	2.09	1.90	1.83	1.8	2.16	1.75				
NT2RM4002362	10.19	5.95	5.50	3.14	3.38	3.88	2.99	2.56	2.32			*	-
NT2RM4002373	3.73	2.27	4.81	3.06	4.43	4.48	1.89	2.78	3.21				
NT2RM4002374	2.46	1.36	2.00	4.92	6.85	2.91	2.01	2.17	2.46				
NT2RM4002376	3.65	2.05	2.36	5.15	3.88	5.04	5.2	2.97	2.99	*	+		
NT2RM4002383	5.41	2.46	3.35	8.94	8.52	7.85	5.76	4.08	7.78	**	+		
NT2RM4002390	7.22	2.53	2.49	3.89	3.09	3.46	2.47	3.20	2.59				
NT2RM4002398	4.68	2.42	2.88	5.08	6.85	4.30	3.82	2.28	3.63				
NT2RM4002409	2.87	2.53	3.04	4.21	5.07	3.80	3.49	3.93	3.64	*	+	*	+
NT2RM4002414	5.03	1.84	3.97	3.80	4.16	6.28	4.49	4.44	4.68				
NT2RM4002438	5.21	2.42	2.20	4.07	3.59	4.94	3.44	3.46	2.5				
NT2RM4002440	4.95	2.33	3.53	5.69	5.26	3.20	3.34	4.02	4.39				
NT2RM4002446	6.41	3.72	3.77	5.16	5.23	4.99	5.81	3.91	5.57				
NT2RM4002450	7.34	5.13	5.19	4.41	3.88	3.16	3.9	3.82	4.13				
NT2RM4002452	4.76	3.56	2.63	3.31	4.00	4.75	2.58	2.59	2.32				
NT2RM4002457	3.97	2.35	2.27	5.42	4.08	5.14	4.64	3.85	2.87	*	+		
NT2RM4002458	2.05	1.17	1.07	1.55	3.27	2.46	2.27	3.06	1.92				
NT2RM4002460	1.51	0.73	1.48	0.65	1.16	0.85	1.55	1.39	1.26				
NT2RM4002464	2.69	1.95	2.48	3.72	3.71	4.31	2.38	2.92	1.83	**	+		
NT2RM4002479	6.89	5.60	6.27	9.61	8.13	4.62	4.88	6.96	5.42				
NT2RM4002482	35.61	22.59	16.97	21.71	19.69	20.16	30.11	17.88	24.23				
NT2RM4002489	15.59	8.96	10.80	10.87	12.64	11.89	10.58	8.12	11.95				
NT2RM4002493	3.66	2.45	2.96	3.64	2.32	2.09	3.63	3.17	2.29				
NT2RM4002499	39.72	27.06	27.17	54.95	67.76	43.13	21.05	20.01	15.47	*	+		
NT2RM4002504	10.06	5.00	4.83	15.16	13.66	11.30	9.77	10.12	11.17	*	+		
NT2RM4002506	3.00	2.28	3.10	3.05	3.95	4.66	3.19	3.46	3.27				
NT2RM4002510	1.71	1.62	1.42	3.05	3.64	3.86	2.57	2.61	2.07	**	+	*	+
NT2RM4002527	1.36	1.99	1.93	1.99	2.17	2.01	1.62	2.61	1.13				
NT2RM4002532	8.36	3.92	4.29	7.17	9.98	8.89	6.69	5.89	6.32				
NT2RM4002534	5.34	2.37	2.56	3.48	4.24	3.83	3.66	4.16	3.67				

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Table 244

NT2RM4002535	8.63	5.41	4.92	15.46	13.83	13.63	8.73	8.80	8.02	**	+		
NT2RM4002554	3.24	2.37	1.91	1.77	3.57	2.77	2.58	2.42	1.39				
NT2RM4002558	3.05	3.08	3.12	4.82	3.64	4.78	4.67	4.24	3.5	*	+	*	+
NT2RM4002565	4.27	2.27	3.74	8.08	6.46	7.43	4.53	4.18	4.36	**	+		
NT2RM4002567	2.07	1.22	2.13	2.02	9.16	3.14	2.05	3.10	2.71				
NT2RM4002571	4.37	2.84	3.54	4.69	4.81	3.75	4.16	4.57	3.27				
NT2RM4002572	6.03	2.28	2.98	6.08	6.68	4.99	9.74	8.44	9.5			*	+
NT2RM4002577	2.75	1.19	0.59	1.71	1.14	1.51	6.59	4.68	6.71			**	+
NT2RM4002583	3.95	2.68	2.93	2.91	3.44	3.57	3.57	3.67	3.56				
NT2RM4002584	6.72	4.52	4.49	7.70	8.13	5.82	4.85	4.09	4.77				
NT2RM4002593	11.06	6.50	9.20	6.84	5.82	5.78	2.04	3.51	4.47			*	-
NT2RM4002594	4.49	2.50	2.60	5.70	6.28	5.59	4.77	7.23	6.06	*	+	*	+
NT2RM4002604	4.69	2.15	3.00	3.62	4.47	4.27	3.38	3.51	3.57				
NT2RM4002614	2.09	1.88	1.83	3.05	2.85	2.71	1.21	3.15	1.87	**	+		
NT2RM4002616	5.30	2.89	2.15	2.37	1.56	2.52	2.81	1.79	2.9				
NT2RM4002623	8.57	2.95	4.75	3.25	4.49	3.44	2.87	3.18	2.88				
NT2RM4002634	1.64	1.74	1.53	1.95	2.12	2.72	2.59	3.50	2.79			**	+
NT2RM4002636	5.12	3.99	4.07	4.89	3.26	2.51	3.1	3.30	2.24			*	-
NT2RP1000002	4.91	2.69	3.55	5.37	6.59	6.81	5.02	6.11	5.97	*	+		
NT2RP1000006	3.58	2.73	3.36	3.30	5.24	3.97	3.46	5.04	3.59				
NT2RP1000015	0.58	0.54	1.13	1.73	1.75	2.13	1.06	2.60	1.34	**	+		
NT2RP1000018	0.26	0.38	0.59	1.15	1.19	1.44	1.05	2.21	0.52	**	+		
NT2RP1000034	281.35	132.61	141.44	137.16	124.07	106.57	66.03	58.57	54.32				
NT2RP1000035	3.85	3.38	2.73	3.70	4.44	3.26	2.6	2.77	2.19				
NT2RP1000040	1.60	1.01	1.16	1.82	1.72	0.90	1.72	1.93	1.4				
NT2RP1000042	0.16	0.85	0.49	1.42	1.37	0.52	0.89	2.70	1.63				
NT2RP1000048	3.91	1.94	1.67	2.45	3.78	2.00	3.04	5.80	4.69				
NT2RP1000050	2.17	1.06	1.90	2.79	3.16	3.31	1.43	4.06	2.02	*	+		
NT2RP1000056	29.42	14.22	19.60	15.96	16.06	15.82	8.26	10.94	9.03				
NT2RP1000058	1.76	1.01	1.59	2.63	1.51	1.74	0.73	1.28	0.3				
NT2RP1000063	2.86	1.68	1.32	1.33	2.84	1.66	1.17	1.53	1.43				
NT2RP1000068	2.57	1.65	0.98	2.49	2.52	1.99	1.28	2.09	2.14				
NT2RP1000072	111.07	54.80	68.45	57.17	59.96	64.56	51.74	45.59	52.17				
NT2RP1000073	0.97	0.59	0.56	1.83	1.57	2.36	0.84	2.78	1.72	*	+		
NT2RP1000078	3.33	1.48	2.67	2.36	2.30	2.50	1.17	3.68	1.39				
NT2RP1000079	2.67	0.92	1.74	2.69	2.08	2.10	4.5	6.28	4.63			*	+
NT2RP1000080	7.28	4.50	5.28	5.11	5.46	5.42	2.3	4.02	3.44				
NT2RP1000086	4.35	3.00	3.48	3.24	3.23	2.33	1.02	2.72	1.4			*	-
NT2RP1000087	5.00	2.82	2.77	4.73	5.17	3.70	4.25	2.63	3.17				
NT2RP1000089	21.30	13.02	9.99	15.70	10.56	8.76	7.11	5.03	7.52				
NT2RP1000090	62.12	34.52	35.37	65.14	57.48	42.93	29.21	27.16	16.48				
NT2RP1000100	2.17	0.88	1.25	1.24	1.63	1.66	0.75	2.69	2.15				
NT2RP1000101	6.92	3.86	4.62	6.27	8.56	8.35	6.29	5.31	6.14				
NT2RP1000111	3.13	2.02	3.20	4.79	4.46	1.70	2.06	3.98	4.56				
NT2RP1000112	1.19	1.17	1.40	1.98	2.39	2.90	2.08	3.24	1.09	*	+		
NT2RP1000124	2.04	1.79	2.18	5.67	6.32	7.61	0.92	3.26	4.08	**	+		
NT2RP1000125	13.33	6.69	5.55	16.93	13.49	11.53	18.17	14.66	19.62			*	+
NT2RP1000129	8.42	3.01	2.92	5.33	4.43	3.32	3.8	3.24	4.62				
NT2RP1000130	3.80	3.59	3.16	6.14	5.63	6.01	3.49	3.06	4.37	**	+		
NT2RP1000154	2.77	1.66	1.73	4.97	6.35	4.78	3.19	4.61	2.92	**	+		
NT2RP1000163	2.54	1.56	0.69	1.65	3.20	1.85	0.24	3.07	0.88				
NT2RP1000170	1.25	0.62	0.44	1.93	1.94	1.90	0.89	3.09	1.57	**	+		
NT2RP1000174	0.77	0.39	0.59	0.80	1.14	0.73	0.83	1.30	0.25				
NT2RP1000181	15.66	7.51	13.59	20.37	20.72	18.84	8.95	8.78	5.68	*	+		
NT2RP1000191	2.05	1.96	1.05	3.54	1.96	2.31	1.34	1.45	2.86				
NT2RP1000202	1.43	1.24	0.92	2.91	2.20	1.99	0.8	2.37	2.35	*	+		

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Table 245

NT2RP1000239	0.54	0.73	0.33	1.02	1.34	0.58	0.16	1.81	1.18				
NT2RP1000243	0.84	0.90	0.58	2.06	1.73	0.89	0.86	2.41	1.44				
NT2RP1000255	0.75	0.34	1.01	1.49	0.71	0.80	0.75	1.85	0.92				
NT2RP1000259	1.78	1.74	1.10	4.78	3.63	3.84	2.82	4.39	2.57	**	+	*	+
NT2RP1000261	1.08	0.77	0.32	2.74	1.80	1.60	0.7	2.51	1.42	*	+		
NT2RP1000269	12.70	6.05	5.79	12.05	12.78	10.09	7.5	10.31	8.4				
NT2RP1000271	65.05	27.46	27.30	118.92	88.05	70.43	44.58	28.04	22.55				
NT2RP1000272	15.64	8.87	8.62	11.91	10.97	10.04	8.77	5.04	6.08				
NT2RP1000279	3.64	2.60	2.62	4.01	4.52	4.50	3.4	3.60	2.95	*	+		
NT2RP1000290	31.80	25.40	25.59	36.52	40.72	40.15	26.39	22.95	29.24	**	+		
NT2RP1000293	8.90	5.15	6.17	9.07	11.34	10.12	7.62	7.73	8.67				
NT2RP1000300	21.75	19.20	18.07	20.53	28.21	20.72	16.45	24.53	12.12				
NT2RP1000324	12.47	5.32	8.89	10.68	13.57	9.75	6.98	9.83	9.18				
NT2RP1000325	91.19	35.26	49.60	54.44	61.67	55.26	47.32	30.15	44.99				
NT2RP1000326	10.60	7.28	6.00	12.46	8.25	10.43	7.71	8.51	5.43				
NT2RP1000331	13.85	7.24	6.82	12.25	10.31	7.00	5.01	4.72	3.71				
NT2RP1000333	12.54	6.22	6.09	8.86	8.17	8.74	6.53	7.71	7.88				
NT2RP1000336	1.87	1.73	1.02	1.35	1.53	1.21	3.14	2.70	2.83			*	+
NT2RP1000347	2.75	2.10	2.88	2.09	2.48	2.62	1.53	2.25	0.84				
NT2RP1000348	1.47	0.48	0.33	1.45	1.42	2.72	1.13	1.89	0.66				
NT2RP1000349	0.93	0.52	0.64	1.41	1.77	1.72	0.95	0.90	1.19	**	+		
NT2RP1000353	40.50	18.12	20.02	27.21	16.43	19.17	10.71	8.40	12.57				
NT2RP1000356	39.98	22.39	20.90	32.15	26.26	25.06	14.83	10.10	14.28				
NT2RP1000357	13.61	7.81	6.20	11.20	13.90	12.68	8.98	8.00	11.38				
NT2RP1000358	11.64	5.39	5.27	10.20	9.77	8.75	7.77	6.88	9.19				
NT2RP1000360	26.32	15.93	17.17	17.83	19.58	19.99	16.48	15.94	15.67				
NT2RP1000363	22.05	14.66	16.07	21.39	24.54	24.53	22.26	17.18	17.26				
NT2RP1000376	5.84	3.91	5.30	4.51	6.40	6.42	7.18	6.13	5.77				
NT2RP1000386	31.79	21.04	23.39	64.26	64.31	34.90	56.81	60.95	58.22	*	+	**	+
NT2RP1000407	0.29	0.73	0.45	0.62	0.61	0.29	1.08	0.88	0.22				
NT2RP1000409	2.22	1.91	0.68	2.83	3.38	2.80	2.71	1.86	1.7				
NT2RP1000413	7.71	3.51	3.63	7.04	7.63	7.01	5.32	4.65	6.75				
NT2RP1000416	2.07	0.73	0.71	1.73	2.70	2.64	1.38	1.53	1.42				
NT2RP1000418	0.88	0.78	0.91	2.07	1.77	2.03	1.84	2.71	1.4	**	+	*	+
NT2RP1000420	0.51	0.68	0.34	1.31	0.46	1.21	1.33	1.52	0.65				
NT2RP1000434	0.66	0.29	2.53	1.80	1.28	1.15	1.63	2.36	0.97				
NT2RP1000439	13.59	10.41	10.76	8.22	11.99	8.15	6.48	6.20	3.53			*	-
NT2RP1000443	1.67	1.60	1.02	3.09	3.95	2.04	3.35	1.76	1.48				
NT2RP1000447	2.13	0.82	0.90	2.07	1.95	1.21	1.39	1.67	1.12				
NT2RP1000448	1.39	0.47	0.72	0.68	1.75	1.34	1.82	1.77	0.69				
NT2RP1000451	5.40	2.45	1.97	5.69	5.15	3.49	1.66	2.36	1.96				
NT2RP1000458	22.07	12.50	14.79	20.35	29.47	24.03	21.83	19.22	26.03				
NT2RP1000460	19.74	9.97	12.40	17.61	20.40	21.09	17.72	15.83	18.24				
NT2RP1000465	14.77	10.71	12.70	18.32	19.61	21.10	14.71	11.30	11.86	**	+		
NT2RP1000468	3.47	2.54	4.12	7.07	8.07	7.42	3.93	5.61	4.57	**	+		
NT2RP1000470	14.45	6.40	6.23	5.28	6.94	7.41	8.62	6.71	6.97				
NT2RP1000477	0.33	0.76	0.21	0.93	1.49	0.73	0.8	1.04	0.52				
NT2RP1000478	2.01	1.44	1.12	1.74	1.18	2.18	1.98	3.01	1.97				
NT2RP1000481	3.26	1.45	1.19	1.27	1.08	1.24	0.92	2.02	0.85				
NT2RP1000493	1.13	0.65	0.54	1.16	1.49	1.41	1.57	2.12	0.89	*	+		
NT2RP1000513	8.57	3.43	5.13	11.73	10.43	8.69	10.51	9.55	9.33				
NT2RP1000522	9.74	3.47	5.93	6.13	9.61	9.77	8.53	8.00	7.9				
NT2RP1000533	2.49	0.79	1.93	2.45	2.66	3.02	1.21	2.77	1.5				
NT2RP1000544	2.42	0.99	0.69	2.39	1.44	1.14	1.43	1.13	2.11				
NT2RP1000547	0.17	0.54	0.23	0.77	0.69	0.77	0.43	1.67	0.73	*	+		
NT2RP1000551	1.62	1.44	0.64	0.50	0.71	0.60	1.24	2.56	1.59				

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Table 246

NT2RP1000567	1.21	0.33	0.63	1.21	1.30	2.41	2.12	3.42	1.77			*	+
NT2RP1000574	1.82	0.32	0.03	23.76	28.12	20.34	4.23	4.69	3.79	**	+	**	+
NT2RP1000577	1.22	0.49	0.73	1.46	1.85	1.75	1.18	2.92	1.35	*	+		
NT2RP1000579	0.79	0.65	0.57	1.33	1.34	1.32	1.35	2.50	0.76	**	+		
NT2RP1000581	1.36	0.66	1.82	2.04	1.55	1.78	1.95	2.51	1.03				
NT2RP1000593	2.64	0.66	1.75	2.65	2.96	1.71	1.41	0.83	1.4				
NT2RP1000604	11.50	7.94	7.40	3.94	3.98	3.21	2.12	2.31	2.08	*	-	**	-
NT2RP1000609	2.53	2.00	0.54	1.02	1.56	1.09	1.82	2.61	1.48				
NT2RP1000613	1.94	0.88	0.65	1.32	0.99	1.16	0.85	2.58	1.01				
NT2RP1000622	1.32	0.92	0.99	1.13	1.63	1.80	1.57	3.98	2.19				
NT2RP1000627	5.47	2.19	3.87	5.94	4.15	4.81	4.23	6.27	4.91				
NT2RP1000629	1.49	0.86	0.95	1.86	1.84	2.88	2.18	2.88	1.87			*	+
NT2RP1000630	5.89	2.85	5.42	13.99	11.47	13.46	7.36	6.55	7.16	**	+		
NT2RP1000639	2.68	1.18	0.53	1.84	1.97	0.94	1.56	1.83	1.5				
NT2RP1000640	81.74	37.60	35.82	57.27	52.32	39.58	48.18	42.34	41.38				
NT2RP1000646	7.82	4.91	3.97	8.29	9.40	9.31	5.5	5.31	6.52	*	+		
NT2RP1000659	6.71	2.34	3.90	4.05	6.32	6.12	3.31	4.60	4.15				
NT2RP1000674	4.71	2.08	3.93	5.76	7.16	7.25	3.17	4.95	4.5	*	+		
NT2RP1000677	9.51	6.01	6.41	8.66	8.51	8.83	7.33	7.01	8.68				
NT2RP1000679	1.23	0.42	0.82	1.73	1.38	1.63	1.09	2.06	0.76	*	+		
NT2RP1000688	4.67	2.07	2.03	5.85	5.34	3.72	3.1	4.12	2.68				
NT2RP1000689	2.83	0.64	1.04	1.11	1.67	0.84	1.37	0.88	0.83				
NT2RP1000695	1.62	1.12	1.10	1.18	2.39	1.24	1	0.87	0.88				
NT2RP1000701	0.90	0.82	0.62	0.83	0.27	1.25	0.87	1.19	1.4				
NT2RP1000702	0.76	0.35	1.53	0.66	1.47	1.82	0.6	1.47	2.57				
NT2RP1000713	0.23	0.42	0.37	0.34	0.89	0.44	0.17	1.44	1.47				
NT2RP1000721	10.57	6.36	5.67	7.28	13.00	9.92	8.49	9.05	8.17				
NT2RP1000730	2.55	1.65	1.97	4.38	3.90	3.35	1.75	3.65	2.95	*	+		
NT2RP1000733	4.46	2.99	3.71	5.44	5.04	3.14	1.44	3.93	4.16				
NT2RP1000738	28.84	10.50	11.79	17.48	18.85	18.44	15.99	11.65	12.72				
NT2RP1000739	14.40	7.16	8.58	10.60	12.85	8.63	11.15	9.94	11.2				
NT2RP1000740	3.66	1.37	2.15	2.84	4.09	2.86	2.91	2.60	3.23				
NT2RP1000746	1.31	0.85	0.82	1.32	1.26	0.89	1.26	2.13	2.46				
NT2RP1000750	9.51	4.76	5.09	7.09	6.45	6.48	4.95	5.43	4.72				
NT2RP1000751	77.49	46.65	53.99	41.34	32.45	28.11	17.67	20.76	21.6			*	-
NT2RP1000767	1.53	0.63	1.06	1.68	1.34	1.25	1.21	2.74	2.71				
NT2RP1000769	4.65	2.64	3.84	2.57	3.18	2.72	4.13	4.77	3.22				
NT2RP1000780	1.51	0.92	0.80	2.30	1.18	0.64	1.37	0.96	0.77				
NT2RP1000782	5.21	2.12	2.72	11.13	10.26	10.71	6.05	7.66	6.54	**	+	*	+
NT2RP1000796	6.49	4.06	3.11	4.93	5.23	3.73	4.82	3.98	7.13				
NT2RP1000797	11.72	5.77	5.28	6.51	8.45	5.34	7.81	7.98	9.33				
NT2RP1000800	0.13	0.54	1.00	1.07	2.16	1.97	0.82	3.18	1.42	*	+		
NT2RP1000825	3.33	1.37	1.55	2.64	2.23	1.50	1.34	2.32	1.31				
NT2RP1000833	6.35	2.68	2.53	4.24	4.98	4.14	2.29	4.43	2.42				
NT2RP1000834	16.60	5.93	7.79	8.68	7.93	6.33	6.47	7.84	5.03				
NT2RP1000836	1.43	1.06	0.85	1.19	1.20	0.59	2.19	1.50	0.63				
NT2RP1000837	6.20	2.33	2.35	4.62	5.53	5.38	4.6	3.52	3.49				
NT2RP1000846	1.21	0.89	0.89	1.89	2.60	1.73	1.96	1.80	1.08	*	+		
NT2RP1000847	2.27	1.79	1.06	1.99	2.12	2.09	2.78	1.80	2.3				
NT2RP1000851	10.08	6.27	7.87	9.89	12.49	7.13	7.78	9.66	7.43				
NT2RP1000856	9.90	5.85	7.31	20.58	23.87	20.13	15.75	15.89	19.71	**	+	**	+
NT2RP1000860	7.91	5.43	8.96	10.11	6.72	7.04	5.54	7.17	4.85				
NT2RP1000902	2.64	0.85	0.61	5.04	4.02	3.81	3.86	2.25	3.35	*	+		
NT2RP1000903	7.75	3.79	2.92	4.96	6.61	5.49	5.15	5.13	5.52				
NT2RP1000905	3.44	2.09	1.19	3.49	2.21	2.49	3.41	1.72	2.16				
NT2RP1000915	15.16	7.68	7.64	8.98	6.57	7.27	3.44	4.20	4				

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Table 247

NT2RP1000916	3.20	2.97	0.92	3.11	2.12	2.20	3.16	2.17	2.19				
NT2RP1000921	1.84	1.45	1.78	3.53	2.23	2.78	2.9	2.99	2.53	*	+	**	+
NT2RP1000943	1.83	0.78	1.29	5.94	5.07	4.31	7.05	7.60	6.55	**	+	**	+
NT2RP1000944	3.54	2.52	3.09	5.21	4.55	4.65	2.55	2.42	2.55	**	+		
NT2RP1000947	6.99	4.11	3.31	6.97	6.41	5.03	5.81	4.15	4.54				
NT2RP1000954	5.12	2.35	2.15	5.93	4.95	4.84	4.75	3.63	4.18				
NT2RP1000958	20.62	10.44	1.43	11.21	10.24	6.49	7.05	5.48	7.18				
NT2RP1000959	72.56	35.16	43.30	53.44	48.85	40.35	20.64	19.16	22.61				
NT2RP1000966	36.86	19.10	21.19	22.56	35.39	24.14	15.07	9.91	18.23				
NT2RP1000974	10.91	8.14	8.28	18.92	22.10	19.21	14.69	15.24	13.39	**	+	**	+
NT2RP1000980	3.63	2.59	2.91	3.75	4.02	3.96	2.97	3.22	2.22				
NT2RP1000981	4.96	3.42	4.61	4.59	5.02	3.62	2.94	3.11	2.77			*	-
NT2RP1000988	2.69	1.97	1.73	4.25	5.22	4.19	3.95	3.30	3.66	**	+	*	+
NT2RP1001002	6.75	4.73	2.89	3.13	4.46	2.79	4.86	5.58	5.21				
NT2RP1001004	1.76	1.26	0.75	1.72	1.80	2.22	3.2	2.14	2.89			*	+
NT2RP1001007	1.72	0.91	0.86	2.02	1.84	1.75	3	2.58	3.22			**	+
NT2RP1001011	4.98	3.03	2.17	7.06	8.67	6.46	5.23	4.65	5.76	*	+		
NT2RP1001013	3.60	3.50	3.48	9.46	12.09	7.99	6.88	5.63	8.02	**	+	**	+
NT2RP1001014	3.96	3.16	3.28	4.93	3.71	4.01	3.71	3.05	2.43				
NT2RP1001020	3.23	1.24	1.06	2.23	1.86	1.47	2.29	2.09	1.68				
NT2RP1001023	261.06	118.84	124.95	113.92	104.93	83.66	236.2	219.46	213.5				
NT2RP1001027	12.10	6.08	4.74	9.03	7.91	6.47	4.01	4.15	4.04				
NT2RP1001031	2.17	1.05	0.67	1.79	1.31	1.73	0.62	1.86	1.33				
NT2RP1001033	2.89	1.62	1.96	3.31	4.49	3.57	2.4	3.46	2.46	*	+		
NT2RP1001042	2.56	1.34	2.04	5.44	5.57	4.27	4.68	4.47	4.7	**	+	**	+
NT2RP1001045	55.87	37.46	39.12	31.66	32.21	26.52	26.73	25.41	27.84			*	-
NT2RP1001073	18.17	10.94	13.65	7.43	11.62	10.45	3.3	5.82	3.6			*	-
NT2RP1001079	6.27	4.29	4.83	7.17	5.68	5.81	5.84	5.09	3.64				
NT2RP1001080	4.59	3.36	2.02	3.32	2.67	3.66	3.81	3.01	2.62				
NT2RP1001113	2.09	1.06	0.43	0.85	1.89	1.25	1.74	2.63	1.22				
NT2RP1001159	22.23	15.34	13.51	27.36	29.04	20.75	11.14	12.23	9.12				
NT2RP1001173	2.37	0.91	1.48	10.20	7.72	8.04	6.93	5.00	6.33	**	+	**	+
NT2RP1001176	5.14	3.86	5.35	6.46	6.12	5.31	4.46	5.39	4.12				
NT2RP1001177	3.79	2.64	3.45	7.23	6.84	5.24	5.18	4.11	3.16	*	+		
NT2RP1001185	4.77	2.20	2.83	10.28	7.74	6.42	4.72	4.39	3.75	*	+		
NT2RP1001199	2.06	1.25	1.14	4.62	4.88	3.76	2.05	2.71	1.7	**	+		
NT2RP1001205	19.37	11.82	11.58	17.19	17.16	12.69	6.66	6.05	4.62			*	-
NT2RP1001215	5.66	2.61	2.14	2.79	3.86	3.71	2.65	3.10	2.8				
NT2RP1001225	5.42	2.06	1.65	2.88	2.39	2.40	3.21	4.49	4.21				
NT2RP1001245	3.12	2.43	4.04	4.32	4.51	4.91	3.1	5.42	4.42	*	+		
NT2RP1001247	1.41	0.44	0.55	0.62	0.90	1.10	0.75	2.81	1				
NT2RP1001248	2.68	2.07	1.62	3.98	2.41	2.41	1.39	3.80	1.81				
NT2RP1001253	6.69	3.25	3.71	6.33	4.35	5.83	4.57	5.25	3.74				
NT2RP1001286	3.18	1.26	2.31	4.52	3.67	4.87	3.96	3.81	2.61	*	+		
NT2RP1001294	9.78	2.41	4.54	3.50	4.67	2.27	2.68	1.87	2.59				
NT2RP1001302	8.57	3.22	3.02	3.18	3.24	3.37	2.74	2.23	2.95				
NT2RP1001310	9.73	5.23	5.10	9.63	10.00	7.15	7.46	7.70	6.61				
NT2RP1001311	18.47	7.91	7.87	5.75	8.43	7.25	3.98	5.42	3.54				
NT2RP1001313	10.94	5.16	4.72	12.65	11.32	9.22	3.47	5.55	4.61				
NT2RP1001324	3.38	2.26	1.54	3.44	2.03	2.97	2.03	3.34	1.99				
NT2RP1001349	3.51	1.77	2.13	2.29	2.35	2.91	2.76	4.09	1.76				
NT2RP1001361	9.53	5.57	12.07	15.75	14.43	10.15	3.96	7.68	5.72				
NT2RP1001379	9.49	3.63	4.16	6.43	5.54	3.66	4.65	4.16	4.18				
NT2RP1001385	6.18	2.32	2.60	4.81	6.35	3.73	2.76	3.62	3.67				
NT2RP1001395	5.45	2.82	3.04	4.04	3.63	2.71	4.99	4.64	3.44				
NT2RP1001410	18.25	5.37	10.42	15.62	9.58	11.66	11.21	9.39	10.03				

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Table 248

NT2RP1001424	2.87	1.62	0.72	3.11	2.58	2.58	1.61	3.38	2.21				
NT2RP1001432	2.47	1.17	2.41	2.23	2.48	1.53	1.78	3.14	1.45				
NT2RP1001449	7.62	4.22	5.10	9.69	11.61	8.75	6.99	5.82	6.74	*	+		
NT2RP1001457	4.04	2.37	2.71	3.08	3.14	2.75	2.72	2.61	3.14				
NT2RP1001459	10.76	3.49	3.82	8.95	9.17	5.61	7.87	6.73	6.96				
NT2RP1001466	22.82	9.71	11.08	9.67	7.98	7.40	7.72	5.26	6.18				
NT2RP1001475	6.67	4.07	4.28	8.53	10.26	8.11	4.73	4.80	4.35	*	+		
NT2RP1001482	11.57	4.98	6.24	6.89	5.62	4.62	2.44	2.41	2.61				
NT2RP1001494	1.38	1.05	0.95	2.03	1.52	1.37	0.9	2.19	2.18				
NT2RP1001500	2.19	2.12	1.80	1.11	1.95	1.39	1	2.88	1.81				
NT2RP1001517	1.81	0.96	1.45	2.37	1.81	2.59	1.22	2.90	1.19				
NT2RP1001540	5.66	2.57	3.71	5.28	5.66	5.56	4.29	5.21	3.47				
NT2RP1001543	8.78	3.57	3.35	10.80	11.59	6.71	5.01	4.67	5.34				
NT2RP1001546	21.79	10.60	8.72	53.53	51.38	41.78	29.72	27.77	37.59	**	+	*	+
NT2RP1001550	9.54	5.59	4.56	11.19	14.45	11.40	5.56	6.79	7.13	*	+		
NT2RP1001553	6.39	3.38	2.69	4.45	3.49	2.74	3.6	4.16	2.78				
NT2RP1001555	9.92	5.57	6.23	12.43	10.74	10.45	11.69	18.08	11.64				
NT2RP1001563	4.37	1.97	2.43	3.66	4.03	3.10	1.84	4.08	2.22				
NT2RP1001569	5.25	3.17	2.27	4.32	4.47	4.21	3.54	6.70	3.89				
NT2RP1001584	8.28	4.33	4.71	6.70	8.09	6.25	5.94	7.17	6.75				
NT2RP1001599	7.22	2.05	1.29	32.60	27.43	19.18	6.56	7.36	8.71	**	+		
NT2RP1001616	3.29	0.83	1.26	2.03	2.10	1.09	2.49	2.44	3.45				
NT2RP1001654	19.86	5.14	4.62	10.80	10.51	8.45	6.66	9.40	9.83				
NT2RP1001665	1.29	1.28	0.35	1.08	1.87	1.90	0.74	2.81	0.7				
NT2RP1001679	87.88	43.02	42.15	72.20	73.59	55.81	28.48	41.49	35.04				
NT2RP1001681	21.69	14.86	18.60	13.78	17.18	10.98	7.11	14.27	11.13				
NT2RP1001694	8.51	6.03	4.96	4.21	4.41	2.94	5.31	11.65	6.79				
NT2RP2000001	6.32	1.40	2.79	3.24	2.80	2.62	3.54	4.14	4.08				
NT2RP2000006	2.04	1.48	0.96	4.50	2.92	2.33	2.69	2.50	1.61				
NT2RP2000007	10.09	4.44	5.04	3.97	3.31	4.03	3.55	1.69	1.81				
NT2RP2000008	10.88	5.03	5.27	12.65	14.30	9.35	7.5	5.73	4.32				
NT2RP2000010	1.99	1.02	0.52	2.09	3.06	2.49	2.1	2.41	2.6				
NT2RP2000011	7.02	4.29	5.02	10.56	10.46	8.08	6.55	5.23	6.43	*	+		
NT2RP2000027	3.12	1.86	1.41	5.78	3.32	2.95	2.99	2.41	1.39				
NT2RP2000028	2.89	1.81	1.90	3.51	2.63	2.74	4.34	5.32	5.48			**	+
NT2RP2000032	1.94	1.20	2.03	2.85	3.78	4.04	1.05	2.10	0.96	*	+		
NT2RP2000040	37.68	15.23	16.54	19.89	18.06	16.95	22.42	19.65	16.11				
NT2RP2000042	9.28	3.40	4.33	7.54	7.04	6.30	5.89	6.48	6.12				
NT2RP2000045	10.41	4.33	5.29	6.44	6.23	7.07	5.45	5.93	4.14				
NT2RP2000051	12.68	6.63	7.07	5.35	6.94	5.58	5.26	5.53	4.86				
NT2RP2000054	5.27	3.29	2.87	3.98	5.04	4.42	5.28	3.65	4.48				
NT2RP2000056	4.49	2.47	2.46	3.36	3.01	3.82	3.5	3.62	3.48				
NT2RP2000057	52.52	38.64	47.28	59.49	56.29	50.39	23.72	29.59	31.7			*	-
NT2RP2000067	3.42	1.83	2.49	4.64	3.08	3.41	1.5	3.38	2.02				
NT2RP2000070	8.99	4.22	3.23	5.71	5.95	7.00	8.23	3.07	7.09				
NT2RP2000076	2.83	1.15	1.15	1.86	1.61	1.73	2.7	1.97	2.2				
NT2RP2000077	10.69	4.72	3.55	9.58	8.73	8.11	7.3	4.40	8.28				
NT2RP2000079	4.88	3.21	3.11	8.07	7.12	7.59	4.5	3.56	4.48	**	+		
NT2RP2000088	3.87	3.74	2.96	4.10	4.22	2.91	4.51	4.30	4.17				
NT2RP2000091	3.05	2.14	3.45	10.95	9.06	8.83	4.37	6.05	6.43	**	+	*	+
NT2RP2000092	10.83	5.23	7.63	16.92	17.59	12.32	8.03	11.12	9.14	*	+		
NT2RP2000097	2.33	2.76	2.63	4.90	4.82	3.90	2.22	2.43	2.99	**	+		
NT2RP2000098	10.38	5.79	6.50	5.56	4.26	4.65	2.67	1.61	2.03			*	-
NT2RP2000108	9.83	5.39	6.38	12.17	15.62	9.37	8.01	6.04	4.82				
NT2RP2000114	2.05	1.50	1.13	3.20	1.92	2.20	3.45	2.13	2.56				
NT2RP2000116	5.05	3.16	5.23	7.97	9.36	8.63	7.01	7.36	8.27	**	+	*	+

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Table 249

NT2RP2000119	8.68	3.95	4.21	9.78	9.83	7.70	4.38	5.61	4.76				
NT2RP2000120	6.77	5.63	5.88	9.79	11.11	8.08	7.54	6.05	5.79	*	+		
NT2RP2000126	6.86	4.89	4.70	8.53	5.94	6.57	4.76	5.23	4.11				
NT2RP2000133	3.99	1.70	2.52	3.67	4.08	3.28	3.34	3.20	1.96				
NT2RP2000147	10.14	5.06	4.39	7.57	6.45	7.93	7.96	5.91	7.47				
NT2RP2000153	9.59	4.30	4.77	11.17	12.10	9.91	6.51	6.58	8.83				
NT2RP2000156	8.43	4.96	3.48	10.08	10.36	9.94	5.38	4.40	3.72	*	+		
NT2RP2000157	3.42	2.19	2.41	3.80	5.30	4.72	2.87	2.06	2.91	*	+		
NT2RP2000161	3.63	2.23	2.07	2.95	5.95	3.11	2.97	3.99	3.8				
NT2RP2000168	0.99	0.64	1.00	1.63	1.21	0.85	1.57	2.63	1.12				
NT2RP2000173	5.26	3.38	4.83	5.31	6.20	4.30	6.86	7.09	4.77				
NT2RP2000175	5.66	3.98	5.08	6.59	5.28	4.03	5.09	5.43	4.57				
NT2RP2000178	4.05	2.68	1.96	2.97	4.24	3.15	4.17	4.26	3.99				
NT2RP2000183	10.17	3.83	4.48	9.26	9.55	10.17	7.2	6.57	6.26				
NT2RP2000195	7.49	2.50	2.99	9.64	9.13	9.97	5.54	5.28	4.35	*	+		
NT2RP2000204	61.75	38.58	41.68	97.90	112.72	86.99	46.74	43.39	38.72	**	+		
NT2RP2000205	3.47	1.89	2.20	5.10	3.54	4.32	2.79	2.79	2.7				
NT2RP2000208	3.13	2.58	1.85	5.38	5.41	5.54	3.65	4.43	4.57	**	+	*	+
NT2RP2000224	10.06	4.94	5.26	13.62	13.47	11.09	7.3	8.43	8.25	*	+		
NT2RP2000230	10.44	5.32	7.82	4.62	4.88	4.53	6.76	7.92	6.25				
NT2RP2000231	15.70	8.92	8.46	8.81	11.88	10.86	12.38	9.81	14.32				
NT2RP2000232	3.82	2.08	1.56	2.18	2.93	2.14	2.17	3.16	3.23				
NT2RP2000233	3.92	2.50	2.55	3.87	3.62	3.14	4.2	5.00	3.42				
NT2RP2000239	5.63	2.55	4.01	2.51	2.65	1.68	2.58	2.65	2.15				
NT2RP2000240	2.65	0.99	1.49	3.74	2.57	2.17	1.29	3.46	1.94				
NT2RP2000248	2.07	1.21	1.92	5.23	4.26	2.91	2.54	3.82	2.58	*	+		
NT2RP2000256	2.45	1.19	2.67	4.07	3.99	4.15	2.35	4.00	2.51	*	+		
NT2RP2000257	4.01	2.58	4.00	7.82	7.06	6.67	4.5	7.31	5.28	**	+		
NT2RP2000258	4.50	2.39	2.97	2.52	3.60	4.01	2.36	1.90	2.05				
NT2RP2000261	5.05	1.91	1.66	2.79	3.32	2.35	3.34	3.46	3.43				
NT2RP2000270	4.76	3.28	4.00	7.87	7.75	6.15	4.27	5.23	5.14	**	+		
NT2RP2000274	1.79	1.60	1.36	2.19	2.83	2.80	2.75	3.55	2.34	*	+	*	+
NT2RP2000277	2.75	1.21	1.42	2.17	1.68	1.96	1.92	2.84	2.38				
NT2RP2000279	0.41	1.31	1.45	1.18	1.47	1.06	1.2	2.43	1.11				
NT2RP2000283	3.37	2.23	2.52	5.72	4.12	4.64	3.18	4.04	2.42	*	+		
NT2RP2000288	5.70	4.02	4.20	8.50	6.14	8.35	4.51	3.57	3.55	*	+		
NT2RP2000289	6.80	5.85	3.10	6.12	5.47	3.78	3.88	3.57	4.36				
NT2RP2000297	11.76	5.46	4.79	20.39	23.99	16.10	8.54	7.85	6.17	*	+		
NT2RP2000298	4.88	2.68	4.30	8.97	6.69	7.77	3.27	4.79	4.52	*	+		
NT2RP2000310	3.32	1.70	1.94	1.61	2.82	2.27	1.42	3.61	2.47				
NT2RP2000327	2.70	2.09	1.98	2.16	2.54	2.15	1.73	3.66	2.67				
NT2RP2000328	9.99	5.11	5.84	9.30	7.53	6.17	5.88	5.38	4.93				
NT2RP2000329	6.52	3.59	6.38	14.80	8.75	11.24	11.8	13.63	15.25	*	+	**	+
NT2RP2000333	2.61	2.37	2.88	3.29	2.69	3.44	2.94	4.19	2.52				
NT2RP2000337	1.84	1.24	0.70	1.53	2.14	1.62	1.08	1.19	1.29				
NT2RP2000346	6.13	3.16	4.39	6.09	6.33	4.39	5.29	3.87	4.75				
NT2RP2000357	4.83	1.57	2.53	4.81	4.10	3.76	2.25	2.94	2.98				
NT2RP2000358	4.05	2.01	1.43	3.71	5.44	4.47	2.33	3.23	3.82				
NT2RP2000366	3.62	3.12	2.58	3.24	4.65	4.15	3.46	5.12	4				
NT2RP2000369	3.68	3.14	3.25	7.30	6.97	6.80	16.68	15.91	21.03	**	+	**	+
NT2RP2000376	16.50	7.18	10.26	12.72	14.14	12.56	11.16	13.27	14.04				
NT2RP2000394	3.97	3.08	4.07	2.94	3.29	3.97	2.41	3.13	3.01				
NT2RP2000396	14.08	6.54	5.86	11.48	9.74	7.82	9.11	5.57	11.18				
NT2RP2000412	7.77	4.65	2.97	6.62	7.16	4.26	3.14	4.29	4.91				
NT2RP2000414	18.85	9.88	9.70	17.32	11.45	11.38	9.42	7.23	10.75				
NT2RP2000420	2.85	2.26	2.25	4.04	3.82	1.85	2.03	3.71	2.9				

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Table 250

NT2RP2000422	4.34	2.42	2.61	4.23	4.79	3.97	2.48	4.12	3.58					
NT2RP2000426	25.72	16.73	17.55	38.01	37.89	27.90	28.44	35.63	32.72	*	+	*	+	
NT2RP2000428	8.81	5.15	7.26	4.95	7.26	4.98	5.88	6.67	7.85					
NT2RP2000438	6.31	4.25	6.08	7.20	6.52	5.26	4.94	5.80	4.64					
NT2RP2000447	4.41	2.06	2.07	4.91	3.95	2.02	2.15	2.90	4.07					
NT2RP2000448	7.83	4.29	4.32	8.83	10.57	6.61	6.83	6.72	9.81					
NT2RP2000459	3.66	2.01	1.92	4.90	4.18	3.40	3.04	3.12	2.39					
NT2RP2000479	1.93	0.77	1.02	3.37	3.48	3.07	1.64	3.13	2.2	**	+			
NT2RP2000498	3.73	1.64	2.79	6.08	6.58	5.26	3.06	4.66	3.3	*	+			
NT2RP2000503	0.99	0.59	0.90	1.83	1.74	0.79	1.01	2.91	0.59					
NT2RP2000510	1.06	0.59	0.92	1.09	1.85	1.43	0.94	2.45	1.3					
NT2RP2000514	1.41	1.10	1.00	1.62	1.02	0.66	0.8	2.20	1.21					
NT2RP2000516	2.96	2.89	1.64	2.85	2.86	3.71	3.31	2.30	4					
NT2RP2000523	3.99	1.92	2.37	1.57	3.10	1.25	3.93	1.39	1.65					
NT2RP2000533	8.58	5.78	6.04	9.66	6.29	7.70	8.46	6.89	6.1					
NT2RP2000540	3.70	1.50	1.36	1.88	3.29	2.35	3	2.34	2.25					
NT2RP2000547	4.21	3.25	2.00	3.94	5.17	3.32	3.43	3.90	3.44					
NT2RP2000557	6.17	3.16	5.21	9.43	7.58	8.00	4.94	5.68	5.75	*	+			
NT2RP2000558	6.82	5.39	2.81	8.42	7.99	7.74	3.91	5.66	3.66					
NT2RP2000564	3.37	1.73	2.60	5.24	4.86	4.91	2.08	2.76	4.62	**	+			
NT2RP2000565	10.89	3.85	5.45	5.34	4.15	3.62	5.93	5.18	4.1					
NT2RP2000583	12.11	7.48	7.41	14.37	9.94	10.68	9.35	8.42	9.2					
NT2RP2000591	1.21	1.15	0.59	1.83	2.04	1.49	1.94	1.98	1.05	*	+			
NT2RP2000599	1.47	1.25	1.53	1.16	1.55	1.34	1.22	2.03	0.81					
NT2RP2000601	2.53	1.94	2.56	4.22	3.80	2.72	5.23	4.02	4.33			**	+	
NT2RP2000603	3.39	2.35	1.65	2.95	3.86	3.73	3.27	3.61	3.79					
NT2RP2000610	8.35	6.25	7.50	11.79	10.08	10.19	6.69	6.74	5.04	*	+			
NT2RP2000614	96.26	103.19	118.68	120.08	119.37	64.42	36.46	62.71	38.98			**	-	
NT2RP2000616	6.76	3.07	4.14	4.68	4.17	3.26	5.28	4.32	4.63					
NT2RP2000617	8.33	3.91	4.08	4.27	5.55	4.60	5.01	3.15	4.64					
NT2RP2000623	4.48	1.59	1.85	3.07	2.65	2.79	2.55	2.58	1.9					
NT2RP2000634	2.21	1.66	0.95	4.67	6.41	3.91	3.28	3.56	3.18	*	+	*	+	
NT2RP2000636	2.78	1.86	2.23	5.39	5.75	3.65	5.59	4.74	6.43	*	+	**	+	
NT2RP2000638	21.16	12.92	16.03	4.08	3.49	3.77	3.77	2.86	3.58	**	-	**	-	
NT2RP2000644	4.37	1.59	2.30	6.98	6.00	7.24	4.21	4.56	3.58	*	+			
NT2RP2000649	7.14	4.82	5.18	7.37	7.32	4.24	9.38	7.32	6.55					
NT2RP2000652	3.51	2.62	3.37	2.59	3.37	3.58	3.42	2.20	3.62					
NT2RP2000656	2.66	3.06	2.65	4.78	6.50	7.33	2.65	3.45	3.99	*	+			
NT2RP2000658	0.93	1.13	0.36	1.13	1.33	1.51	1.68	1.25	0.75					
NT2RP2000663	4.22	2.97	3.08	9.06	10.89	6.58	6.13	6.43	9.35	*	+	*	+	
NT2RP2000664	23.91	17.42	14.73	9.66	12.53	10.44	7.05	5.83	8.31			*	-	
NT2RP2000668	5.30	2.81	4.65	6.71	5.59	4.69	6.21	4.52	4.52					
NT2RP2000678	0.48	0.48	0.42	0.75	0.94	0.64	0.81	1.41	0.39	*	+			
NT2RP2000694	2.29	2.24	2.05	19.86	17.58	12.78	4.53	4.69	3.6	**	+	**	+	
NT2RP2000704	6.91	3.49	2.43	6.07	5.63	5.83	4.96	5.30	4.17					
NT2RP2000710	9.01	4.65	4.93	4.63	5.99	4.41	2.4	3.05	3.57					
NT2RP2000712	8.69	3.86	3.32	7.90	11.98	9.71	4.72	4.64	4.82					
NT2RP2000715	2.82	2.17	1.75	4.86	5.63	4.47	3.49	4.30	2.59	**	+			
NT2RP2000720	4.75	3.62	3.91	5.03	5.10	4.87	4.06	4.30	4.01					
NT2RP2000731	2.07	0.87	1.19	1.70	1.63	1.57	2.2	2.35	1.11					
NT2RP2000739	4.43	3.04	3.85	4.97	5.04	12.49	4.91	4.00	4.7					
NT2RP2000748	2.01	0.84	1.62	3.67	2.92	3.60	1.71	2.82	2.4	*	+			
NT2RP2000749	18.07	9.30	9.03	17.51	22.01	17.32	13.66	13.69	16.17					
NT2RP2000758	6.82	2.65	3.39	7.55	7.28	7.11	5.45	4.30	5.82					
NT2RP2000764	6.06	3.40	3.08	3.96	3.81	2.89	3.82	5.32	3.35					
NT2RP2000766	4.46	2.57	3.04	28.36	19.71	19.14	14.72	13.56	10.75	**	+	**	+	

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Table 251

NT2RP2000777	29.85	20.42	21.91	16.22	17.42	15.02	12.37	12.07	13.5			*	-
NT2RP2000786	8.23	5.22	4.46	10.55	9.74	7.80	11.68	12.09	10.59			*	+
NT2RP2000793	14.01	7.42	10.26	12.19	18.41	17.74	12.21	12.81	15.75				
NT2RP2000796	6.25	2.57	4.14	5.05	5.14	3.86	3.27	4.71	3.04				
NT2RP2000809	7.70	5.02	4.14	9.32	10.55	8.44	6.87	4.85	6.03	*	+		
NT2RP2000812	6.41	3.65	3.75	7.05	6.14	5.86	4.83	5.04	3.67				
NT2RP2000814	2.40	1.13	1.50	2.03	1.96	1.78	0.9	2.54	1.09				
NT2RP2000816	5.89	1.17	2.01	3.48	3.06	4.82	3.84	4.28	3.29				
NT2RP2000818	2.61	0.71	0.86	3.13	3.87	2.75	2.08	1.63	3.25				
NT2RP2000819	2.57	1.24	1.34	1.88	1.49	1.77	1.81	2.05	1.32				
NT2RP2000841	2.46	0.72	1.21	2.94	1.98	3.02	1.06	2.75	1.48				
NT2RP2000842	1.34	0.54	1.09	1.95	1.45	1.71	2.84	2.70	1.53			*	+
NT2RP2000845	12.78	5.61	3.57	11.56	12.23	11.13	7.34	7.10	8.72				
NT2RP2000863	2.24	1.48	1.52	2.02	1.72	1.96	1.61	2.25	1.68				
NT2RP2000880	10.87	4.76	7.03	10.28	10.84	10.60	7.87	8.04	7.97				
NT2RP2000892	3.07	1.45	2.10	2.15	3.52	2.03	2.6	3.34	2.68				
NT2RP2000894	2.45	1.27	1.87	2.80	3.03	2.60	3.77	5.13	5.17			**	+
NT2RP2000903	2.42	1.74	2.17	15.91	10.43	12.06	3.76	4.80	3.91	**	+	**	+
NT2RP2000906	2.89	1.95	2.70	4.14	5.17	4.16	3.32	2.67	4.12	*	+		
NT2RP2000910	2.79	1.53	2.66	6.17	5.30	4.67	3.71	4.07	3.28	**	+	*	+
NT2RP2000931	32.13	11.92	13.53	39.97	39.93	28.59	17.58	15.27	16.3				
NT2RP2000932	4.21	2.31	2.05	7.96	6.87	4.87	4.36	3.76	4.67	*	+		
NT2RP2000938	19.54	10.59	13.57	13.71	16.06	13.76	9.46	10.81	12.03				
NT2RP2000943	4.61	2.00	2.25	2.99	4.17	3.48	6.66	6.59	6.2			*	+
NT2RP2000957	2.25	1.38	1.92	2.45	2.33	2.46	1.28	3.48	2.23				
NT2RP2000958	6.62	2.75	4.11	5.71	4.71	5.65	4.44	6.65	3.45				
NT2RP2000959	5.43	1.74	2.79	6.81	7.31	5.96	7.7	6.58	8.28	*	+	*	+
NT2RP2000965	8.62	7.11	7.91	6.90	6.39	7.29	4.61	4.19	4.83			**	-
NT2RP2000970	6.70	2.82	2.67	8.85	8.32	8.60	5.68	4.48	4.57	*	+		
NT2RP2000973	3.87	3.35	2.21	3.68	3.61	1.94	3.33	3.24	2.43				
NT2RP2000985	4.15	2.39	2.33	2.87	4.28	3.35	2.71	2.53	3.95				
NT2RP2000987	2.36	1.40	1.29	2.94	3.30	3.87	2.43	3.02	3.28	*	+	*	+
NT2RP2000997	3.92	3.46	2.91	6.76	6.13	8.29	6.06	7.63	6.82	**	+	**	+
NT2RP2001024	3.02	2.00	2.80	4.39	4.00	3.80	2.57	2.72	3.03	*	+		
NT2RP2001028	1.53	1.61	1.49	3.31	2.89	2.16	1.09	3.10	1.56	*	+		
NT2RP2001036	8.99	5.09	6.28	14.47	12.09	13.66	6.21	7.37	8.86	**	+		
NT2RP2001039	2.38	1.24	0.84	2.83	2.64	1.64	1.85	1.41	1.82				
NT2RP2001044	3.60	1.75	2.33	3.81	3.95	2.60	1.92	3.42	3.51				
NT2RP2001056	8.76	6.20	3.80	10.38	10.96	8.29	5.85	5.19	6.9				
NT2RP2001065	11.06	6.53	6.66	6.07	7.52	5.67	4.84	4.18	3.98				
NT2RP2001067	3.97	2.56	1.95	4.29	2.72	3.44	1.28	3.38	2.55				
NT2RP2001070	6.27	3.18	2.94	8.92	8.75	6.08	5.11	6.42	3.18				
NT2RP2001081	7.29	3.39	2.85	9.20	10.42	10.02	6.26	8.11	6.41	*	+		
NT2RP2001087	2.47	2.17	1.24	3.46	5.06	3.87	2.98	3.13	3.05	*	+	*	+
NT2RP2001094	0.61	0.13	0.10	1.14	0.70	0.35	0.83	0.86	1.21			*	+
NT2RP2001119	6.84	4.46	3.47	7.70	9.69	7.83	4.19	5.13	8.84	*	+		
NT2RP2001127	5.97	3.17	2.14	8.14	7.01	6.94	3.37	5.51	5.47	*	+		
NT2RP2001133	6.80	4.14	3.76	7.22	8.84	6.01	3.82	6.62	4.59				
NT2RP2001137	4.85	2.38	2.65	2.75	3.98	3.93	2.74	5.27	3.23				
NT2RP2001142	3.86	1.91	2.02	3.11	3.09	2.46	1.97	4.83	1.3				
NT2RP2001149	4.02	1.34	2.11	3.88	2.95	3.29	1.85	2.88	2.53				
NT2RP2001168	13.95	5.65	7.80	16.05	15.12	13.54	11.11	11.37	10.13				
NT2RP2001173	2.96	1.32	1.35	7.72	6.56	4.53	4.19	3.26	2.72	*	+		
NT2RP2001174	4.49	3.17	1.74	5.69	5.38	5.09	5.65	3.56	3.21				
NT2RP2001184	7.71	4.21	4.96	7.15	6.32	5.98	5.09	5.61	5.63				
NT2RP2001196	1.68	0.99	1.05	1.56	1.51	1.49	1.6	1.79	2.14				

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Table 252

NT2RP2001200	3.43	3.44	2.46	6.55	4.88	4.21	3.59	2.77	3.29				
NT2RP2001218	3.11	1.72	2.13	3.51	3.65	3.23	2.31	2.98	3.88				
NT2RP2001223	5.06	2.55	3.61	3.72	4.59	2.27	3.19	3.20	3.06				
NT2RP2001226	12.72	7.29	8.85	12.01	9.47	7.65	11.46	8.46	11.8				
NT2RP2001227	6.22	4.18	3.44	6.26	5.08	5.75	7.03	4.88	5.64				
NT2RP2001232	7.29	3.90	3.93	7.87	8.17	8.48	7.39	5.90	4.44				
NT2RP2001233	14.76	8.17	8.10	14.08	19.00	21.01	13.52	10.12	10.65				
NT2RP2001245	3.69	2.29	2.63	3.56	3.59	3.28	3.42	3.62	4.39				
NT2RP2001246	2.35	0.80	3.09	3.34	4.44	4.13	4.38	7.67	6.87			*	+
NT2RP2001268	5.55	3.73	6.74	8.43	9.77	9.29	5.65	6.17	7.45	*	+		
NT2RP2001270	14.16	9.13	9.94	14.63	14.49	8.30	11.4	14.47	14.26				
NT2RP2001276	2.24	1.82	0.94	3.36	2.75	2.46	3.31	2.32	2.92				
NT2RP2001277	3.77	1.80	1.15	7.12	6.46	6.90	6.6	4.91	5.92	**	+	*	+
NT2RP2001290	3.82	2.12	2.26	5.58	9.49	5.69	6.49	4.65	4.63	*	+	*	+
NT2RP2001295	3.75	1.96	2.66	4.93	5.60	3.83	3.62	3.11	3.56				
NT2RP2001297	104.94	62.95	78.61	112.57	111.95	109.12	28.51	42.30	59.76				
NT2RP2001301	6.22	5.96	7.50	7.48	6.39	7.90	5.94	7.38	6.32				
NT2RP2001312	16.14	10.26	15.91	20.56	19.30	16.72	18.23	19.30	23.86				
NT2RP2001327	8.14	6.35	5.95	5.76	7.30	7.36	7.73	8.61	9.09				
NT2RP2001328	18.42	9.64	9.66	24.64	22.08	22.34	13.94	10.86	12.67	*	+		
NT2RP2001341	17.63	7.30	6.72	12.36	9.62	10.30	8.25	8.97	14.65				
NT2RP2001347	17.63	11.15	9.87	16.21	14.33	12.17	10.57	9.73	12.31				
NT2RP2001366	10.12	8.31	6.45	18.92	23.58	18.36	11.75	11.32	14.59	**	+	*	+
NT2RP2001378	8.29	6.95	6.58	6.49	8.22	6.02	7.98	9.16	9.41				
NT2RP2001381	4.07	2.97	3.94	2.90	3.52	4.42	2.95	2.69	2.85				
NT2RP2001388	3.41	3.63	3.35	6.25	9.01	7.41	5.95	6.27	6.62	**	+	**	+
NT2RP2001391	210.40	161.64	144.04	393.09	492.35	288.04	175.7	224.46	230.6	*	+		
NT2RP2001392	7.04	3.01	3.58	4.59	5.33	4.71	6.14	5.70	5.27				
NT2RP2001394	9.60	6.22	4.32	15.24	15.30	14.78	8	5.76	7.4	**	+		
NT2RP2001397	15.57	11.63	10.83	8.23	11.47	9.12	4.18	3.62	3.82			**	-
NT2RP2001400	2.42	2.39	2.33	4.87	6.19	6.06	7.4	8.87	13.18	**	+	*	+
NT2RP2001408	5.20	3.88	3.54	7.39	10.57	7.94	7.53	7.30	6.48	*	+	**	+
NT2RP2001420	4.15	2.99	3.26	8.92	7.75	7.19	4.98	4.32	3.55	**	+		
NT2RP2001423	3.65	2.45	3.55	6.47	6.38	4.42	6.23	5.04	5.49	*	+	*	+
NT2RP2001427	4.90	3.28	3.58	5.81	6.42	5.73	4.13	4.89	4.51	*	+		
NT2RP2001428	4.31	2.09	2.32	7.25	7.90	5.77	3.53	5.08	3.14	*	+		
NT2RP2001436	3.76	2.25	2.26	8.78	8.61	8.75	5.22	4.80	6.42	**	+	*	+
NT2RP2001440	3.29	2.41	1.73	3.63	4.88	4.33	2.34	3.35	3.86	*	+		
NT2RP2001445	2.95	1.26	2.68	2.98	3.78	3.07	2.47	3.15	2.23				
NT2RP2001449	2.88	2.13	1.40	3.15	3.39	4.62	2.6	3.60	1.97				
NT2RP2001450	4.05	2.94	3.13	3.77	4.91	3.85	3.71	4.15	3.13				
NT2RP2001467	2.37	1.91	2.75	5.44	4.55	6.16	5.15	4.88	3.4	**	+	*	+
NT2RP2001469	10.04	7.34	9.26	5.41	8.75	6.36	6.52	6.42	6.37			*	-
NT2RP2001480	6.23	4.15	2.86	6.30	5.94	4.07	6.36	5.86	4.85				
NT2RP2001495	14.26	10.91	10.35	11.90	13.38	11.11	12.39	11.10	12.13				
NT2RP2001499	4.67	3.29	2.95	6.59	7.16	8.76	5.49	6.33	5.02	**	+	*	+
NT2RP2001506	4.89	3.71	3.86	7.29	8.04	7.88	5.96	6.72	7.88	**	+	*	+
NT2RP2001508	6.85	6.36	6.72	17.18	14.22	13.59	7.65	11.84	6.81	**	+		
NT2RP2001511	11.59	6.20	8.17	12.86	12.37	12.22	11.15	9.45	10.6				
NT2RP2001514	6.61	4.54	5.10	6.50	5.89	6.49	5.87	6.17	7.22				
NT2RP2001520	2.37	1.99	2.43	3.12	2.75	2.57	4.35	3.09	2.57				
NT2RP2001526	12.96	5.00	5.99	26.60	29.55	19.41	14.77	8.09	13.41	*	+		
NT2RP2001529	8.76	6.16	5.20	6.03	7.62	5.55	4.77	5.25	10.17				
NT2RP2001536	3.16	2.19	1.50	3.33	3.18	2.23	2.35	2.79	2.24				
NT2RP2001538	75.84	48.30	57.88	103.08	97.23	96.04	48.73	42.09	45.9	*	+		
NT2RP2001547	5.37	2.86	3.64	4.76	4.73	4.52	3.5	4.96	4.64				

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Table 253

NT2RP2001560	6.39	4.64	4.20	5.82	7.13	5.81	3.38	4.66	5.13				
NT2RP2001562	4.89	3.58	3.48	6.44	6.82	4.81	4.71	5.39	5.07				
NT2RP2001566	7.48	4.52	5.51	7.16	5.92	8.75	7.73	7.60	6.5				
NT2RP2001569	14.82	5.79	9.60	21.83	22.56	14.28	10.25	9.70	10.1				
NT2RP2001576	10.55	5.49	5.69	8.15	9.33	7.45	8.98	9.68	8.51				
NT2RP2001581	56.76	28.34	28.83	65.72	65.95	57.58	33.46	29.31	29.57				
NT2RP2001597	6.52	3.84	3.20	6.75	8.45	4.27	5.43	7.30	6.46				
NT2RP2001601	1.39	1.22	0.85	2.84	5.69	3.38	1.83	3.28	2.5	*	+	*	+
NT2RP2001613	0.98	1.39	1.71	1.95	1.58	2.25	1.57	2.65	2.69				
NT2RP2001628	3.83	3.04	3.39	4.74	7.75	4.57	4.66	5.20	3.94				
NT2RP2001634	9.71	7.65	8.42	9.38	5.92	8.18	7.57	6.78	7.74				
NT2RP2001635	6.36	3.48	2.24	6.23	7.58	4.38	4.88	3.74	2.85				
NT2RP2001660	2.86	2.10	1.03	7.27	5.03	4.32	4.44	3.32	7.02	*	+		
NT2RP2001662	9.75	5.05	6.57	13.09	11.75	8.88	7.01	6.63	7.59				
NT2RP2001663	3.29	2.74	2.56	3.86	4.83	6.87	3.87	4.11	4.21			**	+
NT2RP2001672	3.92	2.66	2.42	6.76	8.23	7.05	3.9	5.21	5.15	**	+	*	+
NT2RP2001675	2.35	2.00	2.38	1.25	1.56	1.93	1.59	2.56	2.41	*	-		
NT2RP2001677	6.62	5.40	3.75	5.38	8.63	6.75	8.06	7.03	7.46				
NT2RP2001678	3.81	2.77	2.79	5.76	5.75	5.77	3.78	5.60	5.43	**	+		
NT2RP2001683	1.31	1.34	1.35	2.92	5.85	2.75	1.53	1.74	1.61			**	+
NT2RP2001699	10.48	4.46	4.39	9.39	8.26	5.63	7.71	4.72	6.45				
NT2RP2001707	6.36	2.69	3.12	4.80	5.89	4.38	5.21	3.89	4.02				
NT2RP2001720	4.31	2.23	2.64	5.76	5.81	5.36	2.53	3.30	4.19	*	+		
NT2RP2001721	5.95	3.63	4.33	4.87	4.91	5.43	4.03	4.62	4.71				
NT2RP2001740	9.64	7.71	6.71	10.42	9.86	6.60	4.64	5.42	6.18				
NT2RP2001748	8.04	6.16	5.85	6.53	8.57	9.79	7.32	7.38	8.28				
NT2RP2001755	8.56	5.19	5.01	5.45	6.63	4.59	3	4.11	4.45				
NT2RP2001762	3.51	1.45	1.56	4.01	2.49	1.10	1.33	1.59	1.38				
NT2RP2001768	10.52	5.70	5.26	8.83	8.48	7.75	7.16	7.38	7.69				
NT2RP2001769	10.19	4.14	4.34	4.02	3.67	3.86	2.04	3.80	3.12				
NT2RP2001784	3.41	2.66	3.05	4.40	6.83	4.24	3.51	4.60	5.21				
NT2RP2001805	8.47	4.44	5.36	7.33	9.55	7.18	6.45	7.26	6.85				
NT2RP2001813	0.85	0.76	1.30	1.56	0.97	1.22	1.03	2.43	0.53				
NT2RP2001817	3.31	2.32	3.38	2.20	3.73	2.38	1.83	3.68	1.91				
NT2RP2001818	9.15	4.97	5.99	7.22	8.04	4.90	5.14	6.97	4.17				
NT2RP2001837	6.67	3.70	3.89	10.21	8.70	8.64	6.67	5.27	5.41	*	+		
NT2RP2001839	8.94	4.07	4.05	8.65	8.01	5.90	7.01	4.33	4.71				
NT2RP2001861	3.92	3.91	2.96	5.38	4.82	4.41	3.85	3.89	4.28	*	+		
NT2RP2001869	3.96	3.68	2.84	5.29	6.76	6.36	4.79	4.96	8.38	**	+		
NT2RP2001876	5.26	4.39	3.67	5.40	6.52	6.44	4.25	3.45	3.89	*	+		
NT2RP2001878	2.96	2.08	2.84	3.77	3.75	3.70	4.02	3.19	4.69	*	+		
NT2RP2001881	3.61	3.23	3.04	4.01	3.35	3.50	1.51	1.79	2.14			**	-
NT2RP2001883	14.84	8.25	6.92	8.52	8.12	7.84	10.33	7.28	8.44				
NT2RP2001884	13.60	7.36	6.43	4.80	5.47	5.55	7.44	5.61	6.14				
NT2RP2001885	4.58	2.98	2.92	4.56	5.26	4.27	4.8	4.09	3.45				
NT2RP2001898	5.25	3.59	4.61	5.09	5.82	4.63	4.24	6.45	7.13				
NT2RP2001900	3.76	2.05	3.66	6.01	5.52	2.71	3.58	3.82	6.81				
NT2RP2001903	26.27	19.19	22.63	20.41	23.55	21.60	18.49	17.64	17.95				
NT2RP2001907	6.26	4.16	3.66	9.32	10.90	7.90	6.73	6.46	7.59	*	+		
NT2RP2001915	2.75	1.61	1.89	3.01	6.15	2.73	2.2	4.12	4.37				
NT2RP2001921	13.96	7.17	5.50	7.19	5.36	4.44	6.09	4.12	4.96				
NT2RP2001926	2.31	1.57	1.52	6.10	5.30	3.82	6.1	3.59	5.57	*	+	*	+
NT2RP2001933	7.86	5.07	6.52	8.86	5.68	6.54	7.83	5.74	7.63				
NT2RP2001936	1.63	0.95	0.99	1.17	2.42	2.36	1.86	2.55	1.83				
NT2RP2001943	51.19	30.10	31.53	33.01	35.70	30.61	29.07	28.57	30.35				
NT2RP2001946	3.26	2.65	3.35	3.35	3.83	4.97	4.68	3.30	3.45				

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Table 254

NT2RP2001947	4.91	3.61	5.81	3.96	7.23	5.13	4.97	5.37	4.61				
NT2RP2001948	3.08	1.21	4.06	4.99	4.92	1.65	1.37	3.34	8.7				
NT2RP2001956	15.21	7.64	6.12	7.09	9.06	8.60	13.91	9.28	14.64				
NT2RP2001969	8.23	4.55	5.29	5.46	6.80	5.70	8.22	5.90	10.07				
NT2RP2001976	2.14	2.20	2.33	1.64	3.47	2.44	1.48	2.24	2.16				
NT2RP2001978	4.60	3.86	2.35	6.96	6.45	5.14	6.22	4.96	6.39	*	+	*	+
NT2RP2001985	3.92	3.42	3.57	5.93	6.65	5.91	5.3	5.09	5.9	**	+	**	+
NT2RP2001991	1.73	1.46	2.57	3.16	4.44	3.93	3.02	3.02	2.07	*	+		
NT2RP2001997	3.98	3.95	3.94	5.87	6.12	4.91	4.68	4.05	3.66	*	+		
NT2RP2002015	78.11	51.57	65.21	141.26	146.10	108.68	76.93	62.92	81.97	**	+		
NT2RP2002017	3.82	3.00	1.73	4.92	6.18	4.74	4	3.36	3.11	*	+		
NT2RP2002025	9.38	5.00	3.82	6.47	6.74	7.41	7.27	7.03	6.73				
NT2RP2002030	14.24	9.95	8.14	32.58	35.24	33.11	14.46	16.78	20.02	**	+		
NT2RP2002032	7.60	6.08	6.71	7.52	10.42	7.21	9.78	7.83	10			*	+
NT2RP2002033	10.00	6.88	8.54	14.32	18.25	17.32	8.01	10.19	9.71	**	+		
NT2RP2002041	1.30	1.42	1.01	2.33	2.65	2.99	2.24	3.22	3.54	**	+	*	+
NT2RP2002046	2.29	2.31	3.63	4.90	5.83	4.05	4.05	4.50	4.31	*	+	*	+
NT2RP2002047	5.55	4.39	6.12	3.39	3.21	2.86	3.07	2.96	1.09	*	-	*	-
NT2RP2002050	8.38	3.98	6.12	10.46	10.43	10.14	8.27	8.23	7.23	*	+		
NT2RP2002052	6.47	4.41	3.60	6.50	9.32	5.86	4.66	4.62	6.58				
NT2RP2002058	3.62	2.82	3.02	3.46	3.52	2.23	2.78	3.89	2.56				
NT2RP2002060	6.58	3.14	4.55	4.58	5.81	5.66	5.55	7.36	5.35				
NT2RP2002063	1.56	1.90	1.51	3.69	1.67	1.86	2.22	2.63	1.71				
NT2RP2002066	5.03	3.37	4.61	4.73	5.21	5.32	7.33	6.17	4.62				
NT2RP2002070	0.79	0.79	0.34	1.28	2.20	1.05	0.97	2.47	0.94				
NT2RP2002076	3.86	2.57	2.52	3.36	3.56	2.78	2.73	4.09	2.15				
NT2RP2002078	5.54	3.35	3.42	13.66	10.39	8.08	7.93	6.64	6.4	*	+	*	+
NT2RP2002079	5.14	3.23	1.70	5.80	4.94	6.51	3.67	4.05	3.99				
NT2RP2002099	7.45	3.48	2.47	4.21	4.13	3.43	3.32	4.93	4.92				
NT2RP2002105	5.64	3.25	3.05	3.88	4.16	3.68	4.68	5.62	4.37				
NT2RP2002115	0.92	0.69	0.55	1.83	1.20	1.32	0.97	2.15	0.81	*	+		
NT2RP2002124	2.28	1.30	1.91	4.70	4.64	3.30	3.98	3.75	2.5	*	+	*	+
NT2RP2002137	2.93	1.88	1.87	2.18	3.16	2.61	3.4	4.11	2.95				
NT2RP2002139	4.33	3.54	3.42	3.56	4.04	4.02	5.23	4.66	5.13			*	+
NT2RP2002154	5.53	2.76	1.92	4.83	6.57	3.88	4.83	4.72	5.4				
NT2RP2002155	279.79	155.93	163.22	222.28	242.49	184.60	219.6	179.59	177.9				
NT2RP2002172	4.14	2.59	2.22	3.81	3.52	4.02	3.34	4.90	3.32				
NT2RP2002185	4.32	3.52	2.95	4.55	4.64	4.41	4.65	5.42	5.45			*	+
NT2RP2002188	11.41	5.54	8.75	9.54	13.32	9.41	7.96	10.55	9.63				
NT2RP2002192	3.64	3.48	3.53	4.30	3.68	3.71	1.91	3.83	2.29				
NT2RP2002193	3.15	2.72	2.77	3.68	4.01	3.41	3.89	3.36	4.16	*	+	*	+
NT2RP2002208	2.07	2.36	2.72	6.19	4.41	5.19	4.33	5.08	2.51	**	+		
NT2RP2002219	4.17	1.29	1.62	2.78	4.30	2.60	1.31	1.97	1.84				
NT2RP2002231	2.75	2.39	1.20	3.02	3.57	1.95	2.15	1.47	2.21				
NT2RP2002232	5.59	1.67	2.23	5.04	5.05	3.28	3.82	4.55	3.16				
NT2RP2002235	7.15	4.93	3.90	3.84	3.33	2.89	4.86	6.74	5.47				
NT2RP2002239	23.74	15.37	16.41	23.91	26.96	19.68	8.59	12.98	10.06				
NT2RP2002252	9.96	4.94	5.61	5.48	5.08	6.39	5.19	6.06	5.88				
NT2RP2002256	1.33	1.22	1.37	1.71	2.37	2.14	1.73	2.95	1.47	*	+		
NT2RP2002257	2.29	1.76	1.74	4.11	5.09	2.83	4.04	4.42	3.81	*	+	**	+
NT2RP2002259	3.72	2.30	2.90	6.32	3.45	2.90	3.06	3.48	1.66				
NT2RP2002264	2.47	1.33	1.14	6.07	7.37	5.74	2.09	3.51	3.03	**	+		
NT2RP2002267	8.31	4.57	4.68	12.59	14.87	10.14	12.21	9.31	10.07	*	+	*	+
NT2RP2002270	7.39	4.62	5.64	7.88	7.73	8.65	3.38	3.42	4.07				
NT2RP2002281	8.20	4.58	6.60	7.60	8.32	8.02	5.18	6.11	4.33				
NT2RP2002288	5.39	5.46	4.44	3.41	3.45	3.50	3.57	3.54	3.96	**	-	*	-

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Table 255

NT2RP2002292	13.36	8.93	10.00	7.24	12.33	7.03	8.51	6.90	8.43				
NT2RP2002299	4.86	3.21	3.87	7.31	5.99	7.44	5.79	6.94	6.46	*	+	*	+
NT2RP2002304	3.12	1.09	1.07	3.72	6.64	4.48	2.39	2.10	2.14	*	+		
NT2RP2002312	3.00	2.02	1.91	4.87	5.25	3.26	3.11	3.70	3.89	*	+	*	+
NT2RP2002316	2.57	2.29	2.38	6.74	6.43	5.78	3.25	3.23	4.39	**	+	*	+
NT2RP2002325	2.17	2.03	1.50	3.32	3.39	2.92	1.65	3.11	3.18	**	+		
NT2RP2002333	6.45	4.83	4.75	7.88	10.32	7.81	5.66	5.80	6.3	*	+		
NT2RP2002371	4.90	4.23	3.63	9.29	8.56	8.25	9.75	10.58	7.26	**	+	**	+
NT2RP2002373	5.37	4.02	2.70	5.83	10.05	6.25	5.7	8.27	6.72				
NT2RP2002381	0.73	0.29	0.85	0.79	0.90	2.57	1.16	2.65	1.41				
NT2RP2002385	7.34	2.40	2.24	6.24	3.86	3.39	5.09	3.89	4.74				
NT2RP2002394	1.71	0.33	0.18	1.03	1.49	1.31	0.28	1.27	2.19				
NT2RP2002408	2.38	1.66	1.45	4.45	2.73	2.67	1.95	4.44	3.16				
NT2RP2002409	29.85	16.62	15.12	29.12	39.51	28.40	19.16	20.28	16.59				
NT2RP2002424	3.78	2.45	1.98	3.14	4.67	3.25	3.81	5.82	3.46				
NT2RP2002426	5.16	3.36	3.05	8.68	9.29	8.07	5.5	8.86	7.03	**	+	*	+
NT2RP2002429	6.36	5.02	5.09	9.72	12.33	8.37	9.84	17.67	16.81	*	+	*	+
NT2RP2002437	3.49	2.56	3.29	4.17	7.17	4.10	3.26	6.17	5.32				
NT2RP2002439	11.07	5.27	5.30	11.81	8.46	7.22	11.52	9.36	7.78				
NT2RP2002442	6.40	2.74	3.03	4.62	5.05	4.46	4.75	2.98	3.74				
NT2RP2002457	2.28	2.49	1.70	3.54	4.01	3.48	4.07	3.72	3.08	**	+	*	+
NT2RP2002464	5.19	2.78	3.13	3.90	4.79	4.00	5.08	3.74	4				
NT2RP2002475	3.58	3.74	3.05	8.04	7.22	4.99	7.48	6.02	7.62	*	+	**	+
NT2RP2002479	3.49	2.33	2.32	3.60	4.32	2.72	2.92	2.66	5.14				
NT2RP2002487	4.86	2.73	2.49	4.04	4.25	4.00	3.16	3.11	3.07				
NT2RP2002498	2.48	0.99	1.21	3.47	2.96	2.55	1.35	1.52	1.58				
NT2RP2002503	13.02	6.05	8.78	12.14	16.89	12.87	9.04	8.81	7.66				
NT2RP2002504	6.63	3.00	4.84	4.05	6.27	4.67	6.68	4.71	5.18				
NT2RP2002510	15.40	9.87	11.00	12.38	17.28	17.15	18.56	12.92	13.19				
NT2RP2002520	1.61	1.78	1.33	4.08	3.77	4.83	3.97	4.73	4.31	**	+	**	+
NT2RP2002527	11.26	7.87	9.14	12.36	15.57	11.93	8.08	6.87	9.06				
NT2RP2002533	15.80	10.32	13.55	16.21	16.47	14.65	18.71	12.94	18.73				
NT2RP2002537	6.78	4.47	5.46	7.12	8.21	8.66	4.34	3.85	6.54	*	+		
NT2RP2002542	11.84	6.86	7.87	24.97	24.70	21.27	12.25	9.81	10.65	**	+		
NT2RP2002546	3.51	1.75	1.39	2.49	2.71	2.52	4.4	3.54	3.7				
NT2RP2002549	8.05	4.99	5.19	5.57	6.51	7.45	6.2	3.49	5.35				
NT2RP2002564	13.08	7.54	8.36	11.61	12.09	10.41	11.1	8.10	13.89				
NT2RP2002591	9.73	4.99	4.71	11.69	11.90	10.05	7.9	7.42	7.09				
NT2RP2002595	5.43	4.01	5.43	9.33	7.85	7.01	6.61	6.19	7.33	*	+	*	+
NT2RP2002602	4.82	4.74	4.84	5.43	11.27	8.16	5.69	6.45	7.55			*	+
NT2RP2002606	5.86	3.02	3.06	8.03	9.33	3.93	3.99	4.72	6.99				
NT2RP2002609	4.71	2.92	3.43	5.18	4.82	3.59	3.34	4.09	4.4				
NT2RP2002618	4.82	3.33	2.74	6.13	4.63	4.67	4.95	4.51	4.42				
NT2RP2002621	10.26	6.84	5.48	15.22	14.98	13.05	11.07	8.62	10.72	*	+		
NT2RP2002643	4.22	2.96	3.21	5.73	8.43	4.77	4.53	4.98	4.94			*	+
NT2RP2002672	4.36	3.45	3.37	8.96	12.04	8.60	8.5	8.50	11.85	**	+	**	+
NT2RP2002673	2.97	2.38	1.11	7.44	9.35	7.43	5.4	7.46	8.29	**	+	**	+
NT2RP2002674	1.07	1.16	1.07	0.86	1.66	1.60	1.52	2.10	1.72			*	+
NT2RP2002686	3.43	3.39	4.42	4.11	5.80	4.25	4.81	4.16	5.05				
NT2RP2002688	13.80	10.26	10.39	17.41	16.88	13.34	9.74	11.51	8.03				
NT2RP2002695	6.80	3.06	3.92	5.81	7.30	4.59	7.03	4.43	5.61				
NT2RP2002701	6.95	4.89	4.37	8.51	9.98	9.57	8.2	7.53	9.25	*	+	*	+
NT2RP2002706	4.89	2.72	3.50	5.60	7.16	5.82	4.64	4.20	5.97	*	+		
NT2RP2002710	42.99	27.04	33.49	47.10	50.09	39.86	54.16	44.21	55.65			*	+
NT2RP2002721	7.76	5.23	6.54	9.71	10.64	8.40	10.35	8.03	8.87	*	+		
NT2RP2002727	0.98	1.45	0.99	2.09	1.15	2.50	2.3	2.04	1.73			*	+

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Table 256

NT2RP2002734	4.55	3.02	5.80	12.41	12.84	10.69	6.86	8.07	7.85	**	+	*	+
NT2RP2002736	3.63	2.27	2.67	2.07	2.02	2.04	2.87	2.60	2.01				
NT2RP2002740	2.59	1.02	0.94	3.18	2.63	2.29	2.78	2.96	1.96				
NT2RP2002741	5.52	4.27	3.15	7.73	8.99	8.94	4.51	5.06	7.43	**	+		
NT2RP2002750	7.28	6.29	4.77	14.35	17.57	18.80	8.32	9.26	7.61	**	+		
NT2RP2002752	11.68	7.46	7.74	12.78	17.74	15.50	11.31	10.02	12.22	*	+		
NT2RP2002753	11.55	5.48	11.53	10.53	6.13	11.57	7.42	7.93	9.43				
NT2RP2002760	8.78	4.40	4.62	7.89	8.63	6.01	6.34	6.38	7.33				
NT2RP2002769	3.29	2.63	2.68	3.72	6.64	6.67	2.86	4.11	3.55	*	+		
NT2RP2002778	9.07	6.03	9.70	7.44	6.87	7.92	6.93	7.76	4.98				
NT2RP2002791	6.58	4.82	4.00	9.50	14.75	9.25	8.23	6.79	7.02	*	+		
NT2RP2002800	6.57	4.20	5.63	10.46	11.33	12.38	5.4	8.07	7.04	**	+		
NT2RP2002805	1.48	1.18	0.66	2.57	1.66	1.18	2.89	3.53	1.96			*	+
NT2RP2002811	5.70	5.54	4.77	8.54	7.13	7.69	6.53	7.67	6.08	**	+		
NT2RP2002824	9.12	5.93	7.91	13.68	13.22	9.65	9.82	10.22	11.6	*	+		
NT2RP2002839	3.89	2.03	2.96	3.87	4.52	3.28	3.17	3.43	3.41				
NT2RP2002845	2.29	1.84	1.77	4.04	4.31	4.72	3.6	4.26	3.16	**	+	**	+
NT2RP2002857	0.99	1.45	1.80	1.98	2.27	1.76	2.36	3.14	1.89				
NT2RP2002862	11.21	6.20	5.58	10.84	12.86	10.44	6.99	7.12	10.71				
NT2RP2002880	5.70	4.03	2.74	3.50	4.84	3.87	4.05	5.72	5				
NT2RP2002885	6.90	4.59	4.82	5.83	6.45	4.16	3.34	4.76	3.08				
NT2RP2002891	5.76	3.80	3.33	5.44	6.69	6.13	4.92	4.49	5.35				
NT2RP2002907	4.12	1.98	2.30	4.77	3.91	2.49	2.25	3.24	2.04				
NT2RP2002925	3.23	2.04	2.18	4.98	4.44	5.21	3.38	2.81	4.67	**	+		
NT2RP2002927	14.45	8.55	11.84	14.25	14.86	13.10	10.66	9.50	13.04				
NT2RP2002928	1.42	1.26	2.32	3.26	2.52	3.14	1.44	1.91	1.88	*	+		
NT2RP2002929	6.54	3.13	3.18	6.60	7.00	5.63	5.25	5.85	5.87				
NT2RP2002934	5.87	2.70	3.00	3.46	2.95	4.09	3.58	3.88	3.47				
NT2RP2002939	6.87	3.02	3.14	4.78	4.45	4.28	3.95	4.36	3.63				
NT2RP2002942	4.16	2.79	3.25	6.95	8.21	6.01	4.14	5.76	4.58	**	+		
NT2RP2002954	3.73	2.07	3.02	3.75	4.03	3.04	2.28	3.89	5.22				
NT2RP2002959	5.43	4.36	4.62	6.19	7.91	6.08	3.63	5.75	5.03	*	+		
NT2RP2002974	2.77	2.53	1.82	5.32	4.88	3.20	3.66	3.70	3.24	*	+	*	+
NT2RP2002976	1.81	1.66	2.46	4.07	3.02	2.77	2.16	2.65	2.13	*	+		
NT2RP2002979	10.96	6.09	6.26	13.05	14.90	10.76	8.18	9.68	7.32				
NT2RP2002980	8.71	5.49	6.33	14.65	15.05	11.66	8.24	9.16	9.26	**	+		
NT2RP2002986	8.28	6.07	5.22	8.21	6.48	6.46	9.09	7.74	9.39				
NT2RP2002987	6.13	3.28	3.28	8.77	8.51	7.89	4.85	7.00	9.15	*	+		
NT2RP2002988	34.52	23.01	24.20	21.24	19.88	21.98	15.82	15.65	16.56			*	-
NT2RP2002993	4.35	3.19	4.08	2.57	3.44	2.83	3.21	3.84	2.8				
NT2RP2003000	6.81	5.24	5.01	12.83	14.50	14.13	6.77	6.65	8.42	**	+		
NT2RP2003008	3.03	1.86	2.21	2.77	3.21	3.26	2.46	3.49	5.58				
NT2RP2003020	7.91	3.15	3.03	14.51	13.63	11.55	10.67	9.71	9.8	**	+	*	+
NT2RP2003032	4.25	3.36	3.04	5.65	7.30	4.26	5.14	2.86	5.02				
NT2RP2003034	8.64	4.19	5.82	12.73	13.68	11.86	9.6	7.30	8.21	**	+		
NT2RP2003042	3.77	2.17	2.53	3.68	4.54	3.65	3.09	3.66	3.89				
NT2RP2003050	2.09	1.93	2.12	2.58	4.04	3.16	2.04	3.12	2.84	*	+		
NT2RP2003060	6.89	6.04	6.20	6.11	6.61	6.02	4.64	5.08	4.58			**	-
NT2RP2003073	5.10	4.79	4.81	10.73	11.79	9.58	6.83	8.25	4.87	**	+		
NT2RP2003099	3.77	3.26	2.86	5.64	6.07	7.01	4.27	4.57	5.19	**	+	*	+
NT2RP2003108	3.73	1.70	0.71	4.43	4.78	3.41	2.53	3.13	3.98				
NT2RP2003115	12.63	7.03	6.49	10.94	5.30	4.75	6.51	5.99	10.91				
NT2RP2003117	9.96	4.65	5.66	15.04	15.48	11.38	8.83	7.84	6.17	*	+		
NT2RP2003121	3.53	2.40	1.92	4.30	5.00	3.18	3.72	4.52	4.42			*	+
NT2RP2003125	5.32	2.20	2.34	3.41	4.18	3.51	3.6	4.31	3.11				
NT2RP2003127	3.09	3.27	3.35	3.25	3.63	2.74	2.3	4.46	3.68				

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Table 257

NT2RP2003129	3.68	2.64	1.93	5.72	5.89	5.75	3.03	4.40	2.82	**	+		
NT2RP2003137	2.40	2.79	2.71	6.74	6.38	5.76	4.22	6.41	4.31	**	+	*	+
NT2RP2003138	6.42	2.67	2.97	5.99	6.92	3.98	5.12	3.06	1.92				
NT2RP2003146	4.44	2.51	1.78	3.73	3.26	2.77	3.76	2.57	1.66				
NT2RP2003148	9.10	6.45	5.51	11.73	13.86	11.19	8.71	8.13	7.46	*	+		
NT2RP2003150	3.26	2.20	1.35	8.65	2.99	4.86	3.92	2.84	8.35				
NT2RP2003157	7.49	3.86	3.67	8.41	10.43	9.55	4.96	6.45	5.87	*	+		
NT2RP2003158	1.98	1.89	2.17	2.26	3.00	2.46	2.43	2.76	2.85			*	+
NT2RP2003161	1.04	1.33	0.76	2.12	4.38	4.18	1.59	2.84	8.91	*	+		
NT2RP2003164	2.83	1.78	1.70	2.90	2.78	2.57	2.53	2.97	2.44				
NT2RP2003165	4.31	2.10	2.06	5.98	4.84	6.84	5.12	3.81	4.72	*	+		
NT2RP2003177	3.18	2.52	2.22	3.53	2.99	3.63	4.35	2.80	2.79				
NT2RP2003179	4.54	3.39	3.36	5.90	7.70	7.29	4.85	4.79	6.24	**	+		
NT2RP2003194	16.94	9.59	9.74	7.86	8.77	6.84	7.23	6.50	9.93				
NT2RP2003206	0.19	0.73	0.54	2.02	2.10	1.11	1.07	1.15	1.17	*	+	*	+
NT2RP2003210	5.52	2.50	2.65	2.94	4.61	3.60	3.44	3.99	4.15				
NT2RP2003227	2.55	1.52	2.78	3.96	4.66	3.48	2.52	3.60	4.44	*	+		
NT2RP2003228	5.50	4.11	4.96	4.07	4.64	3.51	3.63	3.86	2.66				
NT2RP2003230	1.04	1.41	1.38	3.75	3.72	3.44	8.77	4.96	7.21	**	+	**	+
NT2RP2003231	6.83	5.52	4.87	9.61	7.64	6.47	5.75	5.89	8.09				
NT2RP2003237	4.46	2.56	2.35	5.51	7.13	6.33	3.56	4.31	3.67	*	+		
NT2RP2003239	4.50	2.01	3.71	6.44	6.32	5.76	4.01	4.23	4.42	*	+		
NT2RP2003243	5.46	3.20	3.57	7.44	6.11	7.58	5.91	6.40	3.87	*	+		
NT2RP2003265	5.61	3.24	3.60	7.47	8.92	7.01	5.38	4.10	6.74	*	+		
NT2RP2003267	3.97	3.06	3.71	7.15	8.86	6.88	4.28	4.40	5.84	**	+		
NT2RP2003272	5.37	3.98	5.63	6.49	6.56	6.62	7.54	6.51	7.61	*	+	*	+
NT2RP2003277	9.14	5.91	4.66	7.52	10.35	9.11	9.97	7.77	15.8				
NT2RP2003280	3.01	2.25	1.41	4.02	6.71	7.68	6.13	4.20	7.59	*	+	*	+
NT2RP2003286	3.53	1.84	2.37	2.62	3.15	2.83	2.96	2.70	4.01				
NT2RP2003293	6.85	4.64	6.03	12.22	12.54	11.97	6.66	5.15	8.8	**	+		
NT2RP2003295	4.81	3.25	3.18	3.96	8.36	5.27	4.16	4.98	3				
NT2RP2003297	1.97	1.06	1.42	2.82	3.09	2.49	1.97	1.89	1.68	*	+		
NT2RP2003300	5.99	4.89	4.68	7.75	7.40	7.47	7.28	9.19	9.08	**	+	*	+
NT2RP2003302	4.65	3.24	4.39	8.90	10.20	7.29	4.36	7.27	5.11	**	+		
NT2RP2003307	1.67	1.09	0.57	2.24	1.67	2.40	2.82	1.84	1.76				
NT2RP2003308	3.09	2.17	1.85	4.09	5.19	2.83	3.04	2.74	3.16				
NT2RP2003311	6.85	3.58	2.13	4.65	6.66	4.36	3.88	3.65	4.23				
NT2RP2003329	3.07	1.86	1.87	3.19	5.07	3.49	3.77	3.82	5.96				
NT2RP2003339	2.38	1.55	1.29	2.90	3.98	3.91	2.69	3.47	2.24	*	+		
NT2RP2003345	1.83	1.44	1.40	1.51	1.52	1.92	2.28	2.65	1.28				
NT2RP2003347	1.48	2.10	1.67	2.03	5.75	1.76	2.44	3.10	4.09			*	+
NT2RP2003367	1.26	0.98	1.42	1.39	1.59	1.55	1.21	2.14	1.04				
NT2RP2003369	3.82	2.31	1.37	1.62	2.10	1.87	3.19	2.85	1.99				
NT2RP2003383	7.18	3.57	4.41	16.30	14.96	15.98	8.79	9.62	11.29	**	+	*	+
NT2RP2003390	9.92	6.14	6.73	11.71	12.19	9.52	7.92	9.43	8.34				
NT2RP2003391	35.23	21.64	23.50	36.95	36.23	27.51	23.69	17.29	17.85				
NT2RP2003393	2.40	1.57	1.83	4.13	5.18	3.56	3.96	4.34	3.87	*	+	**	+
NT2RP2003394	4.02	2.41	2.76	12.16	9.99	10.68	6.12	6.15	3.96	**	+		
NT2RP2003401	2.33	1.80	1.86	3.02	4.68	2.41	3.02	4.51	3.57			*	+
NT2RP2003403	1.23	1.40	1.41	3.20	3.23	4.51	3.04	3.80	3.41	**	+	**	+
NT2RP2003433	8.96	4.52	3.52	6.71	5.66	5.39	7.4	6.01	5.01				
NT2RP2003445	3.20	3.09	2.41	6.94	6.16	6.94	13.01	11.43	14.04	**	+	**	+
NT2RP2003446	5.05	4.02	2.72	4.09	6.31	3.82	5.45	4.95	5.35				
NT2RP2003456	4.21	2.96	2.69	10.80	8.14	8.43	6.15	5.44	4.71	**	+	*	+
NT2RP2003466	5.26	3.68	3.82	5.95	5.44	4.60	3.82	5.23	9				
NT2RP2003469	3.53	2.12	2.45	3.89	4.69	5.28	2.75	4.01	3.09	*	+		

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Table 258

NT2RP2003470	11.59	7.42	9.22	28.44	23.50	24.05	11.29	12.07	8.19	**	+		
NT2RP2003471	0.69	0.28	0.53	1.86	1.08	1.71	2.23	2.31	0.86	*	+		
NT2RP2003480	15.63	7.31	7.47	13.91	14.92	13.14	9.58	7.59	11				
NT2RP2003495	6.78	5.33	4.65	5.96	5.20	6.08	4.27	5.58	4.14				
NT2RP2003499	3.16	1.30	1.31	2.42	1.62	2.16	3.79	4.26	2.53				
NT2RP2003505	2.95	2.52	1.64	4.06	3.25	3.65	2.65	3.70	2.81	*	+		
NT2RP2003506	4.36	2.44	2.89	4.61	6.57	3.32	3.86	4.37	5.74				
NT2RP2003511	5.80	4.98	5.36	9.63	8.04	5.73	6.43	6.77	8.36			*	+
NT2RP2003513	3.23	2.52	3.10	3.94	3.00	3.76	2.27	3.48	3.18				
NT2RP2003517	1.52	0.95	2.01	2.87	2.13	1.37	2.66	3.16	3.17			*	+
NT2RP2003522	21.16	8.31	12.55	21.51	17.78	15.40	9.2	5.69	8.01				
NT2RP2003525	6.58	6.05	5.00	12.44	12.64	12.83	8.86	7.54	7.95	**	+	*	+
NT2RP2003533	7.73	4.59	4.51	11.94	12.52	10.34	6.62	8.25	8.72	**	+		
NT2RP2003541	9.89	7.73	6.72	8.34	7.49	6.40	6.78	6.83	5.85				
NT2RP2003543	4.46	3.26	2.49	5.01	7.76	4.19	6.57	7.85	7.39			**	+
NT2RP2003545	6.37	3.24	4.48	2.58	2.60	1.05	1.96	3.63	2.3				
NT2RP2003559	1.78	1.16	2.25	3.59	3.08	3.14	2.24	2.88	3.16	*	+		
NT2RP2003564	1.65	1.70	1.81	2.44	3.74	2.88	2.97	3.23	1.66	*	+		
NT2RP2003565	9.14	3.08	4.12	8.63	10.17	6.24	4.03	4.24	3.56				
NT2RP2003567	7.44	5.21	4.96	7.20	9.00	7.04	7.75	6.53	4.86				
NT2RP2003575	5.24	1.86	2.00	2.78	2.67	1.70	1.73	2.24	4.67				
NT2RP2003576	208.36	132.21	112.56	100.63	118.10	86.36	71.48	50.82	50.69			*	-
NT2RP2003579	56.28	38.17	48.67	28.49	15.58	24.16	19.34	17.93	21.34	*	-	**	-
NT2RP2003581	4.71	3.22	3.45	3.09	5.04	4.47	3.46	3.82	4.77				
NT2RP2003587	8.55	4.99	7.99	8.79	9.50	8.44	7.38	8.78	13.4				
NT2RP2003590	11.27	7.70	8.07	4.15	4.86	4.77	3.73	6.36	4.84	*	-	*	-
NT2RP2003593	9.63	4.82	5.47	13.80	9.75	5.79	6.89	8.08	6.91				
NT2RP2003596	3.20	2.89	2.89	6.00	8.78	7.99	4.62	4.90	7.08	**	+	*	+
NT2RP2003599	8.81	5.81	5.81	8.37	10.49	10.48	10.61	8.00	12.61				
NT2RP2003600	3.15	1.54	2.36	3.63	5.05	4.21	2.91	3.54	3.28	*	+		
NT2RP2003604	8.61	4.63	5.27	5.66	7.11	7.00	5.84	5.70	5.33				
NT2RP2003629	0.93	0.41	0.97	1.80	1.56	1.57	0.76	2.29	1.4	*	+		
NT2RP2003630	3.31	2.56	2.95	6.23	8.50	6.34	5.52	5.72	4.54	**	+	**	+
NT2RP2003643	16.50	10.48	12.66	12.59	15.91	12.75	9.42	11.38	10.03				
NT2RP2003655	4.54	2.17	1.95	4.91	4.47	3.19	4.31	4.99	6.38				
NT2RP2003664	7.29	4.58	3.44	9.78	13.11	10.33	7.53	12.65	18.19	*	+		
NT2RP2003668	7.64	3.93	2.99	7.77	11.11	7.27	3.61	4.49	4.92				
NT2RP2003687	3.50	2.00	2.53	2.44	3.28	2.52	1.34	3.20	1.86				
NT2RP2003691	3.51	2.23	2.36	4.83	5.26	4.14	2.6	3.93	3.34	*	+		
NT2RP2003702	4.72	3.23	2.91	5.75	5.42	5.03	3.29	5.65	2.48	*	+		
NT2RP2003704	3.03	1.02	1.33	3.00	4.19	2.96	1.48	4.19	2.8				
NT2RP2003706	0.54	0.54	0.40	1.92	1.23	0.53	1.37	2.50	2.1			*	+
NT2RP2003713	3.77	2.04	1.68	4.89	3.40	3.69	3.54	1.79	2.29				
NT2RP2003714	16.93	11.05	8.85	15.34	13.25	10.73	6.94	5.43	4.92				
NT2RP2003727	9.17	5.59	4.98	8.92	8.98	7.11	5.82	4.15	6.45				
NT2RP2003737	4.49	2.62	2.06	3.80	4.50	3.26	2.92	3.29	5.35				
NT2RP2003751	0.82	0.97	1.07	1.33	1.62	0.98	1.33	0.88	0.72				
NT2RP2003760	3.61	2.60	1.42	4.28	5.22	4.19	4.75	3.97	7.45	*	+		
NT2RP2003764	4.43	3.65	3.32	3.81	3.64	3.20	3.86	3.12	8.26				
NT2RP2003769	3.03	1.62	1.45	3.28	5.14	3.51	3.96	2.62	2.26				
NT2RP2003770	11.88	6.14	5.72	10.96	9.10	9.34	9.86	5.90	7.19				
NT2RP2003777	8.28	5.95	4.45	12.14	8.07	7.31	6.16	4.05	5.91				
NT2RP2003781	6.93	4.17	4.88	6.60	9.83	10.25	6.27	5.64	6.39				
NT2RP2003785	5.07	3.24	3.30	5.65	5.69	5.57	6.33	7.73	14.42	*	+		
NT2RP2003793	9.26	6.02	4.92	6.26	7.16	5.41	4.28	4.76	5.16				
NT2RP2003806	6.44	4.78	6.02	12.68	12.04	12.13	5.52	7.88	5.99	**	+		

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Table 259

NT2RP2003825	9.16	5.63	6.57	17.27	18.54	12.04	6.67	8.08	14.03	*	+		
NT2RP2003840	10.64	4.89	5.66	8.31	7.78	5.93	7.12	5.91	8.06				
NT2RP2003857	12.72	6.86	6.25	8.31	8.84	9.18	7.95	6.05	8.74				
NT2RP2003859	6.93	3.73	2.73	12.12	10.40	13.45	5.71	3.90	6.36	**	+		
NT2RP2003871	3.42	3.01	2.13	9.67	10.18	8.65	5.24	4.53	5.97	**	+	*	+
NT2RP2003876	7.74	4.51	4.43	5.67	8.07	7.43	4.37	5.53	5.6				
NT2RP2003878	4.47	2.22	2.10	3.89	4.71	3.64	3.95	3.56	4.06				
NT2RP2003885	5.69	2.59	2.76	3.73	7.92	5.39	4.25	4.87	6.01				
NT2RP2003898	10.09	7.67	7.33	11.75	12.18	9.75	5.01	8.03	5.65				
NT2RP2003902	10.41	8.37	6.78	8.14	9.71	9.88	7.68	5.42	8.06				
NT2RP2003912	13.81	9.98	7.42	16.63	17.90	13.52	10.9	14.66	13.18				
NT2RP2003931	3.74	1.68	1.44	2.28	2.88	2.54	2.24	1.94	2.65				
NT2RP2003940	18.24	10.75	11.51	44.72	39.79	24.81	16	14.58	19.02	*	+		
NT2RP2003950	3.98	2.45	3.31	3.52	4.06	3.60	3	3.05	3.52				
NT2RP2003952	5.00	3.18	4.24	4.00	4.74	3.20	2.55	2.62	4.33				
NT2RP2003968	13.52	6.81	6.24	9.83	14.58	9.98	4.25	4.49	10.21				
NT2RP2003976	5.76	3.40	2.77	10.86	15.30	22.19	5.6	7.99	7.6	*	+		
NT2RP2003981	5.81	3.89	2.20	4.65	4.94	4.43	4.88	3.67	4.28				
NT2RP2003984	11.22	7.15	6.30	8.47	13.43	9.96	9.18	9.47	16.24				
NT2RP2003986	11.50	5.47	4.61	14.29	15.56	15.24	7.95	7.99	8.32	*	+		
NT2RP2003988	5.84	4.44	3.08	11.21	13.07	8.96	7.35	4.72	6.91	**	+		
NT2RP2004013	19.46	11.40	12.00	20.33	26.92	19.32	8.59	11.59	12.13				
NT2RP2004014	5.88	5.77	8.06	11.00	14.73	13.84	6.02	5.49	4.74	**	+		
NT2RP2004036	4.76	2.41	3.64	4.63	4.19	5.70	3.7	3.95	3.26				
NT2RP2004041	2.79	3.61	3.30	4.01	6.06	4.15	3.2	4.29	4.43				
NT2RP2004042	4.23	3.45	2.82	4.59	3.59	5.00	3.97	2.94	3.64				
NT2RP2004049	5.52	3.09	3.20	5.68	4.82	4.18	3.14	3.78	3.4				
NT2RP2004060	6.54	4.19	4.75	5.31	7.44	5.90	6.84	5.31	6.57				
NT2RP2004066	7.62	3.57	3.11	8.07	8.17	6.09	3.54	4.23	4.08				
NT2RP2004069	2.46	2.35	2.84	3.73	4.30	3.52	3.02	4.14	4.07	**	+	*	+
NT2RP2004076	1.40	1.15	1.26	2.49	2.65	1.93	1.27	2.46	1.33	**	+		
NT2RP2004080	2.70	2.23	2.55	3.88	5.93	4.96	4.18	5.58	4.25	*	+	*	+
NT2RP2004081	2.74	2.99	2.36	3.72	4.51	3.72	1.45	3.28	1.61	*	+		
NT2RP2004098	10.83	5.42	4.87	10.62	9.37	7.52	6.04	4.69	6.05				
NT2RP2004108	15.24	8.74	6.82	24.00	21.97	22.21	10.22	12.30	14.43	**	+		
NT2RP2004124	5.29	4.13	3.63	5.87	5.42	5.25	4.18	2.84	4.23				
NT2RP2004130	9.77	7.17	7.05	9.85	13.14	10.78	12.57	13.32	11.04			*	+
NT2RP2004133	11.24	7.82	7.31	10.46	12.30	8.54	8.71	9.42	8.83				
NT2RP2004141	4.33	2.78	3.55	5.05	6.27	4.10	3.83	4.25	5.14				
NT2RP2004142	3.53	1.25	3.26	3.70	5.10	5.11	2.84	4.94	3.66				
NT2RP2004152	2.68	1.78	2.43	4.24	5.04	5.23	2.05	2.34	1.5	**	+		
NT2RP2004165	21.03	8.19	8.39	7.87	8.05	7.98	5.38	6.52	6.22				
NT2RP2004170	7.13	4.37	2.78	6.23	7.89	6.07	5.24	5.06	3.73				
NT2RP2004172	3.69	2.25	1.50	2.50	3.71	2.71	2.83	3.52	1.97				
NT2RP2004176	7.84	4.13	3.67	5.48	5.12	4.33	5.56	7.38	6.12				
NT2RP2004179	6.87	2.52	2.41	5.35	4.30	3.84	3.98	4.72	4.2				
NT2RP2004187	3.69	2.64	1.86	5.62	6.94	5.86	3.38	4.90	4.03	**	+		
NT2RP2004190	2.07	2.03	2.45	3.29	3.28	2.78	5.06	5.55	4.18	*	+	**	+
NT2RP2004194	6.67	3.78	5.18	7.29	8.60	7.46	5.61	6.42	7				
NT2RP2004196	20.28	5.85	8.55	16.34	14.05	15.75	7.78	7.99	8.4				
NT2RP2004205	10.63	6.42	6.10	11.21	13.23	11.22	6.53	6.15	7.63				
NT2RP2004207	4.42	3.24	2.70	3.44	4.24	3.84	3.13	3.26	3.82				
NT2RP2004226	4.97	4.89	4.35	4.76	5.20	4.65	3.73	3.67	3.35			**	-
NT2RP2004232	2.49	1.77	2.98	3.76	4.69	3.30	2.85	3.10	2.15	*	+		
NT2RP2004239	4.49	3.56	3.79	6.17	7.37	6.14	4.15	5.46	4.58	**	+		
NT2RP2004240	6.30	3.45	4.77	13.34	11.74	9.18	6.02	6.36	6.66	*	+		

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Table 260

NT2RP2004242	4.01	3.66	4.18	4.80	6.97	3.56	2.91	4.22	3.72				
NT2RP2004245	4.75	2.29	3.26	4.55	5.39	2.63	3.01	2.48	2.79				
NT2RP2004270	18.23	8.30	7.67	19.68	17.41	13.31	11.69	12.72	8.05				
NT2RP2004300	3.69	2.58	2.90	3.43	6.04	3.65	2.47	3.40	4.86				
NT2RP2004304	6.67	2.88	6.27	10.77	12.81	11.19	6.73	6.65	7.62	**	+		
NT2RP2004313	3.69	3.44	2.33	4.32	4.99	4.51	2.56	4.15	4.27	*	+		
NT2RP2004316	4.16	1.43	2.32	4.51	4.31	4.04	2.43	3.50	4.17				
NT2RP2004321	15.92	11.27	11.28	36.60	56.46	33.80	10.57	12.49	9.91	*	+		
NT2RP2004336	2.22	1.97	1.95	1.98	2.72	1.41	1.95	2.65	2.2				
NT2RP2004339	18.02	10.18	7.42	25.42	25.92	20.21	14.54	10.64	9.51	*	+		
NT2RP2004347	6.36	3.28	2.51	3.98	5.62	3.33	2.91	2.22	3.77				
NT2RP2004364	7.25	3.84	3.16	7.45	10.83	6.50	5.33	5.38	5.14				
NT2RP2004365	3.92	1.67	1.92	3.47	3.94	3.44	1.64	2.60	3.66				
NT2RP2004366	3.77	1.94	2.27	3.01	4.43	2.63	2.6	3.92	2.96				
NT2RP2004373	2.38	2.55	1.79	5.73	5.73	2.95	2.28	3.83	3.83				
NT2RP2004375	14.49	9.73	10.51	9.34	13.60	9.23	5.43	7.02	8.38				
NT2RP2004389	6.54	5.30	4.58	4.64	5.83	5.40	4.4	4.73	4.62				
NT2RP2004392	28.46	15.89	13.93	32.21	29.99	20.99	14.28	13.07	11.38				
NT2RP2004396	12.58	7.77	8.62	10.01	8.33	7.76	2.74	2.93	6			*	-
NT2RP2004399	7.37	3.73	4.44	6.18	6.63	5.28	3.66	5.23	7.06				
NT2RP2004400	3.45	1.87	1.89	5.43	5.79	4.47	2.84	3.98	3.76	*	+		
NT2RP2004404	11.50	7.62	6.89	11.66	13.80	10.35	8.27	8.35	9.19				
NT2RP2004410	11.23	11.38	11.20	17.64	15.77	17.12	11.2	18.45	13.95	**	+		
NT2RP2004412	4.89	2.82	3.13	4.05	4.86	3.06	2.32	3.89	3.43				
NT2RP2004414	6.08	2.18	5.00	3.14	3.56	2.80	1.59	3.95	2.41				
NT2RP2004425	2.01	1.60	1.70	2.43	4.37	2.34	2.53	1.37	3.45				
NT2RP2004447	3.57	2.63	1.82	4.60	4.54	3.34	3.94	3.07	2.46				
NT2RP2004463	11.21	7.40	6.24	12.62	8.89	9.28	9.29	8.97	10.07				
NT2RP2004476	4.90	3.15	2.20	5.47	5.87	6.15	2.61	3.85	5.36	*	+		
NT2RP2004488	5.90	4.58	3.55	4.28	5.12	3.55	2.91	3.17	2.6				
NT2RP2004490	4.32	3.15	2.55	3.51	4.12	4.44	2.62	3.95	8.62				
NT2RP2004495	12.24	5.83	8.88	11.24	10.73	8.49	9.47	11.08	18.95				
NT2RP2004512	5.33	2.48	2.45	3.28	4.26	3.70	3.48	2.44	3.06				
NT2RP2004523	10.16	5.01	3.79	10.11	8.70	10.80	6.51	6.83	6.35				
NT2RP2004524	3.86	3.51	2.47	5.08	4.81	4.16	5.08	3.55	3.98	*	+		
NT2RP2004536	11.38	9.71	7.82	9.14	12.16	9.03	6.49	7.82	9.84				
NT2RP2004538	38.06	30.58	30.32	62.14	68.91	71.97	40.07	32.51	41.6	**	+		
NT2RP2004548	5.50	4.46	3.74	10.83	12.12	12.54	4.81	5.53	8.83	**	+		
NT2RP2004551	3.34	1.83	3.26	4.96	5.20	3.92	2.98	2.39	13.41	*	+		
NT2RP2004556	8.58	7.04	6.71	15.74	11.77	13.75	8.42	10.11	9.77	**	+		
NT2RP2004568	19.23	11.22	8.88	15.82	10.64	12.31	13.87	9.13	9.97				
NT2RP2004580	7.17	4.71	2.64	11.67	9.76	7.99	7.1	5.36	6.59	*	+		
NT2RP2004585	10.92	6.41	6.18	10.89	10.92	9.49	8.51	7.18	15.75				
NT2RP2004587	2.30	1.65	0.84	2.47	1.80	1.78	1.76	1.48	2.46				
NT2RP2004594	5.87	5.87	4.84	5.34	8.13	4.27	3.88	5.17	7.53				
NT2RP2004600	1.88	2.05	1.13	2.29	2.11	2.15	1.86	2.50	1.01				
NT2RP2004602	4.95	4.31	4.04	9.75	8.80	8.23	5.05	5.03	6.56	**	+		
NT2RP2004606	11.77	11.03	6.62	13.49	15.68	9.80	18.35	17.80	17.2			**	+
NT2RP2004614	7.71	4.83	3.32	3.55	3.54	4.41	5.21	3.79	4.38				
NT2RP2004648	6.00	3.54	2.10	4.35	4.65	3.29	4.52	3.41	7.33				
NT2RP2004655	13.74	9.02	8.53	4.81	7.79	4.98	3.5	4.03	6.04			*	-
NT2RP2004664	6.11	4.51	4.83	11.64	9.59	6.61	6.34	6.03	5.86				
NT2RP2004670	3.00	2.33	2.81	3.65	3.96	4.05	3.26	3.38	4.44	**	+		
NT2RP2004675	5.69	3.74	5.15	11.77	11.28	10.21	5.45	4.84	5.26	**	+		
NT2RP2004681	5.04	3.65	4.78	6.53	9.83	7.35	6.37	6.72	6.63	*	+	**	+
NT2RP2004689	2.24	1.16	1.68	3.06	4.60	6.68	1.3	2.45	1.72	*	+		

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Table 261

NT2RP2004709	5.18	3.25	1.93	12.66	12.56	10.94	5.12	4.16	3.85	**	+		
NT2RP2004710	5.83	4.70	2.80	7.69	7.61	6.76	4.34	3.44	4.54	*	+		
NT2RP2004721	11.13	7.44	7.40	6.68	9.65	8.99	11.35	9.52	13.55				
NT2RP2004736	6.31	5.30	5.26	8.14	9.36	7.77	6.53	5.39	5.85	**	+		
NT2RP2004743	2.77	1.82	1.65	5.65	6.03	4.15	4.87	6.71	5.76	**	+	**	+
NT2RP2004750	8.14	5.64	6.27	13.53	14.23	13.30	8.05	8.74	9.81	**	+		
NT2RP2004755	11.30	7.99	8.26	16.42	20.16	17.92	10.59	13.63	13.47	**	+		
NT2RP2004767	6.21	2.89	4.95	9.44	8.05	8.14	4.7	6.19	4.36	*	+		
NT2RP2004768	9.61	3.95	2.60	2.99	2.03	1.57	2.24	1.57	1.49				
NT2RP2004775	2.25	2.07	1.48	4.36	5.01	5.07	4.16	3.75	3.44	**	+	**	+
NT2RP2004791	14.05	7.61	6.73	8.91	10.03	9.17	7.11	6.72	8.15				
NT2RP2004794	41.53	28.26	27.09	43.02	36.69	32.68	39.95	33.86	41.52				
NT2RP2004795	3.77	2.11	2.19	3.89	7.37	3.74	3.78	5.26	5.25			*	+
NT2RP2004799	5.43	1.93	3.24	6.30	6.15	4.50	3.93	5.78	3.84				
NT2RP2004802	4.83	2.53	3.34	7.41	6.03	5.58	2.16	3.27	3.61	*	+		
NT2RP2004810	3.12	1.86	2.24	8.72	9.56	6.30	5.77	5.46	6.09	**	+	**	+
NT2RP2004816	4.85	3.14	2.65	6.62	9.96	5.26	6.09	3.65	4.78				
NT2RP2004837	13.44	8.28	7.12	11.51	16.25	16.53	19.77	16.72	17.56			*	+
NT2RP2004841	2.64	1.81	1.21	3.03	4.37	3.11	1.94	3.01	1.95				
NT2RP2004847	16.48	11.83	12.45	15.24	18.08	16.57	16.4	14.80	14				
NT2RP2004861	1.52	1.27	1.44	3.27	3.09	3.21	1.26	1.81	1.52	**	+		
NT2RP2004897	1.25	0.88	1.99	3.40	2.11	1.91	1.21	2.22	1.75				
NT2RP2004932	10.00	7.17	11.03	13.12	14.42	13.51	9.72	9.64	9.65	*	+		
NT2RP2004933	1.78	1.31	1.88	3.51	3.60	2.84	3.51	3.18	3.33	**	+	**	+
NT2RP2004936	4.87	2.22	1.77	6.48	8.16	3.31	4.73	2.49	2.48				
NT2RP2004951	5.43	2.53	1.87	3.02	4.24	3.02	2.87	3.70	11.67				
NT2RP2004959	8.45	5.08	5.37	8.17	7.86	9.93	4.85	5.55	4.46				
NT2RP2004961	5.21	3.54	2.31	7.99	9.20	8.11	4.59	5.46	6.53	**	+		
NT2RP2004962	4.01	2.64	2.72	5.11	4.60	4.41	3.88	3.76	3.58	*	+		
NT2RP2004966	2.57	2.53	3.68	2.80	3.88	2.77	2.12	3.33	4.07				
NT2RP2004967	2.23	2.61	2.86	7.50	6.79	8.12	3.33	4.64	3.83	**	+	*	+
NT2RP2004974	1.95	1.80	1.93	2.56	3.12	2.39	3.76	2.94	0.71	*	+		
NT2RP2004978	6.88	2.95	2.57	5.63	7.09	3.07	4.98	3.62	3.21				
NT2RP2004982	1.90	1.58	1.47	6.52	6.96	3.08	1.22	2.05	1.93	*	+		
NT2RP2004985	24.53	11.76	13.37	30.81	35.00	31.74	21.76	19.69	22.43	*	+		
NT2RP2004999	4.87	3.06	2.28	6.14	7.08	4.89	3.19	4.04	3.16				
NT2RP2005000	3.68	2.30	2.22	2.75	3.93	3.69	1.87	3.37	3.49				
NT2RP2005001	3.57	1.78	2.11	2.93	4.06	3.83	3.59	4.32	2.86				
NT2RP2005003	4.67	3.07	2.71	7.63	8.71	7.19	5.69	5.10	6.02	**	+	*	+
NT2RP2005012	6.73	4.06	6.10	5.56	7.80	5.46	4.68	6.28	4.92				
NT2RP2005018	7.22	3.93	3.53	6.32	10.68	5.74	4.63	4.62	5.01				
NT2RP2005020	17.60	10.40	7.54	8.46	8.34	5.63	6.22	5.13	5.78				
NT2RP2005022	4.95	2.69	3.66	5.26	6.40	4.90	4.15	3.47	4.07				
NT2RP2005027	22.97	13.64	17.61	9.34	8.66	7.21	22.54	22.24	24.2	*	-		
NT2RP2005031	1.59	1.04	2.13	1.35	2.05	1.82	1.32	2.27	2.73				
NT2RP2005035	12.28	9.78	9.98	17.38	24.50	17.61	24.38	23.70	30.68	*	+	**	+
NT2RP2005037	3.95	3.48	2.80	4.77	7.93	4.42	2.77	3.83	4.79				
NT2RP2005038	1.07	1.01	1.27	2.71	2.99	1.89	1.22	3.15	1.8	*	+		
NT2RP2005048	8.09	4.51	4.12	7.64	8.60	7.45	7.59	5.31	4.79				
NT2RP2005069	25.41	8.17	11.97	37.61	33.07	31.21	30.69	32.10	38.73	*	+	*	+
NT2RP2005073	4.93	2.00	2.06	7.13	4.92	3.75	2.76	2.91	4.07				
NT2RP2005097	4.59	2.92	2.93	3.87	3.63	3.16	2.4	2.61	2.69				
NT2RP2005108	3.21	2.75	1.61	3.23	2.96	2.92	1.57	2.62	2.37				
NT2RP2005116	9.11	5.71	5.87	6.08	9.75	7.92	7.26	7.17	8.23				
NT2RP2005126	8.28	8.63	9.53	6.69	10.50	10.65	4.18	6.96	4.15			*	-
NT2RP2005135	3.79	3.03	2.85	3.91	5.50	2.16	3.03	4.16	3.27				

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Table 262

NT2RP2005139	3.84	1.72	1.31	3.14	3.97	2.27	2.16	2.35	2.71				
NT2RP2005140	6.44	3.34	1.76	2.06	2.19	1.94	1.62	2.45	4.48				
NT2RP2005144	7.59	4.23	3.57	8.56	9.25	7.68	4.75	8.24	8.15				
NT2RP2005147	3.33	1.34	1.33	2.20	2.64	3.04	4.92	2.37	1.84				
NT2RP2005148	4.87	2.83	2.05	4.55	5.06	4.19	2.73	4.23	3.35				
NT2RP2005159	3.35	2.32	2.38	3.01	3.13	3.18	2.03	3.88	1.9				
NT2RP2005162	3.09	1.68	1.72	3.70	3.44	2.30	2.24	3.35	2.16				
NT2RP2005163	25.94	15.25	17.25	21.49	24.77	28.25	17.62	25.86	21.18				
NT2RP2005168	4.54	2.65	2.28	2.25	4.03	2.91	2.1	1.69	2.5				
NT2RP2005181	9.05	4.31	4.53	4.26	4.18	3.03	3.8	2.76	3.1				
NT2RP2005204	8.22	7.14	6.39	7.26	7.87	6.45	7	4.58	3.93				
NT2RP2005219	6.43	4.48	4.74	6.61	6.15	4.27	4.15	5.58	7.21				
NT2RP2005227	6.13	3.78	3.14	9.09	11.14	7.97	3.82	5.07	8.88	*	+		
NT2RP2005237	27.33	18.84	15.64	23.79	22.48	23.44	22.52	21.69	18.11				
NT2RP2005239	3.74	1.34	1.71	2.73	2.86	2.63	2.66	2.69	2.3				
NT2RP2005247	2.49	2.14	1.98	4.28	4.68	4.69	2.63	2.43	2.5	**	+		
NT2RP2005254	9.04	3.29	3.29	8.47	7.53	8.80	7.01	6.79	4.08				
NT2RP2005270	4.99	2.71	2.82	6.57	6.85	4.80	6.2	6.16	8.3			*	+
NT2RP2005276	9.47	6.54	6.31	10.41	11.77	12.24	5.39	7.57	7.48	*	+		
NT2RP2005287	4.80	3.96	2.36	5.91	7.62	8.20	5.51	5.27	7.29	*	+		
NT2RP2005288	3.78	1.10	1.91	4.67	4.69	3.22	2.56	2.68	2.46				
NT2RP2005289	3.95	2.82	3.63	10.36	10.31	13.45	7.04	9.38	8.68	**	+	**	+
NT2RP2005293	4.69	3.98	2.48	2.80	6.37	4.36	1.98	2.19	8.18				
NT2RP2005315	4.50	2.51	3.53	6.84	5.84	6.72	4.55	3.38	3.33	*	+		
NT2RP2005322	8.85	3.21	3.77	5.49	9.42	5.85	5.53	11.41	21.87				
NT2RP2005325	13.28	7.03	7.32	9.81	8.97	5.93	11.14	10.62	11.49				
NT2RP2005336	12.73	6.78	5.54	13.58	10.27	12.67	8.85	6.83	5.91				
NT2RP2005343	6.02	1.89	2.05	7.45	9.65	7.01	10.08	10.85	12.82	*	+	**	+
NT2RP2005344	1.85	1.66	1.47	2.08	2.88	1.92	2.74	2.45	3.15			**	+
NT2RP2005347	4.37	2.71	1.89	5.25	5.00	4.78	3.35	2.93	2.34				
NT2RP2005354	12.00	6.61	6.14	17.43	12.77	12.49	8.48	9.88	9.01				
NT2RP2005358	4.88	3.45	2.64	4.51	4.14	3.14	3.97	2.53	1.99				
NT2RP2005360	7.88	5.76	2.39	6.48	5.68	6.59	4.31	3.84	6.35				
NT2RP2005378	18.33	8.81	8.98	11.83	10.64	10.23	12.69	11.85	15.35				
NT2RP2005391	11.21	5.99	4.87	8.42	9.50	6.15	7.72	6.42	7.6				
NT2RP2005393	7.14	5.04	4.09	7.19	7.55	7.32	5.14	5.24	6.8				
NT2RP2005407	4.70	3.27	2.59	4.12	5.86	4.29	4.19	4.07	6.46				
NT2RP2005419	2.03	2.94	2.38	2.87	3.30	2.26	2.46	2.93	2.38				
NT2RP2005425	3.16	1.77	1.43	6.79	4.57	5.63	3.84	5.07	4.35	*	+	*	+
NT2RP2005429	5.40	3.41	3.71	7.74	6.15	6.01	3.54	4.45	2.89	*	+		
NT2RP2005436	11.49	5.63	5.95	16.34	13.38	12.70	9.59	8.94	10.22	*	+		
NT2RP2005441	2.64	2.24	1.49	4.39	3.02	4.62	2.37	2.61	2.65	*	+		
NT2RP2005442	6.72	3.80	3.11	6.35	6.53	5.07	6.08	5.33	7.07				
NT2RP2005444	14.62	10.40	7.75	7.08	9.17	7.55	7.37	6.88	8.45				
NT2RP2005453	1.54	2.20	1.49	7.95	9.47	8.01	8.67	8.44	9.15	**	+	**	+
NT2RP2005457	15.76	12.87	16.87	26.94	13.90	21.92	12.51	12.21	12.15				
NT2RP2005458	1.63	1.87	2.03	5.92	5.93	3.89	2.67	3.64	6.17	**	+		
NT2RP2005463	4.65	3.64	4.43	7.72	7.84	5.33	6.02	6.93	5.84	*	+	-	+
NT2RP2005464	11.98	9.14	6.68	11.62	10.20	8.75	5.59	3.86	4.74			*	-
NT2RP2005465	4.57	3.64	2.60	8.98	7.23	8.68	2.44	5.04	5.3	**	+		
NT2RP2005472	10.01	4.28	4.30	7.95	7.14	5.73	3.03	3.71	5.35				
NT2RP2005476	5.22	3.10	3.30	10.18	12.60	10.12	5.36	4.72	5.84	**	+		
NT2RP2005490	5.25	3.96	4.56	6.13	9.22	5.46	5.31	3.92	5.71				
NT2RP2005491	15.97	8.85	12.00	4.52	5.86	4.78	8.53	10.16	9.41	*	-		
NT2RP2005495	2.68	2.26	2.48	2.05	3.65	3.42	3.01	4.37	2.75				
NT2RP2005496	9.04	5.08	6.06	16.30	11.28	12.12	9.01	10.34	6.32	*	+		

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Table 263

NT2RP2005498	6.78	2.60	2.45	2.62	6.63	3.50	3.33	3.34	4.18				
NT2RP2005501	4.44	2.53	2.65	2.38	4.12	2.69	2.07	3.28	2.78				
NT2RP2005506	5.72	4.30	3.10	5.43	9.55	6.10	24.52	21.82	25.02			**	+
NT2RP2005509	6.91	5.58	4.63	12.32	11.78	9.14	5.34	8.99	8.48	*	+		
NT2RP2005514	3.36	2.23	2.33	3.96	5.18	4.19	3.03	4.16	4.55	*	+		
NT2RP2005520	10.34	5.10	5.86	6.07	8.22	5.46	3.87	3.79	3.08				
NT2RP2005525	6.12	4.01	5.33	8.58	7.75	8.13	5.26	8.01	5.47	*	+		
NT2RP2005531	0.65	1.10	1.57	2.33	1.56	1.74	1.49	2.39	1.21				
NT2RP2005535	36.57	17.31	21.13	93.90	73.03	67.87	27.53	17.14	25.99	**	+		
NT2RP2005539	10.87	6.53	4.81	8.43	9.17	6.85	6.76	6.87	5.25				
NT2RP2005540	2.81	2.63	2.81	7.15	6.27	5.67	4.42	5.46	9.74	**	+		
NT2RP2005541	5.40	3.42	2.70	8.82	9.81	10.04	7.49	7.37	5.44	**	+	*	+
NT2RP2005549	3.91	1.98	1.81	3.23	3.51	2.41	2.43	3.46	2.97				
NT2RP2005555	3.52	2.33	3.66	6.38	7.55	5.49	7.54	10.56	6.47	*	+	*	+
NT2RP2005557	7.00	5.12	11.72	16.35	11.47	12.41	6.34	5.80	8.04				
NT2RP2005581	5.51	4.09	4.45	13.70	13.23	10.54	6.26	5.62	5.86	**	+		
NT2RP2005586	7.40	3.49	4.35	2.55	4.08	2.63	1.67	2.60	2.43				
NT2RP2005597	6.16	4.97	3.02	4.57	4.34	4.57	4.67	4.40	5.08				
NT2RP2005600	4.06	2.52	2.53	3.83	4.26	3.10	2.47	4.00	2.95				
NT2RP2005605	13.12	8.01	6.74	12.67	14.30	12.26	6.96	7.51	8				
NT2RP2005614	9.18	5.27	8.25	16.39	16.00	13.57	10.11	8.70	9.2	**	+		
NT2RP2005620	4.07	2.65	2.40	3.99	3.40	3.40	2.45	3.61	2.26				
NT2RP2005622	9.20	6.36	7.23	6.07	7.94	5.76	4.64	4.67	6.34				
NT2RP2005632	3.64	3.42	2.57	5.77	4.33	3.82	2.82	3.85	3.3				
NT2RP2005635	3.95	2.73	2.06	3.40	4.38	2.94	2.4	2.42	3.18				
NT2RP2005637	2.20	1.05	1.68	13.21	4.02	4.55	2.2	2.55	5.6				
NT2RP2005640	3.47	1.55	1.53	2.16	1.23	2.22	1.96	2.66	2.84				
NT2RP2005645	6.42	3.67	2.99	5.68	11.68	7.34	5.29	6.74	5.73				
NT2RP2005651	4.09	3.02	3.19	6.89	11.77	5.52	3.81	4.33	6.7				
NT2RP2005654	5.50	3.61	4.20	6.10	7.84	5.96	4.19	5.64	4.96				
NT2RP2005666	4.54	3.08	3.45	5.18	6.63	4.14	4.25	3.69	7.2				
NT2RP2005669	6.09	5.35	5.64	8.34	9.73	9.01	4.66	6.00	6.82	**	+		
NT2RP2005670	2.87	2.37	1.87	5.75	5.68	2.37	1.68	2.33	3.03				
NT2RP2005671	10.41	3.42	4.33	5.10	6.32	3.51	3.46	4.47	6.12				
NT2RP2005675	11.31	4.30	4.30	8.54	8.22	4.79	7.64	6.94	9.43				
NT2RP2005683	9.32	5.43	5.87	8.08	9.48	5.92	5.85	4.94	4.56				
NT2RP2005690	3.18	1.30	1.52	3.24	4.46	3.75	2.33	3.71	3.54				
NT2RP2005694	4.33	2.30	2.18	4.82	3.54	4.62	3.22	3.77	3.78				
NT2RP2005701	22.21	13.84	17.86	22.12	25.56	24.08	18.18	17.70	22.41				
NT2RP2005712	2.84	3.06	3.02	3.90	3.94	3.10	1.15	2.49	1.88			*	-
NT2RP2005719	2.26	1.27	0.73	3.09	3.04	2.67	2.23	1.46	2.56	*	+		
NT2RP2005722	11.76	8.52	5.52	18.21	24.59	18.10	8.26	9.21	12.37	*	+		
NT2RP2005723	4.68	2.75	2.29	7.35	6.52	3.86	4.39	4.70	2.79				
NT2RP2005726	5.41	2.39	2.73	5.77	4.51	4.16	3.27	4.19	3.67				
NT2RP2005729	5.30	2.58	2.08	6.82	6.27	4.01	3.21	5.54	3.89				
NT2RP2005731	0.50	0.60	0.63	1.06	1.43	0.80	0.71	2.81	0.87	*	+		
NT2RP2005732	8.98	3.61	4.01	6.71	6.46	5.79	4.23	7.06	7.16				
NT2RP2005737	10.83	8.16	10.12	14.65	17.80	12.60	12.9	11.51	9.06	*	+		
NT2RP2005741	5.83	2.63	2.65	3.36	3.80	2.41	3.96	2.72	3.47				
NT2RP2005748	3.52	1.63	2.33	2.18	2.64	1.48	3.11	2.62	2.38				
NT2RP2005752	5.37	3.43	3.73	6.46	5.65	5.66	6.55	3.67	3.82				
NT2RP2005753	22.04	14.07	18.05	15.96	24.14	20.59	21.63	18.25	19.82				
NT2RP2005763	6.73	2.47	2.52	3.25	3.61	3.70	1.84	3.88	3.22				
NT2RP2005767	2.43	2.60	2.16	6.91	6.56	7.20	3.36	3.03	4.12	**	+	*	+
NT2RP2005773	15.62	10.12	12.99	19.66	19.02	17.26	17.15	13.07	15.8	*	+		
NT2RP2005774	10.33	5.72	6.91	21.21	24.60	21.03	9.42	7.55	8.22	**	+		

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Table 264

NT2RP2005775	4.39	1.98	1.42	2.12	2.56	2.56	2.19	2.08	1.67				
NT2RP2005781	5.85	3.98	3.29	6.76	5.57	5.04	4.75	3.50	4.17				
NT2RP2005784	11.14	6.73	5.29	8.15	8.38	8.40	7.85	8.40	10.24				
NT2RP2005789	4.85	3.33	3.28	5.63	7.04	4.46	3.88	3.70	4.09				
NT2RP2005799	1.71	1.81	1.37	3.76	5.36	2.16	2.16	2.19	2.43			*	+
NT2RP2005804	6.19	3.18	3.30	4.57	7.49	6.42	5.55	5.88	4.72				
NT2RP2005812	3.92	3.04	2.54	4.78	6.17	3.21	2.98	4.18	4.04				
NT2RP2005815	2.54	2.17	3.20	3.81	3.69	2.58	2.35	2.98	1.88				
NT2RP2005835	14.04	7.44	6.79	14.50	10.00	10.84	9.86	7.11	11.61				
NT2RP2005841	6.35	3.23	3.13	5.70	4.93	4.82	5.84	3.68	4.27				
NT2RP2005853	3.23	3.29	2.96	6.28	6.53	5.74	4.87	4.09	5.28	**	+	*	+
NT2RP2005857	8.95	4.28	4.74	6.65	7.52	6.19	1.63	2.12	1.8				
NT2RP2005859	5.38	4.41	5.54	4.28	5.42	3.86	2.87	3.84	3.87			*	-
NT2RP2005860	3.02	1.60	2.64	2.92	4.01	2.37	2.32	4.74	1.81				
NT2RP2005863	4.66	2.88	2.88	3.96	3.85	3.93	2.02	2.05	1.69				
NT2RP2005868	3.44	1.57	1.65	4.52	4.28	2.97	2.38	3.85	2.89				
NT2RP2005876	13.61	7.01	5.40	17.03	13.16	6.91	8.8	8.61	107				
NT2RP2005878	6.92	4.37	4.13	11.06	12.33	11.73	5.81	7.81	6.82	**	+		
NT2RP2005883	1.59	1.56	1.08	3.31	2.84	2.42	3.91	4.53	4.86	**	+	**	+
NT2RP2005886	8.60	4.98	6.40	10.11	11.16	11.42	6.19	6.08	5.43	*	+		
NT2RP2005887	5.47	3.26	3.97	12.05	12.81	9.32	13.75	10.35	15.02	**	+	**	+
NT2RP2005890	7.74	6.08	7.50	6.23	6.35	4.71	2.57	2.56	1.86			**	-
NT2RP2005901	3.39	2.76	2.57	3.81	4.07	4.20	2.43	3.04	3.13	*	+		
NT2RP2005902	1.86	0.89	1.33	3.39	3.77	2.15	2.13	2.79	3.13	*	+	*	+
NT2RP2005908	9.46	5.71	4.03	9.28	7.93	10.45	6.03	6.26	6.92				
NT2RP2005927	7.43	5.84	5.10	9.51	9.65	7.14	3.72	5.75	4.41				
NT2RP2005933	6.32	4.20	3.63	5.57	7.02	4.50	3.29	2.73	4.08				
NT2RP2005941	9.03	6.94	7.01	7.65	13.07	8.78	10.41	9.47	5.87				
NT2RP2005942	3.02	2.03	1.79	3.90	4.09	3.96	2.56	2.68	2	*	+		
NT2RP2005946	6.57	4.95	5.93	3.90	3.86	3.27	2.5	2.94	2.41	*	-	**	-
NT2RP2005970	12.30	10.25	11.94	15.87	16.05	15.06	14.9	13.37	14.97	**	+	*	+
NT2RP2005980	3.71	2.65	2.25	7.90	7.37	4.49	4.13	4.23	2.71	*	+		
NT2RP2005994	5.01	2.60	2.01	2.75	4.22	1.07	2.23	3.11	2.43				
NT2RP2006004	2.32	1.82	1.35	2.43	4.21	2.56	2.36	3.37	2.03				
NT2RP2006013	4.44	2.15	4.45	6.09	6.99	3.28	4.68	5.22	4.41				
NT2RP2006023	21.60	12.40	20.04	37.44	49.33	45.44	22.61	22.79	24.39	**	+		
NT2RP2006028	5.34	3.20	3.73	4.07	4.23	2.81	3.39	4.81	5.42				
NT2RP2006038	0.34	0.06	1.28	0.43	0.83	3.61	0.25	1.80	0.18				
NT2RP2006042	8.65	5.14	6.93	7.32	7.79	6.34	7.56	7.82	9.4				
NT2RP2006043	5.05	2.75	2.80	12.32	12.87	10.73	8.05	8.08	7.82	**	+	**	+
NT2RP2006052	2.31	2.64	1.44	1.42	2.55	2.98	1.26	2.10	2.6				
NT2RP2006057	3.69	1.67	1.24	3.57	3.44	2.48	2.2	3.85	3.27				
NT2RP2006064	12.49	6.77	9.83	12.13	10.85	6.00	10.28	6.81	5.57				
NT2RP2006068	3.25	3.63	2.31	8.60	6.86	6.64	4.6	5.09	2.54	**	+		
NT2RP2006069	1.08	0.69	0.92	0.88	1.74	0.95	0.92	1.48	1.42				
NT2RP2006071	2.73	3.23	2.31	5.07	7.66	5.45	2.92	4.00	2.55	*	+		
NT2RP2006090	3.70	1.69	2.79	3.57	5.20	3.82	3.74	3.63	2.49				
NT2RP2006092	3.65	2.47	2.47	3.19	3.41	3.44	2.36	2.80	2.77				
NT2RP2006097	24.23	9.76	10.66	21.53	18.65	14.12	10.2	9.65	12.96				
NT2RP2006098	4.17	2.27	1.77	4.26	4.04	2.86	4.03	6.51	3.5				
NT2RP2006099	4.48	2.99	2.12	5.82	5.86	5.18	3.32	4.84	3.86	*	+		
NT2RP2006100	3.88	1.55	1.83	3.98	4.92	3.85	2.1	3.68	2.65				
NT2RP2006103	10.54	3.86	5.78	3.37	2.55	1.88	2.21	3.36	1.85				
NT2RP2006106	8.45	4.11	4.04	6.45	5.69	6.30	4.48	6.29	4.22				
NT2RP2006127	9.00	6.34	7.56	9.10	8.66	7.24	9.22	10.10	8.49				
NT2RP2006134	1.55	1.02	1.47	1.76	1.82	1.93	1.55	2.52	1.29	*	+		

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Table 265

NT2RP2006141	5.76	3.11	3.17	3.84	5.50	4.54	3.67	3.75	3.95				
NT2RP2006166	7.93	5.66	5.17	12.63	13.99	9.56	6.76	6.08	6.36	*	+		
NT2RP2006176	4.45	2.26	1.67	6.40	4.88	5.22	2.44	3.34	5.68	*	+		
NT2RP2006181	1.58	1.06	1.00	1.37	3.24	3.22	1.23	2.94	1.73				
NT2RP2006184	23.94	15.54	16.09	22.96	21.00	23.09	17.11	19.55	14.56				
NT2RP2006186	1.68	1.14	2.35	2.02	3.74	1.74	1.23	3.31	1.82				
NT2RP2006196	4.74	3.02	3.70	6.83	6.02	5.77	4.04	5.17	3.91	*	+		
NT2RP2006199	2.29	2.59	2.52	3.33	3.50	4.30	2.88	2.76	2.12	*	+		
NT2RP2006200	4.29	2.63	1.43	3.59	5.59	2.06	3.12	2.50	2.5				
NT2RP2006210	59.40	41.07	36.68	33.45	39.27	22.58	11.72	8.31	9.47			**	-
NT2RP2006219	3.75	1.76	1.64	3.39	3.29	2.82	2.17	1.88	4.22				
NT2RP2006224	5.72	3.72	4.01	5.11	6.26	6.39	3.82	3.77	4.2				
NT2RP2006237	5.09	3.91	5.00	9.00	7.92	10.28	5.01	5.76	5.27	**	+		
NT2RP2006238	3.42	2.16	1.78	4.42	4.29	2.44	2.31	3.01	1.89				
NT2RP2006258	9.12	5.55	6.28	6.08	7.62	7.68	6.35	6.07	3.93				
NT2RP2006261	1.75	2.42	1.14	2.06	2.49	1.87	1.21	1.75	2.67				
NT2RP2006269	23.86	9.30	9.53	15.39	18.13	13.53	12.46	10.61	15.67				
NT2RP2006275	4.68	2.71	2.12	3.99	3.20	2.45	2.89	2.81	3.34				
NT2RP2006282	7.12	3.89	6.34	8.17	11.45	9.25	4.48	4.87	2.85	*	+		
NT2RP2006302	4.86	2.69	3.31	10.51	10.47	9.06	10	9.83	3.76	**	+		
NT2RP2006312	8.45	5.62	5.99	10.60	10.03	9.84	7.18	6.51	5.02	*	+		
NT2RP2006320	3.62	2.45	1.39	4.62	5.47	5.86	2.21	4.05	3.23	*	+		
NT2RP2006321	1.99	1.78	2.42	3.22	4.24	2.52	1.97	3.17	2.07				
NT2RP2006323	1.30	0.75	0.38	1.35	1.65	0.69	0.19	2.09	2.6				
NT2RP2006333	2.18	0.70	0.66	2.51	1.88	1.17	1.49	1.76	2.35				
NT2RP2006334	3.73	1.40	1.47	2.69	3.03	2.34	0.81	2.29	2.95				
NT2RP2006338	2.65	1.82	1.03	3.45	4.02	2.81	1.6	3.69	2.93				
NT2RP2006339	2.37	1.54	1.37	3.09	2.39	1.47	1.2	2.47	2.21				
NT2RP2006355	1.01	0.99	0.71	2.16	2.25	1.72	1.94	2.95	0.87	**	+		
NT2RP2006365	1.51	1.66	1.15	3.16	4.39	3.70	1.83	4.13	1.9	**	+		
NT2RP2006374	16.70	8.19	7.22	17.36	18.00	12.60	10.86	13.62	9.02				
NT2RP2006393	4.85	2.17	2.52	8.54	10.40	8.85	5.98	6.32	6.15	**	+	*	+
NT2RP2006394	2.02	1.64	1.69	3.46	1.86	1.52	3.53	1.56	2.54				
NT2RP2006400	1.99	1.74	1.43	2.29	2.67	2.67	2.79	1.32	1.33	*	+		
NT2RP2006411	36.13	23.40	20.23	18.85	35.68	22.21	26.26	22.92	21.44				
NT2RP2006429	3.49	1.96	1.56	18.22	22.80	21.81	7.61	6.72	8.71	**	+	**	+
NT2RP2006435	2.88	2.61	2.07	4.19	4.16	3.86	3.51	3.02	3.91	**	+		
NT2RP2006436	4.50	2.57	2.37	11.47	10.14	10.45	15.06	14.83	12.68	**	+	**	+
NT2RP2006441	5.48	3.11	4.37	12.23	11.44	10.95	9.38	9.44	9.01	**	+	**	+
NT2RP2006447	3.63	2.74	2.87	7.53	5.11	1.37	2.09	1.56	0.94			*	-
NT2RP2006454	3.45	1.48	1.32	2.04	2.21	2.24	3.02	1.84	0.51				
NT2RP2006455	3.08	1.02	1.42	3.46	1.52	2.11	2.25	1.46	1.25				
NT2RP2006456	3.43	1.56	1.38	1.87	3.29	2.20	1.39	3.00	3.52				
NT2RP2006464	7.78	4.38	3.90	5.55	4.82	4.88	3.6	3.54	5.67				
NT2RP2006467	5.66	2.72	2.67	10.90	8.83	10.03	7.29	6.50	9.64	**	+	*	+
NT2RP2006472	7.44	3.78	3.97	8.69	8.19	8.22	5	4.65	10.62				
NT2RP2006474	8.86	5.98	7.97	27.71	30.65	24.91	30	37.03	33.44	**	+	**	+
NT2RP2006475	5.74	3.11	2.17	15.80	11.04	13.89	8.72	6.46	9.93	**	+	*	+
NT2RP2006476	14.81	5.32	5.83	6.07	6.15	5.06	6.6	4.52	6.65				
NT2RP2006501	10.57	4.49	3.64	10.98	10.15	9.25	4.35	4.19	5.76				
NT2RP2006512	10.18	4.42	5.26	7.98	9.45	6.77	5.81	5.75	6.47				
NT2RP2006526	2.38	0.63	1.13	1.33	3.17	1.44	1.31	2.50	2.57				
NT2RP2006527	6.04	4.50	5.90	6.98	6.77	8.30	6.37	6.06	6.05				
NT2RP2006534	1.08	0.58	0.52	1.10	1.90	2.81	1.51	1.54	1.55			*	+
NT2RP2006537	7.96	4.17	4.11	12.78	11.80	12.98	5.84	7.01	9.26	**	+		
NT2RP2006543	2.53	2.49	1.25	3.82	3.98	2.63	5.74	3.55	4.9			*	+

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Table 266

NT2RP2006554	2.93	1.44	1.64	4.14	5.11	5.65	3.05	2.87	4.34	**	+		
NT2RP2006565	2.42	3.04	1.97	5.84	7.27	4.73	5.76	4.50	8.32	*	+	*	+
NT2RP2006571	15.53	8.80	8.87	9.19	10.25	5.31	9.49	9.09	15.1				
NT2RP2006573	3.03	1.23	1.11	3.74	3.96	3.02	2.6	2.13	2.11				
NT2RP2006598	5.73	3.98	4.61	7.93	8.72	6.43	5.28	3.71	6.12	*	+		
NT2RP2006601	37.52	34.93	32.64	41.04	41.47	32.68	27.39	28.66	36.43				
NT2RP3000002	3.95	2.25	3.29	4.37	7.61	7.60	3.47	4.83	7.96	*	+		
NT2RP3000011	4.07	2.64	1.62	5.92	4.70	5.14	3.96	3.12	4.24	*	+		
NT2RP3000014	3.17	3.00	2.39	9.14	11.05	8.39	7.15	7.48	8.57	**	+	**	+
NT2RP3000016	9.66	5.49	5.68	6.73	6.36	7.49	4.75	5.66	6.35				
NT2RP3000022	4.96	2.03	2.47	3.53	3.43	2.45	3.24	3.89	7.1				
NT2RP3000024	12.74	9.32	13.69	28.77	37.69	22.23	11.49	12.80	14.79	*	+		
NT2RP3000031	4.64	2.28	2.98	4.90	4.09	5.50	4.12	3.94	3.26				
NT2RP3000034	4.51	3.69	3.49	3.95	4.58	4.75	3.38	3.05	3.23				
NT2RP3000037	15.49	9.32	10.69	13.56	14.15	12.81	7.78	9.45	8.16				
NT2RP3000040	2.98	2.45	1.73	1.43	1.95	2.12	0.99	2.09	2.1				
NT2RP3000041	10.75	6.47	4.78	19.57	16.79	13.38	9.67	7.12	9.17	*	+		
NT2RP3000046	5.16	2.85	2.89	6.40	9.13	5.39	4.23	3.75	6.16				
NT2RP3000047	6.44	3.75	3.07	4.50	4.32	4.37	3.44	4.24	4.69				
NT2RP3000049	3.94	3.36	1.85	3.67	6.35	6.22	5.02	4.43	8.2				
NT2RP3000050	7.94	4.67	6.52	13.03	15.60	12.76	7.92	7.66	10.86	**	+		
NT2RP3000051	6.26	3.23	4.99	9.29	9.59	8.78	5.46	7.17	6.65	**	+		
NT2RP3000054	6.09	3.47	4.38	5.67	6.99	5.26	5.01	4.84	5.62				
NT2RP3000055	3.24	2.73	0.81	4.89	4.66	2.53	2.67	2.43	3.79				
NT2RP3000056	2.70	3.24	1.60	2.60	3.66	2.74	3.75	2.94	3.3				
NT2RP3000059	4.21	2.87	2.12	3.45	3.50	3.02	3.35	3.22	4.21				
NT2RP3000063	7.78	5.44	6.74	6.64	5.14	7.47	6.5	8.34	4.12				
NT2RP3000068	1.30	1.86	2.21	1.64	3.20	2.26	2.1	3.07	3.12				
NT2RP3000069	3.21	2.16	2.26	10.79	10.68	7.75	8.64	7.90	7.98	**	+	**	+
NT2RP3000072	2.08	1.15	1.36	3.34	2.75	2.73	2.05	3.07	2.12	*	+		
NT2RP3000080	12.90	8.84	11.62	14.83	16.14	12.41	14.4	11.56	12.15				
NT2RP3000085	4.82	2.44	2.00	2.73	3.07	3.01	2.95	2.26	2.49				
NT2RP3000087	12.35	7.36	5.97	19.26	20.25	18.12	12.89	8.99	10.11	**	+		
NT2RP3000092	2.83	2.11	1.59	4.04	2.45	1.56	2.71	2.87	2.87				
NT2RP3000109	1.75	1.89	2.71	5.02	4.39	3.90	1.58	3.14	1.97	**	+		
NT2RP3000119	10.48	4.74	6.30	7.48	8.15	6.85	5.44	7.67	7.52				
NT2RP3000125	9.53	6.24	6.75	10.54	13.59	12.33	7.17	8.82	6.83	*	+		
NT2RP3000131	13.37	7.84	8.67	12.43	13.75	13.12	11.27	10.91	10.26				
NT2RP3000134	8.39	4.00	4.04	11.86	8.47	11.09	6.57	5.88	5.18	*	+		
NT2RP3000137	7.33	3.86	4.11	4.55	10.23	5.70	5.38	4.77	5.25				
NT2RP3000142	8.58	2.85	3.30	8.25	6.01	4.98	4.9	4.68	4.51				
NT2RP3000148	6.50	3.03	2.82	4.77	5.93	4.35	4.39	4.87	3.31				
NT2RP3000149	7.40	4.34	3.38	4.95	6.06	4.71	3.65	4.88	5.43				
NT2RP3000163	5.34	2.10	2.73	5.49	7.84	4.53	2.61	3.70	2.68				
NT2RP3000168	17.73	9.34	8.35	13.43	12.52	14.26	15.5	18.99	23.37				
NT2RP3000169	2.79	1.47	1.93	3.28	2.66	2.80	2.69	4.02	3.92				
NT2RP3000171	30.99	20.17	24.95	41.61	37.53	33.55	22.47	25.44	33.88	*	+		
NT2RP3000172	5.29	2.13	2.18	3.70	4.85	1.88	2.31	1.91	2.23				
NT2RP3000186	16.37	8.43	6.94	11.35	12.10	6.88	5.69	5.57	6.97				
NT2RP3000197	2.96	2.49	2.66	5.21	6.67	3.78	2.54	2.96	3.64	*	+		
NT2RP3000201	11.54	5.67	6.73	11.59	11.99	10.04	5.11	5.52	10.33				
NT2RP3000204	3.53	2.05	1.72	2.68	3.65	3.34	1.75	3.41	1.98				
NT2RP3000207	4.88	2.36	2.46	3.16	3.56	3.29	4.1	5.13	6.04				
NT2RP3000216	8.62	6.38	5.44	6.42	8.59	6.54	8.63	6.16	7.72				
NT2RP3000220	2.88	1.23	2.50	2.75	3.70	2.71	2.57	3.23	2.33				
NT2RP3000221	4.47	2.97	2.52	4.75	5.82	4.37	3.89	3.79	4.34				

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Table 267

NT2RP3000232	7.80	2.59	4.87	14.07	13.78	10.58	4.43	6.16	6.42	*	+		
NT2RP3000233	4.29	2.04	3.30	4.16	4.02	3.58	3.88	4.05	3.95				
NT2RP3000234	5.82	3.69	3.99	6.88	6.24	5.76	5.09	5.25	5.52				
NT2RP3000235	4.07	2.16	2.75	4.46	3.39	3.79	3.35	4.56	3.36				
NT2RP3000239	7.80	3.65	4.61	5.36	6.98	5.05	3.92	4.89	7.01				
NT2RP3000247	2.30	1.21	1.95	2.12	2.01	2.94	1.85	3.86	2.35				
NT2RP3000251	8.89	5.54	6.24	11.87	10.35	8.87	9.19	9.33	7.77				
NT2RP3000252	15.04	4.46	4.08	9.00	9.21	5.83	5.52	5.10	6.74				
NT2RP3000255	5.13	2.85	2.23	3.53	3.93	3.32	2.12	2.52	4.46				
NT2RP3000262	7.20	3.34	3.67	7.23	8.28	5.67	4.7	4.54	3.81				
NT2RP3000266	13.99	6.47	5.93	16.36	16.88	13.38	9.91	14.29	13.15				
NT2RP3000267	4.19	1.73	1.51	3.08	4.17	2.39	2.28	3.19	2.31				
NT2RP3000271	7.47	3.16	2.85	7.84	6.39	5.57	3.5	5.30	3.75				
NT2RP3000278	3.14	2.04	3.02	4.79	6.42	5.26	3.22	5.70	4.21	**	+		
NT2RP3000281	7.14	3.51	4.30	9.39	7.57	6.94	6.62	8.48	7.76				
NT2RP3000292	2.43	1.31	1.46	1.66	2.08	1.80	2.97	2.36	1.82				
NT2RP3000299	3.32	1.72	2.64	3.50	2.85	1.65	3.49	2.65	2.85				
NT2RP3000304	7.20	4.06	3.87	3.27	5.90	6.50	4.23	4.68	5.46				
NT2RP3000310	9.88	5.44	4.97	10.57	8.79	8.65	8.38	7.53	9.91				
NT2RP3000312	4.71	2.11	3.36	4.19	4.91	4.91	2.11	3.53	4.02				
NT2RP3000320	9.82	2.79	5.46	8.18	6.79	9.80	7.95	7.10	16.94				
NT2RP3000322	30.65	18.22	26.99	58.85	49.93	31.40	36.14	39.97	34.74			*	+
NT2RP3000324	2.18	1.49	1.41	2.10	2.20	2.50	2.87	1.62	1.63				
NT2RP3000326	4.07	2.09	2.65	6.40	4.79	6.20	5.05	3.50	3.68	*	+		
NT2RP3000329	8.08	3.03	2.39	13.04	10.42	8.93	5.43	5.08	6.48	*	+		
NT2RP3000330	6.13	3.81	4.47	3.99	4.93	3.61	5.76	6.52	5.37				
NT2RP3000333	3.58	1.99	1.19	2.09	2.88	2.04	2.14	2.57	2.31				
NT2RP3000341	13.34	6.74	7.40	16.98	14.13	16.48	11.16	11.51	12.58	*	+		
NT2RP3000344	2.19	2.15	1.77	2.27	1.91	1.50	1.56	1.76	2.32				
NT2RP3000345	0.88	0.64	0.51	3.07	2.22	3.27	0.95	0.77	2.11	**	+		
NT2RP3000348	112.18	53.12	48.19	87.36	67.82	76.37	170.4	141.05	175.2			*	+
NT2RP3000350	13.69	7.30	6.99	9.25	9.00	7.77	7.42	5.74	8.01				
NT2RP3000359	10.64	6.49	5.35	19.00	17.38	16.68	15.5	13.49	16.08	**	+	*	+
NT2RP3000361	10.35	4.92	4.34	11.24	6.97	7.55	6.16	6.69	7.28				
NT2RP3000366	7.65	3.30	4.82	9.45	14.23	10.18	10.84	11.42	12.66	*	+	**	+
NT2RP3000378	4.91	3.67	4.88	5.34	6.49	6.00	4.34	4.99	3.64				
NT2RP3000384	6.56	5.43	5.50	8.93	9.13	11.76	6.91	6.90	7.16	*	+	*	+
NT2RP3000389	14.26	10.15	11.05	22.04	27.40	18.38	12.47	13.44	23.39	*	+		
NT2RP3000393	5.27	3.15	2.77	4.98	4.37	4.43	4.32	3.00	3.71				
NT2RP3000395	121.26	84.54	65.25	98.14	119.90	103.24	32.56	26.84	40.17			*	-
NT2RP3000397	3.69	4.24	2.44	2.76	4.13	3.97	3.48	2.62	4.13				
NT2RP3000398	6.97	4.09	4.94	8.35	10.97	6.66	5.51	6.21	5.86				
NT2RP3000403	4.82	3.83	4.35	9.87	12.59	8.19	6.65	6.56	8.79	*	+	*	+
NT2RP3000418	4.00	2.62	2.61	8.58	12.65	8.62	5.36	6.28	7.5	**	+	*	+
NT2RP3000424	5.08	4.11	3.96	14.10	16.88	10.90	8.47	7.77	7.95	**	+	**	+
NT2RP3000427	2.50	1.80	2.77	5.73	6.63	8.27	3.99	5.02	3.87	**	+	*	+
NT2RP3000431	3.51	2.32	1.35	4.97	4.03	2.77	4.39	4.52	3.47				
NT2RP3000433	4.48	3.35	3.32	4.96	5.89	5.97	3.9	4.05	4.56	*	+		
NT2RP3000436	11.10	6.79	5.78	9.34	10.99	9.24	10.36	9.52	16.87				
NT2RP3000439	5.21	2.28	3.00	3.90	7.56	3.69	3.69	4.00	3.42				
NT2RP3000441	1.19	0.92	0.83	1.64	2.07	1.50	2.8	3.37	2.81	*	+	**	+
NT2RP3000444	2.26	2.00	1.85	2.13	2.91	3.48	2.82	2.26	2.53				
NT2RP3000448	3.48	2.24	3.61	8.12	11.89	8.40	5.13	4.03	6.51	**	+		
NT2RP3000449	5.49	2.45	3.20	2.67	4.04	3.28	1.61	2.66	1.96				
NT2RP3000451	5.47	3.68	2.74	2.86	3.50	4.17	4.01	4.24	4.31				
NT2RP3000456	4.82	4.21	3.70	3.94	5.59	4.96	4.41	3.70	5.42				

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Table 268

NT2RP3000460	6.78	3.61	3.73	8.08	8.65	7.41	13.4	12.29	10.37	*	+	**	+
NT2RP3000471	6.95	4.34	4.50	7.79	8.60	6.26	4.55	7.24	5.12				
NT2RP3000477	21.65	12.36	9.87	23.85	19.48	15.72	11.17	14.00	11.16				
NT2RP3000478	7.29	4.54	5.34	13.47	15.94	11.73	8.07	4.43	7.92	**	+		
NT2RP3000481	0.63	0.59	0.73	1.35	1.95	1.38	0.46	2.40	1.02	*	+		
NT2RP3000484	1.55	0.72	1.25	1.68	2.10	2.87	1.12	2.90	1.09				
NT2RP3000487	5.07	1.99	2.06	3.79	5.91	4.35	2.41	2.16	2.61				
NT2RP3000512	6.71	4.34	3.46	3.23	5.10	5.08	2.77	4.20	4.93				
NT2RP3000523	27.58	15.65	17.30	17.42	22.63	15.01	11.77	10.31	9.03				
NT2RP3000526	2.57	1.90	3.01	5.30	4.16	4.98	2.88	5.37	3.11	**	+		
NT2RP3000527	3.80	1.53	2.25	4.05	4.14	5.85	2.46	3.30	2.31				
NT2RP3000531	15.89	10.13	8.97	23.60	23.41	21.43	13.33	15.19	15.55	**	+		
NT2RP3000532	6.87	3.91	4.69	7.54	6.97	6.82	3.54	4.64	3.97				
NT2RP3000542	4.26	2.58	3.40	6.33	6.95	7.50	5.58	5.25	4.09	**	+		
NT2RP3000554	21.26	8.36	10.64	9.79	12.63	8.67	7.85	5.66	7.16				
NT2RP3000561	1.72	1.29	0.49	4.36	4.39	2.75	5.41	6.15	4.61	*	+	**	+
NT2RP3000562	5.35	3.52	2.70	6.24	5.67	6.85	4.69	5.36	4.51	*	+		
NT2RP3000578	2.48	1.13	0.91	1.41	2.33	1.20	1.51	2.72	1.83				
NT2RP3000582	2.70	1.06	2.14	1.55	1.76	2.00	1.13	2.91	1.43				
NT2RP3000584	3.87	1.71	2.00	3.83	3.38	4.15	1.95	3.50	3.43				
NT2RP3000586	4.68	3.18	3.48	5.21	5.82	4.88	4.06	4.66	4.73	*	+		
NT2RP3000590	3.21	1.61	2.30	2.02	1.87	2.52	1.95	2.50	2.25				
NT2RP3000592	2.67	1.26	1.45	1.25	2.76	1.46	1.33	1.90	1.13				
NT2RP3000596	20.65	9.80	8.82	23.94	26.59	16.13	11.86	9.91	14.07				
NT2RP3000599	3.31	1.41	2.33	3.96	4.14	2.63	2.43	4.34	3.3				
NT2RP3000603	4.81	2.59	2.37	5.30	5.93	6.54	3.73	4.56	4.65	*	+		
NT2RP3000605	2.51	1.85	1.50	3.30	3.59	2.96	2.17	4.09	3.29	*	+		
NT2RP3000607	7.51	5.55	8.79	5.67	5.09	3.67	3.76	3.78	3.57			*	+
NT2RP3000616	2.94	0.94	1.60	3.25	4.41	3.35	2.18	3.01	2.34				
NT2RP3000621	4.36	2.30	3.65	4.44	7.67	4.30	4.7	5.31	5.41				
NT2RP3000622	6.01	4.28	3.80	5.09	7.11	5.45	5.08	3.73	3.94				
NT2RP3000624	7.72	5.67	3.32	6.67	8.14	5.52	5.24	3.13	5.14				
NT2RP3000628	7.54	4.50	3.20	10.58	21.80	10.94	10.01	5.74	10.27				
NT2RP3000631	16.09	7.17	9.25	14.57	17.16	15.18	7.31	8.71	8.97				
NT2RP3000632	7.31	3.75	5.02	6.89	10.18	9.21	4.07	4.61	4.79				
NT2RP3000638	7.68	5.11	4.32	4.07	4.85	4.59	5.9	6.86	5.24				
NT2RP3000644	19.00	10.57	14.03	22.53	22.68	23.63	19.34	20.74	17.56	*	+		
NT2RP3000645	22.63	12.76	16.07	25.22	24.49	30.53	19.65	22.44	19.81				
NT2RP3000652	25.30	13.23	15.28	45.18	43.44	33.63	16.17	15.59	14.77	*	+		
NT2RP3000658	10.87	4.38	5.61	9.08	8.70	4.57	4.84	5.59	6.4				
NT2RP3000660	7.86	3.20	4.43	11.71	10.96	7.67	5.63	5.73	5.08				
NT2RP3000661	5.33	3.07	4.20	8.73	10.09	5.63	4.67	5.28	4.19				
NT2RP3000665	6.64	1.93	2.75	5.80	4.45	4.67	4.17	5.21	4.12				
NT2RP3000676	8.20	4.06	3.78	8.46	10.33	8.20	6.83	8.27	6.88				
NT2RP3000677	4.44	2.49	3.08	10.60	15.84	15.84	2.62	4.06	2.32	**	+		
NT2RP3000681	16.25	8.48	11.24	17.10	13.94	12.61	11.39	15.24	10.7				
NT2RP3000683	10.17	2.34	3.24	19.41	15.14	11.09	6.65	5.82	9.12	*	+		
NT2RP3000685	7.81	3.42	2.68	6.13	4.88	5.09	4.14	3.91	7.49				
NT2RP3000690	3.45	1.81	2.38	2.69	3.42	3.19	1.6	4.35	4				
NT2RP3000698	3.44	1.71	1.90	3.98	4.36	3.04	3.05	5.26	3.03				
NT2RP3000708	8.35	3.44	2.85	6.09	5.53	5.09	2.92	4.17	5.63				
NT2RP3000719	6.12	2.90	4.00	7.25	5.34	4.25	3.6	5.95	3.12				
NT2RP3000721	4.08	2.25	2.01	4.97	4.56	3.47	2.13	3.08	2.89				
NT2RP3000728	2.25	0.64	0.87	2.34	2.75	2.13	0.67	2.18	0.8				
NT2RP3000730	1.35	0.93	1.10	1.92	2.14	1.30	2.2	1.20	1.35				
NT2RP3000733	4.35	2.50	1.71	6.01	6.36	4.79	3.49	3.48	2.85	*	+		

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Table 269

NT2RP3000735	2.00	1.20	0.61	2.06	0.92	1.03	2.17	1.47	1.63				
NT2RP3000736	3.46	3.21	3.33	4.48	4.58	3.34	3.43	2.28	2.96				
NT2RP3000739	15.24	8.34	8.12	11.53	11.36	10.77	13.58	12.81	14.45				
NT2RP3000742	15.14	9.63	9.98	14.05	14.60	13.15	13.09	11.17	13.06				
NT2RP3000753	4.09	1.46	2.26	4.87	6.45	3.41	1.81	3.35	5.41				
NT2RP3000759	4.36	3.02	3.28	9.27	10.72	9.10	9.4	9.92	12.65	**	+	**	+
NT2RP3000789	6.97	3.15	3.19	2.62	3.38	3.33	2.9	2.77	2.91				
NT2RP3000815	3.08	1.87	2.78	5.08	5.91	5.79	4.34	3.06	3.33	**	+		
NT2RP3000818	7.88	5.88	4.83	9.79	13.01	13.93	8.4	7.38	10.56	*	+		
NT2RP3000820	6.70	4.35	2.57	15.50	20.24	18.97	5.35	5.01	5.38	**	+		
NT2RP3000821	6.58	4.20	3.95	5.67	6.08	4.63	5.13	4.56	4.66				
NT2RP3000825	0.66	0.26	0.38	1.28	1.09	2.20	0.44	1.29	0.44	*	+		
NT2RP3000826	14.31	7.15	8.00	20.59	14.43	14.08	24	29.57	29.39			**	+
NT2RP3000836	8.67	4.78	5.47	15.61	15.21	9.41	7.61	8.53	8.85	*	+		
NT2RP3000838	69.68	35.31	38.08	62.74	50.92	57.55	114.4	92.67	110.6			*	+
NT2RP3000839	3.11	1.70	2.32	2.00	3.56	1.87	3.03	1.30	2.5				
NT2RP3000841	4.62	3.46	2.85	4.30	8.16	5.93	4.11	3.68	3.13				
NT2RP3000845	4.22	3.31	3.16	4.56	7.12	4.56	4.69	3.53	11.01				
NT2RP3000847	8.01	5.03	4.67	11.17	12.10	10.61	8.29	6.56	5.96	**	+		
NT2RP3000848	4.58	2.34	3.27	5.39	6.00	5.09	3.72	3.05	5.42	*	+		
NT2RP3000850	7.12	3.32	4.95	11.87	12.25	13.21	7.48	7.20	7.92	**	+		
NT2RP3000852	2.41	2.02	3.14	2.50	3.10	2.98	1.15	2.04	2				
NT2RP3000859	11.57	6.45	2.66	9.86	9.35	7.35	6.51	5.86	6.19				
NT2RP3000861	12.29	5.70	6.74	20.57	26.68	20.53	8.96	8.46	14.99	**	+		
NT2RP3000862	10.74	6.85	6.61	6.87	7.71	5.23	6.09	5.39	7.24				
NT2RP3000865	2.61	2.77	1.86	4.46	4.70	3.49	3.05	2.82	3.22	*	+		
NT2RP3000866	3.65	3.07	3.41	3.79	4.93	3.08	2.95	3.92	4.36				
NT2RP3000868	6.63	4.07	4.55	6.52	6.19	4.40	5.59	4.36	6.01				
NT2RP3000869	7.38	5.89	6.47	6.37	7.71	6.66	5.72	5.36	5.4				
NT2RP3000871	2.80	1.69	2.21	3.13	2.44	2.63	2.19	2.91	2.3				
NT2RP3000875	6.14	2.07	3.11	2.15	2.68	3.67	3.92	2.74	3.62				
NT2RP3000895	3.27	2.20	2.57	3.83	6.39	6.15	3.73	2.67	3.88	*	+		
NT2RP3000900	9.85	5.60	5.12	11.99	12.50	10.94	7.71	7.19	8.22	*	+		
NT2RP3000901	5.01	2.45	2.11	6.45	8.36	6.11	4.49	5.69	7.42	*	+		
NT2RP3000903	2.28	1.60	1.75	4.44	6.62	5.24	4.43	2.98	3.76	**	+	*	+
NT2RP3000904	2.30	1.61	2.05	2.19	1.89	3.97	2.54	3.22	2.14				
NT2RP3000907	9.61	6.08	7.44	8.62	11.64	8.56	8.91	8.78	9.69				
NT2RP3000913	7.70	2.80	3.71	8.25	8.06	6.91	5.87	6.50	4.94				
NT2RP3000917	10.36	7.31	5.72	9.00	16.41	11.45	7.56	6.56	8.24				
NT2RP3000919	5.76	4.04	3.02	5.13	7.71	4.25	4.75	6.45	6.91				
NT2RP3000921	3.51	1.70	2.76	4.60	7.92	2.75	6.8	3.67	4.11				
NT2RP3000942	9.61	5.52	5.34	12.62	14.38	12.46	6.8	6.53	7.24	*	+		
NT2RP3000968	103.66	58.95	83.91	147.53	158.89	133.89	55.3	53.20	43.04	*	+		
NT2RP3000974	3.04	1.59	2.65	3.97	5.03	4.21	2.71	3.66	2.41	*	+		
NT2RP3000980	39.62	20.55	29.98	6.47	9.37	6.00	4.91	6.99	8.46	*	-	*	-
NT2RP3000984	5.29	4.18	5.73	10.16	10.11	7.87	6.25	8.85	4.44	**	+		
NT2RP3000994	3.63	2.42	1.96	4.75	5.40	3.69	3.58	4.22	3.83				
NT2RP3001001	3.47	2.25	3.10	3.83	2.41	2.13	2.68	3.98	2.58				
NT2RP3001004	1.80	1.40	1.87	2.71	2.31	1.48	2.16	4.18	3				
NT2RP3001007	4.63	2.03	2.66	14.00	6.75	8.49	6.39	6.25	5.07	*	+	*	+
NT2RP3001012	5.10	1.75	3.11	5.04	4.34	5.34	2.86	4.75	2.29				
NT2RP3001042	5.71	3.43	4.72	5.27	4.96	3.88	3.98	3.86	2.98				
NT2RP3001044	7.02	3.73	5.60	14.85	12.04	12.37	9.89	10.94	7.73	**	+	*	+
NT2RP3001048	2.35	1.96	3.94	3.25	4.98	4.26	3.16	2.56	3.24				
NT2RP3001050	11.91	8.75	3.68	7.09	10.52	7.57	19.34	10.54	18.84				
NT2RP3001055	19.61	12.87	10.53	9.87	9.64	7.47	11.2	7.71	10.89				

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Table 270

NT2RP3001057	8.67	4.03	5.93	19.26	14.18	12.30	8.42	6.94	7.2	*	+		
NT2RP3001061	5.88	4.01	4.14	7.75	9.70	8.03	5.42	6.19	4.88	*	+		
NT2RP3001069	9.78	4.93	5.43	13.99	17.62	14.76	9.74	9.96	12.86	**	+		
NT2RP3001074	8.31	4.57	4.04	11.86	10.34	7.95	6.59	7.36	7.45				
NT2RP3001078	5.34	2.26	4.49	9.51	7.77	7.53	5.94	3.60	5.02	*	+		
NT2RP3001081	3.83	2.45	4.20	6.12	3.89	6.40	3.56	5.22	3.4				
NT2RP3001084	5.54	2.82	2.70	2.36	4.10	1.78	2.85	2.45	3.36				
NT2RP3001095	1.93	1.69	1.44	3.80	3.49	3.25	2.25	2.83	2.47	**	+	*	+
NT2RP3001096	4.61	2.92	2.43	5.50	5.58	4.69	7.37	7.57	7.11			**	+
NT2RP3001097	9.61	7.40	9.00	12.56	12.16	11.92	6.67	6.88	9.12	**	+		
NT2RP3001107	6.04	4.02	3.50	4.89	5.87	4.23	3.8	4.49	5.02				
NT2RP3001109	6.26	3.05	4.30	3.18	4.47	2.65	2.28	2.72	1.85				
NT2RP3001111	4.22	3.38	2.92	4.13	5.15	4.60	4.36	4.69	3.98				
NT2RP3001112	28.16	25.89	21.28	24.06	17.68	24.85	10.06	10.75	13.22			**	+
NT2RP3001113	1.79	0.99	0.62	1.34	2.23	1.54	1.11	1.24	1.25				
NT2RP3001115	3.88	1.85	2.25	7.26	3.45	2.57	3.4	3.91	4.67				
NT2RP3001116	3.94	1.69	1.56	4.63	3.42	2.74	3.29	4.13	4.33				
NT2RP3001119	9.02	6.38	5.74	6.52	9.40	7.53	6.04	4.43	6.5				
NT2RP3001120	11.82	5.87	8.94	18.20	12.33	18.08	8.42	9.14	10.96	*	+		
NT2RP3001126	3.38	2.35	3.59	5.64	8.45	7.51	8.01	7.65	6.3	*	+	**	+
NT2RP3001127	1.21	0.67	1.51	2.88	2.70	1.71	4.11	3.13	5.1	*	+	**	+
NT2RP3001133	7.23	4.12	5.49	7.95	8.82	7.67	4.57	6.00	4.72				
NT2RP3001140	2.84	1.04	1.66	3.30	3.99	3.19	1.56	2.10	3.38	*	+		
NT2RP3001147	7.62	3.19	3.51	4.05	4.82	4.29	0.77	2.87	1.63				
NT2RP3001150	5.19	1.79	3.13	6.49	3.73	3.77	3.8	3.66	4.52				
NT2RP3001152	2.12	0.44	0.89	1.69	1.74	1.98	1.83	2.36	2.08				
NT2RP3001155	6.90	4.51	4.25	3.69	4.69	3.75	1.73	3.87	3.96				
NT2RP3001156	2.47	1.68	1.60	2.59	3.59	3.31	2.51	4.84	4.65	*	+		
NT2RP3001159	12.19	5.40	5.34	9.00	9.95	7.35	6.84	6.11	6.14				
NT2RP3001170	7.10	4.60	5.72	9.66	13.09	10.69	5.5	6.89	3.71	*	+		
NT2RP3001176	9.51	3.49	2.75	17.93	12.62	10.20	6.88	5.97	13.3				
NT2RP3001195	6.18	2.83	2.96	6.39	10.42	3.54	4.18	5.32	5.17				
NT2RP3001209	29.33	14.29	10.79	23.50	28.08	21.04	16.75	19.48	15.61				
NT2RP3001214	6.63	3.46	3.32	9.82	10.42	9.38	3.48	5.63	3.56	**	+		
NT2RP3001216	4.48	3.19	3.11	7.11	8.39	8.87	2.58	5.22	3.57	**	+		
NT2RP3001221	1.19	0.31	0.47	1.55	1.56	1.10	1.01	2.22	0.86				
NT2RP3001226	7.00	2.58	2.80	4.50	5.21	4.34	3.95	5.75	3.9				
NT2RP3001230	2.86	1.59	1.71	4.14	3.19	2.63	1.59	3.61	2.59				
NT2RP3001232	4.81	1.38	0.57	1.61	2.09	1.97	2.63	1.53	0.99				
NT2RP3001236	1.71	1.43	0.80	2.59	2.82	2.72	3.58	2.05	2.31	**	+		
NT2RP3001239	2.21	1.46	1.67	2.79	2.29	1.43	3.36	2.12	2				
NT2RP3001240	2.39	2.60	2.79	4.11	6.20	4.44	7.84	6.72	4.74	*	+	*	+
NT2RP3001245	3.14	1.64	2.84	6.19	9.37	6.48	4.16	3.07	4.85	*	+		
NT2RP3001253	4.00	1.90	2.62	6.61	7.24	6.92	3.25	4.04	5.99	**	+		
NT2RP3001259	10.11	5.52	6.66	9.63	10.72	9.87	6.94	7.54	9.1				
NT2RP3001260	1.75	0.60	0.84	2.44	2.65	2.56	1.25	1.75	2.02	*	+		
NT2RP3001264	3.80	0.98	1.35	3.72	2.40	2.94	2.21	1.54	2.06				
NT2RP3001268	5.50	3.38	4.02	7.85	8.76	7.64	4.87	3.66	4.6	**	+		
NT2RP3001271	28.62	19.09	17.03	21.24	19.12	21.60	21.92	16.59	24.45				
NT2RP3001272	5.76	3.32	1.84	5.66	6.83	7.58	3.78	6.70	4.51				
NT2RP3001274	19.11	14.57	13.97	21.86	23.69	19.32	19.59	16.07	21.69	*	+		
NT2RP3001275	3.98	2.12	2.06	4.08	3.88	3.61	4.57	5.00	3.17				
NT2RP3001280	5.95	4.26	3.61	5.15	6.58	6.13	4	4.48	3.31				
NT2RP3001281	4.63	3.14	4.04	6.78	5.25	8.51	3.4	3.74	3.77	*	+		
NT2RP3001288	14.66	10.02	11.01	19.91	17.12	14.80	31.14	30.59	36.12			**	+
NT2RP3001297	4.65	2.39	2.87	6.59	5.46	6.16	4.33	3.73	6.69	*	+		

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Table 271

NT2RP3001300	6.60	4.50	3.63	5.55	5.25	4.91	6.62	5.73	6.77				
NT2RP3001301	4.23	2.95	2.87	6.64	7.54	6.04	6.28	4.21	5.54	**	+		
NT2RP3001307	3.27	2.88	2.97	3.26	3.20	4.09	4.01	4.56	2.31				
NT2RP3001310	14.83	12.54	13.73	16.67	19.61	13.33	4.87	4.68	5.5			**	-
NT2RP3001318	2.74	0.91	1.95	3.13	4.02	2.55	2.31	3.93	2.1				
NT2RP3001322	1.63	0.90	0.90	2.74	1.95	2.82	2.79	4.85	2.34	*	+		
NT2RP3001325	24.22	12.72	10.92	7.56	8.85	7.79	5.36	4.73	4.91				
NT2RP3001338	15.76	12.66	9.88	10.48	14.22	14.25	12.53	9.24	15.76				
NT2RP3001339	4.32	1.49	2.10	2.91	3.84	2.95	3.46	1.89	3.19				
NT2RP3001340	19.62	12.27	15.41	18.07	21.26	18.46	16.08	15.90	21.63				
NT2RP3001341	4.04	2.16	2.75	3.64	4.76	3.69	3.08	3.25	2.32				
NT2RP3001354	12.69	8.27	10.24	14.38	16.19	12.96	8.57	6.12	4.87				
NT2RP3001355	3.39	2.67	2.73	4.52	3.86	4.06	3.69	3.97	3.97	*	+	*	+
NT2RP3001356	2.63	2.41	2.61	3.21	3.25	2.89	2.82	3.46	1.7	*	+		
NT2RP3001359	5.31	3.10	1.88	3.19	6.05	4.15	4.41	3.34	3.75				
NT2RP3001364	6.03	3.09	3.48	5.69	5.56	4.55	3.38	5.70	5.8				
NT2RP3001373	5.46	3.57	2.36	4.41	5.80	3.94	5.01	3.68	6.3				
NT2RP3001374	2.93	1.03	1.18	2.06	2.91	2.46	1.54	1.85	1.14				
NT2RP3001383	6.37	4.77	6.05	9.28	12.56	10.77	4.11	4.30	3.48	**	+	*	-
NT2RP3001384	4.58	2.86	3.25	5.41	5.38	4.60	5.49	4.04	4.15				
NT2RP3001388	3.94	3.65	4.40	11.98	17.15	15.81	10.54	11.04	15.23	**	+	**	+
NT2RP3001392	3.83	1.90	3.17	5.39	4.17	3.84	3.44	3.44	2.66				
NT2RP3001396	2.00	1.30	0.75	2.42	4.93	3.82	4.83	3.81	2.6	*	+	*	+
NT2RP3001398	11.01	6.05	6.28	7.94	10.96	10.36	8.08	7.65	10.79				
NT2RP3001399	8.19	4.25	5.07	7.54	8.60	8.41	4.97	7.59	6.74				
NT2RP3001402	2.09	1.57	1.57	3.12	4.36	4.40	2.46	3.16	5.1	**	+		
NT2RP3001407	9.10	4.59	5.21	13.05	12.91	13.40	7.95	7.65	8.13	**	+		
NT2RP3001416	2.87	2.04	3.00	3.89	8.00	5.00	4.89	5.09	4.41			**	+
NT2RP3001420	5.16	2.34	2.93	5.77	5.70	6.45	3.3	5.56	7.47	*	+		
NT2RP3001425	3.64	1.83	2.78	5.54	5.58	5.80	4.28	4.76	3.32	**	+		
NT2RP3001426	9.63	6.68	3.99	4.77	6.95	7.51	7.14	4.61	7.91				
NT2RP3001427	4.50	3.40	2.04	4.15	3.27	4.34	2.81	4.38	3.95				
NT2RP3001428	4.16	3.58	4.14	7.37	9.48	9.19	4.5	5.96	3.96	**	+		
NT2RP3001429	2.71	0.65	1.93	11.45	6.48	6.19	4.59	7.62	3.98	*	+	*	+
NT2RP3001432	3.34	1.56	1.82	4.80	3.24	3.78	1.92	2.57	3.01				
NT2RP3001439	6.50	4.98	6.18	6.78	9.50	6.94	5.45	6.68	5.8				
NT2RP3001441	4.58	1.98	2.38	4.38	3.89	3.43	3.38	5.92	9.79				
NT2RP3001446	2.76	1.22	2.57	5.62	7.47	6.18	5.44	6.68	4.2	**	+	*	+
NT2RP3001447	8.22	4.12	2.95	6.40	8.22	5.10	3.65	5.93	6.09				
NT2RP3001449	4.73	2.05	2.23	6.25	6.19	5.57	6.13	6.05	7.57	*	+	*	+
NT2RP3001453	6.27	2.66	2.61	7.65	7.63	7.03	4.7	5.93	5.45	*	+		
NT2RP3001457	5.03	2.53	2.21	3.77	4.85	3.80	3.24	4.94	2.94				
NT2RP3001459	2.60	1.82	2.24	2.49	3.26	2.21	2.13	3.94	1.79				
NT2RP3001463	3.43	2.23	2.76	3.05	4.78	3.63	2.47	3.86	2.66				
NT2RP3001466	0.65	0.45	0.93	0.79	1.40	1.78	1.01	1.24	0.81				
NT2RP3001472	5.02	3.77	3.20	8.65	6.87	6.75	5.25	4.56	5.18	*	+		
NT2RP3001475	16.30	4.98	4.56	9.54	12.17	8.13	7.39	5.93	7.4				
NT2RP3001479	11.30	7.78	6.68	11.47	10.59	7.30	7.74	6.55	7.95				
NT2RP3001490	1.44	1.38	1.23	3.68	2.94	3.11	4.42	3.30	2.91	**	+	**	+
NT2RP3001492	3.13	2.23	1.38	5.46	5.82	3.49	2.27	3.77	3.59	*	+		
NT2RP3001495	4.27	2.41	2.48	4.72	5.59	4.95	3.72	4.06	3.66	*	+		
NT2RP3001497	3.41	1.98	2.83	6.14	5.70	4.65	3.85	3.87	3.68	*	+		
NT2RP3001501	3.65	1.22	1.98	4.41	3.90	3.76	3.18	3.14	3.33				
NT2RP3001527	8.81	6.07	6.17	11.31	10.29	10.39	6.88	6.90	7.25	*	+		
NT2RP3001529	9.25	3.58	2.90	11.50	12.88	7.44	5.1	3.82	4.38				
NT2RP3001538	8.31	2.40	2.73	6.50	6.03	5.12	5.17	5.15	4.98				

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Table 272

NT2RP3001539	12.56	6.40	7.00	10.99	10.52	8.15	6.27	6.65	5.19				
NT2RP3001542	3.56	1.19	1.50	6.99	9.11	5.28	2.14	3.06	2.68	*	+		
NT2RP3001549	9.80	7.45	10.38	11.31	10.30	10.04	7.8	5.81	7.76				
NT2RP3001554	3.44	2.57	2.68	4.38	5.21	3.74	3.1	4.12	3.42	*	+		
NT2RP3001560	1.98	0.84	1.82	2.21	1.46	2.33	2.57	1.64	2.81				
NT2RP3001561	7.62	4.57	4.64	6.91	8.11	8.03	7.34	7.68	6.78				
NT2RP3001564	12.59	4.99	5.10	22.94	20.84	14.16	5.83	7.51	11.43	*	+		
NT2RP3001568	10.68	5.54	6.19	6.22	5.75	5.19	2.58	3.78	3.57				
NT2RP3001575	10.33	5.99	5.32	11.60	12.09	8.47	6.09	5.98	6.46				
NT2RP3001580	3.56	1.35	1.99	5.39	3.01	3.50	2.91	3.43	3.66				
NT2RP3001587	9.27	5.60	6.48	9.67	8.64	7.91	3.57	5.67	3.81				
NT2RP3001589	4.49	2.24	2.17	4.59	7.05	6.18	4.42	5.38	3.17	*	+		
NT2RP3001592	4.37	2.01	2.87	4.75	5.39	5.86	3.63	4.01	2.99	*	+		
NT2RP3001607	0.30	0.54	0.84	0.71	1.22	1.55	0.82	2.08	0.53				
NT2RP3001608	7.31	2.87	2.62	6.20	4.67	5.11	3.69	5.29	6.29				
NT2RP3001613	11.75	4.76	3.72	8.30	8.98	5.57	5.89	6.91	7.14				
NT2RP3001619	4.55	2.53	2.20	3.59	4.12	3.29	2.64	4.30	2.99				
NT2RP3001621	7.09	6.13	3.47	2.20	2.82	2.93	1.51	2.76	2.37			*	-
NT2RP3001629	3.07	1.05	1.36	2.67	2.54	2.74	1.29	3.63	1.56				
NT2RP3001630	4.04	2.39	2.24	3.71	3.71	2.59	1.51	3.51	0.99				
NT2RP3001631	24.78	10.11	12.40	17.73	20.88	13.17	4.28	8.91	6.44				
NT2RP3001634	9.27	2.72	5.54	7.96	8.15	7.28	4.29	5.79	4.53				
NT2RP3001642	5.13	3.42	2.92	6.54	7.68	6.47	5.19	3.70	3.73	*	+		
NT2RP3001646	3.27	1.84	0.92	3.18	2.57	2.35	5	2.95	3.44				
NT2RP3001650	3.62	2.89	1.93	2.64	3.29	4.41	2.44	1.58	2.48				
NT2RP3001667	1.93	2.07	1.35	2.81	3.65	4.62	4.85	5.42	7.49	*	+	**	+
NT2RP3001671	7.66	4.46	4.89	5.72	6.98	5.49	3.11	2.99	4.06				
NT2RP3001672	5.04	4.31	3.86	3.93	4.78	3.32	4.59	4.37	7.43				
NT2RP3001676	3.97	2.04	5.02	4.84	5.72	3.79	2.56	2.60	3.1				
NT2RP3001678	5.11	3.61	3.12	4.03	3.95	2.98	4.85	3.51	3.88				
NT2RP3001679	5.80	3.94	3.38	8.40	8.81	5.85	11	8.10	8.4	*	+	*	+
NT2RP3001682	11.08	7.03	6.66	4.48	3.93	2.41	1.86	2.18	2.25	*	-	*	-
NT2RP3001685	5.84	2.49	1.45	5.20	7.06	5.72	3.81	3.24	3.24				
NT2RP3001688	9.98	5.14	4.96	11.67	15.18	13.11	7.75	5.30	4.79	*	+		
NT2RP3001690	6.37	3.50	2.59	4.35	7.48	8.72	4.02	4.96	4.94				
NT2RP3001693	13.26	8.38	9.13	9.74	11.97	8.26	6.72	8.53	7.59				
NT2RP3001696	6.95	4.47	3.30	15.86	17.48	7.56	13.16	12.78	11.08			**	+
NT2RP3001698	6.30	3.93	3.04	7.50	5.16	4.97	10.41	6.02	8.18				
NT2RP3001708	3.49	1.19	1.37	2.49	3.70	3.38	4.25	2.37	2.33				
NT2RP3001712	11.74	6.82	5.41	22.86	35.26	39.54	12.07	11.43	15.14	*	+		
NT2RP3001716	7.22	3.02	4.03	8.79	10.51	6.60	4.73	4.70	5.85				
NT2RP3001724	15.75	4.14	3.21	5.86	6.17	7.63	4.16	4.41	4.61				
NT2RP3001727	8.66	6.49	5.38	14.44	7.82	11.73	11.95	13.12	10.93			*	+
NT2RP3001729	1.93	0.96	0.61	2.40	2.57	2.22	2.16	2.35	2.73	*	+	*	+
NT2RP3001730	6.71	4.57	7.74	11.66	10.98	8.11	6.76	8.86	5.97				
NT2RP3001733	2.88	2.06	0.55	2.95	3.43	1.42	2.02	2.52	2.06				
NT2RP3001737	6.70	4.04	4.02	6.45	5.41	5.38	5.72	3.92	6.08				
NT2RP3001738	10.91	6.90	7.77	7.27	7.41	7.04	6.92	5.83	6.78				
NT2RP3001739	5.34	4.75	4.43	4.78	6.81	5.30	5.03	4.71	6.57				
NT2RP3001742	5.50	3.13	4.00	3.39	9.70	3.77	4.55	5.25	8.02				
NT2RP3001751	13.48	12.01	10.94	15.12	15.40	18.57	7.79	9.88	12.42	*	+		
NT2RP3001752	4.05	3.78	2.59	14.37	14.59	7.40	13.28	13.75	10.73	*	+	**	+
NT2RP3001753	4.22	3.12	2.93	5.12	4.27	8.95	2.67	3.47	2.04				
NT2RP3001754	24.40	11.37	10.27	18.41	20.20	17.55	14.78	11.55	16.09				
NT2RP3001756	3.63	3.86	3.16	12.94	21.73	28.36	7.24	4.83	10.97	*	+		
NT2RP3001764	6.68	4.75	3.99	4.90	5.39	5.66	4.26	4.39	5.91				

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Table 273

NT2RP3001771	3.51	2.93	3.35	3.89	4.06	3.55	3.61	4.21	5.23				
NT2RP3001777	4.09	2.96	3.01	5.51	4.45	3.91	4.86	5.16	6			*	+
NT2RP3001782	2.53	2.57	1.95	6.76	6.36	6.69	4.29	4.57	3.41	**	+	*	+
NT2RP3001792	5.75	4.70	5.90	6.11	8.15	9.14	6.11	4.96	5.99				
NT2RP3001799	4.41	4.21	3.75	7.39	9.01	7.29	5.88	7.01	5.73	**	+	**	+
NT2RP3001819	6.61	3.33	1.74	4.45	5.18	4.58	4.38	3.34	4.47				
NT2RP3001829	60.87	38.63	36.73	56.07	52.70	55.16	28.32	28.08	35.16				
NT2RP3001836	10.17	5.74	4.77	10.85	13.55	11.18	6.57	5.69	7.14				
NT2RP3001839	15.46	12.06	10.35	17.55	22.87	17.91	17.89	15.53	21.32	*	+		
NT2RP3001844	5.39	4.22	4.08	8.68	8.00	8.70	4.83	4.18	5.54	**	+		
NT2RP3001848	8.51	3.03	3.37	7.54	6.39	7.94	7.05	8.18	5.83				
NT2RP3001854	4.31	3.66	2.93	4.93	7.64	5.42	5.84	9.19	10.46			*	+
NT2RP3001855	1.08	0.62	0.41	0.88	3.15	1.50	2.17	1.51	1.24				
NT2RP3001857	8.74	5.14	3.23	3.88	5.79	4.95	4.34	4.47	3.21				
NT2RP3001858	5.96	2.68	3.12	1.87	2.69	2.83	2.52	3.04	2.59				
NT2RP3001861	8.95	6.91	5.65	7.71	8.95	8.02	9.41	9.63	9.39				
NT2RP3001866	1.78	1.67	1.30	2.40	3.59	1.96	3.62	3.94	3.33			**	+
NT2RP3001871	1.22	1.47	1.24	4.28	5.33	4.06	5.94	5.76	6.13	**	+	**	+
NT2RP3001874	2.39	1.48	1.04	1.60	1.73	1.49	2.15	3.07	2.44				
NT2RP3001878	1.89	1.50	2.48	4.52	7.04	3.00	1.74	2.47	2.05				
NT2RP3001885	4.23	3.76	3.61	4.08	6.00	8.45	4.94	5.08	4.08				
NT2RP3001896	3.95	2.31	1.26	4.38	7.80	4.28	4.49	2.83	4.64				
NT2RP3001898	12.61	5.06	3.64	6.11	6.18	5.92	8.68	7.13	11.31				
NT2RP3001899	5.05	3.28	2.34	3.69	5.19	3.08	2.74	3.58	3.91				
NT2RP3001901	12.98	8.89	8.12	8.50	8.51	10.47	8.45	6.54	7.26				
NT2RP3001915	6.53	3.55	4.50	3.73	7.04	4.19	2.46	3.27	3.28				
NT2RP3001926	0.32	0.45	0.32	1.03	1.16	1.31	0.6	2.68	0.45	**	+		
NT2RP3001929	2.79	2.04	3.11	3.82	2.97	3.77	2.42	3.15	2.72				
NT2RP3001931	4.35	3.16	3.68	6.47	4.72	7.93	3.59	3.28	4.34				
NT2RP3001938	7.26	2.97	4.06	7.92	6.46	6.68	4	4.10	3.17				
NT2RP3001943	14.11	5.27	4.51	10.79	10.92	8.33	5.43	5.45	5.13				
NT2RP3001944	3.45	2.33	1.32	2.72	2.97	3.31	3.63	3.49	2.49				
NT2RP3001945	7.29	7.10	5.59	8.17	9.64	11.51	6.42	7.34	6.69	*	+		
NT2RP3001947	4.79	4.51	3.45	5.88	6.32	6.85	5.07	6.05	6.08	*	+	*	+
NT2RP3001949	2.69	1.52	2.67	4.00	3.55	3.46	2.68	2.84	2.52	*	+		
NT2RP3001952	16.48	13.65	16.67	12.37	9.06	10.48	18.01	17.39	16.21	*	-		
NT2RP3001954	5.28	2.86	2.85	5.44	4.55	3.42	3.76	3.67	4.11				
NT2RP3001956	34.22	13.29	14.18	28.43	28.08	22.94	14.79	12.62	14.22				
NT2RP3001967	7.52	2.65	2.30	9.80	9.24	5.06	8.63	5.51	4.88				
NT2RP3001969	7.99	4.86	4.65	5.70	7.31	4.72	3.47	2.46	4.31				
NT2RP3001976	7.58	3.71	3.57	8.43	12.72	10.69	5.69	4.81	4.65	*	+		
NT2RP3001986	4.77	4.42	3.72	5.84	6.16	3.49	3.93	4.27	4.43				
NT2RP3001989	0.59	0.37	0.61	1.26	1.01	1.46	1.37	2.34	1.2	**	+	*	+
NT2RP3002002	4.58	2.14	1.97	6.96	7.70	8.62	3.16	5.19	5.28	**	+		
NT2RP3002004	2.02	1.54	1.44	3.44	3.14	2.45	2.24	2.01	2.64	*	+		
NT2RP3002007	2.30	1.16	1.11	2.63	4.31	2.50	1.57	1.64	1.85				
NT2RP3002014	4.46	3.07	2.32	5.12	6.41	4.59	6.11	3.83	4.25				
NT2RP3002015	7.60	4.06	4.17	6.58	5.55	3.85	6.25	4.00	5.51				
NT2RP3002033	1.85	1.50	1.64	2.80	2.86	2.23	1.62	2.56	2.12	*	+		
NT2RP3002045	1.82	1.00	1.37	1.94	4.75	2.88	1.69	2.27	2.09				
NT2RP3002054	2.00	1.59	0.94	1.90	1.75	2.02	1.61	2.56	2.14				
NT2RP3002056	2.28	1.93	1.78	6.00	7.33	7.83	2.85	2.69	4.61	**	+		
NT2RP3002057	1.99	1.12	1.41	3.14	2.25	1.70	1.48	2.86	1.82				
NT2RP3002061	16.71	9.57	7.36	24.61	19.84	16.31	10.52	9.51	8.46				
NT2RP3002062	2.33	1.47	0.86	3.09	3.51	2.69	1.64	2.02	3.16	*	+		
NT2RP3002063	8.43	3.19	2.56	5.90	5.68	4.65	5.99	6.66	4.47				

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Table 274

NT2RP3002064	5.17	3.05	2.46	4.06	7.44	4.88	4.84	4.54	4.14				
NT2RP3002071	2.33	1.51	1.99	1.86	2.27	1.50	2.16	2.61	2.43				
NT2RP3002073	5.31	4.25	4.41	3.45	4.48	3.77	3.46	5.18	3.88				
NT2RP3002074	3.99	3.21	3.54	3.26	5.35	3.47	3.41	4.15	2.51				
NT2RP3002075	4.75	2.10	2.19	6.52	7.60	4.15	6.03	5.22	5				
NT2RP3002077	8.02	3.34	2.61	6.63	4.07	3.18	5.14	4.74	2.68				
NT2RP3002081	10.07	7.99	7.00	4.79	4.27	3.26	2.76	2.42	1.41	*	-	**	-
NT2RP3002086	4.94	3.90	3.43	7.01	9.40	7.91	6.79	5.61	5.45	**	+	*	+
NT2RP3002094	55.21	38.13	49.40	26.53	35.64	30.76	29.38	24.30	29.05	*	-	*	-
NT2RP3002096	2.03	2.45	2.09	2.34	2.63	1.70	2.31	1.94	2.22				
NT2RP3002097	4.81	2.56	2.66	7.07	9.45	4.39	4.28	5.92	5.09				
NT2RP3002098	1.30	1.49	2.04	3.02	3.52	2.23	1.86	1.80	1.76	*	+		
NT2RP3002102	4.48	2.97	2.73	5.04	5.32	5.08	5.06	4.28	4.93	*	+		
NT2RP3002106	5.41	2.39	2.38	9.26	7.89	8.90	6.1	3.83	3.57	**	+		
NT2RP3002108	6.53	3.49	4.50	3.88	5.75	3.58	3.09	4.07	3.18				
NT2RP3002109	11.23	5.02	4.28	16.19	18.27	13.88	14.35	12.01	12.31	*	+		
NT2RP3002110	23.37	14.84	16.48	34.91	29.71	40.33	23.01	21.75	23.48	*	+		
NT2RP3002113	11.63	9.01	7.67	6.51	7.35	7.47	7.32	7.10	6.45				
NT2RP3002120	1.55	1.48	1.08	2.91	3.24	1.92	2.33	3.13	2.18	*	+	*	+
NT2RP3002121	3.47	2.28	2.84	4.15	6.05	2.79	2.22	3.39	2.01				
NT2RP3002126	11.23	6.99	4.03	8.17	8.24	7.23	16.66	12.35	16.36			*	+
NT2RP3002128	13.16	6.63	6.22	10.39	10.13	7.09	9.73	7.03	10.29				
NT2RP3002130	7.94	5.84	4.52	8.35	9.12	8.25	8.69	6.14	9.87				
NT2RP3002133	7.00	4.13	2.94	10.10	13.02	11.57	10.36	9.95	10.86	**	+	**	+
NT2RP3002136	10.87	7.59	6.07	13.09	20.57	19.22	14.35	15.02	15.43	*	+	**	+
NT2RP3002140	4.41	4.46	5.24	5.99	5.61	7.54	7.49	4.80	5.22				
NT2RP3002142	7.81	6.29	3.94	14.63	15.34	11.73	11.3	15.25	13.24	**	+	*	+
NT2RP3002146	7.61	4.78	4.77	10.91	13.18	6.97	4.8	6.21	4.65				
NT2RP3002147	22.06	11.75	12.01	9.65	10.83	10.56	11.86	8.17	9.38				
NT2RP3002151	14.60	11.05	8.77	13.96	13.74	12.27	8.15	8.64	12.04				
NT2RP3002155	8.16	6.32	4.96	8.79	7.65	4.96	6.19	7.55	7.22				
NT2RP3002156	2.21	1.36	0.96	3.23	3.14	2.36	3.21	3.07	3.25	*	+	*	+
NT2RP3002160	3.98	3.19	1.94	3.32	4.52	5.20	4.3	1.89	4.12				
NT2RP3002163	18.81	11.61	12.16	18.87	21.42	15.74	12.51	9.05	10.05				
NT2RP3002165	6.12	5.16	5.75	6.38	8.10	3.82	6.23	5.63	7.23				
NT2RP3002166	5.72	3.53	1.35	2.95	5.16	3.30	2.3	3.24	3.17				
NT2RP3002173	5.34	3.03	2.78	9.80	6.20	7.21	5.06	5.00	4.94	*	+		
NT2RP3002174	5.68	2.49	1.67	7.29	8.21	9.12	9.02	7.21	12.43	*	+	*	+
NT2RP3002181	9.68	7.50	5.24	4.48	4.92	3.59	2.61	2.36	2.48			*	-
NT2RP3002185	3.81	2.37	1.77	2.88	7.87	3.22	3.57	3.44	2.54				
NT2RP3002193	7.51	6.09	4.76	5.28	9.69	7.23	6.2	5.26	7.9				
NT2RP3002204	2.89	2.47	0.95	9.64	8.53	14.75	4.05	4.67	4.6	*	+	*	+
NT2RP3002244	4.56	5.32	5.18	4.63	6.32	6.34	4.51	3.44	3.59			*	-
NT2RP3002248	8.18	5.72	5.54	14.10	16.32	12.91	11.02	10.26	11.54	**	+	**	+
NT2RP3002253	6.83	4.26	3.08	6.54	5.65	6.66	3.58	3.16	4.05				
NT2RP3002255	44.02	22.63	19.64	26.45	26.34	31.64	17.22	13.77	17.68				
NT2RP3002264	5.83	3.17	2.53	6.13	7.07	6.24	4.47	6.97	4.95				
NT2RP3002267	4.61	2.60	2.31	3.48	4.99	3.73	3.57	2.66	3.09				
NT2RP3002273	14.02	8.03	6.96	15.74	16.07	14.50	9.58	10.63	9.37				
NT2RP3002276	5.72	2.96	3.52	5.50	5.94	5.34	3.99	5.68	5.16				
NT2RP3002281	7.91	5.75	6.50	6.21	6.83	6.47	4.32	5.43	5.21				
NT2RP3002286	2.46	1.62	2.05	3.65	3.52	2.26	2.34	3.39	3.14				
NT2RP3002297	56.91	27.98	24.70	67.63	63.96	45.16	26.65	22.90	25.3				
NT2RP3002301	9.96	5.96	5.15	5.72	8.90	9.72	8.36	7.88	9.26				
NT2RP3002303	10.45	6.01	4.55	8.24	9.49	7.38	8.89	7.75	8.68				
NT2RP3002304	1.01	1.07	1.38	3.55	2.86	2.06	2.84	4.66	2.09	*	+		

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Table 275

NT2RP3002309	6.87	4.15	3.66	6.13	6.93	8.34	2.55	3.41	3.91				
NT2RP3002311	4.05	2.38	2.34	4.56	2.55	3.21	2.05	2.83	2.86				
NT2RP3002315	15.94	11.19	15.32	12.31	8.50	11.56	8.23	8.69	10.92			*	-
NT2RP3002319	1.73	1.09	1.94	2.53	2.43	3.11	2.93	2.04	2.66	*	+		
NT2RP3002324	9.27	3.66	3.72	5.93	9.44	5.66	4.2	5.07	4.43				
NT2RP3002330	9.95	5.32	3.76	4.42	7.75	7.05	6.63	6.18	5.42				
NT2RP3002333	17.93	13.63	12.33	10.81	13.83	11.53	26.44	20.51	21.61			*	+
NT2RP3002337	2.63	1.45	1.52	1.90	1.94	2.01	1.38	3.21	2.65				
NT2RP3002342	15.59	10.64	11.07	10.92	13.50	7.96	9.5	11.72	10.96				
NT2RP3002343	4.86	3.15	3.42	8.66	7.27	7.64	5.82	6.21	6.54	**	+	*	+
NT2RP3002351	2.14	1.87	1.48	1.52	1.49	1.39	1.37	2.50	1.29				
NT2RP3002352	3.51	2.49	2.09	6.56	3.41	4.41	3.67	4.42	2.26				
NT2RP3002353	8.54	2.87	2.50	5.68	7.93	6.04	5.65	4.24	3.09				
NT2RP3002362	10.04	4.71	5.05	6.95	8.81	7.91	8.38	7.04	7.67				
NT2RP3002363	5.45	3.22	2.99	4.20	6.31	4.65	3.29	3.42	4.78				
NT2RP3002377	6.53	3.54	3.81	6.50	6.48	4.79	3.11	4.43	2.57				
NT2RP3002377	16.05	6.92	7.02	15.78	13.73	11.15	9.35	6.37	9.19				
NT2RP3002394	3.83	2.35	2.55	5.43	6.35	4.75	5.11	5.17	5.17	*	+	**	+
NT2RP3002397	1.88	2.06	1.00	2.28	2.42	2.35	2.43	3.20	2.26				
NT2RP3002399	38.89	13.57	16.73	24.89	24.11	20.07	10.95	10.34	11.58				
NT2RP3002402	14.13	6.06	6.64	3.90	7.46	3.60	5.13	2.47	3.86				
NT2RP3002404	2.69	1.41	1.51	4.63	5.57	6.95	5.03	5.62	5.49	**	+	**	+
NT2RP3002410	16.74	9.36	8.24	14.55	17.40	14.68	7.71	8.16	9.6				
NT2RP3002411	5.72	3.09	2.66	5.44	3.76	4.39	3.87	3.60	4.64				
NT2RP3002414	15.70	13.46	15.51	17.50	19.84	20.94	20.31	15.95	17.64	*	+		
NT2RP3002430	5.62	3.03	3.26	4.15	6.68	5.69	3.6	5.22	5.76				
NT2RP3002448	3.21	1.91	1.95	4.68	4.12	2.16	3.43	3.57	3.52				
NT2RP3002454	5.75	3.63	2.88	8.65	10.72	8.12	4.17	6.41	5.11	*	+		
NT2RP3002455	5.96	2.60	2.61	5.44	7.86	5.02	4.61	3.98	4.33				
NT2RP3002456	19.55	5.82	6.70	24.00	22.06	18.49	6.98	7.59	13.81				
NT2RP3002462	10.35	5.72	4.60	11.65	13.73	9.93	5.45	7.13	8.04				
NT2RP3002469	4.02	2.04	2.37	7.68	7.85	6.75	5.57	6.12	6.98	**	+	**	+
NT2RP3002470	34.16	21.24	23.62	26.50	31.46	31.78	25.6	23.51	18.11				
NT2RP3002484	4.96	4.07	3.20	7.26	8.04	8.64	6.14	7.06	7.03	**	+	*	+
NT2RP3002491	2.02	0.31	0.77	1.88	1.82	1.66	1.79	2.17	2.19				
NT2RP3002494	5.69	5.46	5.09	5.37	5.09	4.28	11.1	14.53	16.58			**	+
NT2RP3002497	7.34	2.87	2.34	7.23	5.25	4.45	4.45	4.17	5.52				
NT2RP3002500	6.11	2.15	1.67	4.34	5.06	2.16	2.18	2.29	5.42				
NT2RP3002501	11.25	5.11	3.44	6.23	6.00	5.47	2.88	5.58	5.46				
NT2RP3002512	7.00	3.26	2.28	5.82	6.08	6.36	2.87	4.61	8.18				
NT2RP3002529	3.20	3.16	1.84	7.16	9.33	8.45	4.14	4.40	5.49	**	+	*	+
NT2RP3002533	7.52	4.47	4.21	12.54	12.31	10.84	8.33	13.60	12.28	**	+	*	+
NT2RP3002539	6.08	4.61	2.98	8.67	11.27	7.39	2.77	5.22	3.99	*	+		
NT2RP3002540	2.20	1.79	1.19	3.09	3.15	2.53	2.67	2.99	2.88	*	+	*	+
NT2RP3002543	14.24	6.52	5.35	11.36	10.19	12.56	10.27	10.96	8.43				
NT2RP3002545	4.03	2.04	1.37	6.55	5.22	5.90	5.61	3.59	2.71	*	+		
NT2RP3002549	2.56	1.25	0.83	5.75	4.78	6.90	5.63	3.95	4.81	**	+	*	+
NT2RP3002552	2.93	2.06	2.41	3.32	5.85	3.49	4.06	3.68	4.2			**	+
NT2RP3002558	7.05	4.19	4.48	9.57	11.91	11.02	10.69	7.40	9.14	**	+	*	+
NT2RP3002565	4.40	2.70	2.23	5.52	4.89	4.10	2.94	2.79	3.23				
NT2RP3002566	4.15	3.12	3.18	4.65	4.50	3.46	4.21	2.25	2.13				
NT2RP3002571	1.43	0.64	1.11	2.38	2.79	1.21	2	1.13	1.01				
NT2RP3002572	5.68	2.77	2.24	4.20	4.73	4.39	4.25	2.73	1.87				
NT2RP3002573	12.53	5.63	5.03	10.21	9.69	14.18	6.47	7.06	5.93				
NT2RP3002577	16.44	10.30	7.27	9.02	16.56	19.10	11.76	11.75	13.42				
NT2RP3002579	5.14	1.77	2.75	2.43	7.06	4.13	4.98	5.48	3.32				

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Table 276

NT2RP3002582	12.31	7.23	7.62	9.16	12.52	12.19	7.07	6.55	8.27				
NT2RP3002587	2.59	1.37	0.54	2.46	2.67	3.02	1.24	1.89	1.22				
NT2RP3002590	10.29	5.66	7.55	5.34	4.92	3.70	2.44	4.30	2.27			*	-
NT2RP3002602	2.82	1.08	1.45	3.79	2.37	2.51	2.16	2.20	1.92				
NT2RP3002603	23.80	12.85	10.83	16.77	16.77	18.88	33.04	20.98	28.78				
NT2RP3002621	5.83	2.17	2.11	2.73	3.73	3.84	3.77	3.43	4.67				
NT2RP3002622	6.46	4.71	3.37	7.18	6.32	5.80	5.41	4.46	6.55				
NT2RP3002624	1.38	1.46	0.86	2.16	2.27	1.71	1.92	2.31	2.23	*	+	*	+
NT2RP3002628	3.88	4.12	4.54	3.93	5.95	4.39	6.01	5.25	6.35			*	+
NT2RP3002629	17.56	11.86	13.81	23.77	21.74	24.60	15.1	15.62	16.2	**	+		
NT2RP3002631	0.65	0.54	0.71	0.74	2.00	0.23	0.47	2.10	1.77				
NT2RP3002647	6.35	4.67	4.32	5.81	4.61	3.54	2.45	3.29	2.94			*	-
NT2RP3002649	13.39	5.95	5.65	10.41	9.34	8.49	5.95	5.93	9.13				
NT2RP3002650	6.81	4.69	4.82	5.81	7.89	6.12	6.83	5.78	9.56				
NT2RP3002652	5.20	4.74	1.12	4.44	5.82	4.44	3.42	3.65	3.38				
NT2RP3002654	16.99	10.82	13.04	8.59	8.02	5.74	6.46	6.13	9.06	*	-	*	-
NT2RP3002657	6.11	3.63	4.64	10.15	11.45	6.16	9.57	10.27	10.97			**	+
NT2RP3002659	1.43	1.66	1.88	2.50	3.07	1.94	1.45	2.43	1.88				
NT2RP3002660	6.69	4.61	2.72	7.71	9.95	6.32	4.86	5.91	5.04				
NT2RP3002663	2.95	2.45	2.08	3.55	3.38	2.69	2.33	2.32	1.43				
NT2RP3002664	4.14	2.04	1.66	3.83	4.46	3.08	3.81	2.61	3.84				
NT2RP3002667	10.84	11.80	12.31	7.37	13.24	10.35	2.54	3.53	3.86			**	-
NT2RP3002671	4.10	3.38	2.05	3.68	4.13	3.09	3.64	4.14	3.95				
NT2RP3002682	6.85	6.11	3.50	9.41	10.82	9.25	7.6	6.54	14.33	*	+		
NT2RP3002684	2.31	2.12	2.06	2.65	2.46	1.95	3.43	3.91	2.52				
NT2RP3002687	0.81	0.83	0.64	1.63	2.27	2.37	2.18	2.59	1.3	**	+	*	+
NT2RP3002688	1.90	1.35	1.30	2.68	10.84	4.31	2.62	3.98	4.96			*	+
NT2RP3002698	1.70	1.54	2.28	2.37	1.97	1.69	2.37	4.37	2.27				
NT2RP3002701	9.13	4.28	3.80	7.31	8.31	6.47	5.76	5.84	9.76				
NT2RP3002705	21.78	18.18	17.66	50.09	57.33	55.80	17.31	19.57	25.8	**	+		
NT2RP3002708	8.43	3.13	4.23	10.00	12.33	16.86	6.66	9.06	8.15	*	+		
NT2RP3002711	10.69	7.85	6.27	14.28	17.41	10.11	7.22	6.34	9.71				
NT2RP3002712	75.48	54.09	63.05	72.21	59.93	49.90	55.73	52.68	50.32				
NT2RP3002713	1.12	1.39	0.99	1.79	1.94	1.51	1.51	1.64	2.24	*	+		
NT2RP3002721	4.73	3.29	3.45	5.55	8.69	5.41	5.47	5.66	7.4			*	+
NT2RP3002722	18.60	15.91	19.67	21.10	20.78	20.71	21.26	14.74	13.19				
NT2RP3002723	20.89	13.71	12.73	18.65	26.94	25.35	23.58	19.98	24.35				
NT2RP3002737	10.83	5.85	5.46	7.36	8.93	8.81	7.12	8.21	8.27				
NT2RP3002738	3.06	2.31	2.46	3.88	2.93	4.58	4.14	4.86	3.57			*	+
NT2RP3002742	78.11	50.55	39.19	56.71	49.99	44.98	24.65	24.79	19.15			*	-
NT2RP3002744	1.91	1.57	1.49	3.37	4.81	3.15	4.58	3.73	2.77	*	+	*	+
NT2RP3002756	2.31	1.24	1.63	1.83	2.14	1.21	1.7	1.60	2.11				
NT2RP3002757	4.69	3.13	4.35	7.14	8.49	8.18	8.15	8.37	8.37	**	+	**	+
NT2RP3002758	7.65	5.42	7.31	13.02	12.93	12.57	12.33	13.43	11.46	**	+	**	+
NT2RP3002762	17.62	11.52	8.02	10.66	16.28	10.88	8.09	6.08	11.34				
NT2RP3002763	5.98	3.76	3.67	4.32	6.42	5.16	4.76	6.11	4.92				
NT2RP3002770	6.69	2.71	1.54	4.12	4.84	3.63	3.88	6.30	6.14				
NT2RP3002771	4.19	4.34	2.59	8.14	7.86	8.58	10.72	12.24	8.84	**	+	**	+
NT2RP3002785	3.87	2.70	2.07	1.69	2.61	1.77	0.79	2.12	2.01				
NT2RP3002790	2.54	1.59	2.82	4.68	4.85	6.90	3.49	4.63	2.59	*	+		
NT2RP3002799	2.06	0.55	1.55	2.25	2.19	2.80	1.65	2.16	2.21				
NT2RP3002801	3.39	2.62	3.03	5.62	4.43	4.91	3.26	3.08	2.61	**	+		
NT2RP3002802	9.76	4.91	4.56	5.83	7.90	5.66	5.83	5.98	7.36				
NT2RP3002810	2.05	2.04	1.36	1.95	2.29	2.16	2.36	3.68	3.36			*	+
NT2RP3002818	1.54	1.82	1.16	0.90	1.59	1.73	1.13	2.06	1.73				
NT2RP3002821	17.00	12.39	12.28	12.51	17.54	13.78	7.96	8.86	8.91			*	-

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Table 277

NT2RP3002823	1.32	1.08	1.04	1.83	2.17	1.81	1.57	3.57	2.5	**	+		
NT2RP3002825	7.13	4.05	4.87	6.63	6.04	8.47	4.09	5.57	4.15				
NT2RP3002829	3.03	2.45	2.63	5.74	5.50	4.90	3	3.82	3.79	**	+		
NT2RP3002831	3.87	3.21	2.77	3.69	2.99	3.89	2.66	2.74	2.29				
NT2RP3002836	14.03	6.74	6.74	9.92	15.02	8.10	13.6	10.55	13.13				
NT2RP3002845	6.06	2.27	2.32	3.35	4.67	5.99	2.22	2.92	5.24				
NT2RP3002852	2.14	1.57	1.15	1.52	1.72	1.72	1.78	2.42	2.44				
NT2RP3002861	4.05	2.12	1.50	1.55	2.01	4.44	1.39	3.44	3.12				
NT2RP3002869	6.92	5.64	4.79	4.48	4.94	3.03	3.48	5.21	5.99				
NT2RP3002874	3.62	2.41	3.09	2.41	2.83	2.25	3.7	5.14	4.58				
NT2RP3002876	6.38	5.46	5.19	8.34	12.34	10.89	6.16	7.19	7.18	*	+		
NT2RP3002877	4.36	2.55	2.24	6.28	5.72	7.39	4.17	3.78	4.69	*	+		
NT2RP3002887	2.31	2.06	1.28	2.41	6.33	3.71	2.23	1.91	2.99				
NT2RP3002900	4.62	3.12	1.94	6.79	7.22	4.89	6.77	4.56	5.42	*	+		
NT2RP3002902	13.48	7.11	7.49	17.13	16.57	10.16	8.66	6.18	6.66				
NT2RP3002909	33.33	17.88	18.92	24.91	27.67	27.33	23.19	23.81	25.55				
NT2RP3002911	2.05	1.51	2.25	2.06	2.34	3.42	1.9	2.88	2.46				
NT2RP3002948	2.87	2.05	2.73	3.15	3.80	3.22	3.02	3.24	4.14				
NT2RP3002953	2.95	2.20	2.80	3.91	2.99	2.13	3.94	4.99	3.35				
NT2RP3002955	3.21	2.28	2.19	2.68	3.66	2.17	2.8	4.04	3.2				
NT2RP3002958	5.15	1.89	1.75	8.65	9.49	5.11	5.86	5.70	7.9				
NT2RP3002969	8.37	4.79	4.07	7.09	7.89	5.99	3.82	5.59	8.02				
NT2RP3002972	2.45	1.77	1.17	3.30	4.53	6.41	2.37	3.50	4.2	*	+		-
NT2RP3002978	3.51	1.12	0.76	1.57	2.29	1.16	1.76	2.22	2.49				
NT2RP3002983	2.09	1.72	1.47	2.93	4.10	4.53	1.5	4.04	1.42	*	+		
NT2RP3002985	2.93	1.24	0.64	1.80	1.57	1.56	1.03	3.24	1.64				
NT2RP3002988	3.04	1.50	1.33	2.69	2.87	2.12	2.09	2.69	1.72				
NT2RP3003000	5.52	4.04	3.47	8.75	7.05	6.47	5.37	5.35	7.11	*	+		
NT2RP3003008	3.30	1.49	1.41	3.13	2.40	2.15	3.61	1.58	2.05				
NT2RP3003012	5.75	2.52	2.34	2.71	2.38	1.98	3.89	1.73	1.65				
NT2RP3003015	3.67	2.39	1.41	2.11	1.98	2.12	2.64	2.73	1.76				
NT2RP3003018	5.19	3.49	2.94	3.09	5.88	7.34	2.45	3.41	8.68				
NT2RP3003028	4.42	2.89	2.76	3.64	5.83	5.34	3.92	2.05	3.21				
NT2RP3003029	5.92	3.71	3.59	6.44	6.11	4.11	7.41	7.78	5.42				
NT2RP3003032	8.58	6.19	7.17	18.73	18.81	11.60	10.2	11.99	14.12	*	+	*	+
NT2RP3003041	0.23	0.21	0.07	0.41	0.42	0.07	0.35	0.34	-0.17				
NT2RP3003044	7.25	3.53	3.53	7.47	6.31	4.80	5.47	4.15	4.63				
NT2RP3003047	14.58	8.48	8.68	11.39	12.06	11.40	11.77	9.28	11.88				
NT2RP3003050	6.53	2.71	3.77	5.22	5.47	3.84	5.66	4.93	4.39				
NT2RP3003053	17.07	9.71	8.94	14.88	15.92	20.90	14.19	12.88	11.32				
NT2RP3003059	2.32	1.74	2.11	2.95	2.30	1.48	1.32	1.45	1.42			*	-
NT2RP3003061	4.13	2.99	2.62	3.51	4.22	2.44	3.64	4.14	3.12				
NT2RP3003068	7.07	5.01	4.05	8.08	8.01	6.86	3.94	4.27	5.35				
NT2RP3003071	7.18	5.69	5.64	19.53	14.10	9.02	3.53	6.99	4.86				
NT2RP3003076	20.24	13.69	11.73	17.25	17.10	20.23	12.75	12.44	19.06				
NT2RP3003078	6.31	1.99	2.60	4.81	6.42	5.61	4.7	3.16	4.19				
NT2RP3003081	5.58	3.59	4.40	7.90	10.09	9.19	6.17	5.95	6.74	**	+	*	+
NT2RP3003090	4.22	2.78	2.81	6.19	7.29	6.41	3.45	3.07	3.62	**	+		
NT2RP3003097	2.80	1.80	2.13	3.12	4.85	3.19	4.18	3.63	2.96			*	+
NT2RP3003098	3.43	1.98	2.02	2.28	3.12	2.15	2.19	2.67	2.43				
NT2RP3003101	5.48	5.07	5.35	6.08	7.76	5.95	4.99	7.09	5.03				
NT2RP3003109	14.31	7.48	6.90	18.37	16.28	14.44	15.14	17.70	14.3				
NT2RP3003121	150.76	6.07	4.19	6.53	16.16	5.37	32.59	5.96	252				
NT2RP3003133	6.04	4.14	3.20	8.62	13.38	13.91	5.16	4.56	8.91	*	+		
NT2RP3003137	10.77	5.97	6.19	4.43	6.11	4.14	3.41	3.49	4.4				
NT2RP3003138	5.81	4.35	3.40	6.66	5.96	5.22	1.99	2.76	2.93				

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Table 278

NT2RP3003139	2.43	1.97	1.82	4.72	6.45	3.81	3.26	3.26	4.15	*	+	*	+
NT2RP3003145	2.66	3.16	2.32	3.58	4.86	4.52	5.45	3.67	3.72	*	+		
NT2RP3003150	4.45	3.91	3.35	3.70	3.28	5.66	5.36	4.59	2.96				
NT2RP3003157	15.45	8.45	11.15	23.44	27.58	18.86	11.74	13.90	10.21	*	+		
NT2RP3003185	3.41	2.15	1.16	2.42	3.21	3.33	3.63	2.51	4.07				
NT2RP3003193	5.13	4.24	4.83	11.32	20.09	13.42	6.1	6.95	8.42	*	+	*	+
NT2RP3003197	3.94	1.73	2.04	2.63	7.18	5.13	2.76	3.02	4.74				
NT2RP3003203	10.74	6.48	7.57	9.78	9.35	10.34	12.74	12.49	16.29			*	+
NT2RP3003204	5.10	4.07	4.28	9.44	9.51	9.35	6.59	6.58	5.8	**	+	*	+
NT2RP3003210	2.87	2.26	2.76	4.58	4.94	5.68	4.02	4.31	4.86	**	+	**	+
NT2RP3003212	3.99	3.41	3.08	11.16	9.44	5.92	5.65	5.21	4.76	*	+	**	+
NT2RP3003213	3.64	1.51	1.06	6.12	6.44	4.09	4.51	3.54	3.74	*	+		
NT2RP3003224	4.97	2.24	2.03	5.15	4.35	3.48	1.88	2.89	5.66				
NT2RP3003226	6.57	4.20	3.82	5.03	7.40	7.29	3.35	4.03	3.53				
NT2RP3003230	5.88	2.80	3.00	5.34	6.53	3.95	6.24	6.52	4.98				
NT2RP3003235	5.68	3.50	3.55	11.57	10.99	8.51	10.86	10.22	8.85	**	+	**	+
NT2RP3003242	2.60	1.56	1.56	2.17	2.65	0.82	2.88	3.62	2.34				
NT2RP3003251	6.96	4.06	5.58	8.26	9.86	10.16	5.03	5.10	5.01	*	+		
NT2RP3003252	3.92	3.17	2.70	4.36	6.32	3.73	3.3	3.53	3.19				
NT2RP3003258	4.44	4.88	5.51	5.73	7.67	6.20	6.76	5.52	8.07				
NT2RP3003260	10.73	5.21	4.49	5.79	7.69	5.80	4.33	3.45	7.99				
NT2RP3003264	3.02	3.32	2.19	15.38	18.88	12.82	6.5	5.90	7.82	**	+	**	+
NT2RP3003273	3.18	1.91	3.15	2.64	2.58	3.24	1.86	3.56	1.93				
NT2RP3003278	3.16	1.06	0.85	1.38	1.88	2.32	0.32	2.37	2.1				
NT2RP3003280	11.26	9.07	8.30	12.96	14.31	12.01	8.63	10.92	9.88	*	+		
NT2RP3003282	2.12	1.63	1.57	3.75	3.52	2.64	2.53	3.71	3.58	*	+	*	+
NT2RP3003290	6.74	3.39	5.29	8.39	9.77	12.47	5.55	7.58	4.52	*	+		
NT2RP3003301	3.39	1.66	2.31	5.80	5.15	3.88	3.51	3.63	2.51	*	+		
NT2RP3003302	4.39	1.94	0.70	3.91	4.34	3.52	1.87	2.40	2.1				
NT2RP3003311	6.06	3.51	2.81	1.70	1.60	1.58	1.38	2.35	2.23				
NT2RP3003312	2.65	1.71	1.08	1.61	2.31	2.14	2.34	3.94	2.4				
NT2RP3003313	2.10	1.55	1.28	2.78	3.32	3.29	2.46	3.52	2.12	**	+		
NT2RP3003327	4.75	3.06	2.77	5.48	4.57	3.91	2.76	4.36	2.87				
NT2RP3003330	2.85	1.28	1.93	2.62	3.38	1.73	2.22	3.78	2.76				
NT2RP3003344	2.79	2.00	1.76	2.66	2.98	3.04	2.26	1.95	1.8				
NT2RP3003346	5.06	3.51	3.24	6.69	7.03	5.74	4.23	5.12	4.21	*	+		
NT2RP3003349	9.03	3.41	4.20	7.42	11.99	8.27	4.03	4.39	5.81				
NT2RP3003353	2.34	1.65	0.86	3.37	3.35	2.15	1.51	2.11	2.73				
NT2RP3003354	28.51	16.58	19.06	32.92	34.54	31.72	24.06	25.56	26.43	*	+		
NT2RP3003368	4.73	3.35	3.40	3.00	5.12	6.89	5.78	4.93	4.85				
NT2RP3003375	7.10	4.96	7.12	8.55	8.55	5.98	2.32	4.29	4.97				
NT2RP3003377	7.20	4.93	4.97	2.66	4.68	3.75	3.7	3.85	3.56				
NT2RP3003384	2.46	2.07	1.01	3.30	3.65	2.66	3.02	2.86	2.88				
NT2RP3003385	5.42	4.79	5.32	4.48	4.42	6.30	6.9	4.85	5.01				
NT2RP3003396	9.36	4.73	3.86	5.45	9.23	6.23	6.71	5.33	6.72				
NT2RP3003403	3.05	1.65	1.51	5.41	4.67	5.69	2.27	2.49	2.78	**	+		
NT2RP3003409	2.84	1.35	2.12	3.28	3.13	1.88	2.79	2.04	3.14				
NT2RP3003411	8.55	4.92	6.03	7.49	10.91	12.20	6.24	6.43	9.99				
NT2RP3003420	4.15	2.44	2.36	6.31	7.10	8.42	3.61	4.27	6.2	**	+		
NT2RP3003425	3.63	2.52	1.95	2.10	3.46	2.62	1.83	3.37	4.24				
NT2RP3003426	9.31	6.11	5.45	12.48	10.53	11.34	9.4	9.12	8.46	*	+		
NT2RP3003427	8.99	4.74	5.99	5.37	7.25	6.52	7.72	5.96	8.43				
NT2RP3003433	9.63	4.28	3.87	11.80	10.94	8.04	5.78	4.80	7.07				
NT2RP3003437	18.34	7.27	6.59	15.83	19.21	15.84	12.02	13.41	15.15				
NT2RP3003448	6.95	4.49	2.68	9.13	8.95	5.55	5.56	5.02	6.11				
NT2RP3003455	8.08	3.54	2.51	10.14	9.73	10.02	5.84	8.37	5.46	*	+		

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Table 279

NT2RP3003462	4.12	2.91	3.40	4.80	6.31	3.84	3.87	5.08	5.3				
NT2RP3003464	2.09	1.93	2.25	2.69	2.89	1.33	2.08	3.11	2.15				
NT2RP3003469	3.14	2.14	3.25	2.94	4.36	3.12	4.25	4.89	4.48			*	+
NT2RP3003473	89.05	73.31	85.12	31.82	60.74	51.48	32.07	37.27	32.95	*	-	**	-
NT2RP3003474	3.72	1.64	1.41	2.81	4.68	2.60	1.76	1.83	5				
NT2RP3003475	5.61	2.84	3.02	4.26	5.48	3.96	3.12	2.86	5.38				
NT2RP3003490	2.57	1.77	0.90	2.92	3.66	2.60	1.94	2.99	7.73				
NT2RP3003491	3.82	1.31	1.56	3.52	3.19	3.71	1.08	3.23	2.23				
NT2RP3003493	32.32	24.24	22.86	18.58	22.23	21.78	10.29	22.93	16.25				
NT2RP3003500	1.40	1.72	1.09	3.53	3.58	2.03	2.25	3.61	2.95	*	+	*	+
NT2RP3003527	2.93	1.02	1.39	2.26	3.40	1.33	1.5	4.37	4.13				
NT2RP3003532	6.83	4.04	4.22	15.20	17.07	14.08	8.23	6.65	7.28	**	+		
NT2RP3003535	1.58	1.03	0.30	1.85	1.07	0.98	1.62	1.27	0.97				
NT2RP3003536	2.90	2.77	1.64	5.15	3.92	4.74	3.97	3.71	2.81	*	+		
NT2RP3003543	4.72	4.39	3.25	5.41	8.08	7.02	5.2	5.49	1.98	*	+		
NT2RP3003549	2.71	2.81	2.37	2.41	3.79	4.08	3.3	2.30	1.66				
NT2RP3003552	1.05	1.06	0.00	1.19	1.29	1.21	0.42	0.50	0.79				
NT2RP3003555	7.69	3.49	4.38	7.36	8.38	9.29	5.4	5.33	4.02				
NT2RP3003559	2.48	1.02	1.13	2.42	2.15	3.37	1.46	1.90	0.56				
NT2RP3003564	6.10	3.28	3.23	6.06	5.72	4.12	4.46	3.78	4.48				
NT2RP3003572	4.33	3.51	2.66	3.48	4.50	3.26	3.67	4.32	2.39				
NT2RP3003576	14.59	6.63	6.37	16.23	21.96	19.84	10.82	10.96	8.97	*	+		
NT2RP3003587	15.06	8.22	7.88	8.40	8.95	10.51	3.86	6.31	3.33				
NT2RP3003589	14.90	11.19	8.98	10.98	18.16	17.00	16.77	16.70	14.61				
NT2RP3003592	6.07	3.40	4.66	3.72	5.45	5.40	3.54	4.53	3.89				
NT2RP3003593	5.28	1.75	2.13	3.76	3.86	7.00	3.06	4.00	2.78				
NT2RP3003614	14.05	8.27	10.10	10.29	8.15	9.17	8.06	7.21	4.02				
NT2RP3003621	3.29	1.07	1.69	2.23	2.27	2.45	2.08	2.77	2.99				
NT2RP3003625	11.53	5.52	5.48	9.50	9.71	7.13	7.18	5.14	5.56				
NT2RP3003627	12.05	7.44	6.80	53.97	42.81	41.76	14.96	15.18	18.14	**	+	*	+
NT2RP3003636	5.65	3.72	2.95	5.93	6.64	5.54	5.93	5.72	5.63				
NT2RP3003642	10.88	8.03	6.37	13.82	13.96	17.20	12.37	12.40	16.41	*	+	*	+
NT2RP3003645	4.17	3.33	1.50	5.78	5.31	6.65	5.06	5.99	4.7	*	+		
NT2RP3003648	3.24	3.31	3.16	4.15	4.43	3.91	5.07	3.21	3.18	**	+		
NT2RP3003649	1.14	1.88	2.86	2.19	4.90	3.66	0.71	3.92	1.08				
NT2RP3003650	8.11	4.45	2.20	4.63	4.76	4.42	3.39	3.56	3.36				
NT2RP3003656	5.22	3.74	1.88	3.30	4.87	4.62	3.45	3.40	2.71				
NT2RP3003659	7.45	4.72	4.52	4.36	6.73	4.25	3.17	3.21	3.03				
NT2RP3003662	9.17	7.44	5.08	10.50	15.08	10.64	9.44	8.85	8.35				
NT2RP3003664	8.73	4.21	6.55	11.31	14.75	9.76	9.24	8.50	9.85				
NT2RP3003665	1.46	2.31	3.07	2.00	3.22	2.55	1.63	2.93	1.01				
NT2RP3003671	3.15	3.24	2.25	2.59	7.96	5.47	2.17	4.14	1.93				
NT2RP3003672	4.15	3.09	2.96	4.72	7.37	5.47	2.79	4.69	3.17	*	+		
NT2RP3003673	4.51	3.32	1.35	5.41	6.14	2.58	4.36	4.67	3.13				
NT2RP3003679	34.38	42.38	35.15	32.46	39.83	37.84	41.64	35.07	42.5				
NT2RP3003680	6.95	3.40	1.56	4.84	3.86	4.38	2.61	3.70	3.96				
NT2RP3003686	5.14	3.55	2.82	3.79	4.38	5.04	4.26	3.62	2.84				
NT2RP3003689	3.80	2.46	2.57	6.17	7.73	5.84	3.57	4.94	3.47	**	+		
NT2RP3003697	1.90	2.24	1.34	1.76	2.19	2.72	2.08	3.11	1.51				
NT2RP3003701	1.92	1.12	1.36	1.56	1.36	1.59	2.02	2.99	1.34				
NT2RP3003704	5.17	3.39	3.77	6.61	6.98	7.53	4.92	5.10	3.69	**	+		
NT2RP3003714	3.30	1.91	1.74	4.60	3.93	3.09	3.44	3.54	1.64				
NT2RP3003716	2.44	2.40	1.34	4.13	2.42	3.98	2.31	2.88	2.92				
NT2RP3003721	4.90	3.12	2.28	4.84	6.16	4.98	4.29	3.50	4.65				
NT2RP3003722	8.02	5.81	5.39	6.08	4.24	4.20	2.09	3.67	2.7			*	-
NT2RP3003726	6.59	6.25	3.44	4.38	3.30	5.00	5.53	4.21	4.73				

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Table 280

NT2RP3003729	3.69	2.88	2.55	4.06	4.92	3.98	2.8	3.60	3.35	*	+		
NT2RP3003731	6.61	4.33	5.75	7.10	14.90	8.06	5.99	7.15	5.75				
NT2RP3003740	4.78	3.50	4.29	5.32	3.89	4.79	4.16	4.89	3.61				
NT2RP3003746	5.36	3.49	2.71	5.20	7.52	3.17	3.94	3.31	4.02				
NT2RP3003749	0.76	0.62	0.17	0.29	1.19	1.12	0.64	1.30	0.75				
NT2RP3003754	5.00	3.26	5.25	7.46	7.69	6.19	5.46	4.91	4.55	*	+		
NT2RP3003759	1.70	0.69	0.73	1.39	1.06	0.48	0.73	2.09	2.41				
NT2RP3003764	7.97	5.68	5.63	6.40	8.69	7.67	5.36	5.99	4.9				
NT2RP3003766	4.56	2.73	2.99	3.97	4.19	3.87	3.96	3.75	3.32				
NT2RP3003767	6.96	5.70	6.63	13.57	9.41	11.81	7.79	9.76	8.37	*	+	*	+
NT2RP3003778	5.19	3.99	4.33	9.90	11.58	8.75	5.62	5.86	5.15	**	+		
NT2RP3003779	13.01	5.97	4.99	6.05	7.93	6.85	7.17	5.72	8.58				
NT2RP3003783	19.26	10.08	8.20	11.73	11.20	13.62	12.33	9.52	7.82				
NT2RP3003787	4.90	2.40	2.22	2.44	3.52	4.85	2.78	3.53	7.22				
NT2RP3003789	5.36	4.73	2.56	3.44	7.01	5.23	5.4	5.55	4.62				
NT2RP3003795	2.17	1.85	1.40	3.14	2.08	3.57	2.46	3.18	2.41				
NT2RP3003799	2.89	2.29	1.32	1.87	1.75	2.53	1.45	2.24	2.66				
NT2RP3003800	3.51	2.88	4.22	3.79	5.81	4.55	3.66	3.45	2.49				
NT2RP3003805	6.47	3.37	3.41	4.89	4.12	5.73	3.59	4.60	4.09				
NT2RP3003809	5.03	1.78	2.92	4.79	3.39	3.28	1.85	3.89	3.58				
NT2RP3003819	20.93	12.43	10.20	22.69	23.35	18.68	16.05	13.33	11.82				
NT2RP3003824	12.10	8.20	9.56	14.53	12.56	14.16	10.06	10.73	7.38	*	+		
NT2RP3003825	22.51	14.11	14.65	13.44	18.74	15.00	10.89	9.86	10.89				
NT2RP3003828	3.66	3.06	2.75	5.51	4.72	4.12	2.65	4.12	4.14	*	+		
NT2RP3003831	2.13	2.74	2.94	4.32	4.71	5.94	3.1	4.50	4.33	*	+		
NT2RP3003833	5.17	2.54	2.51	3.72	3.00	5.07	4.52	4.42	4				
NT2RP3003836	7.43	5.49	5.12	9.64	6.79	8.16	7.54	6.97	9.43				
NT2RP3003842	17.19	8.40	7.68	16.76	16.34	13.12	12.09	8.43	8.61				
NT2RP3003843	11.40	7.50	6.65	20.59	22.26	19.09	11.26	10.84	11.37	**	+		
NT2RP3003844	12.70	8.55	6.42	7.70	6.74	8.49	13.96	12.46	12.2				
NT2RP3003846	3.76	1.97	2.48	4.49	3.48	4.92	2.73	3.31	3.38				
NT2RP3003849	4.75	3.02	2.95	4.08	4.65	4.41	2.89	4.41	5.12				
NT2RP3003862	8.19	5.27	4.97	5.73	7.14	6.59	9.21	6.75	9.43				
NT2RP3003870	8.87	6.42	4.81	9.09	8.35	8.66	8.21	7.03	8.25				
NT2RP3003874	4.83	4.91	4.32	6.66	5.96	5.92	4.88	5.78	3.78	**	+		
NT2RP3003876	8.40	4.71	3.53	8.21	6.66	5.04	3.88	4.35	5.13				
NT2RP3003880	3.42	3.11	2.28	6.01	6.99	4.51	4.71	5.26	4.07	*	+	*	+
NT2RP3003889	1.46	1.88	0.92	1.03	3.20	2.06	0.85	2.31	2.72				
NT2RP3003891	1.54	2.30	0.87	1.75	2.99	2.00	1.08	2.80	2.25				
NT2RP3003914	7.95	4.51	4.21	5.57	7.65	7.02	5.69	6.39	7.2				
NT2RP3003915	1.86	2.20	1.19	1.63	2.60	2.36	2.19	3.03	2.1				
NT2RP3003918	5.05	3.66	2.14	2.83	4.62	2.98	3.63	5.42	5.25				
NT2RP3003920	4.98	4.36	2.71	6.50	6.25	5.72	5.51	6.91	3.85	*	+		
NT2RP3003924	6.49	3.55	2.01	7.69	8.02	5.14	4.31	3.95	7.6				
NT2RP3003932	3.65	2.42	1.71	4.82	7.98	3.41	2.85	3.76	4.41				
NT2RP3003939	2.69	1.67	1.95	3.86	3.92	3.18	2.41	3.31	2.98	*	+		
NT2RP3003940	15.51	8.52	7.81	11.47	11.25	8.35	8.68	9.97	7.23				
NT2RP3003943	3.63	3.38	2.60	2.90	3.77	1.83	2.48	3.48	4.35				
NT2RP3003959	2.34	2.12	1.61	3.04	4.84	3.82	2.42	3.16	4.93	*	+		
NT2RP3003963	6.98	5.43	4.54	7.42	7.40	5.93	6.05	7.92	6.84				
NT2RP3003965	44.37	24.77	31.74	35.84	34.50	26.36	12.7	12.05	15.03			*	-
NT2RP3003972	14.33	10.15	6.83	27.44	20.29	23.76	23.62	15.59	17.39	*	+		
NT2RP3003973	8.15	5.02	3.70	7.18	5.27	4.94	5.3	5.61	3.97				
NT2RP3003979	11.32	8.28	4.38	9.43	15.88	13.30	10.9	7.26	6.82				
NT2RP3003980	10.84	7.99	7.63	8.16	9.43	9.50	5.75	7.95	4.2				
NT2RP3003982	1.33	3.01	1.15	1.21	2.15	2.04	1.21	3.30	0.58				

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Table 281

NT2RP3003989	2.69	2.90	1.66	1.97	4.23	17.93	2.15	5.56	2.09				
NT2RP3003992	4.45	3.19	2.09	6.85	5.45	5.48	2.46	5.01	2.52	*	+		
NT2RP3004000	2.21	2.96	1.05	1.76	3.78	2.06	4.87	2.93	3.16				
NT2RP3004001	10.03	7.36	4.34	11.63	8.96	9.72	6.39	7.58	6.18				
NT2RP3004005	2.84	1.39	1.85	4.23	3.15	3.89	6.12	4.26	2	*	+		
NT2RP3004013	12.35	8.49	6.06	13.19	14.63	10.33	6.81	8.18	5.23				
NT2RP3004016	4.50	2.25	1.85	4.36	3.71	4.81	2.81	2.48	3.43				
NT2RP3004025	4.30	3.53	3.53	4.99	6.65	6.46	4.38	6.03	4.27	*	+		
NT2RP3004030	22.90	14.65	17.74	29.69	32.04	29.24	22.51	18.90	19.9	**	+		
NT2RP3004041	2.52	1.89	2.73	9.78	7.34	7.80	4.71	4.38	4.76	**	+	**	+
NT2RP3004042	14.33	10.61	5.39	8.88	10.41	10.70	11.54	9.64	11.73				
NT2RP3004044	21.83	11.12	9.61	8.22	9.50	8.35	6.17	5.06	6.39				
NT2RP3004051	10.03	6.48	4.32	11.50	10.92	8.70	7.09	5.39	5.97				
NT2RP3004052	8.89	3.73	4.41	8.80	8.69	8.41	6.86	4.66	5.92				
NT2RP3004053	30.17	20.41	22.51	39.10	49.24	42.11	31.51	31.71	33.47	*	+		
NT2RP3004055	4.37	1.71	1.44	3.41	6.47	4.74	2.67	3.05	2.47				
NT2RP3004059	4.35	3.84	2.26	4.57	5.40	6.36	4.38	3.95	3.58				
NT2RP3004063	3.19	5.38	4.25	5.25	3.73	4.82	2.48	4.55	2.33				
NT2RP3004067	20.37	6.61	6.47	9.24	9.55	7.82	8.89	7.62	7.01				
NT2RP3004070	5.14	4.09	2.46	6.23	5.56	5.86	3.96	3.22	4.36				
NT2RP3004075	4.89	3.98	3.09	4.61	4.46	5.82	3.77	3.33	3.83				
NT2RP3004078	6.60	3.72	3.12	5.82	6.46	5.79	5.42	4.95	4.97				
NT2RP3004083	2.32	2.07	2.04	35.55	41.35	31.65	20.9	19.75	24.51	**	+	**	+
NT2RP3004084	4.82	3.89	2.80	2.32	2.21	5.07	2.3	4.34	3.24				
NT2RP3004087	6.30	4.80	3.92	7.31	7.31	7.55	5.02	5.55	6.07	*	+		
NT2RP3004090	3.22	2.13	1.57	4.35	5.08	3.83	3.16	6.01	4.35	*	+		
NT2RP3004093	5.89	4.55	3.16	7.72	8.34	6.85	6.58	5.64	6.63	*	+		
NT2RP3004095	14.57	8.24	7.88	13.27	13.82	13.04	10.11	8.74	11.47				
NT2RP3004102	11.19	6.90	6.93	9.17	11.74	10.70	9.42	7.28	9.35				
NT2RP3004110	34.95	22.41	23.25	26.04	28.26	24.02	16.77	18.06	22.74				
NT2RP3004119	6.91	5.16	5.08	8.05	6.96	6.49	5.73	4.85	4.73				
NT2RP3004125	14.03	10.35	8.98	14.12	16.80	14.86	13.91	11.06	10.62				
NT2RP3004129	3.44	1.56	2.05	2.41	2.99	3.58	2.35	2.48	1.77				
NT2RP3004130	3.67	2.75	3.57	6.28	6.18	5.89	7.37	7.97	5.85	**	+	**	+
NT2RP3004133	8.07	5.45	4.56	6.17	4.98	5.72	6.99	6.13	6.19				
NT2RP3004145	6.56	4.08	2.26	3.88	4.54	4.28	2.91	4.84	3.57				
NT2RP3004148	7.79	6.05	5.54	5.61	5.84	7.93	7.7	7.31	5.13				
NT2RP3004155	3.99	4.60	2.60	5.64	5.29	6.17	3.4	3.66	2.7	*	+		
NT2RP3004165	9.52	6.71	6.33	12.69	13.98	12.98	6.82	6.51	5.79	**	+		
NT2RP3004179	4.17	3.60	3.22	5.35	6.25	6.22	3.75	3.01	3.75	**	+		
NT2RP3004185	2.33	0.68	1.31	1.91	1.20	2.96	1.8	2.34	1.86				
NT2RP3004188	8.37	4.08	5.91	11.26	11.20	6.76	4.54	7.20	6.27				
NT2RP3004189	14.04	5.66	6.06	7.02	12.29	6.24	4.85	4.58	5.6				
NT2RP3004190	11.54	5.42	6.63	7.75	12.77	11.72	5.49	4.47	5.81				
NT2RP3004191	10.44	9.83	8.83	14.00	14.26	11.80	12.41	10.04	10.36	*	+		
NT2RP3004202	2.35	2.27	2.03	3.51	4.57	3.29	3.6	3.97	5.67	*	+	*	+
NT2RP3004205	10.83	6.54	6.41	8.47	10.58	6.84	7.02	6.54	6.67				
NT2RP3004206	3.85	2.53	2.95	2.95	3.06	3.06	4.12	2.99	2.57				
NT2RP3004207	4.93	2.79	3.03	4.73	4.14	4.86	4.28	4.10	5.09				
NT2RP3004209	4.91	2.40	2.89	6.87	6.50	4.96	4.96	5.23	4.63	*	+		
NT2RP3004215	3.55	2.78	2.14	12.42	8.20	7.94	3.86	4.27	5.18	*	+	*	+
NT2RP3004219	16.93	6.45	7.83	7.64	9.11	7.10	7.36	6.55	7.25				
NT2RP3004242	5.13	4.26	3.60	4.45	5.10	4.52	4.84	3.47	2.95				
NT2RP3004246	4.82	4.45	3.64	5.22	7.08	6.18	4.56	5.99	5.39	*	+		
NT2RP3004253	1.98	2.17	2.49	2.39	1.93	2.99	2.38	3.72	5.59				
NT2RP3004258	11.77	7.63	9.50	10.32	13.55	13.92	4.51	6.56	5.46			*	-

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Table 282

NT2RP3004262	4.35	2.96	2.85	2.71	3.57	4.45	4.01	4.72	3.41				
NT2RP3004275	3.72	3.04	2.37	3.29	3.02	3.38	3.39	4.75	1.04				
NT2RP3004282	12.87	5.01	5.72	9.16	11.91	6.32	7.38	7.58	6.69				
NT2RP3004289	3.01	2.85	1.46	6.88	5.77	3.72	2.35	3.31	3.68	*	+		
NT2RP3004294	7.18	3.41	2.73	24.46	29.15	28.18	20.58	15.67	20.34	**	+	**	+
NT2RP3004298	7.07	5.08	3.77	5.00	5.97	6.16	6.4	6.06	5.61				
NT2RP3004309	10.96	7.28	6.61	7.01	8.68	7.42	5.52	6.85	6.57				
NT2RP3004321	11.18	6.12	7.27	9.56	8.71	10.32	7.19	8.23	10.39				
NT2RP3004322	3.28	2.42	1.89	3.12	2.58	3.70	3.77	3.09	3.39				
NT2RP3004332	6.32	6.72	6.36	11.24	8.54	10.03	4.86	8.82	5.48	*	+		
NT2RP3004334	4.49	2.34	2.27	5.43	4.10	3.66	2.44	1.92	2.32				
NT2RP3004336	5.86	3.72	2.08	6.83	9.08	6.19	5.13	6.87	5.49				
NT2RP3004338	11.56	5.52	9.71	8.36	5.67	6.93	5.31	4.61	6.32				
NT2RP3004341	2.24	1.74	1.67	2.56	2.48	3.60	1.13	2.35	3.45				
NT2RP3004345	3.27	3.23	2.25	3.71	4.02	3.88	3.2	3.07	4.38				
NT2RP3004348	8.53	5.32	6.83	14.49	13.97	11.82	7.76	7.80	9.23	**	+		
NT2RP3004349	10.22	7.24	8.20	12.70	11.94	13.01	6.98	7.06	5.47	*	+		
NT2RP3004355	6.08	5.70	3.65	5.80	6.46	7.00	4.88	5.01	4.97				
NT2RP3004356	13.62	7.29	6.71	12.35	15.04	10.32	9.71	9.44	9.13				
NT2RP3004360	7.52	3.61	3.49	4.81	4.04	4.08	2.07	3.17	4.82				
NT2RP3004361	16.01	7.31	5.66	15.99	14.58	14.13	4.38	5.01	4.13				
NT2RP3004374	7.91	4.13	3.84	7.91	7.91	7.64	5.99	5.39	5.89				
NT2RP3004378	26.21	17.19	14.59	10.81	12.69	11.18	6.13	10.86	9.07			*	-
NT2RP3004399	2.04	2.65	1.39	1.42	2.99	2.67	1.58	2.38	2.75				
NT2RP3004405	3.95	3.77	2.00	4.65	7.05	3.79	3.22	5.96	4.47				
NT2RP3004406	7.20	4.61	5.55	5.61	8.40	5.80	5.82	7.89	6.47				
NT2RP3004411	7.77	3.85	3.09	16.41	12.18	7.61	7.04	7.47	10.13				
NT2RP3004424	4.60	1.42	1.67	3.96	3.79	2.00	1.27	3.09	4.78				
NT2RP3004428	7.15	4.01	3.24	6.42	5.85	3.58	6.97	6.90	7.98				
NT2RP3004432	3.82	2.57	0.97	7.56	9.25	7.81	7.72	10.80	9.98	**	+	**	+
NT2RP3004434	9.49	5.09	3.75	6.31	8.59	6.98	5.23	4.83	5.64				
NT2RP3004446	6.23	5.35	3.39	6.60	5.96	4.57	2.58	4.37	4.71				
NT2RP3004451	3.49	1.02	1.26	4.55	6.79	4.04	2.13	3.69	4.46				
NT2RP3004454	3.00	1.25	1.36	2.36	2.23	1.93	1.66	2.42	2.5				
NT2RP3004466	16.12	6.82	7.66	12.66	11.01	12.35	11.52	8.75	10.08				
NT2RP3004470	8.70	6.35	3.18	11.68	12.19	10.86	7.44	7.38	5.56	*	+		
NT2RP3004472	1.89	2.60	1.02	4.08	3.19	3.82	2.45	1.91	1.78	*	+		
NT2RP3004475	4.99	3.80	4.98	4.54	5.61	3.71	4.55	5.07	4.35				
NT2RP3004480	7.66	5.39	3.59	15.02	14.38	12.51	8.01	7.48	6.29	**	+		
NT2RP3004481	4.24	6.01	3.44	3.84	4.84	6.10	5.51	4.88	3.41				
NT2RP3004490	1.09	1.00	1.30	1.59	2.17	1.90	1.13	0.94	0.16	*	+		
NT2RP3004496	11.99	5.64	6.80	14.82	15.35	7.87	12.41	15.48	10.73				
NT2RP3004498	10.57	6.90	5.91	5.39	8.13	7.76	7.22	4.55	5.58				
NT2RP3004503	8.32	5.77	4.24	17.06	17.79	15.82	8.93	7.92	6.72	**	+		
NT2RP3004504	16.66	9.32	8.13	4.90	5.37	6.99	5.11	6.36	4.24				
NT2RP3004505	8.72	5.28	4.61	4.26	5.67	7.97	8.11	8.94	7.62				
NT2RP3004507	4.86	3.25	3.44	5.31	4.59	4.43	2.27	3.02	3.06				
NT2RP3004519	3.79	1.12	1.28	2.61	2.20	3.15	1.55	1.93	1.88				
NT2RP3004524	1.80	1.60	2.36	2.58	1.67	4.26	2.22	2.30	1.3				
NT2RP3004527	1.16	0.95	0.83	1.29	0.90	1.98	0.25	0.54	0.6			*	-
NT2RP3004534	5.79	3.52	3.93	3.26	4.89	7.19	3.48	2.92	3				
NT2RP3004539	14.05	8.61	6.22	8.74	9.46	10.33	9.59	6.77	9.38				
NT2RP3004541	4.42	3.07	2.91	2.08	4.14	2.58	3.82	4.01	3.83				
NT2RP3004544	9.72	3.68	2.35	4.38	6.86	7.17	4.05	5.81	5.64				
NT2RP3004551	3.07	2.54	2.87	4.55	5.33	3.79	4.49	4.42	3.29	*	+	*	+
NT2RP3004552	11.09	5.45	4.69	3.94	6.09	8.11	5.03	5.45	2.94				

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Table 283

NT2RP3004557	9.04	5.56	6.56	5.65	4.56	3.38	5.82	5.13	3.59				
NT2RP3004561	5.68	3.44	3.35	5.27	5.92	3.88	4.61	5.03	4.06				
NT2RP3004566	6.63	6.29	6.33	12.53	11.01	9.47	7.43	8.46	13.57	**	+		
NT2RP3004569	6.44	5.29	4.60	10.37	11.99	10.11	4.46	4.55	4.39	**	+		
NT2RP3004572	3.83	3.21	2.73	4.62	5.78	5.28	4.26	4.30	2.97	*	+		
NT2RP3004578	5.21	3.44	2.27	5.01	7.11	5.48	3.71	3.96	4.42				
NT2RP3004584	3.59	3.64	3.56	3.31	4.74	4.86	3.85	3.43	4.22				
NT2RP3004588	3.87	2.70	2.67	8.15	6.21	6.68	4.64	5.48	4.37	**	+	*	+
NT2RP3004594	7.86	6.82	6.37	5.22	4.81	5.30	4.15	4.02	2.13	*	-	*	-
NT2RP3004603	60.30	35.19	34.71	45.07	50.01	29.71	17.9	21.98	18.08			*	-
NT2RP3004612	6.20	3.05	3.45	4.40	4.92	2.76	4.05	3.39	3.11				
NT2RP3004617	3.07	2.70	1.70	1.60	2.01	3.22	2.53	2.44	1.96				
NT2RP3004618	3.95	2.90	2.07	5.51	5.52	3.64	3.14	3.14	4.18				
NT2RP3004625	5.48	4.10	2.95	5.75	7.50	5.56	7.41	6.90	5.44				
NT2RP3004635	4.31	4.50	4.46	4.30	6.48	5.74	5.58	3.86	3.99				
NT2RP3004640	3.88	3.08	3.28	7.49	7.45	6.73	5.96	5.47	4.27	**	+	*	+
NT2RP3004642	10.28	8.51	8.84	14.09	13.53	15.70	10	10.58	5.55	**	+		
NT2RP3004647	7.16	4.79	5.37	9.93	6.54	8.91	7.81	5.99	5.6				
NT2RP3004652	9.07	6.60	3.76	13.15	12.30	9.92	7.24	7.33	3.44	*	+		
NT2RP3004669	8.16	5.80	4.33	5.00	7.93	5.74	5.7	5.73	5.33				
NT2RP3004670	14.41	12.39	9.32	16.29	20.04	15.04	13.36	13.59	15.01				
NT2RP4000008	15.39	10.91	11.09	13.50	10.87	9.28	9.4	8.75	8.85				
NT2RP4000018	9.99	5.44	8.54	9.01	5.02	7.90	7.84	6.47	7.74				
NT2RP4000023	5.20	4.00	3.38	3.86	2.64	2.61	3.51	4.32	2.67				
NT2RP4000025	5.36	5.89	4.96	8.91	15.04	11.95	12.96	16.75	13.7	*	+	**	+
NT2RP4000035	8.26	5.47	5.42	13.88	11.54	12.72	5.97	11.43	5.65	**	+		
NT2RP4000041	8.69	5.46	1.79	1.69	4.25	2.76	4.28	5.58	4.93				
NT2RP4000049	4.05	2.09	2.36	3.68	4.19	3.53	5.9	5.73	3.33				
NT2RP4000050	3.62	2.75	1.71	2.29	3.50	3.25	3.01	5.38	3.14				
NT2RP4000051	7.84	3.90	4.64	5.71	7.58	5.48	5.27	7.15	5.15				
NT2RP4000063	4.66	2.43	2.44	3.26	2.94	4.77	3.68	5.96	2.61				
NT2RP4000065	4.21	2.76	2.69	4.09	3.65	3.77	3.32	3.08	2.24				
NT2RP4000070	3.16	2.60	2.02	6.63	8.48	9.49	3.2	4.92	3.34	**	+		
NT2RP4000074	1.25	0.65	0.45	1.09	0.95	1.43	1.92	3.35	1.24				
NT2RP4000078	19.45	8.95	8.65	15.20	11.49	10.74	9.98	6.63	6.98				
NT2RP4000080	16.31	10.55	9.31	16.83	24.18	15.57	14.36	10.43	16.69				
NT2RP4000099	48.25	34.08	34.96	222.14	203.11	165.35	108.2	86.72	64.03	**	+	*	+
NT2RP4000102	1.59	3.03	0.75	2.02	3.06	3.50	2.33	2.26	2.57				
NT2RP4000103	2.96	1.87	1.69	2.51	4.74	2.46	2.75	4.73	2.41				
NT2RP4000108	7.32	4.36	4.82	47.03	44.25	37.96	49.26	38.51	49.37	**	+	**	+
NT2RP4000109	12.97	8.34	8.98	9.50	12.20	12.85	13.79	10.89	9.27				
NT2RP4000111	1.66	4.14	1.76	3.30	2.22	1.71	2.22	1.42	3.11				
NT2RP4000112	12.62	5.96	5.20	13.14	12.78	6.27	9.14	9.28	9.82				
NT2RP4000115	6.69	4.45	3.10	4.28	5.71	3.35	6.12	5.23	4.95				
NT2RP4000129	5.85	2.83	2.30	2.80	3.92	3.49	3.8	3.85	2.88				
NT2RP4000137	6.85	6.38	5.53	4.82	7.68	8.16	4.3	6.03	5.81				
NT2RP4000138	31.16	22.51	24.42	13.11	12.17	10.03	14.81	14.41	15.27	**	-	*	-
NT2RP4000141	4.89	2.65	2.93	4.06	3.52	4.29	2.76	4.18	2.03				
NT2RP4000147	2.17	1.29	1.74	2.55	2.46	3.03	2.68	3.29	2.54	*	+	*	+
NT2RP4000150	7.08	4.20	5.06	8.60	7.56	6.25	7.64	8.70	6.48				
NT2RP4000151	7.65	4.77	3.15	5.40	5.42	4.70	5.71	4.77	7.3				
NT2RP4000157	47.42	28.18	24.63	140.24	151.70	90.24	64.55	61.24	48.04	**	+	*	+
NT2RP4000159	2.50	1.76	1.15	1.15	1.62	2.34	1.61	2.61	1.83				
NT2RP4000163	26.39	20.86	16.59	7.91	9.36	8.09	5.61	5.24	4.41	*	-	**	-
NT2RP4000167	3.26	3.04	2.67	3.80	3.99	4.24	2.64	3.85	3.17	**	+		
NT2RP4000171	7.53	5.74	5.41	5.89	7.46	4.62	5.54	5.19	6.82				

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Table 284

NT2RP4000175	26.66	17.23	19.20	12.23	15.62	11.17	16.22	18.62	19.97				
NT2RP4000180	17.71	15.54	16.60	7.75	7.76	10.71	9.21	10.11	9.68	**	-	**	-
NT2RP4000185	14.57	9.35	~5.99	12.31	15.65	9.34	8.25	9.02	7.47				
NT2RP4000192	9.26	5.09	4.80	6.32	4.48	3.65	4.83	4.74	4.23				
NT2RP4000194	3.63	2.75	1.83	3.79	5.80	2.67	3.51	4.32	4.95				
NT2RP4000196	8.18	4.81	3.10	7.96	7.13	5.03	5.27	5.97	5.49				
NT2RP4000210	28.53	18.46	17.26	28.89	37.05	27.38	24.22	22.19	25.95				
NT2RP4000212	12.06	7.92	6.39	16.76	20.50	16.60	12.59	12.83	12.92	*	+		
NT2RP4000214	10.71	7.74	6.94	13.03	16.29	15.56	10.1	11.28	8.66	*	+		
NT2RP4000216	5.44	4.53	4.98	6.46	9.49	6.90	5.75	6.76	4.95				
NT2RP4000218	7.33	2.22	2.67	4.98	4.33	3.81	3.81	4.58	6.27				
NT2RP4000223	19.92	13.17	10.28	22.13	21.62	13.05	22.62	26.76	25.86			*	+
NT2RP4000243	13.18	9.89	7.93	15.15	23.34	10.85	12.84	16.56	15.03				
NT2RP4000246	33.96	22.95	19.51	28.17	27.99	24.14	21.88	39.67	28.61				
NT2RP4000250	7.99	6.43	5.04	12.08	14.24	11.05	12.85	25.59	17.99	**	+	*	+
NT2RP4000256	2.39	2.62	1.51	3.73	3.59	2.62	3.4	5.63	3.02				
NT2RP4000257	47.78	28.06	32.52	17.19	17.58	12.15	20.3	21.14	18.74	*	-		
NT2RP4000259	4.57	3.53	4.63	12.50	13.85	8.56	9.95	10.96	10.32	*	+	**	+
NT2RP4000261	4.69	3.90	2.69	4.69	4.12	2.59	6.07	3.27	3.23				
NT2RP4000262	8.40	4.25	5.05	10.81	7.69	5.18	7.05	4.76	3.22				
NT2RP4000263	2.39	2.26	1.46	3.24	1.78	2.52	2.31	2.43	1.67				
NT2RP4000280	19.84	10.94	16.02	14.51	20.53	17.86	16.38	15.79	14.33				
NT2RP4000286	14.05	12.14	5.20	8.66	7.23	8.18	6.73	10.62	6.93				
NT2RP4000290	4.20	3.07	2.79	5.43	3.58	4.59	3.38	3.10	2.4				
NT2RP4000291	18.51	15.32	18.47	45.30	38.54	34.77	17.5	19.25	13.11	**	+		
NT2RP4000301	2.59	1.81	1.04	2.23	2.98	3.54	2.54	3.49	1.63				
NT2RP4000312	4.56	1.79	4.33	4.54	4.75	3.56	5.14	2.41	5.06				
NT2RP4000321	13.60	6.74	4.54	13.92	11.99	10.85	8.51	8.80	9.62				
NT2RP4000323	3.58	2.53	1.59	2.86	3.50	3.23	2.71	3.60	1.23				
NT2RP4000324	7.25	5.08	2.70	5.19	6.35	3.74	5.48	4.98	4				
NT2RP4000334	13.97	11.43	12.75	30.03	27.15	21.64	10.28	10.30	9.71	**	+	*	-
NT2RP4000343	4.98	3.25	2.65	4.86	5.56	3.68	3.76	4.39	3.15				
NT2RP4000348	3.02	1.79	1.77	4.45	3.35	4.09	4.17	3.46	2.74	*	+		
NT2RP4000349	2.02	3.31	1.01	2.05	0.64	3.58	0.41	1.43	0.27				
NT2RP4000355	10.07	4.28	4.14	7.89	8.66	7.17	5.76	4.78	6.28				
NT2RP4000356	10.81	5.71	5.12	9.75	8.69	6.70	12.73	12.78	15.8			*	+
NT2RP4000360	5.76	3.41	2.25	11.67	15.48	9.10	8.87	7.21	7.44	*	+	*	+
NT2RP4000367	2.23	2.01	1.13	1.88	2.90	1.83	2.17	1.67	2.44				
NT2RP4000370	4.54	3.75	1.61	3.50	4.39	3.20	3.15	3.31	3.03				
NT2RP4000373	4.40	4.53	4.20	4.85	4.38	4.02	3.74	3.46	2.82			*	-
NT2RP4000376	3.46	3.35	3.32	5.35	3.36	3.31	2.76	4.60	2.39				
NT2RP4000381	3.20	2.91	2.81	7.76	5.97	5.48	3.69	3.62	2.58	**	+		
NT2RP4000388	507.68	363.39	334.24	288.84	217.90	196.35	431.3	437.24	362.7				
NT2RP4000390	19.01	14.68	11.68	24.99	29.51	23.19	15.68	13.59	14.64	*	+		
NT2RP4000393	3.40	2.87	1.85	2.59	3.15	3.33	5.06	3.98	3.29				
NT2RP4000398	5.34	4.23	2.50	10.36	14.48	10.01	6.8	5.94	5.69	*	+		
NT2RP4000406	9.30	5.25	6.26	5.59	5.04	6.35	7.54	6.32	4.52				
NT2RP4000407	5.98	4.41	3.78	8.29	7.16	4.70	4.32	5.68	5.13				
NT2RP4000413	1.40	1.18	0.62	0.72	1.57	3.58	1.37	2.49	1.36				
NT2RP4000415	10.74	4.75	5.55	8.27	6.74	8.60	4.84	5.48	2.05				
NT2RP4000417	7.49	5.67	3.62	5.24	6.05	4.58	5.78	5.18	6.52				
NT2RP4000423	10.91	8.43	6.08	17.00	12.75	12.74	5.48	6.12	5.86	*	+		
NT2RP4000424	4.48	2.86	1.81	7.46	7.77	6.37	5.69	7.35	4.76	**	+		
NT2RP4000447	13.10	8.03	11.15	9.03	13.44	9.03	6.38	5.33	5.62			*	-
NT2RP4000448	2.34	1.79	0.84	4.19	6.84	6.98	5.24	4.20	3.76	*	+	*	+
NT2RP4000449	2.70	2.01	2.13	2.07	1.89	2.22	2.41	2.65	1.44				

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Table 285

NT2RP4000453	7.28	6.16	3.48	2.35	2.43	4.15	1.8	4.72	0.91				
NT2RP4000455	1.01	1.01	1.48	2.29	2.70	1.92	2.22	2.27	0.83	*	+		
NT2RP4000456	13.97	7.10	6.36	13.16	13.46	10.68	8.85	8.11	5.28				
NT2RP4000457	6.68	4.82	2.84	3.69	4.73	3.69	4.6	3.98	5.62				
NT2RP4000461	5.28	3.96	3.32	7.87	8.68	6.42	5.85	6.52	5.36	*	+		
NT2RP4000462	8.07	4.05	4.23	7.49	8.39	11.75	6.93	5.29	4.06				
NT2RP4000463	9.18	6.18	6.85	10.59	9.85	9.05	5.78	4.84	4.27				
NT2RP4000471	3.55	1.94	1.96	3.21	3.41	4.25	4.22	4.59	2.95				
NT2RP4000472	3.05	2.42	1.96	12.20	8.76	6.84	4.36	5.24	4.11	*	+	*	+
NT2RP4000476	1.50	1.02	0.85	12.49	11.85	10.88	21.84	18.65	17.71	**	+	**	+
NT2RP4000480	15.36	6.51	5.30	5.47	9.87	5.81	7.44	7.54	5.87				
NT2RP4000481	3.47	2.35	0.78	2.35	2.92	2.36	3.06	3.89	4.07				
NT2RP4000483	2.86	2.52	1.45	2.10	2.49	1.39	3.11	4.18	2.64				
NT2RP4000487	3.11	1.79	1.56	6.59	4.70	2.73	3.7	3.87	2.46				
NT2RP4000496	0.65	2.01	0.43	0.74	1.20	0.89	1.64	1.30	1.26				
NT2RP4000497	6.68	4.62	5.43	14.85	10.68	12.20	7.76	11.46	5.67	**	+		
NT2RP4000498	4.09	1.89	2.15	3.59	3.39	3.97	3.69	5.45	2.91				
NT2RP4000500	3.65	2.95	1.78	3.44	3.70	2.25	3.4	3.63	2.11				
NT2RP4000507	15.14	8.22	5.69	11.50	10.49	7.06	7.7	7.22	9.04				
NT2RP4000515	15.49	10.59	8.57	12.80	13.50	16.10	12.82	10.19	8.69				
NT2RP4000516	7.24	4.39	3.65	20.66	19.29	17.91	10.11	9.21	8.83	**	+	*	+
NT2RP4000517	3.07	2.43	1.84	4.04	5.74	5.81	3.42	4.89	3.38	*	+		
NT2RP4000518	4.18	1.91	2.39	4.28	2.50	2.78	3.19	3.42	2.91				
NT2RP4000519	1.25	1.47	1.18	2.14	1.80	1.86	1.53	2.34	1.09	**	+		
NT2RP4000524	0.66	1.08	0.33	1.66	1.94	1.79	1.87	1.81	1.62	**	+	**	+
NT2RP4000528	1.96	2.16	0.43	1.52	2.71	2.98	1.9	3.84	1.18				
NT2RP4000537	40.32	18.87	17.18	18.72	15.16	10.99	14.21	10.18	11.8				
NT2RP4000541	6.42	4.52	3.64	6.16	5.27	3.57	5.96	5.32	5.79				
NT2RP4000543	7.15	4.38	3.94	5.71	5.28	6.49	7.13	6.85	7.19				
NT2RP4000545	22.00	12.60	11.90	35.02	30.28	28.43	15.85	15.53	13.71	*	+		
NT2RP4000546	3.49	2.74	2.72	5.16	6.84	5.20	2.65	5.26	4.13	*	+		
NT2RP4000549	10.31	6.26	6.97	10.02	6.99	7.06	17.04	10.70	13.71				
NT2RP4000556	4.79	2.38	2.09	2.96	4.95	3.16	3.01	3.93	2.39				
NT2RP4000557	2.43	1.89	1.59	3.06	2.06	2.13	1.6	1.76	2.34				
NT2RP4000558	7.85	4.61	3.47	5.80	4.60	4.48	8.11	4.97	5.07				
NT2RP4000560	11.62	8.43	5.62	16.38	11.32	8.62	10.3	8.86	6.76				
NT2RP4000568	0.86	1.06	0.72	1.99	2.89	2.56	1.2	1.79	1.98	**	+	*	+
NT2RP4000583	9.91	5.21	4.91	9.30	13.09	14.53	6.79	5.52	7.23				
NT2RP4000585	3.74	2.64	3.88	4.44	2.94	3.43	2.78	2.68	3.99				
NT2RP4000588	1.78	1.61	0.91	2.23	3.68	2.01	2.78	3.01	2.89			**	+
NT2RP4000590	7.09	4.23	3.81	4.80	5.51	5.49	5.51	5.97	3.62				
NT2RP4000599	1.53	1.26	0.87	1.24	1.41	1.06	0.44	2.70	0.51				
NT2RP4000603	11.90	6.03	3.85	6.61	6.16	3.84	4.98	5.10	6.79				
NT2RP4000607	9.25	5.54	5.52	6.95	7.07	10.29	4.24	5.47	7.66				
NT2RP4000614	18.95	12.78	10.17	25.67	26.47	23.13	9.33	11.19	9.77	*	+		
NT2RP4000634	4.83	2.61	1.81	7.54	6.71	5.97	5.4	7.61	4.39	*	+		
NT2RP4000638	3.55	2.37	1.27	3.88	3.82	3.28	2.34	4.08	2.48				
NT2RP4000648	3.49	3.15	1.64	4.18	4.00	1.87	2.79	3.50	2.8				
NT2RP4000657	7.42	4.66	4.89	3.76	5.89	4.90	4.79	4.73	4.39				
NT2RP4000691	3.57	4.48	4.25	6.09	7.82	5.58	5.65	7.17	5.49	*	+	*	+
NT2RP4000697	11.06	7.17	4.24	7.59	7.47	5.97	4.38	5.33	7.55				
NT2RP4000704	9.94	4.45	4.08	7.72	7.80	6.93	8.9	11.64	11.09				
NT2RP4000710	39.78	22.43	20.25	37.57	42.17	34.47	22.39	29.16	28.71				
NT2RP4000713	3.09	1.40	0.88	3.21	4.08	3.16	3.3	5.18	2.97				
NT2RP4000724	3.53	1.86	1.77	4.48	4.24	3.42	3.25	6.43	3.91				
NT2RP4000725	4.59	2.50	2.14	3.16	3.33	2.21	3.39	4.06	2.51				

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Table 286

NT2RP4000728	21.11	12.54	13.41	26.39	33.93	29.91	18.2	20.00	17.52	*	+		
NT2RP4000737	2.29	1.59	0.36	2.95	3.74	3.56	1.99	4.28	1.59	*	+		
NT2RP4000739	3.68	1.68	1.40	3.64	3.60	3.19	3.01	1.32	2.06				
NT2RP4000749	4.61	2.23	2.17	5.43	5.08	3.32	3.77	2.84	2.99				
NT2RP4000769	4.46	2.77	1.61	5.35	5.75	3.06	3.69	3.92	2.49				
NT2RP4000774	7.04	3.62	4.69	6.48	7.03	5.14	4.99	3.77	3.67				
NT2RP4000781	1.78	1.82	2.45	2.48	1.82	2.08	1.95	1.67	1.08				
NT2RP4000783	5.52	3.48	3.60	5.32	4.17	5.29	1.54	2.21	1.91			*	-
NT2RP4000787	(0.08)	0.27	0.06	0.45	0.09	1.07	0.1	0.13	-0.1				
NT2RP4000788	7.00	4.42	3.89	7.56	7.52	5.50	5.26	4.25	3.66				
NT2RP4000792	9.90	5.45	5.18	4.82	3.85	3.35	2.89	1.10	1.13			*	-
NT2RP4000809	138.97	85.82	100.50	13.12	12.28	11.89	8.69	10.55	11.51	**	-	**	-
NT2RP4000817	6.53	3.13	3.81	7.81	8.21	7.10	5.75	6.24	6.14	*	+		
NT2RP4000821	10.40	5.88	5.97	8.60	9.00	10.24	19.32	14.83	13.61			*	+
NT2RP4000822	7.54	4.48	4.61	11.43	10.03	11.32	7.11	5.54	4.78	**	+		
NT2RP4000823	6.10	4.87	14.52	6.50	4.58	4.69	17.58	17.55	14.17			**	+
NT2RP4000831	4.53	2.70	1.65	4.00	4.27	4.75	3.68	4.83	3.77				
NT2RP4000833	9.98	4.61	3.88	12.93	9.95	9.75	7.85	6.14	9.61				
NT2RP4000837	16.84	7.67	8.19	4.27	7.04	6.55	7.9	6.72	7.63				
NT2RP4000839	8.09	4.28	3.15	6.64	6.35	8.56	6.01	3.49	4.81				
NT2RP4000846	7.97	4.70	3.74	7.70	5.83	5.14	6.12	4.09	4.55				
NT2RP4000848	5.78	2.64	3.11	8.90	6.26	8.65	7.07	7.56	8.46	*	+	*	+
NT2RP4000855	3.22	3.08	1.54	2.41	2.92	2.82	2.82	2.57	2				
NT2RP4000863	3.79	2.50	2.36	1.24	1.67	1.78	2	2.70	1.71				
NT2RP4000865	9.55	7.40	5.94	26.23	26.54	18.52	8.98	8.90	8.56	**	+		
NT2RP4000873	8.88	4.73	4.97	9.82	9.15	8.69	10.43	4.81	6.51				
NT2RP4000874	5.60	3.25	3.18	4.02	6.09	6.60	5.15	3.17	5.54				
NT2RP4000875	10.06	7.69	6.92	10.24	9.60	8.28	5.61	5.34	4.98			*	-
NT2RP4000878	15.02	8.48	6.31	16.61	14.17	15.37	18.42	13.92	17				
NT2RP4000879	1.68	0.79	0.77	1.38	2.21	2.54	2.35	2.03	1.86			*	+
NT2RP4000880	5.88	4.11	3.04	9.39	7.05	7.35	6.97	5.69	5.31	*	+		
NT2RP4000891	102.85	62.84	77.22	114.50	151.60	104.23	43.98	42.97	34.75			*	-
NT2RP4000894	8.78	5.12	4.69	6.91	6.62	9.49	7.97	4.83	7.88				
NT2RP4000898	0.75	1.23	0.33	0.94	1.28	0.69	1.75	1.00	0.58				
NT2RP4000899	14.91	8.73	9.27	8.87	7.17	6.06	2.92	6.91	6.96				
NT2RP4000907	7.23	4.77	4.04	8.01	14.43	8.65	11.43	9.68	10.25			**	+
NT2RP4000908	3.70	3.82	2.81	5.39	5.05	5.27	4.11	5.22	3.41	**	+		
NT2RP4000910	11.95	5.36	6.97	10.03	8.98	9.73	9.64	9.49	7.69				
NT2RP4000918	10.45	8.95	8.11	12.80	9.01	11.75	7.94	8.71	6.88				
NT2RP4000925	1.77	2.18	1.68	2.08	2.56	3.09	1.91	2.37	0.93				
NT2RP4000927	2.00	0.98	0.64	1.21	1.11	1.91	1.67	2.03	0.45				
NT2RP4000928	8.63	5.13	3.60	5.86	6.72	6.51	5.18	4.85	6.75				
NT2RP4000929	1.61	1.10	1.06	1.59	2.36	1.14	0.96	1.23	1.92				
NT2RP4000946	3.91	2.24	2.26	7.89	6.10	6.89	5.7	5.35	4.43	**	+	*	+
NT2RP4000947	1.12	1.54	1.05	1.80	1.82	0.62	1.3	1.55	0.89				
NT2RP4000949	16.12	8.67	10.24	5.88	3.51	5.79	19.02	19.45	15.95				
NT2RP4000955	9.21	5.55	4.76	5.43	4.34	5.39	4.04	4.48	4.02				
NT2RP4000959	16.07	16.16	17.01	17.30	15.74	18.65	13.76	14.61	12.03			*	-
NT2RP4000962	4.28	2.72	4.02	3.76	4.20	2.99	2.02	3.10	1.89				
NT2RP4000973	6.76	3.78	2.61	4.40	5.08	4.18	8.32	7.27	7.89				
NT2RP4000975	4.74	2.41	1.77	5.26	4.90	3.72	2.88	4.71	4.07				
NT2RP4000979	6.80	3.38	3.74	6.77	5.99	3.62	6.11	4.01	4.79				
NT2RP4000984	3.24	3.46	2.61	2.85	2.49	5.25	1.35	3.81	1.22				
NT2RP4000986	3.13	2.19	3.27	2.70	3.05	3.24	3.2	4.03	2.69				
NT2RP4000988	4.24	3.53	3.97	6.52	7.14	6.40	4.03	5.72	2.89	**	+		
NT2RP4000989	4.55	3.53	3.49	5.18	3.51	4.95	4.91	5.46	4.69			*	+

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Table 287

NT2RP4000990	0.91	1.17	0.68	5.32	4.83	4.20	3.51	3.92	3.51	**	+	**	+
NT2RP4000994	6.03	3.61	2.39	2.73	3.58	3.95	4.94	3.50	5.8				
NT2RP4000996	6.29	4.22	3.37	8.35	8.21	4.36	4.41	5.02	6.24				
NT2RP4000997	61.78	21.49	33.43	48.43	44.30	38.85	25.67	23.78	20.69				
NT2RP4001001	5.72	4.90	3.47	5.67	6.31	7.83	5.36	5.68	6.44				
NT2RP4001004	2.47	1.20	1.29	1.66	1.42	2.31	0.88	2.30	2.26				
NT2RP4001006	6.01	3.42	6.46	5.11	3.94	7.35	4.19	4.92	4.66				
NT2RP4001009	8.55	4.50	6.33	9.69	4.66	6.57	7.89	8.50	7.3				
NT2RP4001010	2.33	1.99	3.31	3.50	2.89	4.49	3.41	2.18	2.22				
NT2RP4001013	24.76	12.16	10.77	11.37	8.47	9.68	9.97	7.96	8.93				
NT2RP4001029	12.87	4.18	5.93	5.61	5.98	4.93	3.75	3.75	3.77				
NT2RP4001036	12.25	7.10	7.56	11.16	11.59	9.83	8.7	8.94	6.61				
NT2RP4001041	12.91	6.26	9.00	10.06	7.34	6.55	5.46	5.13	5.26				
NT2RP4001042	19.25	12.69	10.60	14.77	15.99	12.64	7.69	8.09	6.86				
NT2RP4001046	7.12	4.49	4.11	7.61	7.51	8.81	6.32	5.77	5.49				
NT2RP4001050	2.62	1.51	1.21	2.43	2.08	3.36	1.88	2.76	1.6				
NT2RP4001051	6.34	2.77	3.34	9.61	5.53	9.29	3.29	7.15	4.7				
NT2RP4001057	8.53	5.25	3.91	5.29	5.25	3.31	3.9	2.95	5.29				
NT2RP4001063	10.42	5.01	5.86	6.23	5.90	5.66	7.16	6.14	5.17				
NT2RP4001064	8.38	3.24	3.12	6.83	5.16	4.26	7.84	6.40	8.7				
NT2RP4001067	3.31	1.58	2.32	2.67	2.92	2.43	3.23	3.73	3.54				
NT2RP4001078	4.41	2.35	1.43	3.09	2.15	3.81	2.07	3.77	2.39				
NT2RP4001079	3.33	2.47	3.40	5.24	5.12	4.58	4.51	5.49	6.01	**	+	*	+
NT2RP4001080	1.87	1.13	0.72	2.09	1.21	1.64	1.8	2.65	1.93				
NT2RP4001086	6.48	4.50	4.95	6.91	6.12	6.66	5.1	5.61	4.86				
NT2RP4001095	9.39	3.28	2.95	11.12	8.02	6.83	6.4	5.11	6.99				
NT2RP4001098	8.66	3.42	3.13	5.99	6.59	3.50	4.06	3.58	3.83				
NT2RP4001100	15.58	6.86	5.99	15.36	16.25	10.53	11.07	8.66	10.12				
NT2RP4001105	11.53	6.11	5.68	11.42	12.40	12.53	6.82	8.59	7.03				
NT2RP4001110	4.14	2.11	2.03	3.53	3.73	5.22	7.74	9.16	5.7			*	+
NT2RP4001115	8.23	4.76	5.40	7.44	6.61	6.42	6.49	8.54	8.25				
NT2RP4001117	5.86	2.61	3.66	4.84	5.68	5.67	6.82	7.82	11.35				
NT2RP4001122	4.53	2.89	4.44	5.52	5.25	6.14	3.92	5.33	5.22	*	+		
NT2RP4001123	11.03	6.64	4.19	7.23	8.62	6.22	6.52	4.59	7.16				
NT2RP4001126	12.30	8.14	5.35	14.50	10.35	10.40	6.7	7.95	9.08				
NT2RP4001127	2.67	1.52	0.45	2.09	2.22	1.57	1.96	4.17	3				
NT2RP4001138	3.41	2.11	1.63	1.48	2.64	1.74	2.14	3.24	4.17				
NT2RP4001143	6.89	2.21	3.01	4.13	4.68	5.32	4.17	5.67	5.66				
NT2RP4001148	1.94	1.16	1.16	2.70	2.05	0.60	1.41	3.15	1.62				
NT2RP4001149	4.34	2.11	2.80	3.19	3.00	3.41	3.12	4.58	4.05				
NT2RP4001150	4.09	2.84	2.82	5.63	5.48	6.34	4.62	4.61	4.79	**	+	*	+
NT2RP4001159	8.72	3.82	5.00	5.57	8.96	6.80	7.8	6.33	6.38				
NT2RP4001162	3.97	2.49	1.88	3.46	2.36	3.14	3.98	2.29	2.75				
NT2RP4001170	9.81	5.75	5.29	2.68	3.96	2.23	2.4	2.44	1.3			*	-
NT2RP4001174	6.78	5.08	5.60	9.49	9.90	7.92	7.08	5.86	4.66	*	+		
NT2RP4001175	19.07	9.74	10.40	16.34	17.86	15.79	8.78	8.58	11.27				
NT2RP4001176	62.90	39.84	55.63	104.65	115.71	110.77	63.62	58.35	46.85	**	+		
NT2RP4001184	10.39	5.65	5.39	5.95	4.48	5.41	4.76	4.78	4.24				
NT2RP4001198	10.79	4.11	5.82	13.69	9.03	11.21	14.64	14.06	13.84			*	+
NT2RP4001199	2.92	0.71	0.91	2.99	2.97	1.91	3.68	2.25	2.92				
NT2RP4001206	13.96	4.32	7.41	11.41	10.25	10.46	8.73	9.26	10.42				
NT2RP4001207	3.37	2.92	1.08	2.45	1.58	1.84	2.26	2.66	0.61				
NT2RP4001210	2.36	1.47	2.10	3.13	2.39	1.71	1.5	2.49	2.3				
NT2RP4001213	10.44	5.34	6.49	11.64	9.13	13.58	7.15	5.01	5.42				
NT2RP4001214	0.95	1.06	0.59	2.80	1.54	8.36	1.71	2.54	1.49			*	+
NT2RP4001219	2.55	2.66	2.86	4.42	15.66	4.45	5.58	7.03	5.57			**	+

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Table 288

NT2RP4001228	6.93	2.54	3.03	5.28	9.41	5.96	8.24	4.93	8.37				
NT2RP4001235	6.11	4.31	3.21	5.70	5.94	5.25	5.94	4.41	5.1				
NT2RP4001256	4.51	1.77	2.22	4.07	5.11	4.94	4.27	3.05	2.43				
NT2RP4001257	6.40	4.02	2.26	5.05	5.54	3.44	5.95	5.21	4.31				
NT2RP4001260	5.39	3.07	4.18	8.97	9.59	5.62	5.8	6.24	6.64			*	+
NT2RP4001261	14.65	12.44	12.58	14.19	12.55	13.99	17.34	12.10	15.2				
NT2RP4001274	4.71	4.57	4.07	7.45	6.65	6.76	5.26	6.13	6.26	**	+	*	+
NT2RP4001276	15.31	8.46	8.50	10.61	14.38	10.37	11.44	11.39	8.98				
NT2RP4001283	63.21	34.01	32.33	24.21	25.03	19.31	48.06	42.63	46.56				
NT2RP4001299	15.00	9.02	6.78	6.64	8.24	7.13	7.92	6.14	6.14				
NT2RP4001313	3.06	1.56	1.37	2.51	0.89	2.21	1.62	2.23	2.1				
NT2RP4001315	3.67	2.67	2.40	3.95	5.09	3.45	3.89	3.89	4.16				
NT2RP4001320	9.02	4.65	5.15	9.20	8.51	8.68	15.43	12.65	14.49			**	+
NT2RP4001325	12.74	11.37	11.78	16.64	15.36	9.87	12.12	10.53	7.42				
NT2RP4001336	6.40	4.16	5.13	5.38	3.83	5.19	4.39	4.05	2.52				
NT2RP4001339	3.62	2.24	4.32	4.37	4.09	4.92	3.51	4.78	3.43				
NT2RP4001343	8.44	4.63	3.67	7.94	6.79	5.81	5.7	6.09	6.51				
NT2RP4001344	5.76	3.40	4.09	5.03	5.50	6.54	6.12	6.22	5.58				
NT2RP4001345	6.21	3.12	2.61	3.29	6.07	5.15	4.25	4.33	4.38				
NT2RP4001351	11.92	6.04	5.53	9.86	6.47	8.71	6.54	7.28	6.61				
NT2RP4001353	1.80	1.08	1.42	2.16	2.00	2.04	2.15	2.48	2.23	*	+	*	+
NT2RP4001355	2.54	1.08	2.05	2.40	2.01	1.99	2.51	3.62	2.23				
NT2RP4001367	23.22	13.41	17.84	6.30	4.94	5.47	9.28	11.30	7.57	*	-	*	-
NT2RP4001372	5.35	2.77	2.56	3.34	4.53	3.59	4.57	5.24	5.57				
NT2RP4001373	10.60	5.25	4.77	8.11	9.86	9.53	6.1	5.34	6.98				
NT2RP4001375	5.11	3.33	2.60	2.66	4.56	3.81	2.85	3.42	3.31				
NT2RP4001379	3.86	2.14	2.09	2.83	2.70	4.72	3.26	3.43	2.58				
NT2RP4001381	8.37	5.24	5.75	10.66	11.10	10.55	6.09	7.62	6.54	*	+		
NT2RP4001386	3.36	2.18	2.25	6.41	4.78	6.49	3.68	5.89	3.24	**	+		
NT2RP4001389	10.33	5.90	8.63	13.74	8.10	10.59	13.58	10.92	11.95				
NT2RP4001396	1.51	0.17	0.39	1.10	1.45	1.19	1.43	2.48	0.52				
NT2RP4001407	2.74	1.02	1.62	3.87	3.78	1.98	2.72	2.67	1.52				
NT2RP4001409	7.90	3.42	3.68	8.04	5.25	6.08	3.89	2.35	3.87				
NT2RP4001410	41.71	16.67	20.24	29.88	31.04	31.69	28.88	20.00	22.74				
NT2RP4001414	11.73	6.50	5.48	10.69	11.38	10.17	10.68	8.69	10.89				
NT2RP4001424	3.25	2.51	1.43	4.18	3.70	4.01	2.5	5.15	3.66	*	+		
NT2RP4001433	10.93	1.50	1.13	15.16	15.56	3.13	10.41	4.52	7				
NT2RP4001438	8.06	6.23	6.43	14.12	10.57	11.39	6.77	9.65	7.69	*	+		
NT2RP4001442	5.25	2.76	3.72	6.62	2.55	2.88	2.74	3.33	2.46				
NT2RP4001447	1.94	1.07	2.00	4.12	2.36	3.98	1.68	3.22	0.71	*	+		
NT2RP4001466	13.13	5.79	4.82	7.69	5.30	6.70	2.91	4.53	3.9				
NT2RP4001467	4.50	1.22	1.33	0.82	1.55	1.40	3.66	4.13	3.7				
NT2RP4001472	4.77	3.08	3.33	7.29	7.84	10.23	7.79	8.21	9.21	*	+	**	+
NT2RP4001474	2.86	1.72	1.90	2.18	3.93	2.05	1.94	3.80	3.06				
NT2RP4001483	2.29	1.49	1.84	3.04	2.50	2.14	2.24	3.68	2.54				
NT2RP4001488	5.16	2.65	2.75	5.33	5.10	5.16	4.15	4.07	6.19				
NT2RP4001492	5.93	3.30	2.87	5.58	3.40	4.66	3.78	4.60	5.29				
NT2RP4001498	2.17	1.63	1.33	2.59	1.07	2.19	2.61	1.92	1.74				
NT2RP4001502	36.00	12.08	15.43	15.15	11.96	14.06	11.15	10.06	10.33				
NT2RP4001503	12.74	6.75	6.97	11.88	9.69	8.87	5.71	4.79	6.02				
NT2RP4001507	5.29	3.55	4.09	6.91	8.58	5.74	3.85	4.47	6.06	*	+		
NT2RP4001510	9.01	6.05	7.69	15.28	11.96	14.90	7.45	6.33	7.03	**	+		
NT2RP4001516	6.51	3.15	3.51	3.57	3.42	3.81	3.63	4.76	4.46				
NT2RP4001520	26.12	11.82	16.11	17.96	13.99	17.71	16.8	15.23	12.31				
NT2RP4001523	3.37	1.82	2.58	4.23	3.77	4.26	2.29	4.88	4.21	*	+		
NT2RP4001524	11.16	7.76	6.79	8.80	7.75	9.91	6.38	9.28	5.14				

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Table 289

NT2RP4001529	9.24	4.27	3.42	3.66	4.21	3.95	6.65	3.78	5.28				
NT2RP4001531	7.58	4.22	3.87	4.40	6.79	5.07	4.85	4.25	5.33				
NT2RP4001546	27.96	14.34	13.14	33.50	26.35	22.36	39.72	37.62	23.88				
NT2RP4001547	5.16	3.87	3.59	6.27	5.81	5.41	6.77	5.69	7.74	*	+	*	+
NT2RP4001551	4.66	2.25	2.91	1.72	2.50	2.23	1.06	2.31	2.02				
NT2RP4001555	2.63	1.70	1.48	1.84	1.34	1.78	3.29	2.29	1.99				
NT2RP4001567	4.17	2.21	3.48	5.17	4.12	2.97	3.53	3.55	4.6				
NT2RP4001568	24.66	11.55	19.71	26.48	16.71	27.97	21.61	20.91	21.83				
NT2RP4001569	13.23	7.51	6.17	8.88	7.94	7.65	6.86	6.56	7.44				
NT2RP4001571	3.88	2.14	1.80	4.74	3.69	4.71	3.97	5.20	7.86				
NT2RP4001574	8.96	4.84	4.26	8.19	9.78	5.65	6.26	6.22	8.16				
NT2RP4001575	8.04	4.77	3.76	6.08	7.50	5.82	4.63	5.56	5.85				
NT2RP4001578	11.18	4.73	6.33	7.50	4.87	4.81	7.41	8.00	7.35				
NT2RP4001592	9.35	5.87	4.90	5.95	6.70	4.56	3.37	8.97	5.41				
NT2RP4001593	6.28	4.83	5.72	9.71	12.44	12.90	7.66	7.56	6.44	**	+	*	+
NT2RP4001605	4.40	2.61	3.07	7.26	7.76	5.64	5.16	7.35	8.18	*	+	*	+
NT2RP4001606	13.15	5.10	4.06	9.17	7.65	6.75	3.7	4.31	6.28				
NT2RP4001607	3.47	1.57	1.29	3.76	4.78	2.65	1.67	3.06	4.34				
NT2RP4001610	4.08	2.08	1.47	3.77	3.73	2.68	2.34	4.35	2.92				
NT2RP4001614	2.75	1.07	1.10	2.96	1.97	1.29	2.18	3.56	3.15				
NT2RP4001623	3.08	1.60	1.52	2.58	2.94	2.80	1.24	3.23	2.34				
NT2RP4001626	19.42	15.83	18.19	15.38	17.59	13.04	1.75	4.18	2.95			**	-
NT2RP4001634	4.38	2.77	2.43	4.92	4.36	4.52	1.82	3.51	2.53				
NT2RP4001638	2.68	1.70	0.84	1.98	2.75	2.80	1.64	3.48	1.26				
NT2RP4001644	3.61	2.50	2.30	4.35	3.54	2.45	4.35	2.84	4.05				
NT2RP4001646	20.39	11.21	10.21	30.98	19.98	25.17	21.75	14.88	9.56				
NT2RP4001656	6.55	3.72	4.64	5.20	5.23	4.49	4.29	3.23	2.79				
NT2RP4001666	5.11	3.28	3.35	4.54	4.56	3.95	3.53	3.52	3.5				
NT2RP4001670	7.31	3.77	5.28	4.59	6.96	4.67	4.23	4.15	4.55				
NT2RP4001677	16.68	12.12	14.19	29.06	40.57	32.81	33.86	36.13	36.39	**	+	**	+
NT2RP4001679	11.61	4.52	5.94	19.33	14.25	14.99	8.64	9.90	7.91	*	+		
NT2RP4001695	20.41	7.98	11.64	19.72	19.63	15.23	7.89	9.75	7.32				
NT2RP4001696	6.64	4.27	3.64	4.33	3.58	5.85	4.75	3.99	3.79				
NT2RP4001699	1.63	1.58	0.71	2.91	1.63	2.15	3.74	2.30	2.42				
NT2RP4001717	5.33	4.49	3.61	5.92	6.26	5.39	5.73	6.49	5.79				
NT2RP4001719	3.81	3.40	2.34	4.26	2.94	3.04	4.14	3.43	2.54				
NT2RP4001725	4.09	3.08	1.88	3.37	4.40	3.86	2.62	4.74	3.15				
NT2RP4001726	4.90	3.18	3.91	4.82	4.39	4.14	4.14	5.24	5.01				
NT2RP4001730	0.78	0.69	0.71	1.42	1.12	2.01	0.61	1.16	0.59	*	+		
NT2RP4001739	4.83	2.71	3.87	5.22	3.09	4.63	4.39	5.41	4.57				
NT2RP4001741	10.82	7.34	4.37	12.44	9.41	10.54	7.99	6.39	5.79				
NT2RP4001753	11.73	4.55	5.91	14.42	16.38	12.01	9.64	6.92	8.76				
NT2RP4001760	12.48	7.93	6.76	6.21	7.16	7.70	2.14	2.05	1.86			*	-
NT2RP4001787	45.15	35.87	34.25	46.58	51.77	52.14	19.69	24.09	19.41	*	+	**	-
NT2RP4001790	6.06	3.59	2.88	5.91	6.74	7.08	5.5	5.13	5.27				
NT2RP4001795	25.43	15.84	22.47	18.33	17.56	16.99	11.05	11.79	10.2			*	-
NT2RP4001803	3.51	2.55	1.55	5.77	4.36	4.15	4.43	4.25	2.97	*	+		
NT2RP4001805	4.04	2.46	2.43	5.53	4.54	4.71	3.91	2.59	3.66	*	+		
NT2RP4001809	14.99	9.07	7.27	11.92	10.72	9.25	11.36	11.25	11.16				
NT2RP4001817	16.10	8.59	7.80	8.81	9.92	9.75	5.74	6.19	5.7				
NT2RP4001822	9.90	6.09	4.79	7.82	4.55	6.51	6.73	5.44	6.61				
NT2RP4001823	1.63	1.96	0.82	1.62	2.17	1.74	1.56	1.67	0.88				
NT2RP4001827	5.09	4.68	4.45	4.54	5.32	5.79	7.53	6.64	8.76			*	+
NT2RP4001828	17.04	10.89	10.46	15.89	15.47	13.14	13.38	12.00	9.76				
NT2RP4001836	5.07	3.08	3.80	4.72	5.04	5.75	5.07	4.56	2.8				
NT2RP4001838	6.83	3.89	5.07	5.21	5.01	6.41	4.27	6.56	2.85				

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Table 290

NT2RP4001841	5.15	2.19	2.44	6.33	5.75	3.95	4.94	4.03	3.03				
NT2RP4001849	4.08	2.37	1.90	1.96	2.08	2.74	2.12	3.59	2.22				
NT2RP4001861	19.55	11.05	8.48	18.06	19.21	17.61	12.49	10.31	10.34				
NT2RP4001877	18.38	12.98	11.71	13.65	17.92	15.26	10.17	11.03	9.86				
NT2RP4001879	6.00	4.86	5.20	4.62	6.88	7.55	4.96	6.52	5.75				
NT2RP4001889	3.83	2.48	2.26	4.36	5.15	5.12	3.39	5.09	3.84	*	+		
NT2RP4001893	4.85	2.58	3.31	5.78	4.46	6.55	5.02	4.75	1.96				
NT2RP4001896	4.86	2.86	3.13	4.46	5.44	4.95	3.44	3.93	1.91				
NT2RP4001898	12.63	7.18	6.38	11.85	13.48	14.72	8.27	7.05	8.92				
NT2RP4001901	9.37	5.10	4.58	7.22	7.41	7.58	5.92	5.84	4.25				
NT2RP4001910	44.22	14.42	25.27	36.18	28.56	31.03	15.44	16.11	13.43				
NT2RP4001925	6.01	3.53	4.07	7.13	8.88	6.52	5.38	5.68	3.89	*	+		
NT2RP4001926	5.02	2.32	4.10	6.70	3.01	7.01	3.35	4.83	1.34				
NT2RP4001927	7.81	3.22	8.37	2.90	3.77	4.75	2.11	3.46	2.61				
NT2RP4001931	12.13	7.10	9.23	9.30	11.80	10.57	7.09	9.58	5.89				
NT2RP4001933	7.27	5.93	8.24	33.37	26.48	21.53	12.07	15.48	9.59	**	+	*	+
NT2RP4001938	11.79	6.36	5.51	7.00	8.59	7.23	7.68	7.54	9.66				
NT2RP4001942	19.13	10.55	10.00	11.76	13.07	12.47	8.35	7.90	8.71				
NT2RP4001945	3.39	2.16	1.75	1.10	2.83	1.75	3.88	3.65	3.03				
NT2RP4001946	2.78	2.76	2.10	6.68	5.62	8.03	3.2	4.28	3.28	**	+		
NT2RP4001947	0.70	0.50	0.71	3.55	3.12	4.05	1.69	2.42	0.29	**	+		
NT2RP4001950	52.07	29.14	30.34	3.90	3.31	3.63	2.85	3.53	3.23	*	-	*	-
NT2RP4001953	6.50	3.60	5.67	12.09	12.07	9.95	5.86	6.12	3.31	**	+		
NT2RP4001966	3.87	2.06	1.81	2.93	2.33	3.06	2.56	3.55	1.61				
NT2RP4001970	18.77	7.73	6.33	7.39	9.12	8.12	6.83	7.05	6.87				
NT2RP4001975	16.12	8.35	8.50	16.73	14.58	16.13	21.64	17.08	14.87				
NT2RP4001988	6.11	2.52	2.36	2.17	2.97	2.42	4.05	5.29	6.8				
NT2RP4001996	8.88	6.41	7.06	5.35	6.06	5.33	4.86	5.72	5.5				
NT2RP4002014	5.46	3.70	3.51	5.82	4.28	3.92	5.71	6.94	6.45			*	+
NT2RP4002018	4.51	3.12	2.83	6.79	4.88	5.98	4.66	10.23	5.14	*	+		
NT2RP4002035	6.12	4.46	6.67	7.19	6.57	6.76	5.8	5.73	6.32				
NT2RP4002043	17.40	10.99	15.66	15.62	10.19	12.89	8.93	9.28	8.15			*	-
NT2RP4002046	6.17	4.77	3.90	3.50	9.38	4.20	6.26	5.07	7.72				
NT2RP4002047	14.83	7.78	9.72	12.74	11.88	9.86	4.4	4.88	5.22			*	-
NT2RP4002052	3.82	2.22	2.36	3.72	2.89	4.12	4.34	4.20	5.03			*	+
NT2RP4002056	55.72	38.98	47.46	51.12	52.01	41.19	44.9	38.97	37.38				
NT2RP4002057	17.74	8.34	10.35	10.25	6.84	10.23	9.46	9.43	9				
NT2RP4002058	5.05	3.72	3.60	3.34	2.84	3.35	3.74	3.86	2.96				
NT2RP4002064	2.43	1.64	1.15	2.53	2.72	2.44	2.13	3.96	2.74				
NT2RP4002071	6.91	5.83	6.59	9.94	11.45	10.50	6.83	7.79	5.44	**	+		
NT2RP4002075	5.65	2.21	2.77	1.76	1.64	2.01	1.03	0.80	1.27				
NT2RP4002078	12.20	5.57	6.28	21.16	11.84	9.58	9.34	5.65	7.44				
NT2RP4002081	8.20	4.41	4.38	8.71	5.52	5.98	8.56	5.96	6.86				
NT2RP4002083	1.41	0.64	0.77	1.12	0.92	0.88	1.16	1.92	2.62				
NT2RP4002099	3.50	1.74	2.24	2.98	2.94	2.77	2.69	3.45	2.97				
NT2RP4002106	16.08	11.97	16.65	14.50	11.42	13.37	8.7	8.53	7.16			*	-
NT2RP4002111	14.95	7.66	10.77	13.64	14.70	14.45	16.75	17.55	15.81				
NT2RP4002112	5.99	2.81	3.54	4.57	5.85	6.57	6.12	5.13	4.94				
NT2RP4002116	14.14	7.04	5.48	14.30	12.58	11.93	8.14	4.91	6.09				
NT2RP4002122	15.83	9.46	8.25	6.72	6.57	5.28	1.63	2.27	1.64			*	-
NT2RP4002126	7.11	2.89	3.58	2.17	3.83	2.41	4.77	4.31	5.35				
NT2RP4002133	10.15	4.28	5.52	6.19	8.16	5.73	5.02	6.44	4.79				
NT2RP4002136	13.83	8.55	8.39	5.76	6.14	5.01	5.63	5.28	4.82			*	-
NT2RP4002139	25.38	27.01	30.04	25.35	29.41	24.98	13.23	24.52	19.91				
NT2RP4002174	3.31	1.15	2.46	3.71	3.16	4.15	3.14	5.41	4.47				
NT2RP4002185	10.77	7.55	7.67	15.20	13.59	13.41	10.77	8.24	8.8	*	+		

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Table 291

NT2RP4002186	24.35	16.62	12.92	73.40	68.88	51.66	18.99	20.53	42.77	**	+		
NT2RP4002187	16.88	9.15	8.08	13.25	18.23	17.99	14.62	13.98	23.37				
NT2RP4002188	9.49	5.18	4.64	14.32	14.99	9.78	4.92	6.78	9.43	*	+		
NT2RP4002199	3.33	0.85	1.71	2.01	2.76	1.40	1.46	4.34	2.92				
NT2RP4002206	7.79	3.61	3.56	5.56	5.23	3.75	3.53	5.24	4.66				
NT2RP4002210	3.95	1.94	2.05	3.42	2.86	2.32	2.13	4.76	2.28				
NT2RP4002222	4.87	2.50	3.89	4.48	5.59	3.24	4.1	4.89	3.82				
NT2RP4002241	10.39	8.75	9.34	8.11	10.75	7.80	3.37	5.39	6.12			**	-
NT2RP4002248	5.75	3.15	2.68	4.58	3.49	3.31	6.08	4.55	3.57				
NT2RP4002250	2.77	1.28	0.36	1.28	1.49	1.07	2.02	0.58	1.13				
NT2RP4002259	11.44	4.70	6.93	10.37	10.26	7.96	6.18	7.00	6.72				
NT2RP4002268	9.49	7.15	6.70	7.16	8.97	8.79	12.35	10.44	12.35			*	+
NT2RP4002288	23.22	15.06	19.08	20.88	28.68	23.53	20.32	17.25	20.1				
NT2RP4002290	9.48	5.25	5.05	15.46	15.55	18.46	13.55	11.18	12.37	**	+	*	+
NT2RP4002298	5.94	3.63	4.51	10.11	6.35	12.09	3.11	5.17	4.75				
NT2RP4002306	5.29	2.43	3.39	8.59	7.82	9.25	3.86	4.05	3.61	**	+		
NT2RP4002308	2.50	1.35	1.43	1.70	2.93	1.47	2.72	1.97	2.14				
NT2RP4002336	9.03	4.10	4.50	6.72	4.54	7.26	5.89	4.31	4.91				
NT2RP4002340	0.95	0.34	0.60	0.63	0.88	0.24	1.51	1.53	0.76				
NT2RP4002361	3.28	2.38	1.78	3.90	2.34	2.47	2.23	2.16	1.92				
NT2RP4002367	3.30	2.19	1.54	3.77	4.95	3.32	2.84	2.25	3				
NT2RP4002368	4.21	2.40	3.66	5.83	4.14	3.92	5.91	4.62	3.42				
NT2RP4002377	3.62	4.26	2.84	5.85	2.38	5.20	4.75	3.54	3.33				
NT2RP4002408	29.46	20.49	24.43	3.81	2.37	2.48	1.32	0.66	1.06	**	-	**	-
NT2RP4002425	1.74	1.67	0.75	1.77	1.60	1.39	2.92	1.48	1.25				
NT2RP4002432	8.35	5.60	3.82	5.76	5.85	4.41	8.08	6.14	6.6				
NT2RP4002447	9.10	3.90	3.22	12.78	11.88	10.40	5.91	5.47	6.48	*	+		
NT2RP4002451	2.21	2.30	1.71	3.91	4.29	3.31	5.98	6.15	6.01	**	+	**	+
NT2RP4002461	7.09	5.26	5.72	12.39	9.75	9.13	7.77	8.39	7.06	*	+		
NT2RP4002486	5.84	4.56	5.50	5.14	5.35	4.72	7.44	6.30	6.54			*	+
NT2RP4002517	3.21	2.30	2.48	3.27	2.89	3.72	3.06	3.47	2.44				
NT2RP4002556	10.73	5.00	5.11	11.36	8.97	7.80	4.9	4.20	4.51				
NT2RP4002569	5.60	3.78	2.56	4.11	4.44	3.67	5.29	5.70	3.72				
NT2RP4002587	2.41	1.81	1.87	2.59	3.67	3.36	7.6	6.60	7.95	*	+	**	+
NT2RP4002591	7.42	6.05	5.29	12.68	12.07	10.38	7.78	4.95	7.6	**	+		
NT2RP4002607	6.11	2.67	2.59	6.08	4.47	5.73	3.49	4.31	2.91				
NT2RP4002627	5.30	4.31	4.08	5.45	8.00	6.98	9.55	7.80	7.44			**	+
NT2RP4002628	13.62	7.50	7.90	12.59	11.82	9.24	5.81	7.23	4.46				
NT2RP4002630	3.81	2.47	2.90	6.00	2.15	4.82	6.13	6.96	4.18			*	+
NT2RP4002639	4.77	2.18	3.85	2.27	2.26	2.48	1.79	3.34	1.18				
NT2RP4002641	8.72	3.54	3.33	4.53	5.23	4.41	5.45	5.35	8.22				
NT2RP4002658	39.52	16.53	21.90	10.69	10.22	8.63	12.92	12.25	13.09				
NT2RP4002669	8.68	5.48	3.61	6.49	4.90	5.66	4.3	4.66	5.21				
NT2RP4002677	11.90	7.10	10.78	11.62	13.84	10.32	4.5	5.32	4.63			*	-
NT2RP4002715	6.49	4.85	5.45	16.06	11.33	12.78	11.52	13.89	13.89	**	+	**	+
NT2RP4002750	11.19	4.76	5.94	4.82	3.94	4.94	3.86	3.11	3.58				
NT2RP4002784	5.22	3.74	4.33	6.90	5.66	7.76	7.61	4.05	3.39	*	+		
NT2RP4002791	2.32	2.02	2.01	4.89	4.01	4.73	3.62	3.85	2.33	**	+		
NT2RP4002811	6.07	3.91	2.96	1.95	3.45	3.30	4.41	5.24	4.51				
NT2RP4002830	11.00	4.98	5.60	10.88	8.44	6.08	6.46	6.96	4.35				
NT2RP4002832	2.65	2.09	2.28	3.38	2.40	2.76	1.95	3.23	1.27				
NT2RP4002850	10.22	7.64	6.28	14.24	10.59	11.13	9.28	9.04	5.75				
NT2RP4002874	3.50	2.69	1.87	3.65	3.03	4.18	3.78	5.05	2.68				
NT2RP4002884	17.66	6.25	9.46	10.83	9.85	8.92	15.05	14.77	10.31				
NT2RP4002888	20.83	12.71	14.10	15.29	12.54	11.78	19.91	18.79	15.14				
NT2RP4002891	6.49	3.33	5.04	17.64	15.92	12.46	8.11	7.56	7.35	**	+	*	+

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Table 292

NT2RP4002894	30.47	15.42	16.30	15.33	13.44	13.63	14.61	7.84	11.34				
NT2RP4002896	5.01	2.57	1.03	5.77	4.90	3.35	4.85	5.20	6.5				
NT2RP4002905	3.65	2.18	2.47	3.73	2.63	3.46	2.67	3.64	2.22				
NT2RP4002907	6.79	1.23	2.84	16.01	14.42	10.02	12.06	10.10	6.54	*	+		
NT2RP5003459	65.35	36.44	48.17	27.67	30.09	25.05	9.64	20.91	22.09			*	-
NT2RP5003461	4.58	3.60	3.17	6.87	4.80	7.46	3.05	4.17	2.86	*	+		
NT2RP5003471	5.96	3.26	3.68	5.59	5.78	6.38	36.49	36.45	36.48			**	+
NT2RP5003477	4.19	2.26	3.16	4.58	5.06	6.58	6.46	4.38	3.4				
NT2RP5003487	220.55	93.22	98.28	181.60	187.80	154.38	86.45	85.87	93.23				
NT2RP5003492	7.41	4.46	3.61	6.80	6.09	7.24	6.01	5.67	4.83				
NT2RP5003500	3.73	2.01	1.80	4.33	3.62	5.68	2.91	3.93	3.14				
NT2RP5003506	9.63	4.24	5.17	6.58	8.38	7.49	5.4	7.54	7.66				
NT2RP5003512	2.05	1.82	0.90	1.93	2.76	1.89	1.76	3.04	2.68				
NT2RP5003522	5.00	3.31	4.09	6.05	5.02	4.70	4.69	4.96	3.11		-		
NT2RP5003524	2.66	1.03	1.85	3.05	3.14	2.14	2.01	1.80	0.86				
NT2RP5003527	27.32	17.39	28.11	33.15	29.19	33.15	34.18	28.33	30.99	*	+	*	+
NT2RP5003531	6.09	4.05	3.52	14.63	15.87	11.17	18.91	10.15	13.33	**	+	*	+
NT2RP5003534	4.69	3.24	2.48	4.56	5.46	3.21	3.85	3.74	4.1				
NT2RP6000020	14.93	5.50	7.94	19.43	12.24	14.47	28	17.69	22.01			*	+
NT2RP6000022	2.09	1.92	1.10	2.89	3.69	3.48	1.85	3.95	3.04	*	+		
NT2RP6000050	6.72	2.85	2.69	5.15	4.13	6.91	3.13	4.74	4.15				
NT2RP6000063	4.32	1.86	2.74	4.12	3.95	5.49	4.77	5.84	5.17			*	+
NT2RP6000074	7.65	3.63	3.82	5.82	4.62	5.47	3.91	5.25	4.12				
NT2RP6000083	7.65	4.46	4.22	5.62	7.05	9.12	4.96	6.80	6.49				
NT2RP6000100	8.20	3.69	3.69	11.31	10.03	10.20	5.69	6.11	4.22	*	+		
NT2RP6000123	8.42	4.03	3.87	7.40	6.54	4.76	5.08	5.14	4.33				
NT2RP6000129	5.14	2.45	3.11	3.95	4.30	4.21	3.96	4.16	4.57				
NT2RP6000147	3.79	2.50	3.26	15.24	15.27	11.86	26.48	14.22	25.1	**	+	**	+
NT2RP6000163	1.43	1.14	1.15	3.25	1.30	2.00	1.02	2.54	1.73				
NT2RP6000181	7.19	4.67	4.25	6.16	6.80	4.73	6.67	5.10	6.2				
NT2RP6000182	5.25	3.12	3.43	5.76	4.23	7.79	3.45	3.70	2.44				
OVARC1000001	4.47	2.05	2.92	5.01	4.27	3.71	5.92	4.78	4.37				
OVARC1000003	4.03	2.27	2.17	3.53	4.26	1.98	1.87	2.81	4.16				
OVARC1000004	69.94	45.81	40.28	31.28	33.52	34.13	14.2	20.99	22.91			*	-
OVARC1000006	2.75	1.60	1.91	3.55	3.17	2.27	3.59	3.71	3.52			*	+
OVARC1000013	3.58	2.31	1.87	3.88	4.15	3.20	3.52	4.55	2.95				
OVARC1000014	5.72	2.95	3.69	6.24	6.32	5.61	4.07	4.99	4.34				
OVARC1000017	6.14	3.05	3.33	4.90	5.12	5.05	3.15	5.17	5.31				
OVARC1000026	55.69	36.49	45.68	51.02	60.13	48.46	28.42	36.95	25.22				
OVARC1000035	9.77	8.46	8.93	13.12	14.00	9.30	7.02	5.89	5.3			**	-
OVARC1000037	31.27	16.99	12.47	49.92	39.93	32.59	18.22	25.08	32.08				
OVARC1000058	10.77	5.52	3.11	12.87	13.32	13.63	6.74	5.82	8.66	*	+		
OVARC1000060	3.24	1.54	1.26	3.04	2.70	2.45	2.09	2.66	3.05				
OVARC1000068	2.38	1.15	1.10	3.07	2.77	1.87	1.01	3.23	1.66				
OVARC1000069	4.64	2.24	2.58	7.95	8.04	5.29	4.94	7.33	5.21	*	+		
OVARC1000071	4.18	2.24	2.19	3.21	4.19	2.93	1.32	4.38	1.25				
OVARC1000075	116.66	59.06	70.03	104.67	109.44	102.05	127.1	180.67	194.9			*	+
OVARC1000083	16.13	9.03	10.85	16.27	15.52	17.85	9.32	13.62	11.15				
OVARC1000085	90.31	52.35	57.44	84.93	91.25	74.75	46.89	55.51	55.51				
OVARC1000086	3.63	2.07	4.18	7.09	7.77	8.13	5.87	6.77	6.77	**	+	*	+
OVARC1000087	2.46	0.70	0.93	1.65	1.80	2.44	2.22	3.58	3.58				
OVARC1000090	7.22	4.69	6.24	15.64	14.18	15.90	5.67	9.11	9.11	**	+		
OVARC1000091	3.66	1.42	2.09	5.7	4.57	5.66	4.01	3.77	3.77	*	+		
OVARC1000092	3.91	1.98	2.18	6.09	6.36	8.26	4.35	4.86	4.86	*	+	*	+
OVARC1000105	11.95	8.25	9.35	12.3	11.58	13.87	6.66	8.05	8.05				
OVARC1000106	23.29	10.32	10.91	20.75	17.39	12.69	12.13	18.29	18.29				

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Table 293

OVARC1000109	10.73	4.48	6.00	9.44	8.48	8.37	6.70	8.07	8.07				
OVARC1000113	4.43	3.28	2.32	5.28	7.68	6.28	3.04	3.01	3.01	*	+		
OVARC1000114	4.61	1.82	2.98	6.68	7.59	8.77	4.82	5.56	5.56	*	+		
OVARC1000133	2.28	0.62	2.11	1.97	3.23	1.32	1.31	3.42	3.42				
OVARC1000137	7.57	3.31	3.78	7.45	5.45	6.40	5.03	9.51	9.51				
OVARC1000139	8.5	5.04	5.90	7.42	5.19	7.20	5.43	7.04	7.04				
OVARC1000145	1.66	0.51	1.26	2.03	2.15	2.60	1.95	1.96	1.96	*	+		
OVARC1000148	13.99	5.79	5.64	16.54	19.40	9.14	7.33	8.83	8.83				
OVARC1000151	5.62	2.25	3.47	4.79	5.94	4.15	4.17	6.14	6.14				
OVARC1000157	5.78	3.92	3.63	20.18	23.53	19.12	7.05	10.69	10.69	**	+	*	+
OVARC1000162	1.04	0.27	1.30	1.82	2.05	0.82	1.71	1.67	1.67				
OVARC1000168	6.93	3.43	5.38	9.14	7.70	8.50	5.44	8.50	8.5	*	+		
OVARC1000169	20.78	9.01	10.52	18.85	14.31	18.81	15.67	26.42	26.42				
OVARC1000178	6.27	4.19	5.21	6.05	5.93	6.06	4.30	5.93	5.93				
OVARC1000182	1.08	0.33	0.60	3.18	1.53	2.07	1.58	1.16	1.16	*	+		
OVARC1000186	11.87	6.09	4.34	4.72	8.03	4.57	4.49	8.00	8				
OVARC1000188	6.88	3.30	4.11	6.26	4.11	4.48	4.18	5.80	5.8				
OVARC1000191	2.39	0.93	1.25	1.87	4.24	1.53	1.02	3.43	3.43				
OVARC1000198	7.48	2.50	4.22	12.55	13.51	9.27	4.79	6.14	6.14	*	+		
OVARC1000208	7.66	5.85	6.85	11.11	11.76	10.78	8.71	6.63	6.63	**	+		
OVARC1000209	5.19	2.21	3.10	4.98	5.19	3.99	3.67	6.12	6.12				
OVARC1000212	7.76	3.64	5.91	6.62	4.86	7.78	4.09	6.97	6.97				
OVARC1000216	1.71	1.54	1.80	2.95	1.87	2.06	1.88	2.20	2.2			*	+
OVARC1000240	9.19	4.82	3.93	10.89	11.55	7.32	4.66	6.08	6.08				
OVARC1000241	8.4	2.88	3.50	6.97	5.95	3.69	4.83	5.66	5.66				
OVARC1000249	5.89	2.71	3.55	5.91	5.26	3.50	4.13	5.08	5.08				
OVARC1000254	16.05	11.01	13.12	50.15	59.76	29.83	42.38	33.82	33.82	*	+	**	+
OVARC1000255	5.5	3.14	2.99	5.45	4.17	3.19	3.91	4.30	4.3				
OVARC1000267	8.95	5.90	5.53	9.61	7.91	10.70	8.96	10.59	10.59				
OVARC1000275	0.38	0.28	0.65	1.7	1.69	1.90	10.31	9.09	9.09	**	+	**	+
OVARC1000287	2.16	1.07	1.61	5.38	6.97	4.90	26.09	33.14	33.14	**	+	**	+
OVARC1000288	7.99	3.43	4.43	6.36	6.18	3.91	4.34	4.81	4.81				
OVARC1000298	8.86	6.47	4.36	11.32	12.55	7.25	6.14	7.12	7.12				
OVARC1000302	3.96	1.75	1.50	3.75	4.71	3.28	2.04	3.19	3.19				
OVARC1000304	6.08	4.82	3.98	7.97	7.57	5.26	4.58	6.93	6.93				
OVARC1000307	5.1	1.95	3.30	4.25	2.68	4.18	3.69	3.54	3.54				
OVARC1000309	6.17	3.11	3.95	6.94	5.55	4.98	5.49	5.61	5.61				
OVARC1000312	4.47	2.31	2.62	3.43	3.39	3.03	5.14	4.44	4.44				
OVARC1000313	7.23	3.04	5.41	6.92	6.31	4.37	7.31	10.70	10.7				
OVARC1000321	8.81	5.88	6.66	13.97	15.87	13.56	14.26	12.53	12.53	**	+	**	+
OVARC1000326	3.94	3.57	2.28	3.59	3.18	3.94	3.62	3.71	3.71				
OVARC1000327	4.66	2.13	3.59	7.38	4.82	4.34	3.97	5.68	5.68				
OVARC1000331	6.82	4.80	4.04	7.15	6.72	8.39	4.61	6.40	6.4				
OVARC1000335	5.22	3.45	3.68	6.19	5.78	6.01	4.99	5.32	5.32	*	+		
OVARC1000347	2.86	2.21	1.39	1.74	2.06	3.33	1.79	3.03	3.03				
OVARC1000348	7.01	4.29	4.68	13.43	12.42	16.47	7.65	8.17	8.17	**	+	*	+
OVARC1000363	4.22	3.97	3.08	6.15	6.28	7.74	2.83	4.38	4.38	**	+		
OVARC1000377	2.82	1.76	1.53	3.08	2.53	1.71	0.35	2.23	2.23				
OVARC1000382	5.76	1.98	3.91	4.79	5.06	3.60	4.10	6.90	6.9				
OVARC1000384	6.02	5.30	4.11	6.76	8.20	10.33	8.85	9.44	9.44	*	+	**	+
OVARC1000401	2.8	1.75	1.96	2.86	2.28	2.89	2.67	3.48	3.48				
OVARC1000406	114.78	80.20	88.37	88.01	73.54	119.34	90.62	95.77	95.77				
OVARC1000407	4.6	3.44	3.17	5.58	5.61	8.84	5.08	4.38	4.38				
OVARC1000408	16.3	13.53	12.64	45.51	42.22	49.78	26.85	32.12	32.12	**	+	**	+
VARC1000410	6.71	4.55	5.34	4.6	7.22	6.74	6.55	6.11	6.11				
OVARC1000411	3.32	1.84	2.60	3.91	7.15	2.94	1.78	2.39	2.39				

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Table 294

OVARC1000414	2.94	2.41	3.01	5.83	4.82	5.60	3.16	3.78	3.78	**	+	*	+
OVARC1000420	11.4	6.17	7.59	9.95	9.38	10.06	10.09	13.16	13.16				
OVARC1000421	8.6	6.78	5.53	8.33	7.86	10.75	8.17	6.59	6.59				
OVARC1000427	3.68	2.71	4.36	3.26	4.27	4.49	3.23	3.96	3.96				
OVARC1000431	28.24	22.85	26.14	17.5	18.78	21.85	14.12	15.50	15.5	*	-	**	-
OVARC1000437	4.74	2.97	4.16	5.12	6.15	7.20	4.22	6.60	6.6				
OVARC1000439	7.31	6.90	5.38	7.44	6.69	8.00	6.48	4.83	4.83				
OVARC1000440	10.79	6.84	6.93	7.88	7.24	7.80	6.48	7.22	7.22				
OVARC1000442	5.47	3.48	2.90	10.37	8.05	7.61	4.21	5.71	5.71	*	+		
OVARC1000443	2.37	1.87	2.77	3.52	3.55	4.55	2.82	6.19	6.19	*	+		
OVARC1000461	3.39	2.34	2.79	3.41	2.83	2.56	4.13	3.34	3.34				
OVARC1000465	4.49	3.75	4.70	4.65	4.57	4.49	3.93	2.86	2.86				
OVARC1000466	5.63	3.82	4.46	5.01	4.97	7.62	6.00	5.12	5.12				
OVARC1000467	3.64	2.33	2.91	3.88	3.66	4.53	4.40	4.32	4.32			*	+
OVARC1000470	4.4	2.42	1.89	7.76	7.31	7.37	4.36	3.86	3.86	**	+		
OVARC1000473	5.77	6.12	2.59	5.13	4.08	6.65	4.72	6.17	6.17				
OVARC1000479	10.65	6.40	6.55	8.36	8.23	12.25	7.74	6.99	6.99				
OVARC1000484	7.73	3.54	4.68	14.41	17.12	13.60	11.04	9.93	9.93	**	+	*	+
OVARC1000486	3.13	1.48	1.74	5.56	5.39	7.63	4.10	3.04	3.04	**	+		
OVARC1000496	0.32	0.95	1.13	0.23	0.59	1.74	1.38	0.85	0.85				-
OVARC1000520	0.79	1.22	1.43	1.76	1.97	2.08	2.17	1.68	1.68	*	+	*	+
OVARC1000522	4.89	4.05	3.21	7.99	8.62	12.13	8.58	8.73	8.73	*	+	**	+
OVARC1000526	5.23	3.76	3.40	9.44	8.41	9.79	6.60	6.83	6.83	**	+	**	+
OVARC1000529	8.29	5.03	3.79	8.43	8.08	7.91	6.33	6.00	6				
OVARC1000533	13.85	10.76	9.50	10.46	10.65	9.69	10.80	10.74	10.74				
OVARC1000543	2.14	1.23	0.78	1.99	1.06	1.67	1.34	1.95	1.95				
OVARC1000550	3.95	2.99	2.96	3.41	5.27	5.08	3.89	3.69	3.69				
OVARC1000553	7.96	6.39	6.63	10.34	11.92	12.52	8.20	8.94	8.94	**	+	*	+
OVARC1000556	2.91	2.73	2.33	4.64	4.36	4.57	3.30	5.76	5.76	**	+		
OVARC1000557	1.8	2.00	2.08	3.66	2.89	3.58	2.75	2.23	2.23	**	+		
OVARC1000561	5.49	5.12	4.27	12.79	11.21	12.35	4.34	6.50	6.5	**	+		
OVARC1000564	11	4.97	4.49	6.39	9.03	5.47	5.12	5.72	5.72				
OVARC1000573	3.43	1.54	1.73	4.84	5.71	5.20	3.22	2.70	2.7	**	+		
OVARC1000576	22.35	9.42	12.58	14.84	14.82	13.96	18.96	21.39	21.39				
OVARC1000578	3.78	1.92	1.91	7.25	4.00	7.95	3.26	3.45	3.45	*	+		
OVARC1000581	2.32	0.98	1.31	2.39	2.02	2.50	0.87	2.36	2.36				
OVARC1000586	4.15	3.94	3.82	5.69	4.46	5.03	7.98	9.37	9.37	*	+	**	+
OVARC1000588	3.09	2.32	2.34	6.24	5.07	6.64	3.10	4.00	4	**	+	*	+
OVARC1000605	3.48	1.27	1.57	3.94	3.34	1.96	2.17	3.54	3.54				
OVARC1000622	16.94	7.82	7.29	28.21	27.34	23.72	13.10	15.48	15.48	*	+		
OVARC1000636	7.07	3.14	2.94	8.06	7.46	5.78	4.15	5.40	5.4				
OVARC1000640	1.93	1.10	2.17	2.95	3.95	2.11	1.86	2.87	2.87				
OVARC1000649	6.55	3.47	4.45	4.81	4.28	3.96	4.42	5.10	5.1				
OVARC1000661	8.83	4.09	5.47	7.42	7.41	7.08	6.76	7.35	7.35				
OVARC1000677	5.49	3.25	4.84	5.23	4.19	5.75	3.47	4.95	4.95				
OVARC1000678	3.24	2.45	2.41	6.56	3.68	3.55	3.07	3.23	3.23				
OVARC1000679	2.29	2.05	2.51	5.5	7.69	3.61	2.67	3.02	3.02	*	+	*	+
OVARC1000681	3.04	1.58	2.55	2.83	3.65	2.16	1.27	3.32	3.32				
OVARC1000682	5.34	2.89	3.15	10.89	12.80	6.98	6.81	6.70	6.7	*	+	*	+
OVARC1000689	6.35	2.64	5.24	6.82	5.05	3.15	3.89	5.86	5.86				
OVARC1000700	4.87	2.36	3.84	6.43	6.33	5.87	5.58	3.71	3.71	*	+		
OVARC1000703	6.09	5.10	4.50	10.85	8.68	9.16	5.32	6.24	6.24	**	+		
OVARC1000722	6.99	3.21	3.22	7.7	5.28	6.60	3.85	5.25	5.25				
OVARC1000726	12.55	5.82	7.48	9.62	7.07	8.57	9.99	8.90	8.9				
OVARC1000727	8.32	3.91	3.99	6.93	6.40	4.72	3.99	5.01	5.01				
OVARC1000730	6.1	3.39	3.84	6.3	8.93	6.59	2.98	3.46	3.46				

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Table 295

OVARC1000741	7.47	3.93	4.05	6.71	8.34	4.11	5.58	6.82	6.82				
OVARC1000746	2.7	1.49	1.95	3.42	4.80	3.86	2.21	3.03	3.03	*	+		
OVARC1000764	9.15	7.18	6.73	6.1	5.81	7.27	6.23	6.93	6.93				
OVARC1000769	1.96	2.22	1.65	4.18	3.56	4.40	2.93	2.93	2.93	**	+	**	+
OVARC1000771	3.36	1.52	2.49	4.38	3.35	3.58	3.00	4.34	4.34				
OVARC1000773	223.93	75.55	197.24	131.33	115.24	132.74	69.02	82.73	82.73				
OVARC1000775	5.89	2.38	2.57	10.9	11.89	6.67	5.95	7.36	7.36	*	+		
OVARC1000778	5.16	2.89	2.70	7.19	7.19	4.94	4.21	3.79	3.79				
OVARC1000779	1.34	0.25	1.68	0.81	2.17	1.66	0.98	2.78	2.78				
OVARC1000781	3.01	1.11	1.81	3.21	4.12	3.42	2.43	3.96	3.96				
OVARC1000787	5.12	1.26	2.40	6.21	4.91	6.16	2.68	3.80	3.8				
OVARC1000789	17.92	12.51	11.26	12.68	11.30	14.18	7.52	8.71	8.71				
OVARC1000800	10.27	6.21	6.25	13.32	11.12	11.87	8.07	9.42	9.42	*	+		
OVARC1000802	3.94	1.53	1.34	4.85	5.51	3.97	3.28	3.23	3.23				
OVARC1000810	7.31	2.74	2.89	9.23	8.19	6.66	4.42	6.46	6.46				
OVARC1000811	4.94	1.49	1.98	3.69	5.14	3.20	2.80	3.11	3.11				
OVARC1000814	8.98	4.85	4.30	12.34	14.84	13.49	5.29	9.28	9.28	*	+		
OVARC1000816	5.55	2.23	3.34	6.25	6.38	4.13	4.96	10.86	10.86				
OVARC1000817	0.67	0.84	0.17	1.03	1.43	0.88	1.03	1.18	1.18				
OVARC1000834	7.9	3.52	4.48	7.01	4.99	6.90	5.30	8.11	8.11				
OVARC1000846	8.76	5.89	5.62	13.13	13.07	12.45	7.92	8.86	8.86	**	+		
OVARC1000850	4.55	4.35	3.79	5.06	4.86	6.51	5.09	5.93	5.93			*	+
OVARC1000853	10.26	6.75	7.96	17.45	22.42	13.77	15.27	17.34	17.34	*	+	**	+
OVARC1000862	2.31	1.51	1.67	2.98	3.34	3.48	2.84	3.92	3.92	**	+	*	+
OVARC1000873	5.08	3.94	3.56	7.67	7.81	9.71	8.49	9.22	9.22	**	+	**	+
OVARC1000875	13.15	7.32	6.94	10.33	8.49	11.65	7.63	12.92	12.92				
OVARC1000876	3.56	1.95	2.71	3.83	2.75	3.80	2.91	3.90	3.9				
OVARC1000883	11.24	5.79	7.03	7.42	6.63	8.18	6.12	10.30	10.3				
OVARC1000885	1.99	1.85	0.96	2.91	2.72	4.05	1.81	1.84	1.84	*	+		
OVARC1000886	3.79	3.90	3.30	5.23	4.59	3.88	4.18	4.19	4.19			*	+
OVARC1000890	16.12	9.23	8.22	13.23	13.98	12.06	8.12	8.78	8.78				
OVARC1000891	9.14	4.58	8.52	6.77	7.63	5.67	3.14	5.82	5.82				
OVARC1000897	1.42	0.51	0.89	0.57	0.73	1.37	0.82	2.14	2.14				
OVARC1000912	3.17	1.30	1.93	1.64	2.12	2.69	2.76	3.24	3.24				
OVARC1000914	1.78	1.84	1.59	1.55	2.20	2.36	1.62	3.25	3.25				
OVARC1000915	6.15	3.81	2.82	7.18	8.08	11.76	6.61	6.54	6.54				
OVARC1000916	3.99	3.47	3.85	4.78	5.13	5.34	5.36	5.24	5.24	**	+	**	+
OVARC1000924	3.43	2.14	2.20	3.95	5.25	6.94	3.56	2.87	2.87	*	+		
OVARC1000928	2.3	1.45	1.90	2.94	5.21	2.82	3.59	4.30	4.3			**	+
OVARC1000936	2.24	1.71	1.41	6.64	6.60	5.33	2.20	4.51	4.51	**	+		
OVARC1000937	4.37	3.36	3.65	4.37	4.24	5.18	4.25	6.07	6.07				
OVARC1000945	6.45	6.49	5.55	5.48	7.78	7.98	6.71	7.64	7.64				
OVARC1000948	0.7	1.14	1.80	0.8	1.44	1.73	1.79	1.83	1.83				
OVARC1000956	4.51	3.81	4.84	5.21	4.57	6.49	5.02	4.22	4.22				
OVARC1000959	3.91	3.29	2.51	6.03	6.37	10.71	4.34	3.63	3.63	*	+		
OVARC1000960	15.58	12.49	8.74	25.21	26.65	32.56	13.09	13.48	13.48	**	+		
OVARC1000964	7.4	4.78	4.49	6.36	5.85	5.60	6.26	4.60	4.6				
OVARC1000971	2.15	0.88	1.23	2.29	3.01	2.68	1.01	1.16	1.16	*	+		
OVARC1000975	3.59	2.39	2.50	3.12	3.77	3.56	3.45	3.78	3.78				
OVARC1000976	1.43	1.10	0.67	1.47	1.70	1.61	1.96	1.76	1.76			*	+
OVARC1000981	4.17	3.59	2.08	3.86	4.73	5.67	6.53	5.87	5.87			*	+
OVARC1000982	5.28	3.08	4.53	3.99	3.64	7.26	3.94	5.23	5.23				
OVARC1000984	2.89	2.32	3.02	4.83	4.31	6.06	3.98	4.72	4.72	*	+	**	+
OVARC1000995	6.28	3.58	3.62	10.03	11.01	12.54	6.34	8.81	8.81	**	+	*	+
OVARC1000996	2.44	0.93	1.29	3.23	3.01	2.60	1.59	2.15	2.15	*	+		
OVARC1000999	13.81	7.04	7.16	18.71	16.83	17.82	9.89	10.20	10.2	*	+		

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Table 296

OVARC1001000	10.01	7.69	7.61	19.45	23.56	18.96	10.07	11.74	11.74	**	+	*	+
OVARC1001004	1.03	0.80	0.91	1.57	2.14	1.61	1.90	1.48	1.48	*	+	*	+
OVARC1001010	1.8	1.08	0.56	1.62	1.36	2.03	1.35	1.40	1.4				
OVARC1001011	3.43	2.88	3.13	3.51	3.30	4.55	2.89	3.10	3.1				
OVARC1001030	38.32	24.93	30.71	46.79	41.55	50.96	53.76	59.72	59.72	*	+	**	+
OVARC1001032	1.55	1.32	1.67	3.18	2.58	2.77	2.83	1.37	1.37	**	+		
OVARC1001034	2.4	1.70	2.13	3.14	3.10	3.44	2.01	2.66	2.66	**	+		
OVARC1001038	12.68	9.34	7.92	11.12	13.30	12.41	6.75	6.49	6.49				
OVARC1001040	8.91	6.59	4.66	14.02	14.04	19.13	7.93	7.81	7.81	*	+		
OVARC1001041	6.31	3.56	4.31	8.16	10.01	10.61	5.62	4.95	4.95	*	+		
OVARC1001044	1.81	1.80	2.22	2.71	2.48	2.79	2.22	2.94	2.94	*	+		
OVARC1001049	9.39	8.47	8.39	15.62	16.10	16.18	9.93	8.69	8.69	**	+		
OVARC1001051	57.5	54.01	57.15	51.44	56.52	72.78	36.05	33.73	33.73			**	-
OVARC1001054	1.32	1.27	1.50	2.46	1.80	2.94	1.81	1.58	1.58	*	+	*	+
OVARC1001055	3.77	1.65	2.45	4.24	4.50	2.62	2.94	3.56	3.56				
OVARC1001062	11.74	5.75	4.85	11.81	10.68	10.78	3.12	5.25	5.25				
OVARC1001065	1.99	1.18	1.96	2.64	2.00	1.58	1.32	1.86	1.86				
OVARC1001068	6.51	2.07	3.30	4.91	4.25	4.95	3.64	6.26	6.26				
OVARC1001072	9.32	6.54	7.65	10.21	8.94	9.18	6.17	9.88	9.88				
OVARC1001073	3.46	0.94	2.36	3.97	3.24	3.42	2.17	2.06	2.06				
OVARC1001074	1.75	0.40	1.35	1.71	2.05	2.60	0.86	1.25	1.25				
OVARC1001078	7.1	3.90	5.62	11.77	8.65	7.84	4.87	6.07	6.07				
OVARC1001085	5.2	2.42	3.41	5.59	4.12	3.31	4.28	6.32	6.32				
OVARC1001086	5.76	2.45	2.47	3.85	5.26	3.78	2.15	3.47	3.47				
OVARC1001091	3.91	3.54	2.95	5.93	5.39	4.15	4.20	3.41	3.41	*	+		
OVARC1001092	4.33	2.96	3.51	6.04	6.34	5.50	3.69	5.56	5.56	**	+		
OVARC1001104	1.53	0.53	0.40	1.32	1.57	1.20	0.63	1.14	1.14				
OVARC1001107	9.82	5.46	6.15	6.8	4.45	8.10	6.28	6.79	6.79				
OVARC1001113	4.68	3.14	2.92	4.82	4.00	4.79	2.64	3.74	3.74				
OVARC1001117	6.69	2.96	3.38	8.53	8.56	12.29	4.84	6.35	6.35	*	+		
OVARC1001118	8.12	5.06	4.70	11.61	11.15	10.02	5.36	7.35	7.35	*	+		
OVARC1001125	18.96	12.37	9.61	15.08	18.61	12.67	4.50	5.26	5.26			*	-
OVARC1001129	5.21	3.98	5.45	6.68	4.55	3.29	2.17	3.47	3.47			*	-
OVARC1001132	6.52	3.70	5.55	7.12	8.81	9.06	2.18	2.72	2.72	*	+	*	-
OVARC1001138	16.11	12.56	10.50	16.95	13.15	17.48	16.11	18.55	18.55				
OVARC1001141	5.54	2.36	3.55	4.59	3.46	4.09	3.37	5.02	5.02				
OVARC1001154	5.08	2.38	3.52	7.23	5.71	6.41	6.14	7.71	7.71	*	+	*	+
OVARC1001161	5.7	2.64	4.14	8.62	7.37	7.00	3.80	4.51	4.51	*	+		
OVARC1001162	7.21	3.90	4.19	8.88	8.61	6.05	4.92	4.79	4.79				
OVARC1001163	8.43	4.40	4.84	6.45	6.12	5.05	5.16	8.27	8.27				
OVARC1001167	6.39	2.75	3.96	9.57	10.93	6.52	6.33	5.84	5.84				
OVARC1001169	2.12	0.82	1.00	1.91	2.68	3.48	1.25	1.14	1.14				
OVARC1001170	5.03	2.13	3.01	9.37	9.52	8.69	6.25	6.17	6.17	**	+	*	+
OVARC1001171	13.87	7.94	9.22	17.9	10.00	17.22	8.13	7.41	7.41				
OVARC1001173	6.07	4.57	5.00	13.94	11.16	14.09	6.22	8.18	8.18	**	+	*	+
OVARC1001176	120.6	80.54	85.77	70.13	72.81	62.53	40.27	47.98	47.98			*	-
OVARC1001180	11.62	7.41	6.61	16.44	18.19	11.30	11.76	9.48	9.48				
OVARC1001188	6.48	2.62	2.03	5.02	7.63	5.54	3.93	4.15	4.15				
OVARC1001200	2.22	1.30	1.20	5.74	5.77	3.98	2.73	3.72	3.72	**	+	*	+
OVARC1001202	7.54	4.54	7.94	10.59	9.48	9.04	5.59	7.44	7.44				
OVARC1001206	4.56	1.77	2.35	5.27	2.32	4.40	4.18	3.01	3.01				
OVARC1001209	5.41	4.08	4.25	4.84	4.05	4.40	5.08	5.10	5.1				
OVARC1001219	2.78	1.08	2.61	2.53	1.72	2.02	0.89	2.02	2.02				
OVARC1001222	2.69	0.99	2.05	4.33	4.36	2.81	4.34	4.56	4.56			**	+
OVARC1001232	6.79	3.23	4.22	10.1	7.69	5.83	3.19	6.06	6.06				
OVARC1001240	5.42	2.74	3.04	7.44	8.60	6.15	4.85	5.14	5.14	*	+		

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OVARC1001243	1.72	1.35	1.37	1.54	2.52	1.73	1.36	2.41	2.41				
OVARC1001244	24.7	9.04	13.89	22.81	23.41	15.18	12.84	15.77	15.77				
OVARC1001246	40.74	22.08	30.73	92.94	72.86	54.67	53.93	71.88	71.88	*	+	*	+
OVARC1001247	8.36	4.54	5.70	8.31	7.58	6.86	6.44	6.70	6.7				
OVARC1001260	5.56	1.98	3.43	3.72	4.11	5.56	3.81	5.29	5.29				
OVARC1001261	7.49	5.34	5.88	8.27	8.14	6.50	4.18	3.66	3.66			*	-
OVARC1001268	9.66	6.34	6.78	20.35	19.09	14.70	18.61	12.90	12.9	**	+	*	+
OVARC1001270	2.46	0.92	1.16	1.01	0.99	1.69	1.24	1.98	1.98				
OVARC1001271	7.39	3.05	5.29	8.27	10.72	9.05	7.37	6.66	6.66	*	+		
OVARC1001282	1.01	0.92	0.97	0.97	2.26	1.76	1.02	2.02	2.02				
OVARC1001296	2.46	1.56	1.43	2.56	2.90	3.81	2.32	2.50	2.5				
OVARC1001306	7.3	3.30	5.02	6.03	4.37	5.50	5.45	6.39	6.39				
OVARC1001314	0.91	0.46	0.79	1.37	1.95	2.32	1.59	1.62	1.62	*	+	**	+
OVARC1001316	1.39	0.64	0.79	0.83	1.74	1.83	1.60	1.04	1.04				
OVARC1001329	14.48	8.75	10.68	26.47	22.48	16.87	10.91	14.31	14.31	*	+		
OVARC1001330	5.69	3.01	1.92	3.71	3.31	3.24	2.35	2.85	2.85				
OVARC1001336	5.35	4.02	3.78	4.8	5.04	6.17	4.16	5.22	5.22				
OVARC1001338	3	2.42	3.08	2.63	3.26	3.21	2.60	4.03	4.03				
OVARC1001339	18.39	11.67	11.13	15.76	12.03	15.86	13.83	17.02	17.02				
OVARC1001340	3.7	2.44	2.40	2.48	2.50	2.72	1.64	1.40	1.4			*	-
OVARC1001341	9.61	7.33	5.62	10.7	12.45	13.37	7.41	10.65	10.65	*	+		
OVARC1001342	133.57	112.33	102.75	148.81	134.63	172.83	71.00	44.68	44.68			**	-
OVARC1001344	7.19	4.91	4.20	12.04	11.73	10.02	5.70	6.29	6.29	**	+		
OVARC1001357	1.77	0.51	0.85	0.71	1.22	1.30	1.05	2.71	2.71				
OVARC1001359	12.91	9.14	12.19	10.45	11.07	11.24	11.72	11.75	11.75				
OVARC1001360	1.13	0.79	1.43	0.68	1.47	0.77	1.27	2.96	2.96				
OVARC1001369	3.18	3.27	2.79	3.55	2.73	3.58	3.69	3.39	3.39				
OVARC1001372	2.77	2.30	1.69	2.23	2.48	3.94	3.04	2.69	2.69				
OVARC1001376	2.87	2.00	1.97	5.27	5.80	7.45	3.84	3.47	3.47	**	+	*	+
OVARC1001381	9.02	7.72	5.78	16.38	17.31	19.84	9.24	7.41	7.41	**	+		
OVARC1001391	4.51	2.73	2.85	3.51	4.11	3.13	3.49	3.91	3.91				
OVARC1001392	8.74	6.58	5.89	10.76	13.40	11.71	12.35	14.18	14.18	*	+	**	+
OVARC1001399	8.85	5.58	4.72	7.92	8.25	8.82	4.81	5.40	5.4				
OVARC1001417	2.7	1.43	2.23	1.21	1.52	2.52	2.51	2.99	2.99				
OVARC1001419	4.3	5.24	4.00	3.68	3.86	6.94	5.84	6.00	6			*	+
OVARC1001425	2.29	2.40	2.49	3.29	2.74	4.54	3.29	3.09	3.09			**	+
OVARC1001436	2.31	2.50	1.77	3.81	3.30	4.11	3.38	2.41	2.41	**	+		
OVARC1001442	3.28	3.48	2.35	2.21	3.99	4.48	3.98	3.31	3.31				
OVARC1001451	2.33	1.90	1.35	3.6	3.77	3.76	1.55	1.55	1.55	**	+		
OVARC1001452	3.08	2.65	1.79	3.37	3.43	2.89	2.90	3.86	3.86				
OVARC1001453	1.36	0.57	0.90	1.69	3.97	2.45	2.96	1.73	1.73				
OVARC1001476	9.08	6.86	7.98	15.11	12.70	14.85	28.29	23.49	23.49	**	+	**	+
OVARC1001480	2.63	2.84	2.87	3.18	2.98	4.97	4.13	4.00	4			**	+
OVARC1001489	0.44	0.69	0.81	2.69	2.29	3.27	1.10	4.03	4.03	**	+		
OVARC1001493	1.25	1.74	1.87	2.29	2.11	2.40	3.16	2.54	2.54	*	+	*	+
OVARC1001496	8.58	6.56	5.62	10.89	7.25	13.93	7.36	6.38	6.38				
OVARC1001499	2.77	1.81	1.79	9.3	11.43	8.77	4.71	4.12	4.12	**	+	**	+
OVARC1001506	6.8	3.72	2.93	7.69	8.55	5.52	2.68	3.49	3.49				
OVARC1001509	1.55	1.98	1.98	5.58	4.61	5.41	3.85	2.97	2.97	**	+	*	+
OVARC1001510	1.71	1.36	1.70	2.6	2.03	1.38	0.87	1.95	1.95				
OVARC1001516	4.33	2.50	2.28	4.35	4.41	5.42	3.48	4.66	4.66				
OVARC1001525	1.15	0.47	0.25	2.5	1.57	2.82	0.67	0.87	0.87	*	+		
OVARC1001542	5.12	4.17	4.21	9.27	7.88	7.75	6.26	7.55	7.55	**	+	**	+
OVARC1001544	5.06	4.31	3.88	10.18	11.66	10.16	4.91	5.47	5.47	**	+		
OVARC1001546	4.58	2.37	2.41	4.24	4.04	3.16	5.16	4.17	4.17				
OVARC1001547	3.14	1.52	1.67	3.77	5.22	4.03	1.93	2.91	2.91	*	+		

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Table 298

OVARC1001555	6.13	2.98	2.93	3.66	4.13	4.35	3.24	3.51	3.51				
OVARC1001560	5.27	2.89	4.00	3.57	5.47	3.00	1.86	5.44	5.44				
OVARC1001569	4.31	1.79	2.67	5.77	3.68	6.02	3.66	4.73	4.73				
OVARC1001570	3.15	1.30	2.66	3.39	3.35	3.15	3.14	2.39	2.39				
OVARC1001577	4.77	2.77	4.00	5.05	6.04	4.74	3.79	3.40	3.4				
OVARC1001578	0.13	0.13	0.49	0.11	0.08	0.34	(0.16)	0.33	0.33				
OVARC1001596	6.65	4.15	4.07	12.92	13.04	11.27	13.75	17.88	17.88	**	+	**	+
OVARC1001600	4.44	1.10	1.82	4.64	5.45	5.21	2.46	3.26	3.26				
OVARC1001607	3.4	1.49	1.81	4.77	3.07	3.12	3.27	4.29	4.29				
OVARC1001610	1.98	0.84	1.36	1.63	3.05	2.07	1.29	1.68	1.68				
OVARC1001611	2.19	0.50	1.35	1.78	1.02	1.32	1.66	1.19	1.19				
OVARC1001615	4.22	1.84	2.90	5.28	3.15	3.01	2.44	2.96	2.96				
OVARC1001636	1.51	1.25	1.84	2.49	2.09	2.98	2.73	3.68	3.68	*	+	**	+
OVARC1001668	12.16	5.32	7.43	18.64	16.53	18.49	8.30	9.71	9.71	*	+		
OVARC1001702	8.57	3.96	3.47	6.26	5.42	3.41	3.42	6.27	6.27				
OVARC1001703	3.45	1.33	2.17	2.9	2.76	1.60	1.67	2.48	2.48				
OVARC1001710	12.16	6.40	8.14	12.51	12.10	10.06	5.91	10.48	10.48				
OVARC1001711	3.85	1.19	3.00	4.46	4.77	3.21	3.17	3.47	3.47				
OVARC1001713	3.83	1.81	3.06	4	3.01	2.37	3.41	2.97	2.97				
OVARC1001725	1.76	0.84	1.52	1.59	1.72	1.08	1.90	2.27	2.27				
OVARC1001726	5.39	1.55	3.13	5.82	3.63	5.08	3.26	3.16	3.16				
OVARC1001727	0.29	0.42	1.02	0.81	1.66	2.65	0.38	0.85	0.85				
OVARC1001731	69.09	38.65	38.62	61.15	63.80	29.40	50.44	54.36	54.36				
OVARC1001735	3.44	1.71	2.00	2.93	3.19	1.89	1.63	2.09	2.09				
OVARC1001741	5.73	2.80	4.04	7.5	7.39	7.90	7.54	6.67	6.67	*	+	*	+
OVARC1001745	7.24	4.36	4.49	8.97	10.22	8.41	6.60	5.98	5.98	*	+		
OVARC1001759	1.01	0.86	1.04	1.08	1.84	2.94	2.19	2.25	2.25			**	+
OVARC1001762	8.58	3.74	6.34	5.15	5.47	7.03	4.95	5.82	5.82				
OVARC1001766	9.38	4.99	6.59	7.66	8.01	9.59	6.94	8.67	8.67				
OVARC1001767	3.53	1.57	1.68	5.51	3.61	4.66	1.50	1.77	1.77	*	+		
OVARC1001768	2.87	1.10	1.41	3.92	5.14	2.20	2.97	2.24	2.24				
OVARC1001770	8.73	3.17	3.93	4.79	3.74	3.92	3.08	5.26	5.26				
OVARC1001776	9.28	3.35	3.86	7.43	6.75	3.40	4.83	5.46	5.46				
OVARC1001791	6.37	2.23	2.37	4.77	4.93	3.53	3.51	5.12	5.12				
OVARC1001795	3.33	1.66	2.08	3.57	2.56	3.39	2.70	4.38	4.38				
OVARC1001798	7.18	6.07	6.66	13.95	10.63	12.79	7.22	8.63	8.63	**	+		
OVARC1001802	9.19	4.54	5.70	10.35	10.30	12.39	7.34	10.40	10.4	*	+		
OVARC1001805	4.64	2.74	4.36	2.74	2.72	4.62	3.49	2.65	2.65				
OVARC1001807	8.77	5.93	4.12	6.55	5.33	4.82	5.91	7.39	7.39				
OVARC1001809	6.83	4.86	4.27	6.09	6.40	3.73	5.14	5.48	5.48				
OVARC1001812	4.12	3.13	3.09	7.67	7.95	5.93	3.66	6.68	6.68	**	+		
OVARC1001813	5.43	3.76	2.36	6.97	8.29	5.75	4.00	5.14	5.14				
OVARC1001820	5.44	2.59	2.92	7.68	8.81	9.74	4.50	3.53	3.53	**	+		
OVARC1001828	1.52	0.56	0.82	0.49	1.38	1.06	0.77	2.57	2.57				
OVARC1001833	6.47	2.16	4.12	4.91	4.44	4.92	4.40	5.06	5.06				
OVARC1001839	3.71	1.97	2.01	2.39	2.11	1.77	2.84	1.57	1.57				
OVARC1001846	4.41	2.73	3.00	4.53	4.51	2.44	2.43	1.95	1.95				
OVARC1001849	7.54	4.93	4.04	7.29	7.04	10.00	6.63	6.98	6.98				
OVARC1001861	6.18	3.30	3.37	5.23	6.05	5.82	6.62	5.17	5.17				
OVARC1001873	2.23	3.58	2.82	5.06	4.34	4.98	4.48	5.41	5.41	*	+	*	+
OVARC1001879	6.45	3.48	3.55	6.19	6.28	6.46	4.62	5.20	5.2				
OVARC1001880	8.1	5.60	6.83	9.11	8.57	12.18	8.27	7.92	7.92				
OVARC1001883	2.85	1.41	1.74	4.9	4.51	4.19	2.29	2.05	2.05	**	+		
OVARC1001900	4.98	3.20	2.77	3.89	3.38	3.75	3.72	2.89	2.89				
OVARC1001901	4.87	3.60	3.92	3.84	3.21	3.00	1.68	3.04	3.04				
OVARC1001911	6	4.01	3.43	3.55	3.02	2.97	2.70	4.72	4.72				

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Table 299

OVARC1001916	6.98	5.21	4.19	6.6	6.42	9.56	6.23	7.95	7.95				
OVARC1001928	2.06	0.85	1.79	2.38	2.75	2.84	3.26	4.05	4.05			**	+
OVARC1001937	3.08	3.56	3.08	6.71	6.67	8.66	8.49	10.57	10.57	**	+	**	+
OVARC1001940	2.73	1.83	2.29	2.9	3.41	3.46	2.76	3.64	3.64	*	+		
OVARC1001942	7.33	6.50	6.76	5.22	5.72	6.21	4.66	4.79	4.79	*	-	**	-
OVARC1001943	10.42	8.83	6.98	5.68	5.59	6.08	6.06	4.31	4.31	*	-	*	-
OVARC1001949	10.36	7.25	8.90	17.76	16.95	14.34	7.64	7.78	7.78	**	+		
OVARC1001950	6.51	3.98	3.61	6.85	7.18	5.80	4.70	6.17	6.17				
OVARC1001952	8.93	7.35	6.04	9.34	7.56	8.32	8.80	9.41	9.41				
OVARC1001954	2.25	1.93	2.80	2.22	2.67	3.53	3.43	3.10	3.1			*	+
OVARC1001963	4.35	4.65	3.70	6.06	6.92	7.14	5.20	5.61	5.61	**	+	*	+
OVARC1001983	14.69	9.15	11.07	15.77	13.57	18.65	18.62	19.08	19.08			*	+
OVARC1001987	4.18	3.62	3.23	5.27	5.35	7.29	5.42	5.22	5.22	*	+	**	+
OVARC1001989	4.53	2.66	2.25	6.48	8.72	7.41	3.80	4.09	4.09	*	+		
OVARC1001991	10.96	5.93	5.69	9.46	8.32	6.27	7.05	6.60	6.6				
OVARC1002005	5.4	3.75	4.99	8.51	8.21	8.60	5.67	7.46	7.46	**	+		
OVARC1002044	5.75	6.74	4.12	8.85	9.04	10.30	6.19	6.78	6.78	*	+		
OVARC1002046	11.4	8.29	10.75	14.32	15.39	13.03	16.29	16.11	16.11	*	+	**	+
OVARC1002050	7.01	4.34	4.11	5.04	4.91	6.69	6.80	8.61	8.61				
OVARC1002058	2.46	2.25	3.14	3.04	3.77	4.08	4.59	3.85	3.85			*	+
OVARC1002066	3.19	1.93	3.61	3.32	2.98	4.14	5.23	6.90	6.9			*	+
OVARC1002082	4.87	5.01	3.84	11.38	12.17	13.39	6.27	6.19	6.19	**	+	*	+
OVARC1002091	9.15	5.09	5.80	7.51	5.64	6.50	4.50	6.13	6.13				
OVARC1002092	1.08	0.92	1.01	1.95	2.31	1.47	1.26	2.01	2.01	*	+	*	+
OVARC1002093	10.46	8.34	8.22	9.65	10.46	8.69	6.29	9.67	9.67				
OVARC1002094	3.39	2.34	2.33	2.97	3.73	2.67	2.42	4.62	4.62				
OVARC1002107	4.25	3.34	3.27	6.5	6.62	9.76	3.44	3.77	3.77	*	+		
OVARC1002112	10.9	8.09	8.28	16.78	13.09	25.94	13.30	14.51	14.51			**	+
OVARC1002126	5.65	6.82	6.95	13.64	10.71	12.11	9.13	8.48	8.48	**	+	**	+
OVARC1002127	2.58	2.03	3.02	3.02	3.11	2.31	3.36	3.37	3.37			*	+
OVARC1002138	2.48	2.26	1.89	3.19	3.39	3.93	1.72	2.13	2.13	**	+		
OVARC1002143	1.69	1.30	0.60	1.38	1.56	1.86	1.19	0.95	0.95				
OVARC1002156	1.66	0.93	0.95	1.52	1.87	1.95	2.12	1.74	1.74				
OVARC1002158	2.7	2.62	1.87	2.12	2.65	2.44	2.26	2.68	2.68				
OVARC1002165	7.2	5.63	4.73	11.72	8.43	11.59	6.50	7.88	7.88	*	+		
OVARC1002176	8	8.96	7.89	12.99	11.14	15.46	14.15	11.02	11.02	*	+	*	+
OVARC1002178	1.22	1.02	1.19	6.91	5.74	6.72	4.31	4.39	4.39	**	+	**	+
OVARC1002182	2.89	1.94	1.74	3.43	2.78	3.06	2.40	2.34	2.34				
OVARC1002185	3.07	1.87	2.74	2.77	3.03	2.27	3.08	3.27	3.27				
PLACE1000004	4.13	1.50	2.40	4.62	3.84	3.14	1.43	2.34	2.34				
PLACE1000005	1.35	0.94	1.81	2.1	2.21	3.64	1.75	1.86	1.86				
PLACE1000006	3.24	3.13	3.46	5.32	4.20	5.06	3.54	4.19	4.19	*	+	*	+
PLACE1000007	3.52	1.48	1.95	2.76	2.50	3.15	1.95	2.86	2.86				
PLACE1000014	4.25	3.03	3.71	8.86	8.24	8.01	5.81	6.21	6.21	**	+	**	+
PLACE1000031	2.43	0.83	0.85	3.06	2.75	3.91	2.27	1.91	1.91	*	+		
PLACE1000033	1.29	0.90	0.41	1.55	1.06	1.17	1.59	1.10	1.1				
PLACE1000040	4.49	2.71	2.01	6.89	9.12	6.89	4.66	5.42	5.42	*	+		
PLACE1000048	1.6	1.02	1.34	5.06	4.76	4.04	3.48	3.87	3.87	**	+	**	+
PLACE1000050	5.68	3.49	4.13	5.18	4.97	6.58	3.56	3.95	3.95				
PLACE1000061	158.3	101.17	90.85	157.97	122.81	120.53	58.82	94.38	94.38				
PLACE1000066	24.72	10.40	14.31	13.08	14.83	12.97	11.89	17.52	17.52				
PLACE1000075	3.77	2.50	2.49	11.38	15.88	19.81	6.47	10.82	10.82	**	+	*	+
PLACE1000078	3.4	1.72	2.20	4.82	4.89	6.42	2.94	3.88	3.88	*	+		
PLACE1000081	10.27	4.42	4.34	7.73	8.15	4.92	5.06	4.85	4.85				
PLACE1000086	7.07	5.86	4.84	7.21	7.07	4.90	5.17	6.83	6.83				
PLACE1000094	3.81	2.40	2.03	2.26	2.48	2.45	2.38	2.04	2.04				

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Table 300

PLACE1000101	2.3	2.12	2.61	4.62	5.45	5.31	2.54	3.96	3.96	**	+		
PLACE1000121	3.32	1.82	3.36	3.18	3.46	3.22	4.10	2.97	2.97				
PLACE1000133	22.32	10.62	12.41	24.57	19.93	22.03	9.44	17.41	17.41				
PLACE1000142	3.77	2.94	3.97	3.72	2.78	3.50	4.86	3.02	3.02				
PLACE1000146	12.04	5.71	7.52	11.96	8.63	12.12	6.11	6.64	6.64				
PLACE1000163	10.38	6.77	6.39	8.08	8.26	4.88	8.20	6.01	6.01				
PLACE1000172	2.38	1.36	0.47	1.68	3.26	0.78	1.42	1.36	1.36				
PLACE1000181	4.66	3.09	3.18	5.69	5.41	5.62	4.15	4.68	4.68	*	+		
PLACE1000184	1.13	1.00	1.41	4.73	6.35	6.17	4.40	7.01	7.01	**	+	**	+
PLACE1000185	5.78	3.85	4.83	5.4	6.28	6.49	6.72	6.56	6.56			*	+
PLACE1000198	3.55	2.09	2.55	2.87	3.21	4.22	3.14	3.19	3.19				
PLACE1000213	2.64	0.86	1.73	2.98	2.54	2.75	2.24	2.31	2.31				
PLACE1000214	5.38	1.32	2.03	4.15	4.37	5.82	3.05	3.50	3.5				
PLACE1000220	5.9	3.44	1.89	3.73	2.84	3.93	2.23	3.16	3.16				
PLACE1000231	18.42	11.77	9.30	14.94	14.15	14.87	11.91	14.48	14.48				
PLACE1000236	5.6	2.94	3.19	6.04	6.27	4.87	5.66	5.87	5.87				
PLACE1000245	7.5	5.11	6.34	10.03	9.79	11.42	4.16	7.99	7.99	**	+		
PLACE1000246	5.62	3.38	4.68	6.48	8.30	6.53	8.63	9.43	9.43	*	+	**	+
PLACE1000258	15.61	9.21	10.26	23.89	20.68	20.66	9.91	13.07	13.07	*	+		
PLACE1000288	2.41	2.18	2.21	2.88	1.68	2.31	2.41	3.07	3.07				
PLACE1000292	5.99	4.40	5.17	20.8	17.62	19.45	12.37	20.25	20.25	**	+	**	+
PLACE1000302	1.46	1.42	1.22	6.15	8.89	5.78	5.17	5.07	5.07	**	+	**	+
PLACE1000304	4.47	1.71	1.91	3.89	2.76	3.12	2.80	2.80	2.8				
PLACE1000308	4.91	2.41	1.59	3.39	5.24	3.59	2.01	2.78	2.78				
PLACE1000309	11.75	7.68	5.52	7.14	11.13	6.51	7.34	11.09	11.09				
PLACE1000312	4.15	1.12	1.95	3.37	3.51	3.75	2.70	2.85	2.85				
PLACE1000330	2.07	1.35	1.92	2.05	1.50	2.72	2.22	2.82	2.82			*	+
PLACE1000332	0.54	0.37	0.59	1.08	1.22	2.14	1.43	1.37	1.37	*	+	**	+
PLACE1000347	3.56	1.98	2.82	5.26	6.11	4.66	4.59	5.16	5.16	*	+	*	+
PLACE1000351	5.67	4.34	5.42	8.3	7.13	5.49	4.92	6.31	6.31				
PLACE1000374	9.15	6.32	6.28	12.33	8.13	8.69	5.60	5.63	5.63				
PLACE1000380	8.21	2.59	3.63	4.88	6.57	5.07	4.83	5.60	5.6				
PLACE1000383	3.43	2.31	1.31	2.37	3.17	2.14	2.59	1.96	1.96				
PLACE1000397	4.72	2.15	2.60	3.29	2.51	3.41	2.52	3.33	3.33				
PLACE1000401	8.18	4.62	4.15	5.55	6.29	6.94	5.61	6.88	6.88				
PLACE1000406	5.56	3.08	2.60	5.54	5.34	5.46	3.82	3.45	3.45				
PLACE1000412	3.31	2.01	1.64	4.18	4.67	3.93	2.55	2.54	2.54	*	+		
PLACE1000420	10.38	5.91	5.93	8.64	10.82	10.12	5.86	5.89	5.89				
PLACE1000421	3.59	3.04	2.31	4.45	4.08	3.36	2.89	3.75	3.75				
PLACE1000423	2.95	2.15	1.93	20.49	20.83	20.84	13.81	14.04	14.04	**	+	**	+
PLACE1000424	3	2.12	1.66	4.43	3.32	3.59	1.60	2.52	2.52	*	+		
PLACE1000430	3.63	1.51	1.58	2.45	2.43	3.11	1.57	3.03	3.03				
PLACE1000433	4.59	1.89	2.39	2.55	2.63	3.39	3.84	2.91	2.91				
PLACE1000435	4.53	3.13	3.03	9.09	8.39	8.75	5.45	3.19	3.19	**	+		
PLACE1000437	2.55	2.34	2.51	7.65	7.02	9.50	7.52	8.64	8.64	**	+	**	+
PLACE1000442	12.33	5.94	10.64	23.09	26.07	18.20	10.78	10.42	10.42	*	+		
PLACE1000444	9.31	6.03	5.50	16.99	19.05	17.38	8.02	10.01	10.01	**	+		
PLACE1000453	6.66	4.79	5.00	7.58	6.74	7.37	6.15	9.05	9.05				
PLACE1000456	4.25	3.10	2.24	3.67	3.13	4.02	3.33	4.78	4.78				
PLACE1000465	5.73	3.62	3.38	4.99	3.38	5.47	5.67	4.76	4.76				
PLACE1000481	5.42	4.78	5.17	5.8	8.48	10.90	5.11	5.58	5.58				
PLACE1000492	4.42	2.55	3.57	3.46	5.78	6.28	4.30	4.90	4.9				
PLACE1000508	4.11	3.53	2.58	3.28	3.70	3.99	2.37	3.96	3.96				
PLACE1000512	5.22	2.40	1.36	6.14	5.78	4.97	4.87	4.74	4.74				
PLACE1000540	2.6	2.41	1.99	4.78	4.15	4.34	1.97	1.70	1.7	**	+		
PLACE1000541	6.4	6.38	5.54	8.78	7.96	6.93	7.44	11.12	11.12	*	+	*	+

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Table 301

PLACE1000546	3.29	1.94	2.26	2.05	2.11	2.19	2.74	2.01	2.01				
PLACE1000547	5.79	5.41	5.37	8.99	6.38	9.62	5.74	8.94	8.94	*	+		
PLACE1000560	3.31	3.53	2.48	3.26	3.84	4.27	3.25	2.77	2.77				
PLACE1000562	5.48	3.54	4.16	6.47	7.13	6.86	5.29	6.77	6.77	*	+		
PLACE1000564	2.28	2.89	3.32	2.89	4.25	5.04	4.28	3.71	3.71			*	+
PLACE1000583	10.76	7.63	6.51	18.65	16.27	17.87	10.12	7.24	7.24	**	+		
PLACE1000587	7.2	4.11	4.88	9.4	11.04	9.29	6.85	6.39	6.39	*	+		
PLACE1000588	7.89	4.98	4.13	9.54	8.74	6.18	7.91	6.38	6.38				
PLACE1000596	7.64	7.46	10.08	8.78	8.56	8.98	4.59	7.82	7.82				
PLACE1000599	5.52	4.56	3.15	8.04	7.54	8.14	4.12	5.23	5.23	**	+		
PLACE1000605	4.13	3.66	3.53	4.62	5.26	5.10	5.59	5.89	5.89	**	+	**	+
PLACE1000610	3.95	3.19	2.63	4.04	4.12	4.83	3.09	3.87	3.87				
PLACE1000611	1.33	4.36	3.21	2.64	5.18	3.62	3.25	4.05	4.05				
PLACE1000626	3.93	3.49	2.73	5.31	3.91	4.11	4.05	3.66	3.66				
PLACE1000633	2.72	3.21	2.28	6.49	6.56	3.99	3.45	2.66	2.66	*	+		
PLACE1000636	2.12	1.92	1.69	2.35	1.07	2.86	1.27	1.58	1.58				
PLACE1000653	2.8	1.22	1.84	2.02	2.53	1.75	1.81	4.26	4.26				
PLACE1000656	9.31	7.34	8.14	10.31	10.47	9.31	12.81	14.00	14			**	+
PLACE1000663	1.27	0.67	0.99	1.89	1.74	1.74	1.26	1.65	1.65	*	+		
PLACE1000706	11.24	11.57	11.40	19.1	16.63	21.24	10.14	12.25	12.25	**	+		
PLACE1000712	1.84	3.33	4.09	6.55	4.54	5.89	4.64	6.19	6.19	*	+	*	+
PLACE1000716	2.94	0.83	1.14	1.67	1.91	1.48	1.97	1.39	1.39				
PLACE1000740	3.04	1.05	2.32	2.9	2.88	3.09	2.84	2.88	2.88				
PLACE1000748	6.27	3.34	3.42	5.4	6.40	3.86	2.84	3.25	3.25				
PLACE1000749	12.36	6.45	8.51	10.43	9.17	13.07	10.01	13.44	13.44				
PLACE1000751	2.38	1.17	1.02	4.52	3.07	2.68	4.21	4.95	4.95			**	+
PLACE1000755	2.51	1.55	1.57	3.46	3.45	4.83	2.60	2.77	2.77	*	+		
PLACE1000769	2.21	1.01	1.04	2.25	2.24	3.89	2.18	2.07	2.07				
PLACE1000778	5.1	3.19	2.79	4.88	3.83	3.91	3.55	2.38	2.38				
PLACE1000785	8.86	6.54	5.09	10.87	11.53	8.38	4.96	7.33	7.33				
PLACE1000786	4.27	4.46	2.71	4.67	3.49	4.67	3.76	4.74	4.74				
PLACE1000793	6.19	3.54	4.79	9.71	9.92	9.47	5.31	5.48	5.48	**	+		
PLACE1000795	9.72	4.72	5.55	4.52	4.48	3.39	4.32	4.67	4.67				
PLACE1000798	1.9	1.59	2.33	3.4	3.26	3.47	1.64	2.26	2.26	**	+		
PLACE1000812	2.3	2.38	1.85	3.32	3.27	4.96	2.41	3.24	3.24	*	+		
PLACE1000823	7.01	4.40	5.61	12.77	10.75	11.18	7.00	5.92	5.92	**	+		
PLACE1000825	6.13	3.73	3.27	7.05	6.77	5.20	4.28	5.79	5.79				
PLACE1000838	5.14	3.45	2.78	6.34	7.02	4.42	12.05	18.19	18.19			**	+
PLACE1000841	3.14	5.34	2.01	3.49	3.92	2.49	3.35	1.76	1.76				
PLACE1000843	4.46	2.15	3.63	4.5	6.77	4.11	1.87	4.89	4.89				
PLACE1000849	10.82	6.77	8.57	8.51	10.69	9.82	7.58	11.02	11.02				
PLACE1000856	2.83	1.51	2.02	3.37	2.62	2.73	2.59	1.96	1.96				
PLACE1000863	9.64	6.13	6.86	5.2	5.82	6.39	5.18	5.81	5.81				
PLACE1000876	7.89	4.38	5.88	7.14	5.51	8.48	7.94	7.18	7.18				
PLACE1000899	3.08	2.81	1.69	4.08	4.67	3.67	3.31	2.41	2.41	*	+		
PLACE1000907	16.44	10.14	7.86	22.19	25.12	16.66	7.95	11.86	11.86				
PLACE1000909	3.62	1.21	1.15	2.54	4.35	1.92	1.98	2.37	2.37				
PLACE1000912	6.9	3.41	4.10	5.35	5.89	5.24	4.38	4.49	4.49				
PLACE1000914	3.46	1.48	2.11	2.59	3.24	2.71	3.41	2.78	2.78				
PLACE1000918	0.79	0.41	0.85	0.84	1.40	1.52	0.67	1.33	1.33				
PLACE1000927	3.51	2.64	4.51	6.98	7.67	10.76	8.88	8.80	8.8	*	+	**	+
PLACE1000931	2.76	1.60	7.19	4.08	3.69	6.22	3.38	2.86	2.86				
PLACE1000944	2.02	1.08	0.51	4.48	5.07	3.55	3.07	1.96	1.96	**	+		
PLACE1000948	3.27	0.90	1.90	2.66	2.46	1.89	1.91	1.97	1.97				
PLACE1000958	2.75	1.53	1.51	2.98	2.99	3.11	3.17	4.29	4.29			*	+
PLACE1000972	6.67	4.02	6.08	7.27	8.73	6.46	4.61	7.73	7.73				

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Table 302

PLACE1000977	2.41	2.94	1.04	2.67	2.65	2.73	2.52	2.72	2.72				
PLACE1000979	9.34	4.89	6.74	13.62	13.31	16.23	7.57	8.33	8.33	**	+		
PLACE1000986	4.3	2.25	2.59	5.14	4.48	5.42	4.23	5.38	5.38	*	+		
PLACE1000987	7.13	4.86	5.70	7.21	6.57	6.09	7.59	7.62	7.62				
PLACE1001000	4.76	2.74	3.26	8.41	15.56	9.19	5.75	6.47	6.47	*	+	*	+
PLACE1001007	7.63	3.72	2.80	5.05	4.48	4.63	4.14	4.58	4.58				
PLACE1001010	2.3	1.89	2.06	3.44	3.64	3.65	1.96	2.59	2.59	**	+		
PLACE1001015	2.92	1.68	1.34	3.1	2.61	2.85	2.90	4.52	4.52				
PLACE1001016	7.21	2.36	3.51	5.03	5.51	6.32	4.81	4.26	4.26				
PLACE1001022	3.86	2.81	2.95	4.41	2.88	3.07	2.80	2.90	2.9				
PLACE1001024	3.88	2.20	3.13	2.3	2.95	4.59	2.73	3.68	3.68				
PLACE1001036	5.16	2.56	3.47	6.09	4.65	5.59	4.01	4.38	4.38				
PLACE1001038	28.81	14.88	16.16	21.4	17.66	19.48	21.32	28.28	28.28				
PLACE1001048	3.36	1.96	1.23	2.27	1.42	1.71	1.83	3.38	3.38				
PLACE1001054	7.9	5.99	5.59	6.24	6.31	4.84	4.36	6.39	6.39				
PLACE1001062	7.2	5.87	4.94	11.02	9.95	11.12	6.47	7.34	7.34	**	+		
PLACE1001063	1.41	1.69	1.15	2.65	3.68	3.53	1.70	3.59	3.59	**	+		
PLACE1001076	2.26	0.97	1.04	1.44	1.83	1.65	2.02	2.26	2.26				
PLACE1001081	12.46	8.57	9.92	15.12	11.87	13.36	10.20	12.65	12.65				
PLACE1001088	2.63	1.81	1.14	3.01	3.83	4.04	1.79	3.12	3.12	*	+		
PLACE1001092	6.88	3.43	3.30	7.95	6.98	7.48	8.10	6.69	6.69				
PLACE1001098	3.19	4.37	2.61	7.39	7.22	4.69	3.98	5.42	5.42	*	+		
PLACE1001100	4.67	2.56	3.28	9.14	7.82	8.01	4.36	9.43	9.43	**	+		
PLACE1001104	4.42	3.38	3.50	3.41	4.47	4.62	3.50	5.47	5.47				
PLACE1001114	6.37	3.02	3.19	9.14	6.05	8.38	4.84	6.58	6.58				
PLACE1001118	8.99	8.41	8.16	18.03	15.27	17.69	9.35	8.27	8.27	**	+		
PLACE1001123	3.67	2.98	3.43	6.53	5.15	5.14	7.08	8.09	8.09	*	+	**	+
PLACE1001136	6.74	4.90	3.41	11.43	11.92	9.20	6.63	6.95	6.95	*	+		
PLACE1001144	5.3	3.83	2.70	9.8	6.14	5.78	3.32	5.22	5.22				
PLACE1001147	6.12	3.41	3.43	6.85	6.67	6.42	5.03	6.28	6.28				
PLACE1001148	3.16	1.95	1.69	2.9	2.48	3.03	1.39	4.13	4.13				
PLACE1001159	1.33	1.09	1.58	2.28	2.10	1.76	1.96	4.06	4.06	*	+	*	+
PLACE1001168	1.82	0.78	1.16	1.62	1.75	2.87	2.70	3.06	3.06			**	+
PLACE1001171	2.35	1.34	1.61	1.46	3.10	2.35	2.90	1.94	1.94				
PLACE1001183	1.79	2.36	1.72	2.21	1.23	3.26	2.19	2.54	2.54				
PLACE1001185	5.46	4.74	4.40	6.41	7.88	5.56	6.42	6.55	6.55			**	+
PLACE1001201	6.18	4.83	3.75	5.34	5.15	4.77	3.30	2.90	2.9				
PLACE1001229	9.82	5.35	4.18	9.24	10.40	7.25	8.28	8.97	8.97				
PLACE1001231	9.55	4.73	5.18	5.83	6.30	4.83	3.56	5.51	5.51				
PLACE1001238	5.01	3.11	3.77	6.38	5.60	5.68	4.47	4.58	4.58	*	+		
PLACE1001241	2.02	1.58	1.43	2.15	2.00	2.71	2.20	2.62	2.62			*	+
PLACE1001242	20.17	17.27	18.47	18.81	15.90	19.20	22.68	25.15	25.15			**	+
PLACE1001247	9.52	6.34	6.64	10.32	8.10	12.11	5.62	8.24	8.24				
PLACE1001250	3.73	2.44	3.14	5.42	5.19	6.97	2.55	3.26	3.26	*	+		
PLACE1001257	6.68	5.11	2.77	13.34	10.34	12.61	4.57	6.16	6.16	**	+		
PLACE1001272	6.36	4.10	3.44	7.49	6.51	5.32	5.11	6.14	6.14				
PLACE1001279	2.31	1.92	1.89	3.68	2.64	2.53	2.56	2.17	2.17				
PLACE1001280	2.63	3.05	1.70	3.8	3.92	4.33	2.23	2.86	2.86	*	+		
PLACE1001294	1.16	0.01	1.04	3.47	4.82	2.72	5.00	5.65	5.65	*	+	**	+
PLACE1001295	4.29	3.95	3.46	3.47	3.85	3.06	4.31	5.32	5.32				
PLACE1001300	2.58	2.11	2.36	2.54	2.70	1.93	2.20	3.72	3.72				
PLACE1001304	6.77	5.82	8.24	17.77	13.08	18.60	7.86	9.34	9.34	**	+		
PLACE1001311	5.16	4.21	2.93	10.01	8.67	7.40	5.99	7.20	7.2	**	+	*	+
PLACE1001323	7.17	3.76	3.29	11.33	10.13	10.10	6.13	5.77	5.77	*	+		
PLACE1001325	2.41	1.50	1.58	5.07	4.29	3.56	1.94	2.67	2.67	**	+		
PLACE1001340	8.91	4.41	6.17	8	8.54	6.15	5.24	8.59	8.59				

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Table 303

PLACE1001344	2.76	1.50	1.35	2.41	3.45	2.46	1.70	2.00	2				
PLACE1001351	3.23	1.94	2.24	3.49	3.29	3.25	2.62	4.03	4.03				
PLACE1001366	4.38	2.83	2.63	5.26	5.03	5.59	4.18	3.48	3.48	*	+		
PLACE1001377	2.21	0.95	1.13	1.75	2.13	2.07	1.20	1.68	1.68				
PLACE1001383	3.71	1.90	1.47	3.95	6.26	1.71	1.64	2.49	2.49				
PLACE1001384	3.18	2.05	1.78	4.94	5.31	4.83	2.21	2.83	2.83	**	+		
PLACE1001387	4.38	2.11	2.54	3.04	2.86	4.24	2.34	3.05	3.05				
PLACE1001395	1.59	1.26	1.15	3.65	3.08	5.18	3.82	2.99	2.99	*	+	**	+
PLACE1001399	11.87	6.31	8.20	17.43	15.28	22.75	13.01	12.96	12.96	*	+		
PLACE1001401	1.52	0.25	1.01	1.14	0.80	1.79	1.18	1.33	1.33				
PLACE1001407	6.8	4.32	5.87	3.76	3.93	5.36	10.73	10.24	10.24			**	+
PLACE1001412	5.12	1.76	2.22	3.71	2.25	2.65	2.13	1.31	1.31				
PLACE1001414	15.81	9.44	8.70	18.1	13.15	13.80	12.97	12.27	12.27				
PLACE1001416	4.85	3.13	3.24	4.86	3.47	4.68	3.85	4.04	4.04				
PLACE1001433	34.75	27.32	25.94	41.44	46.72	44.79	20.21	24.82	24.82	**	+		
PLACE1001440	3.36	1.52	3.50	3.58	3.41	4.36	3.30	2.97	2.97				
PLACE1001456	2.82	2.23	1.05	4.35	4.43	4.27	3.77	3.38	3.38	*	+		
PLACE1001464	1.12	0.36	0.61	1.11	1.20	1.53	4.05	3.36	3.36			**	+
PLACE1001468	1	1.48	0.93	1.65	1.22	1.79	1.02	0.92	0.92				
PLACE1001484	5.54	3.35	3.73	7.43	7.35	10.20	3.71	4.16	4.16	*	+		
PLACE1001500	8.54	6.02	4.38	7.39	7.18	5.61	5.36	6.08	6.08				
PLACE1001502	6.06	4.35	3.12	4.46	5.05	4.69	4.11	4.84	4.84				
PLACE1001503	6.09	4.19	3.41	7.11	7.79	6.61	4.97	5.70	5.7	*	+		
PLACE1001505	20.88	12.93	14.68	15.96	17.98	17.32	9.92	14.48	14.48				
PLACE1001513	6.48	3.77	5.22	5.72	3.68	4.54	4.27	6.65	6.65				
PLACE1001516	10.93	7.17	9.57	12.22	8.39	12.84	8.43	11.33	11.33				
PLACE1001517	5.77	3.37	4.96	7.37	4.67	6.00	5.80	4.89	4.89				
PLACE1001523	23.41	10.77	16.66	12.24	9.55	12.27	10.99	12.94	12.94				
PLACE1001526	7.32	4.41	2.62	6.04	11.01	4.64	4.47	5.72	5.72				
PLACE1001534	4	1.96	2.04	4.38	6.28	3.78	3.64	3.03	3.03				
PLACE1001536	2.83	1.23	1.62	1.76	3.23	2.47	2.13	1.81	1.81				
PLACE1001545	36.23	12.22	23.79	37.99	57.83	39.02	33.62	43.32	43.32				
PLACE1001551	6.66	3.51	3.07	3.77	5.41	4.65	3.22	3.12	3.12				
PLACE1001564	1.35	0.83	1.14	1.76	1.17	1.28	1.94	2.02	2.02			**	+
PLACE1001570	0.93	0.34	0.64	2.16	2.60	4.80	1.89	2.31	2.31	*	+	**	+
PLACE1001571	7.95	4.12	4.74	8.82	11.30	11.21	6.14	8.15	8.15	*	+		
PLACE1001595	11.96	8.35	6.84	10.3	8.39	8.08	8.16	6.97	6.97				
PLACE1001602	10.71	5.17	5.52	7.59	10.40	7.10	3.81	6.12	6.12				
PLACE1001603	2.7	2.04	2.99	5.01	5.83	4.53	3.42	3.10	3.1	**	+		
PLACE1001608	2.44	2.10	2.41	3.4	4.03	5.05	2.95	3.88	3.88	*	+	*	+
PLACE1001610	5.43	4.80	5.73	13.88	9.92	13.14	7.65	8.25	8.25	**	+	**	+
PLACE1001611	3.56	2.47	3.24	3.84	3.75	5.73	3.92	3.82	3.82				
PLACE1001629	6.48	3.78	4.26	6.9	3.97	6.33	1.49	1.62	1.62			*	-
PLACE1001632	8.49	4.09	6.12	10.6	10.02	12.44	6.25	8.12	8.12	*	+		
PLACE1001634	3.06	1.40	1.54	5.61	6.76	4.47	2.48	4.23	4.23	*	+		
PLACE1001637	4.89	3.35	2.51	2.97	3.72	3.26	3.61	4.38	4.38				
PLACE1001640	6.92	2.46	2.49	7.67	8.87	5.84	4.54	7.69	7.69				
PLACE1001655	3.46	2.83	2.76	2.95	2.85	2.93	2.12	2.26	2.26			*	-
PLACE1001672	3.35	1.68	2.29	4.35	2.93	3.76	4.49	2.60	2.6				
PLACE1001676	1.74	0.78	2.18	1.12	1.17	2.29	1.50	2.79	2.79				
PLACE1001683	8.62	6.71	9.02	11.78	10.73	12.96	10.63	12.86	12.86	*	+	*	+
PLACE1001691	5.26	3.63	4.10	12.07	10.05	6.33	3.77	5.16	5.16	*	+		
PLACE1001692	4.42	2.12	2.27	4.86	5.36	4.90	4.07	3.26	3.26				
PLACE1001705	8.07	4.26	3.08	6.53	6.17	7.84	4.62	7.50	7.5				
PLACE1001716	3.8	1.68	2.70	3.78	4.85	3.53	4.66	5.71	5.71			*	+
PLACE1001720	1.91	1.29	2.34	3.39	3.22	2.45	2.24	3.40	3.4	*	+		

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Table 304

PLACE1001728	1.5	1.02	0.69	1.1	0.60	1.41	1.40	1.39	1.39					
PLACE1001729	6.79	3.57	3.61	3.84	3.10	4.27	2.54	6.08	6.08					
PLACE1001739	9.94	5.41	6.00	8.04	5.84	6.73	6.37	6.11	6.11					
PLACE1001740	1.57	0.32	0.49	0.97	1.11	1.42	1.06	0.82	0.82					
PLACE1001745	5.8	3.72	3.68	4.06	4.53	4.47	4.22	4.88	4.88					
PLACE1001746	3.57	1.52	1.71	4.99	5.18	6.01	3.66	5.62	5.62	*	+	*	+	
PLACE1001748	4.5	2.90	2.37	5.53	4.76	3.57	3.80	5.19	5.19					
PLACE1001753	3.51	2.28	3.04	2.88	3.35	3.77	3.11	5.17	5.17					
PLACE1001756	12.16	6.46	7.86	8.59	7.90	8.09	4.55	8.41	8.41					
PLACE1001760	8.72	4.93	5.18	11.47	11.77	9.41	7.48	10.20	10.2	*	+			
PLACE1001767	6.27	4.18	2.75	5.86	5.81	6.64	5.16	5.97	5.97					
PLACE1001771	1.84	1.98	1.82	2.36	2.85	5.41	2.31	1.87	1.87					
PLACE1001775	1.14	0.68	0.37	2.02	1.85	1.82	2.01	0.97	0.97	**	+			
PLACE1001777	17.14	13.64	18.62	21.05	26.38	21.12	40.01	76.23	76.23			*	+	
PLACE1001781	2.45	1.71	2.59	2.44	2.81	2.52	2.91	5.33	5.33					
PLACE1001783	4.43	2.58	2.66	2.32	3.33	2.65	2.54	4.19	4.19					
PLACE1001786	1.74	1.05	1.30	1.23	1.66	1.40	1.26	1.69	1.69					
PLACE1001788	5.13	2.94	2.51	5.8	4.90	5.17	4.40	3.27	3.27					
PLACE1001795	2.72	1.91	2.58	4.69	4.12	5.43	5.56	6.85	6.85	**	+	**	+	
PLACE1001799	3.74	3.45	3.29	3.65	3.39	3.75	3.22	5.05	5.05					
PLACE1001810	2.43	0.99	1.08	2.55	2.52	2.29	2.26	1.22	1.22					
PLACE1001817	6.6	4.05	4.21	9.77	8.48	6.29	8.47	8.36	8.36			*	+	
PLACE1001821	3.26	2.45	2.55	4.22	4.44	5.51	4.69	7.27	7.27	*	+	*	+	
PLACE1001836	4.29	2.26	1.81	2.56	3.00	3.57	2.41	2.93	2.93					
PLACE1001844	1.78	2.16	1.61	2.8	3.57	4.27	2.87	4.20	4.2	*	+	*	+	
PLACE1001845	2.41	1.41	2.18	4.39	5.00	4.06	2.82	2.33	2.33	**	+			
PLACE1001858	4.51	4.42	4.15	7.53	6.22	8.84	4.27	3.55	3.55	*	+			
PLACE1001869	3.09	2.60	2.08	2.74	2.72	3.73	1.99	3.40	3.4					
PLACE1001890	2.77	2.42	1.39	7.46	6.18	5.66	5.49	5.13	5.13	**	+	**	+	
PLACE1001897	2.18	2.26	1.85	6.69	5.35	5.34	8.97	9.82	9.82	**	+	**	+	
PLACE1001902	31.17	17.00	21.61	32.58	37.84	31.63	15.20	15.90	15.9					
PLACE1001904	3.92	3.02	3.25	2.81	3.73	3.19	4.96	4.49	4.49			*	+	
PLACE1001907	5.11	3.84	3.69	6.62	6.43	7.96	4.32	5.12	5.12	*	+			
PLACE1001910	1.87	3.06	2.35	3.3	3.81	3.68	14.39	26.30	26.3	*	+	**	+	
PLACE1001912	2.63	0.79	1.20	4.38	3.77	3.71	2.02	2.67	2.67	*	+			
PLACE1001918	10.38	7.15	8.90	11.66	9.55	15.16	10.15	14.11	14.11					
PLACE1001920	2.53	1.11	1.05	1.68	3.07	1.48	1.79	0.84	0.84					
PLACE1001928	8.17	4.57	3.74	7.72	5.90	6.65	3.44	4.51	4.51					
PLACE1001930	2.19	1.43	2.13	1.81	3.19	3.67	2.17	2.30	2.3					
PLACE1001949	2.08	1.14	1.41	2.07	1.98	1.77	1.69	2.05	2.05					
PLACE1001959	1.52	1.78	2.06	2.37	1.77	2.84	1.64	2.36	2.36					
PLACE1001969	4.16	2.19	2.62	4.17	4.18	4.94	2.88	2.78	2.78					
PLACE1001974	9.4	3.65	4.39	13.34	9.00	13.23	6.71	10.90	10.9					
PLACE1001981	1.69	1.37	1.20	2.64	1.90	2.12	1.52	1.67	1.67	*	+			
PLACE1001983	5.62	5.76	3.72	4.29	4.58	4.62	6.62	4.70	4.7					
PLACE1001989	5.11	2.90	3.88	7.82	6.79	6.73	3.99	4.04	4.04	*	+			
PLACE1002004	8.3	4.91	5.56	11.8	13.71	13.04	6.33	7.42	7.42	**	+			
PLACE1002008	14.39	6.47	3.72	18.67	18.94	18.14	8.81	8.95	8.95	*	+			
PLACE1002015	8.41	6.18	4.44	7.71	7.18	8.85	8.17	7.96	7.96					
PLACE1002044	1.09	1.29	1.71	3.03	2.76	2.81	3.27	3.06	3.06	**	+	**	+	
PLACE1002046	3.04	2.60	2.80	3.24	2.46	4.89	3.21	2.77	2.77					
PLACE1002052	1.9	0.59	1.24	2.33	1.00	2.14	1.49	1.25	1.25					
PLACE1002066	6.22	4.18	2.39	10.6	9.81	10.78	7.57	8.32	8.32	**	+	*	+	
PLACE1002072	4.3	3.28	3.34	7.74	8.18	6.54	4.13	5.29	5.29	**	+			
PLACE1002073	4.41	2.63	2.33	3.9	3.18	3.49	2.87	3.67	3.67					
PLACE1002080	9.31	4.83	4.67	8.96	9.64	10.72	7.21	6.98	6.98					

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Table 305

PLACE1002081	1.99	0.89	1.77	2.72	4.23	2.35	2.10	2.07	2.07				
PLACE1002090	14.44	6.66	9.78	10.42	12.14	11.62	5.32	7.78	7.78				
PLACE1002095	6.66	3.83	6.14	8.67	7.29	9.40	5.73	7.69	7.69				
PLACE1002102	11.71	6.09	6.01	11.63	6.93	8.62	6.39	8.11	8.11				
PLACE1002109	2.46	1.22	1.40	2.6	4.68	2.17	2.82	2.11	2.11				
PLACE1002115	3.01	0.88	0.58	1.13	2.98	1.33	0.18	1.10	1.1				
PLACE1002119	18.69	14.15	17.17	28.94	38.25	31.55	24.25	29.45	29.45	**	+	**	+
PLACE1002140	7.37	4.29	6.46	6.39	6.75	7.33	4.91	5.86	5.86				
PLACE1002150	2.02	1.18	2.19	3.93	4.63	3.78	3.27	2.55	2.55	**	+		
PLACE1002153	6.36	3.80	4.46	7.01	6.47	4.93	5.54	4.93	4.93				
PLACE1002157	2.68	1.47	1.39	4.12	3.06	4.68	2.90	3.69	3.69	*	+	*	+
PLACE1002163	7.63	2.62	3.61	7.02	7.14	5.85	5.07	6.08	6.08				
PLACE1002168	4.33	2.82	2.86	4.8	4.18	3.05	4.14	4.00	4				
PLACE1002170	2.98	1.54	1.88	1.56	1.84	1.46	1.96	1.92	1.92				
PLACE1002171	13.45	7.42	8.57	6.89	9.10	5.13	2.02	3.14	3.14			*	-
PLACE1002180	1.81	0.89	1.51	3.13	3.65	3.26	1.39	2.44	2.44	**	+		
PLACE1002184	2.38	1.68	1.24	6.52	7.00	7.36	6.04	5.01	5.01	**	+	**	+
PLACE1002200	3.74	3.15	2.61	3.65	2.78	3.93	3.98	4.06	4.06				
PLACE1002205	1.24	0.51	0.69	2.33	2.64	4.75	1.98	1.74	1.74	*	+	*	+
PLACE1002213	8.87	4.30	5.26	10.21	8.63	11.56	6.15	7.84	7.84				
PLACE1002219	1.89	0.82	0.74	1.44	2.66	1.62	0.97	0.77	0.77				
PLACE1002227	4.82	2.81	1.66	4.34	4.54	4.85	2.92	3.36	3.36				
PLACE1002253	3.86	2.60	1.93	1.41	2.78	1.93	2.88	2.14	2.14				
PLACE1002256	1.83	0.92	1.11	2.87	3.97	2.85	1.91	3.59	3.59	*	+	*	+
PLACE1002259	3.19	1.70	1.57	6.62	7.59	6.60	5.13	4.07	4.07	**	+	*	+
PLACE1002285	1.77	0.92	0.70	2.37	1.34	1.10	1.30	2.28	2.28				
PLACE1002301	3.7	3.54	3.53	4.57	5.90	8.65	6.82	8.88	8.88			**	+
PLACE1002310	2.48	1.29	1.37	3.99	3.09	4.29	7.69	9.72	9.72	*	+	**	+
PLACE1002311	3.44	2.13	1.55	3.07	3.48	2.34	2.76	2.45	2.45				
PLACE1002319	4.6	2.18	2.82	2.38	2.25	2.70	1.39	2.13	2.13				
PLACE1002329	4.19	2.99	2.11	3.47	3.41	5.33	3.47	4.66	4.66				
PLACE1002333	1.41	1.34	1.43	2.55	1.71	1.03	1.08	1.25	1.25			*	-
PLACE1002342	3.55	2.39	2.93	7.53	5.67	7.31	3.57	4.06	4.06	**	+		
PLACE1002343	3.11	2.65	3.16	2.86	3.12	2.88	2.90	5.44	5.44				
PLACE1002355	3.89	1.69	1.70	3.76	3.03	3.60	3.29	2.58	2.58				
PLACE1002358	3.55	2.39	2.49	3.8	3.99	2.81	2.23	2.70	2.7				
PLACE1002359	8	4.42	4.71	3.91	5.64	5.32	4.07	5.01	5.01				
PLACE1002374	14.74	8.20	8.86	9.64	10.72	8.98	11.09	14.20	14.2				
PLACE1002376	7.57	5.16	5.69	9.15	8.50	11.00	8.02	8.55	8.55	*	+	*	+
PLACE1002379	3.61	3.25	3.56	3.36	3.66	3.11	4.20	4.20	4.2			**	+
PLACE1002386	5.82	2.32	2.77	4.29	2.48	5.32	6.23	7.32	7.32			*	+
PLACE1002395	5.61	3.00	2.85	4.9	4.34	4.62	4.54	4.04	4.04				
PLACE1002399	2.61	1.20	1.56	3.06	2.87	4.76	3.56	3.31	3.31			*	+
PLACE1002407	4.59	2.71	2.96	2.81	2.75	3.28	1.95	2.26	2.26				
PLACE1002433	5.13	3.15	3.02	4.68	5.35	5.03	2.23	2.89	2.89				
PLACE1002437	3.54	1.57	2.70	3.76	3.24	3.17	2.59	4.55	4.55				
PLACE1002438	1.21	1.24	1.22	1.63	1.79	2.23	2.23	2.71	2.71	*	+	**	+
PLACE1002446	5.14	2.19	2.50	4.51	3.25	4.13	6.69	7.98	7.98			*	+
PLACE1002447	2.92	2.41	2.19	1.36	3.06	1.99	2.41	2.93	2.93				
PLACE1002450	1.44	2.03	1.72	3.08	3.13	3.49	2.56	2.00	2	**	+		
PLACE1002462	2.28	1.70	1.59	1.95	1.67	3.14	1.58	2.39	2.39				
PLACE1002465	3.1	2.98	2.42	2.1	3.45	3.05	2.13	2.02	2.02			*	-
PLACE1002474	2.91	2.82	2.76	8.43	9.88	7.40	6.02	7.81	7.81	**	+	**	+
PLACE1002477	8.13	3.74	5.00	11.28	9.50	9.10	9.42	12.59	12.59	*	+	*	+
PLACE1002493	1.9	2.19	1.21	1.77	1.63	1.93	2.11	3.26	3.26				
PLACE1002497	2.74	1.52	2.43	1.73	1.95	2.51	2.01	3.14	3.14				

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Table 306

PLACE1002499	3.87	1.99	3.01	5.9	5.94	5.28	3.14	5.21	5.21	**	+		
PLACE1002500	3.82	3.46	3.57	5.63	5.50	7.08	4.28	4.54	4.54	**	+	**	+
PLACE1002514	2.68	2.18	1.93	2.67	2.24	2.48	3.81	2.98	2.98			*	+
PLACE1002518	3.35	3.89	3.09	9.93	9.60	8.45	4.26	3.29	3.29	**	+		
PLACE1002529	1.4	1.36	1.04	1.77	2.14	1.22	1.26	1.64	1.64				
PLACE1002532	8.72	6.46	7.19	6.81	6.68	6.18	7.67	10.12	10.12				
PLACE1002536	4.9	1.91	3.90	5.09	4.55	3.56	4.82	3.96	3.96				
PLACE1002537	3.14	1.37	1.42	3.63	3.37	4.11	2.67	3.94	3.94	*	+		
PLACE1002539	3.39	2.92	3.22	4.41	4.54	5.47	3.82	4.68	4.68	*	+	*	+
PLACE1002547	5.53	5.37	5.59	8.39	7.22	9.28	8.89	10.18	10.18	**	+	**	+
PLACE1002571	4.43	2.94	4.05	4.84	4.88	7.44	3.32	5.08	5.08				
PLACE1002578	5.19	3.96	3.76	12.25	10.98	12.86	5.35	7.25	7.25	**	+	*	+
PLACE1002583	1.66	0.32	1.44	1.04	1.08	1.16	1.18	0.97	0.97				
PLACE1002591	3.86	2.09	2.10	2.84	2.83	2.65	2.44	2.62	2.62				
PLACE1002598	3.84	2.11	2.49	1.35	1.31	2.14	2.05	2.70	2.7				
PLACE1002604	2.65	2.17	1.64	2.8	3.94	3.24	2.45	2.54	2.54				
PLACE1002612	8.01	6.63	6.63	12.1	11.80	12.23	8.71	11.33	11.33	**	+	*	+
PLACE1002625	2.58	1.69	1.51	2.59	2.61	4.00	1.54	3.25	3.25				
PLACE1002638	2.18	2.76	3.22	4.42	3.44	3.29	2.42	3.06	3.06				
PLACE1002655	3.25	4.16	4.18	10.46	6.84	7.33	3.29	5.31	5.31	*	+		
PLACE1002665	4.13	3.33	2.98	6.38	8.85	5.64	3.53	3.33	3.33	*	+		
PLACE1002685	5.53	3.42	2.72	4.03	3.03	3.10	2.10	4.59	4.59				
PLACE1002692	8.81	6.44	4.56	11.47	12.80	10.48	5.21	5.98	5.98	*	+		
PLACE1002714	6.78	4.06	3.36	6.88	8.05	6.09	4.05	4.56	4.56				
PLACE1002721	6.84	4.40	5.49	7.7	6.58	8.37	3.72	4.94	4.94				
PLACE1002722	0.74	0.78	0.84	1.77	1.11	1.67	0.84	1.69	1.69	*	+		
PLACE1002726	3.49	5.71	5.81	8.46	6.47	7.89	5.02	5.08	5.08				
PLACE1002756	3.26	2.58	3.14	6.13	6.45	6.35	3.62	4.77	4.77	**	+	*	+
PLACE1002768	3.97	1.25	1.67	3.3	2.50	2.51	2.78	3.00	3				
PLACE1002772	1.35	0.09	0.96	0.92	1.25	1.40	1.29	1.37	1.37				
PLACE1002775	14.42	7.79	9.64	10.55	11.21	17.27	12.36	11.82	11.82				
PLACE1002780	1.98	1.39	1.23	1.94	2.57	3.18	3.07	5.79	5.79			*	+
PLACE1002782	3.02	0.85	1.61	1.99	1.37	3.05	1.65	1.52	1.52				
PLACE1002794	2.49	1.48	2.20	1.75	2.76	3.63	2.18	2.11	2.11				
PLACE1002795	1.27	0.70	0.60	1.08	1.69	1.49	0.76	0.93	0.93				
PLACE1002811	3.67	1.25	0.81	2.9	2.86	1.50	2.33	2.50	2.5				
PLACE1002815	5.44	2.94	2.29	7.27	15.00	10.36	12.84	16.74	16.74	*	+	**	+
PLACE1002816	8.2	3.96	3.92	6.25	6.25	6.46	5.01	6.23	6.23				
PLACE1002822	3.34	1.86	2.08	2.36	4.04	3.46	2.71	3.36	3.36				
PLACE1002833	7.79	2.79	4.10	8.87	10.15	5.51	5.02	6.82	6.82				
PLACE1002834	10.13	4.35	5.31	13.91	16.58	13.43	4.69	8.55	8.55	*	+		
PLACE1002835	10.05	3.42	5.57	6.59	4.99	6.00	6.06	6.48	6.48				
PLACE1002839	1.69	0.45	1.30	1.57	1.51	2.09	0.58	1.24	1.24				
PLACE1002851	0.76	0.42	0.82	8.19	10.42	3.82	2.14	3.56	3.56	*	+	**	+
PLACE1002853	2.74	1.59	0.90	3.41	5.47	2.91	2.59	4.00	4				
PLACE1002881	6.4	4.73	3.84	9.33	10.46	8.15	5.45	5.65	5.65	*	+		
PLACE1002901	24.97	13.25	21.58	24.2	26.27	27.37	19.88	33.42	33.42				
PLACE1002904	1.92	2.64	1.54	1.71	2.53	1.56	1.90	1.68	1.68				
PLACE1002905	3.55	1.81	2.93	4.92	3.38	5.48	3.25	4.03	4.03				
PLACE1002908	3.03	1.68	2.53	3.06	3.13	3.59	2.41	3.70	3.7				
PLACE1002911	17.43	10.47	13.64	12.95	9.50	14.36	14.97	14.68	14.68				
PLACE1002941	4.78	1.82	1.86	3.71	4.48	2.93	2.39	2.15	2.15				
PLACE1002950	9.17	5.50	4.49	8.77	14.38	6.75	5.85	4.90	4.9				
PLACE1002955	30.87	12.83	9.17	24.34	31.40	20.44	28.45	32.62	32.62				
PLACE1002958	12.6	6.07	8.49	13.92	20.27	16.63	20.63	26.24	26.24	*	+	**	+
PLACE1002962	1.57	0.87	0.79	1.15	2.51	1.72	1.24	1.43	1.43				

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Table 307

PLACE1002967	5.1	2.51	3.09	6.76	6.45	5.80	4.18	4.06	4.06	*	+		
PLACE1002968	1.23	0.90	0.78	1.96	2.73	1.63	1.67	2.25	2.25	*	+	**	+
PLACE1002976	14.62	6.59	8.58	14.43	17.61	21.24	10.88	15.26	15.26				
PLACE1002991	9.09	3.33	5.17	10.69	10.94	9.19	4.59	4.38	4.38				
PLACE1002993	4.97	3.72	3.40	7.49	6.57	6.94	4.40	4.67	4.67	**	+		
PLACE1002996	4.17	2.53	2.14	3.73	3.53	2.43	2.53	3.20	3.2				
PLACE1003010	14.09	9.21	8.66	11.39	9.01	12.05	11.70	11.85	11.85				
PLACE1003025	3.37	1.92	1.25	3.12	3.46	2.82	2.56	2.83	2.83				
PLACE1003027	2.78	1.30	1.63	3.36	4.14	4.94	2.51	3.33	3.33	*	+		
PLACE1003044	5.29	2.38	3.63	5.05	4.60	4.39	4.30	3.74	3.74				
PLACE1003045	1.31	0.14	0.41	1.12	0.74	1.58	0.92	1.66	1.66				
PLACE1003052	5.81	2.44	2.52	4.24	6.72	5.03	2.74	4.06	4.06				
PLACE1003083	1.98	0.63	0.30	1.59	1.48	1.45	1.09	1.36	1.36				
PLACE1003085	8.86	4.56	4.41	4.48	5.13	3.76	5.79	5.25	5.25				
PLACE1003092	4.95	2.80	2.49	4.61	7.21	5.11	3.15	5.59	5.59				
PLACE1003097	2.48	1.08	1.75	2.13	2.19	3.46	1.83	1.87	1.87				
PLACE1003100	5.55	3.04	3.54	4.48	2.63	4.78	3.66	4.38	4.38				
PLACE1003108	2.43	2.01	1.88	3.79	4.20	5.56	3.02	3.15	3.15	*	+	**	+
PLACE1003115	5.59	4.45	4.08	5.2	3.47	4.38	3.94	4.36	4.36				
PLACE1003120	9.1	5.05	6.99	11.92	11.69	8.39	4.33	5.35	5.35				
PLACE1003135	7.15	3.42	2.81	2	1.71	2.50	1.33	2.53	2.53				
PLACE1003136	9.4	3.19	5.96	7.56	7.72	8.01	6.80	8.18	8.18				
PLACE1003141	1.43	1.20	0.97	1.12	1.71	2.12	1.29	2.62	2.62				
PLACE1003145	1.17	1.98	1.88	1.29	0.85	1.19	1.52	2.74	2.74				
PLACE1003147	3.88	1.84	2.10	3.04	3.09	5.16	2.94	6.44	6.44				
PLACE1003153	2.04	1.22	1.34	1.76	3.27	2.50	1.12	2.13	2.13				
PLACE1003163	5.21	2.54	2.21	3.71	2.70	3.59	1.58	3.29	3.29				
PLACE1003172	17.21	13.29	11.63	20.51	17.81	16.21	12.82	14.76	14.76				
PLACE1003174	1.86	0.95	0.96	2.33	2.68	2.13	2.07	2.85	2.85	*	+	*	+
PLACE1003176	1.87	0.85	0.99	0.69	1.79	1.46	1.77	2.02	2.02				
PLACE1003181	2.42	1.29	1.30	1.36	1.88	1.93	2.33	2.76	2.76				
PLACE1003184	4.02	2.35	1.57	1.09	1.42	1.68	2.02	2.95	2.95				
PLACE1003190	12.59	7.17	8.42	3.7	4.03	4.95	5.55	3.22	3.22	*	-	*	-
PLACE1003200	0.16	0.08	0.11	0.98	0.55	0.76	0.91	1.63	1.63	**	+	**	+
PLACE1003205	10.63	4.75	4.99	13.42	19.02	15.56	5.60	9.62	9.62	*	+		
PLACE1003209	1.33	0.58	0.91	1.06	1.71	1.13	1.44	1.84	1.84			*	+
PLACE1003214	3.74	1.92	0.96	2.48	3.08	2.07	2.80	1.58	1.58				
PLACE1003229	4.01	2.47	1.89	4.67	6.17	5.71	3.46	3.20	3.2	*	+		
PLACE1003238	0.55	1.29	0.72	1.01	1.04	1.42	1.89	4.82	4.82			*	+
PLACE1003249	4.21	2.68	2.29	5.89	6.34	7.49	3.21	4.18	4.18	**	+		
PLACE1003256	15.42	10.76	11.86	18.06	20.59	21.48	20.54	17.58	17.58	*	+	*	+
PLACE1003258	1.59	3.70	0.75	1.91	1.78	1.15	1.24	1.39	1.39				
PLACE1003279	5.6	4.25	1.88	7.33	8.87	7.26	3.36	5.26	5.26	*	+		
PLACE1003294	5.96	3.04	2.55	5.19	4.93	5.17	2.65	4.69	4.69				
PLACE1003296	3.69	1.73	1.93	4.06	3.41	2.82	2.94	3.29	3.29				
PLACE1003297	6.38	2.82	3.60	6.92	8.35	6.63	3.36	5.38	5.38				
PLACE1003302	6.92	3.76	5.11	9.34	12.52	9.10	7.08	7.90	7.9	*	+		
PLACE1003334	0.67	1.10	1.68	2.93	3.55	4.00	2.24	3.22	3.22	**	+	*	+
PLACE1003337	10.11	6.39	4.50	7.53	11.58	10.30	6.19	6.17	6.17				
PLACE1003342	1.8	1.54	1.48	1.86	2.85	3.11	2.71	3.37	3.37			**	+
PLACE1003343	0.54	0.36	0.34	0.71	0.79	1.22	0.47	0.55	0.55	*	+		
PLACE1003344	24.27	18.53	13.01	17.74	21.43	22.39	17.02	18.57	18.57				
PLACE1003353	17.73	10.09	9.18	16.17	17.86	14.13	8.53	9.79	9.79				
PLACE1003361	5.88	2.41	3.54	11.34	11.94	9.89	3.99	5.89	5.89	**	+		
PLACE1003366	6.48	3.29	5.05	6.5	8.30	6.96	4.61	4.25	4.25				
PLACE1003369	2.89	2.16	1.46	3.79	2.79	2.98	2.58	2.98	2.98				

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Table 308

PLACE1003372	4.86	3.69	3.10	6.36	6.08	6.40	5.24	6.26	6.26	*	+	*	+
PLACE1003373	4.59	2.14	1.77	6.44	8.87	7.14	3.34	3.58	3.58	*	+		
PLACE1003375	1.64	2.20	2.31	1.72	2.46	2.62	1.19	1.43	1.43			*	-
PLACE1003378	2.12	1.60	1.04	2.23	1.84	1.68	2.18	2.69	2.69				
PLACE1003383	2.45	1.53	0.51	2.22	2.04	0.76	1.14	1.36	1.36				
PLACE1003394	8.16	3.88	4.89	10.77	12.17	8.54	8.17	10.02	10.02	*	+		
PLACE1003401	3.67	0.79	0.99	1.2	1.46	1.82	0.45	1.86	1.86				
PLACE1003405	6.01	6.00	6.98	4.76	7.61	8.04	6.47	7.65	7.65				
PLACE1003407	4.49	4.04	3.71	5.05	5.22	5.15	5.12	5.61	5.61	*	+	**	+
PLACE1003420	4.75	4.07	3.59	7.55	10.89	8.12	4.15	6.01	6.01	*	+		
PLACE1003428	2.19	2.41	3.05	3.29	4.02	4.47	2.16	2.43	2.43	*	+		
PLACE1003432	7.17	3.85	3.68	4.37	7.22	7.66	3.81	6.34	6.34				
PLACE1003438	9.06	3.37	4.39	5.86	7.12	5.43	5.87	7.15	7.15				
PLACE1003452	3.13	1.08	2.21	1.29	5.01	2.29	2.22	2.52	2.52				
PLACE1003454	8.4	4.68	5.18	7.33	6.34	9.17	4.92	7.46	7.46				
PLACE1003455	13.75	5.01	6.05	6.83	8.91	9.83	8.45	9.21	9.21				
PLACE1003456	7.28	4.38	4.13	10.64	12.00	13.60	7.62	7.20	7.2	**	+		
PLACE1003460	7.84	3.76	6.10	10.15	7.44	7.77	6.55	7.66	7.66				
PLACE1003478	3.33	0.56	0.93	2.01	1.78	1.24	0.65	0.96	0.96				
PLACE1003484	7.55	4.57	2.88	11.32	16.35	7.83	7.21	9.47	9.47				
PLACE1003493	14.03	6.96	6.73	11.22	11.97	14.63	9.74	9.34	9.34				
PLACE1003503	42.11	19.93	34.28	29.63	36.26	35.89	25.50	29.49	29.49				
PLACE1003505	2.24	1.06	0.89	0.91	0.90	1.59	2.08	1.73	1.73				
PLACE1003516	1.01	0.49	0.89	2.17	2.40	2.58	1.68	1.86	1.86	**	+	**	+
PLACE1003519	39.78	23.99	30.04	55.6	50.01	57.71	22.97	28.09	28.09	*	+		
PLACE1003520	45.85	22.30	34.27	66.52	30.94	72.87	38.79	44.73	44.73				
PLACE1003521	1.43	0.65	0.89	2.33	3.32	0.95	2.10	3.87	3.87			*	+
PLACE1003525	15.69	8.19	8.09	12.57	19.45	12.58	15.38	18.26	18.26				
PLACE1003528	126.72	75.71	77.51	102.34	128.72	89.84	56.09	57.39	57.39				
PLACE1003529	10.31	6.25	7.90	10.63	11.63	11.54	9.31	9.78	9.78				
PLACE1003537	3.45	1.76	2.18	3.36	4.60	3.48	5.58	5.15	5.15			**	+
PLACE1003549	3.96	2.80	3.67	4.57	2.88	5.08	2.97	4.32	4.32				
PLACE1003553	6.15	2.35	3.07	4.85	4.12	5.00	3.14	3.29	3.29				
PLACE1003566	5.25	2.36	2.80	5.45	5.03	6.90	4.92	5.27	5.27				
PLACE1003568	1.39	1.43	0.56	1.66	1.56	1.27	1.01	0.83	0.83				
PLACE1003573	2.04	1.89	1.09	2.09	2.81	1.71	1.61	1.69	1.69				
PLACE1003575	3.94	2.36	1.55	4.2	5.03	5.48	3.67	2.41	2.41	*	+		
PLACE1003583	1.25	0.21	0.91	0.63	1.54	1.28	1.19	0.85	0.85				
PLACE1003584	3.17	2.52	1.33	5.76	4.75	5.94	2.30	3.30	3.3	**	+		
PLACE1003592	6.37	4.34	3.44	8.54	12.20	11.57	7.98	8.85	8.85	*	+	*	+
PLACE1003593	0.73	1.09	0.64	1.3	1.69	1.81	0.49	1.57	1.57	*	+		
PLACE1003594	16.13	4.42	11.69	14.87	17.87	21.56	10.51	11.29	11.29				
PLACE1003596	5.64	5.18	5.93	10.49	15.28	7.57	7.20	9.60	9.6			*	+
PLACE1003598	13.48	8.08	6.25	8.41	8.96	8.69	7.81	8.78	8.78				
PLACE1003602	3.72	2.13	1.45	3.5	3.57	3.37	2.64	3.45	3.45				
PLACE1003605	18.39	10.93	10.02	16.96	17.66	21.30	9.74	14.50	14.5				
PLACE1003611	3.07	0.86	1.19	2.62	2.97	3.49	1.69	2.05	2.05				
PLACE1003618	2.42	0.71	0.96	1.64	1.41	1.56	1.78	2.12	2.12				
PLACE1003625	3.62	1.30	2.39	3.11	4.04	4.15	3.30	3.49	3.49				
PLACE1003626	13.07	5.94	8.16	14.48	13.10	14.74	12.62	11.51	11.51				
PLACE1003630	3.48	2.42	1.94	3.18	3.39	2.97	3.11	3.27	3.27				
PLACE1003635	2.04	1.03	1.44	2.07	2.17	2.34	1.81	1.67	1.67				
PLACE1003638	3.27	2.36	1.79	4.52	4.52	3.82	3.33	3.31	3.31	*	+		
PLACE1003644	3.31	2.33	2.10	5.21	5.95	5.73	4.05	4.05	4.05	**	+	*	+
PLACE1003654	4.23	1.54	1.89	1.81	2.78	2.00	0.89	2.32	2.32				
PLACE1003656	2.23	0.80	1.38	1.4	1.47	1.90	1.48	2.10	2.1				

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Table 309

PLACE1003660	3.6	2.90	2.17	3.69	3.98	5.22	2.65	3.15	3.15				
PLACE1003669	3.72	1.83	1.76	4.6	5.24	5.00	3.90	4.38	4.38	*	+		
PLACE1003670	15.52	7.07	8.39	9.52	9.26	10.68	8.82	8.03	8.03				
PLACE1003671	4.94	3.13	2.14	3.75	4.23	3.08	3.20	4.09	4.09				
PLACE1003697	3.08	0.80	1.06	3.54	2.83	2.50	7.26	8.03	8.03			**	+
PLACE1003704	11.2	5.78	7.63	14.43	11.92	13.54	6.97	9.55	9.55	*	+		
PLACE1003709	4.98	0.98	1.82	0.79	0.50	1.26	1.00	1.96	1.96				
PLACE1003711	5.06	3.03	2.94	3.49	4.07	3.66	3.26	4.30	4.3				
PLACE1003723	4.06	2.93	3.32	6.92	5.34	6.03	4.19	5.65	5.65	**	+	*	+
PLACE1003724	9.61	5.81	6.68	10.85	14.36	13.13	7.86	7.40	7.4	*	+		
PLACE1003737	1.82	0.70	1.20	1.4	2.78	1.47	0.99	1.14	1.14				
PLACE1003738	4.42	2.23	2.32	2.25	3.92	3.77	2.75	4.94	4.94				
PLACE1003742	4.22	2.78	3.39	5.61	5.88	6.94	5.65	8.11	8.11	*	+	*	+
PLACE1003744	10.38	5.06	4.96	6	6.16	5.58	7.58	7.15	7.15				
PLACE1003758	2.34	1.24	1.52	3.36	2.67	2.23	1.96	3.95	3.95				
PLACE1003760	12.25	10.24	12.40	34.22	35.40	36.07	24.12	29.73	29.73	**	+	**	+
PLACE1003762	3.15	2.22	1.75	4.15	5.03	5.81	2.19	3.25	3.25	*	+		
PLACE1003765	3.6	2.58	2.17	4.49	5.32	6.00	3.44	2.48	2.48	*	+		
PLACE1003768	2.32	0.82	0.97	3.88	3.45	2.85	1.41	2.13	2.13	*	+		
PLACE1003771	1.14	0.42	0.47	3.82	4.60	4.57	2.76	2.88	2.88	**	+	**	+
PLACE1003772	15.91	10.99	11.28	22.4	31.67	17.46	9.36	14.35	14.35				
PLACE1003783	1.42	1.64	0.56	2.3	1.57	1.94	2.32	2.86	2.86			*	+
PLACE1003784	1.03	0.77	0.68	0.97	1.55	1.05	1.26	0.82	0.82				
PLACE1003788	1.09	0.76	0.74	1.58	0.81	1.20	1.20	1.12	1.12				
PLACE1003795	3.57	3.15	3.29	4.82	6.11	5.73	4.14	3.97	3.97	**	+	**	+
PLACE1003827	4.25	3.25	4.26	3.97	4.73	4.26	4.86	4.32	4.32				
PLACE1003833	5.49	4.93	3.72	7.29	6.79	7.39	4.43	6.36	6.36	*	+		
PLACE1003839	15.63	9.41	9.25	19.2	21.48	17.62	11.21	10.43	10.43	*	+		
PLACE1003845	7.01	4.24	4.12	7.35	7.87	5.86	10.74	9.90	9.9			**	+
PLACE1003850	8.77	5.05	5.31	6.16	11.18	6.64	4.92	6.94	6.94				
PLACE1003852	1.98	0.95	1.19	2.52	2.43	1.55	2.10	2.14	2.14				
PLACE1003858	1.86	1.56	1.42	0.9	3.73	1.64	1.18	2.61	2.61				
PLACE1003861	3.4	2.90	2.88	4.73	4.58	4.45	3.62	4.50	4.5	**	+	*	+
PLACE1003864	2.18	1.73	1.70	2.15	2.33	2.94	1.58	1.90	1.9				
PLACE1003870	6.85	4.56	2.90	9.94	13.82	9.81	3.57	5.78	5.78	*	+		
PLACE1003885	3.97	2.09	1.62	4.09	4.19	2.32	1.33	1.78	1.78				
PLACE1003886	6.25	3.53	4.72	4.17	5.68	4.34	4.84	5.28	5.28				
PLACE1003888	2.5	2.14	1.29	2.33	2.24	2.51	1.57	1.20	1.2				
PLACE1003892	0.63	0.82	0.35	1.2	1.75	1.76	1.12	1.37	1.37	*	+	*	+
PLACE1003900	2.12	3.11	2.67	2.84	3.42	2.21	3.08	3.08	3.08				
PLACE1003902	2.67	2.85	2.44	2.17	3.06	3.38	2.09	2.93	2.93				
PLACE1003903	3.07	2.52	2.90	2.6	2.59	4.30	2.16	2.90	2.9				
PLACE1003915	2.93	1.59	2.90	5.14	5.88	4.52	4.31	3.51	3.51	*	+		
PLACE1003918	6.79	4.23	4.22	10.17	14.99	6.89	4.36	4.29	4.29				
PLACE1003923	2.38	0.83	1.07	2.53	2.23	1.52	2.50	2.86	2.86				
PLACE1003932	6.11	3.09	2.41	4.35	4.43	3.41	2.40	3.60	3.6				
PLACE1003936	3.26	3.57	2.07	4.2	6.78	4.35	2.70	3.36	3.36				
PLACE1003966	2.8	1.71	1.81	3.31	3.64	3.17	2.63	3.00	3	*	+		
PLACE1003968	3.23	5.15	4.73	6.02	6.25	7.79	6.80	6.11	6.11	*	+	*	+
PLACE1004018	3.13	3.22	4.15	3.49	4.47	4.76	3.66	5.03	5.03				
PLACE1004020	8.8	4.07	3.96	10.35	11.19	10.96	7.35	8.57	8.57	*	+		
PLACE1004028	2.58	0.63	1.65	1.41	1.48	2.22	1.55	1.12	1.12				
PLACE1004034	14.58	6.23	5.10	4.38	6.92	4.97	2.01	1.93	1.93				
PLACE1004042	13.64	6.23	8.71	10.86	12.72	14.34	11.39	17.16	17.16				
PLACE1004078	4.38	2.37	2.45	5.69	4.75	6.84	3.40	5.09	5.09	*	+		
PLACE1004103	7.95	4.34	4.17	15.49	14.70	18.99	9.99	10.73	10.73	**	+	*	+

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Table 310

PLACE1004104	2.15	1.27	0.85	1.43	1.39	2.13	1.09	2.01	2.01					
PLACE1004113	4.08	1.68	3.31	4.6	4.46	4.54	3.36	3.05	3.05					
PLACE1004114	2.54	0.84	0.51	1.58	2.53	1.82	2.42	1.88	1.88					
PLACE1004118	1.98	1.29	1.42	1.63	4.01	2.38	1.61	2.11	2.11					
PLACE1004128	12.83	9.07	9.04	8.02	8.50	9.63	5.06	6.17	6.17			*	-	
PLACE1004130	2.24	2.05	1.32	1.83	3.44	3.33	2.12	1.72	1.72					
PLACE1004149	18	9.56	12.62	22.09	23.13	25.79	15.85	17.31	17.31	*	+			
PLACE1004156	8.66	4.78	4.97	11.23	13.14	12.83	5.87	8.14	8.14	*	+			
PLACE1004160	31.97	23.56	27.55	20.37	16.69	25.95	28.83	35.50	35.5					
PLACE1004161	12.19	6.98	6.65	7.81	8.30	9.68	8.49	8.65	8.65					
PLACE1004166	10.59	4.49	3.61	8.56	19.40	8.04	5.20	7.58	7.58					
PLACE1004168	9.22	3.40	4.94	7.74	9.05	6.39	5.52	5.88	5.88					
PLACE1004170	0.56	0.65	1.17	2.02	1.70	2.28	1.72	2.24	2.24	**	+	**	+	
PLACE1004178	5.68	2.50	3.59	4.97	6.58	6.01	4.61	7.20	7.2					
PLACE1004183	4.44	2.26	4.45	5.52	5.64	5.63	4.08	3.85	3.85					
PLACE1004197	1.06	1.17	1.74	1.07	1.49	1.13	2.10	1.67	1.67					
PLACE1004199	9.96	6.47	8.63	4.5	6.39	5.99	10.80	9.20	9.2					
PLACE1004203	6.09	3.61	5.37	4.74	4.70	4.68	5.77	5.62	5.62					
PLACE1004242	7.53	2.60	2.25	8.1	9.90	6.46	4.60	5.49	5.49					
PLACE1004249	25.51	14.54	13.20	20.9	26.96	19.21	17.71	21.13	21.13					
PLACE1004255	1.02	0.75	0.36	0.86	1.57	1.36	0.69	1.07	1.07					
PLACE1004256	4.42	1.01	3.09	9.24	13.36	13.94	12.44	10.96	10.96	**	+	**	+	
PLACE1004257	4.54	1.21	1.79	4.96	4.55	4.58	3.59	4.84	4.84					
PLACE1004258	3.59	2.38	2.35	2.98	2.70	2.85	3.20	2.02	2.02					
PLACE1004270	3.93	3.24	3.36	3.85	4.28	6.05	3.70	3.05	3.05					
PLACE1004272	4.04	2.85	3.28	3.85	5.74	5.17	3.42	6.23	6.23					
PLACE1004273	83.7	57.27	49.34	101.5	84.19	78.07	49.24	46.63	46.63					
PLACE1004274	2.95	0.92	1.52	1.53	2.26	1.62	1.54	1.70	1.7					
PLACE1004277	4.89	3.63	3.77	5.98	6.33	5.84	3.49	5.35	5.35	*	+			
PLACE1004279	4.14	2.37	2.56	4.12	4.89	5.01	2.41	5.41	5.41					
PLACE1004282	4.87	1.71	2.16	3.7	2.78	3.26	3.33	4.30	4.3					
PLACE1004284	5.6	3.43	5.55	7.94	7.12	9.08	5.18	6.08	6.08	*	+			
PLACE1004289	4.45	2.76	2.32	4.87	4.64	6.03	3.57	3.74	3.74					
PLACE1004299	3.82	1.87	1.73	3.07	2.88	4.42	3.05	2.95	2.95					
PLACE1004302	2.2	0.86	0.90	1.74	3.32	2.03	1.19	1.35	1.35					
PLACE1004305	3.85	2.26	1.59	1.85	1.24	2.43	2.28	2.58	2.58					
PLACE1004316	5.43	2.71	3.07	1.96	3.30	2.21	2.72	4.32	4.32					
PLACE1004322	1.43	0.69	0.73	1.49	2.28	1.46	1.11	2.06	2.06					
PLACE1004325	13.88	6.16	7.35	9.82	9.01	12.35	11.00	10.37	10.37					
PLACE1004332	3.01	1.40	1.75	1.66	1.82	2.98	2.54	3.00	3					
PLACE1004336	9.91	5.69	5.62	10.43	10.12	10.42	6.74	8.77	8.77					
PLACE1004346	3.07	2.03	1.73	2.75	2.78	2.82	1.63	2.50	2.5					
PLACE1004358	17.58	10.51	10.45	12.26	12.55	14.79	12.38	16.11	16.11					
PLACE1004376	21.68	10.31	10.00	13.3	12.08	12.35	12.00	16.69	16.69					
PLACE1004384	3.8	1.61	2.13	4.74	4.70	5.37	3.12	3.81	3.81	*	+			
PLACE1004385	1.9	0.86	0.50	0.57	1.48	1.53	0.60	1.25	1.25					
PLACE1004388	3.6	1.83	1.85	3.69	4.57	4.12	1.57	1.95	1.95					
PLACE1004405	0.61	1.07	0.82	0.21	0.91	1.17	2.14	2.86	2.86			**	+	
PLACE1004407	5.17	3.33	4.50	6.41	4.17	7.01	4.80	3.58	3.58					
PLACE1004424	1.66	0.59	0.46	0.66	0.44	2.14	0.23	0.46	0.46					
PLACE1004425	1.47	0.52	1.48	2.94	3.61	2.12	1.72	2.14	2.14	*	+			
PLACE1004427	2.86	1.31	1.07	1.87	2.05	1.81	1.96	3.44	3.44					
PLACE1004428	3.96	2.20	1.76	4.03	5.57	4.86	3.58	3.24	3.24					
PLACE1004433	6.32	3.82	4.97	5.63	4.68	5.19	2.95	4.99	4.99					
PLACE1004435	7.56	3.49	4.09	10.74	10.16	12.36	5.74	11.13	11.13	*	+			
PLACE1004437	7.97	3.59	4.68	4.42	7.20	5.02	5.17	3.07	3.07					

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Table 311

PLACE1004441	3.25	1.90	2.33	4.32	4.15	5.16	3.84	4.52	4.52	*	+	*	+
PLACE1004446	1.76	2.09	0.72	1.34	1.42	1.87	2.28	2.32	2.32				
PLACE1004450	0.76	0.23	0.38	0.96	1.30	0.99	0.73	0.72	0.72	*	+		
PLACE1004451	2.04	1.05	0.94	1.87	2.71	1.33	1.83	2.40	2.4				
PLACE1004456	13.14	7.90	8.58	15.19	13.06	9.85	9.75	13.11	13.11				
PLACE1004458	1.13	0.48	0.38	2.8	2.09	3.55	9.05	9.62	9.62	*	+	**	+
PLACE1004460	1.24	0.45	0.57	1.15	1.35	1.69	1.34	1.71	1.71			*	+
PLACE1004467	6.23	3.77	6.46	8.7	9.58	9.65	5.25	4.76	4.76	*	+		
PLACE1004471	7.06	5.28	5.80	10.51	12.81	16.26	6.17	7.08	7.08	*	+		
PLACE1004473	1.57	1.48	1.06	1.91	1.92	2.41	1.84	1.43	1.43	*	+		
PLACE1004475	17.9	8.89	9.13	27.5	24.29	13.71	28.08	20.33	20.33			*	+
PLACE1004482	2.18	1.39	1.16	1.98	2.90	3.51	2.75	3.78	3.78			*	+
PLACE1004491	0.74	0.46	0.72	0.47	1.01	0.56	0.69	1.94	1.94				
PLACE1004492	33.34	16.09	17.54	17.67	22.65	21.39	20.85	24.45	24.45				
PLACE1004506	5.1	3.77	3.89	3.53	5.30	4.79	5.63	7.41	7.41			*	+
PLACE1004507	2.94	1.98	2.25	1.75	2.11	1.80	2.62	3.67	3.67				
PLACE1004510	2.01	2.57	2.33	4.62	4.58	4.58	3.18	2.57	2.57	**	+		
PLACE1004516	1.04	0.43	0.32	0.6	0.82	1.51	0.69	1.14	1.14				
PLACE1004518	5.88	3.35	1.73	3.03	3.63	1.95	4.27	3.46	3.46				
PLACE1004519	3.55	1.36	2.17	1.53	2.33	1.77	1.26	1.42	1.42				
PLACE1004520	4.8	1.73	3.29	3.58	4.49	2.98	3.20	4.60	4.6				
PLACE1004530	7.81	5.59	5.82	2.93	4.17	2.72	3.17	3.36	3.36	*	-	*	-
PLACE1004545	0.98	1.24	0.71	1.02	1.35	1.28	1.23	1.48	1.48				
PLACE1004547	3.48	2.58	2.62	3.89	3.59	4.14	3.27	6.00	6	*	+		
PLACE1004548	5.32	3.02	2.13	5.34	7.57	7.29	2.74	4.90	4.9				
PLACE1004550	4.75	3.89	2.55	4.32	5.77	4.11	3.73	5.54	5.54				
PLACE1004551	2.21	1.18	1.01	2.32	3.16	1.67	1.47	1.73	1.73				
PLACE1004559	1.69	0.68	1.41	2.2	2.41	1.95	1.58	1.77	1.77	*	+		
PLACE1004562	7.92	4.63	4.61	12.8	13.69	12.24	11.70	16.91	16.91	**	+	*	+
PLACE1004564	5.08	3.48	2.94	3.43	4.16	2.75	2.50	3.03	3.03				
PLACE1004604	1.61	1.65	0.87	1.96	1.66	1.23	6.31	2.27	2.27				
PLACE1004611	6.51	4.71	3.22	13.38	14.72	11.15	6.91	6.89	6.89	**	+		
PLACE1004629	3.8	3.23	3.16	7.62	7.80	6.85	5.92	7.19	7.19	**	+	**	+
PLACE1004630	4.43	7.59	4.92	4.3	3.84	5.63	3.88	4.82	4.82				
PLACE1004637	9.71	8.66	5.16	8.97	5.26	6.98	6.87	7.85	7.85				
PLACE1004645	34.24	15.91	17.01	26.16	30.73	32.52	15.81	17.34	17.34				
PLACE1004646	3.38	1.74	3.32	3.28	4.81	3.28	2.79	2.82	2.82				
PLACE1004648	14.4	8.71	8.36	10.69	11.92	11.82	11.67	15.16	15.16				
PLACE1004655	41.73	23.86	25.42	40	42.96	45.63	19.14	24.74	24.74				
PLACE1004658	4.07	3.17	2.80	4.22	4.91	5.38	4.38	3.84	3.84	*	+		
PLACE1004664	2.14	1.15	0.86	2.2	2.05	3.93	1.74	1.79	1.79				
PLACE1004672	11.36	7.67	9.44	13.22	15.37	20.21	6.56	12.23	12.23	*	+		
PLACE1004674	6.89	4.27	3.73	8.23	11.59	6.63	7.24	9.33	9.33			*	+
PLACE1004681	5.36	2.49	2.37	3.93	6.34	2.28	3.03	2.81	2.81				
PLACE1004686	4.25	1.52	2.69	8.28	8.25	8.23	3.83	5.37	5.37	**	+		
PLACE1004690	27.35	18.33	25.68	19.28	26.77	23.31	7.55	15.04	15.04			*	-
PLACE1004691	4.78	2.55	2.69	4.7	7.55	6.34	2.68	5.61	5.61				
PLACE1004693	3.07	1.09	1.84	2.44	2.98	3.35	2.53	3.19	3.19				
PLACE1004701	23.69	11.94	19.76	25.99	21.50	33.00	23.49	24.31	24.31				
PLACE1004705	5.61	4.43	3.93	4.87	5.07	5.49	3.83	4.06	4.06				
PLACE1004708	9.98	7.05	4.96	7.36	17.22	7.73	12.21	12.77	12.77			*	+
PLACE1004716	5.47	2.91	3.32	5.79	8.69	5.11	4.23	4.07	4.07				
PLACE1004722	1.53	1.35	1.55	1.7	3.73	3.67	0.90	2.30	2.3				
PLACE1004736	16.73	9.74	14.43	13.11	17.99	18.80	11.66	17.15	17.15				
PLACE1004737	2.18	1.67	1.79	1.43	3.14	3.32	1.37	1.80	1.8				
PLACE1004740	6.4	3.17	4.45	6.16	4.57	7.19	5.04	5.92	5.92				

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Table 312

PLACE1004743	2.83	1.69	1.62	2.65	2.30	3.35	1.64	2.59	2.59				
PLACE1004751	3.88	2.76	2.71	4.3	4.81	6.07	2.16	4.03	4.03	*	+		
PLACE1004757	6.62	2.79	3.38	5.64	5.36	5.13	4.59	3.33	3.33				
PLACE1004761	1.53	0.69	0.99	1.89	2.90	1.43	1.17	2.01	2.01				
PLACE1004773	6.07	1.81	3.15	5.28	4.05	5.04	3.00	3.37	3.37				
PLACE1004775	0.59	0.48	0.41	0.54	0.33	0.45	0.35	1.11	1.11				
PLACE1004777	2.87	1.56	1.63	3.6	3.28	3.27	3.12	2.18	2.18	*	+		
PLACE1004793	1.91	0.67	0.75	1.6	1.01	2.08	1.33	1.74	1.74				
PLACE1004796	11.15	4.76	6.53	15.2	11.67	18.12	12.53	11.15	11.15	*	+		
PLACE1004804	2.49	2.83	3.47	3.45	3.93	5.58	2.84	4.15	4.15				
PLACE1004813	1.83	1.78	1.19	2.06	4.34	2.04	2.93	2.61	2.61			**	+
PLACE1004814	15.6	8.20	7.30	20.97	26.56	22.14	11.65	11.36	11.36	*	+		
PLACE1004815	2.09	1.04	1.32	4.73	4.30	3.56	2.27	2.36	2.36	**	+		
PLACE1004816	3.22	1.11	2.11	2.58	2.27	3.19	1.56	4.07	4.07				
PLACE1004824	10.16	4.47	7.27	17.15	18.66	21.40	8.53	11.08	11.08	**	+		
PLACE1004827	3.25	1.26	2.36	5.76	5.15	4.86	3.26	3.82	3.82	**	+		
PLACE1004836	2.02	0.78	1.32	3.29	3.51	3.51	1.36	2.69	2.69	**	+		
PLACE1004838	3.17	2.09	1.89	2.78	2.46	3.36	1.52	3.28	3.28				
PLACE1004840	1.23	0.56	0.64	2.27	3.76	2.10	1.40	1.24	1.24	*	+		
PLACE1004842	5.48	1.99	1.07	1.39	1.40	2.34	2.69	3.06	3.06				
PLACE1004850	3.11	1.83	1.19	2.34	1.99	1.83	2.00	3.44	3.44				
PLACE1004868	1.78	1.97	1.38	1.05	1.30	0.94	1.18	1.52	1.52	*	-		
PLACE1004885	4.12	2.86	3.03	6.17	4.95	6.21	2.81	3.69	3.69	*	+		
PLACE1004886	1.77	1.59	1.70	1.43	1.55	1.82	2.32	4.30	4.3			*	+
PLACE1004887	25.24	11.67	14.76	21.81	38.02	28.05	8.65	10.31	10.31				
PLACE1004896	2.33	1.72	1.45	4.61	4.55	3.16	5.89	7.01	7.01	*	+	**	+
PLACE1004900	9.03	4.30	5.53	9.31	10.97	9.80	5.74	6.69	6.69				
PLACE1004902	15.98	5.16	8.41	6.64	13.40	8.82	7.56	8.91	8.91				
PLACE1004904	2.63	1.32	1.15	1.84	2.37	1.90	3.74	3.50	3.5			*	+
PLACE1004911	1.14	3.11	1.00	4.23	0.30	0.65	0.27	1.36	1.36				
PLACE1004913	2.14	1.21	1.21	2.7	1.96	3.02	1.97	4.39	4.39				
PLACE1004918	1.11	0.31	1.10	1.32	1.60	1.48	0.91	1.02	1.02				
PLACE1004930	3.51	2.35	1.88	1.71	2.51	2.60	1.12	1.41	1.41				
PLACE1004934	2.04	1.42	1.26	1.7	2.74	2.49	1.45	1.52	1.52				
PLACE1004937	5.11	2.46	1.95	3.63	3.54	3.36	2.75	2.15	2.15				
PLACE1004949	4.03	1.71	2.54	6.88	7.76	8.45	5.04	9.82	9.82	**	+	*	+
PLACE1004969	3.48	2.29	1.51	2.73	3.17	3.01	2.31	4.32	4.32				
PLACE1004970	0.79	0.82	0.40	0.36	1.00	0.91	0.81	2.69	2.69				
PLACE1004972	1.78	1.50	1.56	2.23	2.38	3.07	1.16	2.50	2.5	*	+		
PLACE1004974	3.63	3.03	1.68	3.41	3.31	2.59	1.64	1.70	1.7				
PLACE1004975	4.46	3.12	2.44	4.13	3.11	5.49	3.51	3.95	3.95				
PLACE1004979	4.8	5.17	3.63	8.89	10.47	10.51	5.50	6.33	6.33	**	+	*	+
PLACE1004982	12.69	7.06	8.29	13.78	13.06	8.17	7.03	8.87	8.87				
PLACE1004985	2.12	0.35	0.79	2.05	1.96	1.11	0.99	3.21	3.21				
PLACE1005003	3.67	1.05	1.88	1.3	2.66	1.79	0.59	2.43	2.43				
PLACE1005004	1.24	1.06	1.30	1.55	1.31	1.17	1.68	1.83	1.83			**	+
PLACE1005005	8.08	4.02	3.41	8.61	8.51	8.54	5.01	5.29	5.29				
PLACE1005011	2.2	1.69	2.79	3	3.06	5.33	3.11	2.57	2.57				
PLACE1005026	2.34	1.90	2.06	1.86	2.01	2.93	1.82	1.53	1.53			*	-
PLACE1005027	4.99	3.43	4.26	7.85	11.24	9.53	3.37	5.57	5.57	**	+		
PLACE1005031	6.43	2.62	2.97	5.45	4.09	3.20	3.04	3.84	3.84				
PLACE1005036	7.51	3.86	5.10	9.33	12.02	7.99	3.66	4.98	4.98				
PLACE1005041	0.87	0.69	0.58	1.76	1.87	1.43	1.58	1.91	1.91	**	+	**	+
PLACE1005046	7.09	3.32	3.54	11.1	10.13	10.18	4.94	5.99	5.99	**	+		
PLACE1005047	3.57	1.97	1.47	3.2	3.87	3.39	2.49	3.04	3.04				
PLACE1005052	4.36	2.90	3.32	3.11	2.49	4.07	4.21	4.75	4.75				

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Table 313

PLACE1005055	1.93	1.90	2.25	2.55	3.80	3.83	1.39	2.30	2.3	*	+		
PLACE1005066	3.73	3.53	2.95	3.62	2.74	3.71	4.65	6.92	6.92			*	+
PLACE1005077	1.88	0.74	0.51	1.94	2.30	1.62	1.19	1.27	1.27				
PLACE1005085	5.35	2.26	1.94	7.82	9.01	6.89	4.04	4.10	4.1	*	+		
PLACE1005086	8.18	4.09	4.61	8.82	11.72	8.88	4.94	5.91	5.91				
PLACE1005088	48.83	27.68	29.69	27.61	39.82	34.65	26.01	25.68	25.68				
PLACE1005089	2.42	1.38	1.99	2.77	2.07	2.49	2.33	3.56	3.56				
PLACE1005101	6.75	6.64	8.03	8.45	9.96	12.39	8.67	10.11	10.11			*	+
PLACE1005102	5.88	7.51	8.49	11.05	10.78	12.60	9.73	9.59	9.59	*	+	*	+
PLACE1005108	5.63	4.27	3.64	12.01	12.87	10.10	5.64	5.46	5.46	**	+		
PLACE1005110	6.84	3.16	2.29	5.61	4.42	2.27	2.47	3.96	3.96				
PLACE1005111	2.32	1.43	0.52	2.8	3.48	1.64	1.69	1.48	1.48				
PLACE1005123	20.53	8.57	10.06	12.54	14.07	10.45	7.24	8.30	8.3				
PLACE1005124	3.92	2.40	2.02	3.08	6.72	4.08	3.28	3.46	3.46				
PLACE1005128	10.6	9.42	9.74	12.9	15.61	15.03	14.09	17.89	17.89	**	+	**	+
PLACE1005130	4.63	4.42	3.58	6.21	6.12	6.60	2.90	3.62	3.62	**	+		
PLACE1005141	11.53	6.88	7.85	10.2	11.46	13.07	6.08	6.65	6.65				
PLACE1005146	2.66	2.45	2.31	3.79	4.23	2.90	1.91	2.35	2.35	*	+		
PLACE1005152	4.31	1.32	1.78	5.23	4.05	4.11	2.87	2.37	2.37				
PLACE1005157	3.17	1.71	2.58	3.61	2.97	3.04	1.83	2.24	2.24				
PLACE1005162	5.03	1.44	2.16	4.55	5.47	5.51	3.63	3.97	3.97				
PLACE1005170	1.73	0.31	0.62	1.61	1.26	1.41	1.34	1.72	1.72				
PLACE1005176	1.61	0.38	0.68	1.16	1.34	1.12	1.06	1.60	1.6				
PLACE1005181	0.5	0.24	0.53	1.19	0.87	2.59	0.77	1.26	1.26			*	+
PLACE1005184	4.44	1.78	2.90	7.9	7.10	9.09	4.75	4.64	4.64	**	+		
PLACE1005186	6.95	2.41	3.82	3.37	3.80	2.87	3.22	3.68	3.68				
PLACE1005187	3.14	1.53	1.03	3.09	5.30	4.21	2.97	2.82	2.82				
PLACE1005189	5.93	2.53	2.32	3.58	5.81	4.44	5.57	5.74	5.74				
PLACE1005193	6.13	3.49	3.63	4.29	4.51	4.47	3.64	4.00	4				
PLACE1005200	4.37	1.39	2.33	2.59	3.60	1.69	2.29	2.95	2.95				
PLACE1005206	2.34	0.51	1.37	1.54	2.19	3.01	1.80	1.98	1.98				
PLACE1005216	1.38	0.71	1.11	2.26	2.41	2.76	2.43	3.73	3.73	**	+	**	+
PLACE1005223	4.29	2.34	2.64	6.04	7.76	7.97	4.06	6.10	6.1	**	+		
PLACE1005225	19.66	8.09	9.52	16.05	21.00	13.76	8.27	9.44	9.44				
PLACE1005232	8.02	4.04	2.69	6.94	10.56	7.61	5.96	6.58	6.58				
PLACE1005239	5.38	1.20	2.07	5.01	3.78	2.93	2.36	3.31	3.31				
PLACE1005243	5.32	3.76	4.72	5.19	5.09	5.33	3.34	5.82	5.82				
PLACE1005250	3.75	1.12	1.85	3.16	3.89	3.16	2.16	2.84	2.84				
PLACE1005261	2.07	0.70	1.90	2.25	2.05	1.77	2.13	1.93	1.93				
PLACE1005266	1.9	0.95	1.09	2.57	2.39	2.64	2.14	1.90	1.9	*	+		
PLACE1005271	5.66	2.63	3.94	8.71	9.11	8.37	4.71	5.02	5.02	**	+		
PLACE1005277	3.05	0.82	0.70	2.46	4.32	1.50	1.02	2.07	2.07				
PLACE1005287	6.59	3.30	3.94	10.35	15.42	7.57	8.69	8.45	8.45			*	+
PLACE1005299	22.18	11.98	9.53	18.56	24.11	17.96	21.90	22.45	22.45				
PLACE1005305	5.96	2.44	4.52	8.17	10.96	9.42	8.88	11.22	11.22	*	+	**	+
PLACE1005307	3.74	1.42	2.86	4.85	5.32	3.53	2.69	4.11	4.11				
PLACE1005308	3.94	1.81	2.45	3.16	2.71	2.64	2.67	2.60	2.6				
PLACE1005313	1.8	1.22	2.93	1.89	0.89	2.76	1.70	1.69	1.69				
PLACE1005320	2.05	0.78	1.58	1.96	1.63	3.04	1.42	1.54	1.54				
PLACE1005327	3.57	2.45	2.12	2.64	6.29	3.81	4.41	6.45	6.45			*	+
PLACE1005331	4	2.27	3.11	3.34	6.04	3.03	3.28	2.86	2.86				
PLACE1005335	9.31	5.05	4.18	8.68	7.24	5.98	5.53	6.95	6.95				
PLACE1005336	3.13	1.45	2.61	5.52	6.69	4.80	4.00	4.81	4.81	*	+	*	+
PLACE1005351	30.75	16.28	19.31	14.85	14.56	18.13	32.39	30.68	30.68				
PLACE1005366	3.38	2.74	2.56	10.21	9.37	10.62	9.15	9.50	9.5	**	+	**	+
PLACE1005373	4.26	1.58	2.70	3.39	2.69	4.82	2.63	3.29	3.29				

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Table 314

PLACE1005374	5	2.10	2.77	8.04	11.61	11.01	4.31	6.01	6.01	**	+		
PLACE1005383	8.86	3.18	3.37	5.63	6.03	4.19	5.25	6.23	6.23				
PLACE1005388	2.57	0.54	0.31	2.75	1.56	0.89	2.61	1.22	1.22				
PLACE1005409	5.48	3.06	2.63	7.59	8.06	6.25	3.31	4.02	4.02	*	+		
PLACE1005410	6.76	2.97	3.65	5.66	8.24	5.17	9.00	11.77	11.77			*	+
PLACE1005426	4.46	1.72	1.45	2.27	1.48	1.00	3.43	3.54	3.54				
PLACE1005431	4.56	2.63	2.58	4.42	5.14	6.40	5.57	6.50	6.5			*	+
PLACE1005453	3.55	1.77	2.09	4.33	4.49	5.14	1.74	3.20	3.2	*	+		
PLACE1005467	5.64	2.78	2.70	6.57	5.73	4.48	5.05	4.51	4.51				
PLACE1005471	3.36	0.50	1.20	3.42	3.09	2.65	2.30	3.64	3.64				
PLACE1005476	5.15	1.54	1.43	2.43	2.59	1.89	1.59	3.01	3.01				
PLACE1005477	2.24	1.35	1.27	5.66	7.05	5.00	4.23	7.05	7.05	**	+	*	+
PLACE1005480	1.93	1.39	1.29	1.24	1.52	1.24	1.31	1.75	1.75				
PLACE1005481	2.22	1.41	1.51	2.73	2.46	3.04	1.87	2.00	2	*	+		
PLACE1005494	1.24	0.38	0.90	0.8	0.90	0.66	0.80	1.98	1.98				
PLACE1005495	4.56	1.60	1.71	3.4	2.67	2.72	2.06	1.93	1.93				
PLACE1005497	8.06	4.83	3.69	4.42	2.88	4.07	9.50	10.40	10.4			*	+
PLACE1005499	4.76	1.36	1.66	2.69	4.07	3.13	5.56	5.51	5.51				
PLACE1005502	2.69	0.87	1.10	2.75	3.41	2.24	1.89	4.02	4.02				
PLACE1005513	1.27	0.71	0.80	3.5	2.88	3.38	1.95	3.18	3.18	**	+	*	+
PLACE1005515	2.84	0.81	0.90	1.12	0.96	1.43	2.38	3.90	3.9				
PLACE1005519	7.14	2.92	5.14	2.37	3.46	3.11	2.55	3.35	3.35				
PLACE1005526	2.06	1.07	1.41	1.41	2.39	1.85	1.31	2.23	2.23				
PLACE1005528	6.82	2.99	3.77	7.7	10.09	11.05	4.64	5.96	5.96	*	+		
PLACE1005530	4.98	2.54	2.80	2.85	5.04	3.55	3.48	2.83	2.83				
PLACE1005536	4.27	3.13	1.98	6.1	4.77	1.67	4.10	3.87	3.87				
PLACE1005539	3	1.66	1.31	3.17	3.20	2.66	1.69	3.05	3.05				
PLACE1005543	2.3	1.25	1.18	4	3.96	4.38	3.55	3.32	3.32	**	+	**	+
PLACE1005544	6.06	3.23	2.89	3.81	4.11	4.35	4.12	5.12	5.12				
PLACE1005550	8.49	4.71	5.86	4.53	4.75	4.40	2.14	3.57	3.57				
PLACE1005554	1.55	0.76	0.94	1.77	1.45	1.38	2.99	1.56	1.56				
PLACE1005557	3.3	1.97	2.34	3.4	5.03	3.76	3.56	3.17	3.17				
PLACE1005563	1.99	2.09	0.76	1.69	2.10	1.89	2.11	1.69	1.69				
PLACE1005569	4.54	2.73	2.52	4.62	4.22	2.24	2.63	3.22	3.22				
PLACE1005574	1.43	0.92	0.87	2.29	2.41	2.10	0.45	0.99	0.99	**	+		
PLACE1005584	1.32	0.88	0.93	1.31	1.40	1.67	1.68	4.67	4.67				
PLACE1005590	2.53	3.81	2.63	3.18	2.75	3.39	4.08	5.93	5.93			*	+
PLACE1005595	2.91	2.55	3.00	2.96	2.39	3.53	3.75	3.64	3.64			**	+
PLACE1005601	2.77	1.99	2.02	2.52	2.79	3.50	2.97	3.86	3.86			*	+
PLACE1005603	0.9	0.55	0.69	0.87	1.06	0.76	1.27	1.79	1.79			*	+
PLACE1005604	4.18	2.56	1.82	4.89	4.83	6.27	2.39	1.93	1.93	*	+		
PLACE1005611	2.64	2.26	1.19	5.02	2.53	3.51	2.64	2.53	2.53				
PLACE1005622	2.15	1.96	1.00	2.49	2.91	2.25	1.48	2.00	2				
PLACE1005623	4.29	1.35	2.10	3.3	3.81	3.92	2.17	2.70	2.7				
PLACE1005630	6.26	3.63	2.27	4.66	6.06	5.41	4.45	5.87	5.87				
PLACE1005639	1.47	1.40	2.08	1.45	2.40	2.84	0.78	1.78	1.78				
PLACE1005646	5.91	4.51	5.24	4.63	5.74	5.46	4.51	5.47	5.47				
PLACE1005647	0.51	0.39	0.52	1.16	1.74	1.90	2.41	4.04	4.04	**	+	**	+
PLACE1005648	5.72	4.93	6.25	15.18	16.23	16.45	5.58	7.21	7.21	**	+		
PLACE1005653	3.3	1.90	0.82	3.94	5.11	4.03	2.85	2.07	2.07	*	+		
PLACE1005656	2.07	1.04	0.59	1.23	2.09	0.91	1.88	0.45	0.45				
PLACE1005659	4.14	1.56	2.46	2.97	4.17	2.22	1.44	2.31	2.31				
PLACE1005660	5.27	3.90	2.60	4.31	5.01	2.96	3.33	4.29	4.29				
PLACE1005664	4.13	4.07	4.07	5.57	5.47	4.07	5.14	6.25	6.25			**	+
PLACE1005666	0.97	1.45	1.51	3.22	3.91	4.93	3.26	2.77	2.77	**	+	**	+
PLACE1005669	4.53	2.92	2.87	6.24	4.95	7.16	3.36	4.69	4.69	*	+		

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Table 315

PLACE1005682	2.11	2.05	2.13	4.34	3.23	4.41	1.89	2.15	2.15	**	+		
PLACE1005698	4.64	2.14	3.28	3.89	3.92	4.16	1.91	2.53	2.53				
PLACE1005708	25.78	13.70	10.51	13.88	16.18	11.27	14.00	14.43	14.43				
PLACE1005725	3.83	1.42	2.33	2.34	3.92	2.04	4.70	4.61	4.61			*	+
PLACE1005727	8.48	2.60	3.97	5.4	4.41	4.96	2.49	2.57	2.57				
PLACE1005730	3.57	0.90	1.62	1.95	2.02	2.00	2.05	2.95	2.95				
PLACE1005736	4.39	2.36	2.88	8.34	10.28	9.63	5.13	7.81	7.81	**	+	*	+
PLACE1005739	2.31	1.03	1.11	1.47	1.17	1.64	2.22	2.15	2.15				
PLACE1005745	9.25	5.63	5.40	10.32	14.44	8.66	7.38	8.69	8.69				
PLACE1005752	4.63	2.11	0.91	2.57	2.97	2.88	2.25	2.86	2.86				
PLACE1005755	0.83	0.18	0.42	0.66	1.88	0.66	0.70	0.93	0.93				
PLACE1005756	14.63	7.31	9.39	22.2	25.42	27.72	29.92	35.68	35.68	**	+	**	+
PLACE1005760	7.89	3.72	4.80	10.59	12.05	10.96	9.45	9.92	9.92	*	+	*	+
PLACE1005763	3.86	1.70	3.26	6.59	6.36	6.88	4.43	4.28	4.28	**	+		
PLACE1005768	6.14	3.01	5.24	7.97	7.90	8.87	6.22	5.90	5.9	*	+		
PLACE1005771	7.62	3.12	5.03	7.4	7.32	9.76	6.04	6.48	6.48				
PLACE1005783	3.63	1.45	2.35	2.79	4.79	2.04	2.34	3.07	3.07				
PLACE1005799	6.45	3.16	3.38	5.32	4.64	3.49	5.15	5.23	5.23				
PLACE1005802	5.01	1.66	1.63	4.46	8.45	4.41	2.49	4.79	4.79				
PLACE1005803	11.48	4.59	6.77	9.23	10.65	9.39	6.53	8.91	8.91				
PLACE1005804	1.62	0.72	0.84	1.97	2.36	1.93	2.21	2.56	2.56	*	+	*	+
PLACE1005813	10.74	3.23	5.61	11.66	8.19	9.55	6.52	6.57	6.57				
PLACE1005815	5.12	2.48	3.85	7.34	9.35	11.87	4.89	5.17	5.17	*	+		
PLACE1005828	5.16	3.37	3.80	8.35	8.98	9.59	4.86	6.29	6.29	**	+		
PLACE1005833	3.06	1.35	1.59	18.69	21.23	11.91	28.00	30.88	30.88	**	+	**	+
PLACE1005834	1.93	0.65	0.55	4	6.43	2.66	1.50	2.50	2.5	*	+		
PLACE1005835	5.07	4.66	2.88	5.05	7.51	3.87	4.83	4.52	4.52				
PLACE1005836	3.75	1.63	2.11	2.62	6.42	3.23	2.73	2.06	2.06				
PLACE1005845	4.98	1.86	2.24	4.26	4.56	2.61	2.60	3.15	3.15				
PLACE1005850	4.23	2.74	2.58	5.55	4.59	5.10	2.95	3.19	3.19	*	+		
PLACE1005851	1.83	0.96	1.69	2.54	2.84	4.11	1.02	0.85	0.85	*	+		
PLACE1005856	4.08	1.29	7.53	4.1	2.89	3.39	1.78	2.05	2.05				
PLACE1005875	3.56	1.05	0.65	5.19	5.82	3.59	3.48	3.10	3.1				
PLACE1005876	4.08	3.91	2.72	2.79	2.82	2.10	2.04	2.27	2.27			*	-
PLACE1005878	5.27	2.13	2.19	4.92	3.53	2.84	3.83	3.82	3.82				
PLACE1005880	3.44	0.96	1.32	2.14	2.64	2.46	2.97	4.34	4.34				
PLACE1005884	1.76	0.52	0.55	1.39	1.77	1.41	2.43	2.29	2.29			*	+
PLACE1005890	2.04	0.70	0.65	1.41	1.86	1.52	1.88	2.21	2.21				
PLACE1005898	2.99	2.09	1.71	4.94	3.42	2.88	2.46	3.27	3.27				
PLACE1005913	5.71	2.57	3.76	7.83	8.39	8.51	3.79	4.62	4.62	*	+		
PLACE1005921	10.98	4.34	4.34	9.34	8.32	8.81	6.16	6.43	6.43				
PLACE1005923	57.96	26.97	25.39	4.09	4.25	2.49	3.95	3.48	3.48	*	-	*	-
PLACE1005925	2.51	0.91	2.14	3.11	3.71	2.82	1.93	2.80	2.8				
PLACE1005927	6.09	2.70	1.89	3.69	4.68	4.01	3.18	5.73	5.73				
PLACE1005932	1.82	0.71	0.41	1.33	1.76	1.08	1.15	1.54	1.54				
PLACE1005934	3.84	2.41	2.72	6.26	7.11	6.43	3.93	5.30	5.3	**	+	*	+
PLACE1005936	2.29	0.78	1.05	1.64	1.78	1.51	1.47	1.36	1.36				
PLACE1005939	6.69	4.35	3.92	5.44	5.46	3.73	16.40	25.30	25.3			**	+
PLACE1005951	5.63	2.39	2.32	4.86	4.02	3.74	3.42	3.43	3.43				
PLACE1005953	2.92	1.24	0.96	2.51	1.78	2.30	1.15	2.55	2.55				
PLACE1005955	3.7	1.62	1.62	2.35	3.61	2.40	3.03	3.07	3.07				
PLACE1005966	3.38	0.65	1.08	1.86	2.32	2.12	2.02	2.80	2.8				
PLACE1005968	10.55	5.64	5.72	7.48	5.88	6.36	5.68	7.85	7.85				
PLACE1005975	10.44	5.19	8.44	12.95	14.63	15.64	8.66	16.92	16.92	*	+		
PLACE1005990	3.19	1.43	1.58	2.28	2.05	1.79	1.80	3.26	3.26				
PLACE1005997	64.81	36.05	40.42	54.4	53.64	53.12	27.58	33.55	33.55				

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Table 316

PLACE1006002	8.53	4.41	5.77	19.13	16.78	16.67	8.23	9.69	9.69	**	+		
PLACE1006003	6.88	5.62	5.05	3.42	5.00	5.45	4.05	7.43	7.43				
PLACE1006011	4.72	2.78	3.04	3.63	3.41	3.26	2.90	3.61	3.61				
PLACE1006017	4.17	1.57	1.37	3.12	3.78	3.87	3.13	4.29	4.29				
PLACE1006037	8.36	3.71	4.44	4.09	4.76	4.29	2.99	4.73	4.73				
PLACE1006040	13.34	8.65	10.10	9.09	7.82	11.18	9.13	10.46	10.46				
PLACE1006063	4.18	2.39	2.46	2.52	3.00	2.07	2.59	2.91	2.91				
PLACE1006071	3.1	2.05	2.07	1.68	2.75	3.43	1.83	2.76	2.76				
PLACE1006073	3.97	2.14	1.81	6.25	6.16	5.43	3.65	5.10	5.1	*	+		
PLACE1006074	4.44	2.36	2.42	6.36	6.76	5.83	2.98	4.13	4.13	*	+		
PLACE1006076	1.24	0.92	1.14	3.37	4.38	2.74	2.16	3.59	3.59	**	+	*	+
PLACE1006079	4.64	2.47	2.65	3.89	4.84	4.04	4.58	5.85	5.85				
PLACE1006093	1.06	0.90	1.72	1.34	1.63	0.86	2.10	2.38	2.38			*	+
PLACE1006116	2.79	1.95	1.97	2.66	2.53	2.69	3.38	3.33	3.33			*	+
PLACE1006119	2.59	2.94	2.87	5.28	4.68	6.57	3.23	3.84	3.84	**	+	*	+
PLACE1006129	2.82	1.25	0.50	2.84	2.73	3.10	3.07	1.53	1.53				
PLACE1006139	7.84	6.54	4.25	6.48	5.34	5.86	6.94	4.78	4.78				
PLACE1006143	2.36	1.84	1.60	4.6	3.86	4.22	1.68	3.18	3.18	**	+		
PLACE1006157	2.84	1.26	1.64	2.25	2.35	1.82	1.52	2.36	2.36				
PLACE1006159	1.74	1.38	1.27	2.48	3.25	2.76	3.72	4.61	4.61	**	+	**	+
PLACE1006164	0.77	0.31	0.34	1.19	1.94	1.20	1.01	0.99	0.99	*	+	*	+
PLACE1006167	6.97	5.82	7.53	6.63	9.38	9.10	8.80	7.88	7.88				
PLACE1006170	3.23	2.05	2.23	3.8	5.15	4.56	3.39	4.89	4.89	*	+	*	+
PLACE1006181	4.1	2.72	3.53	6.41	6.16	6.21	5.86	6.48	6.48	**	+	**	+
PLACE1006187	0.5	0.33	0.10	0.86	0.82	1.09	0.66	0.49	0.49	*	+		
PLACE1006195	3.24	1.23	1.17	2.67	2.87	2.14	2.62	1.30	1.3				
PLACE1006196	8.03	2.93	3.80	5.31	7.47	6.96	4.75	3.79	3.79				
PLACE1006197	7.57	3.83	6.49	6.35	7.27	5.99	3.44	4.86	4.86				
PLACE1006198	2.55	1.19	1.79	2.81	2.56	2.19	0.91	2.46	2.46				
PLACE1006205	0.84	0.89	1.05	0.57	0.49	1.57	0.74	1.36	1.36				
PLACE1006208	2.19	1.80	3.16	5	4.18	5.05	7.99	4.42	4.42	**	+		
PLACE1006211	24.46	16.10	17.64	12.62	6.69	13.24	6.25	5.01	5.01			**	-
PLACE1006219	3.37	2.25	3.36	4.14	6.29	3.89	6.74	5.53	5.53			**	+
PLACE1006223	1.64	1.06	2.11	4.34	4.03	4.26	2.35	1.45	1.45	**	+		
PLACE1006225	1.79	1.20	1.26	2	1.95	1.83	1.23	1.27	1.27				
PLACE1006236	1.44	1.01	1.87	3.01	4.09	1.96	1.59	2.02	2.02				
PLACE1006239	1.72	1.00	1.18	2.46	2.48	2.60	1.22	3.24	3.24	**	+		
PLACE1006245	3.4	2.04	2.24	3.29	3.77	3.95	2.39	2.28	2.28				
PLACE1006246	2.78	1.91	2.09	2.77	4.35	3.44	2.43	1.97	1.97				
PLACE1006248	1.93	1.11	1.30	3.09	2.89	3.27	2.22	1.63	1.63	**	+		
PLACE1006262	3.84	0.83	1.42	2.66	2.88	1.75	2.15	1.21	1.21				
PLACE1006269	3.04	1.04	0.97	1.76	1.81	1.87	1.28	1.88	1.88				
PLACE1006275	7.22	3.03	3.50	4.21	3.01	5.50	3.90	5.68	5.68				
PLACE1006277	2.96	1.17	2.13	3.73	2.55	2.62	1.86	2.11	2.11				
PLACE1006288	11.06	5.08	6.39	7.42	7.01	7.05	7.31	9.33	9.33				
PLACE1006290	2.57	0.88	2.08	1.76	1.36	2.22	3.49	3.56	3.56			*	+
PLACE1006298	4.88	1.93	2.02	5.27	5.25	6.12	2.74	3.06	3.06				
PLACE1006311	0.92	0.15	0.41	0.82	0.31	0.81	2.11	2.64	2.64			**	+
PLACE1006318	4.74	1.72	2.13	3.2	4.07	2.67	3.29	3.63	3.63				
PLACE1006325	9.29	2.77	3.97	3.52	11.00	5.12	4.02	5.45	5.45				
PLACE1006331	4.1	2.50	3.35	6.3	7.84	7.16	3.59	5.15	5.15	**	+		
PLACE1006335	4.07	1.71	1.37	3.4	2.75	3.34	2.92	1.94	1.94				
PLACE1006357	1.19	0.25	0.48	0.63	0.90	0.73	0.68	1.54	1.54				
PLACE1006360	5.46	2.85	2.81	3.84	5.35	5.87	2.18	2.76	2.76				
PLACE1006364	2.49	1.09	1.52	2.96	1.99	3.19	1.91	2.29	2.29				
PLACE1006365	0.49	0.34	1.09	1.19	1.22	2.88	0.94	1.48	1.48				

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Table 317

PLACE1006368	8.01	4.14	3.31	4.49	6.87	3.91	2.14	3.48	3.48				
PLACE1006371	3.39	1.39	1.67	3.81	5.96	2.01	3.24	1.56	1.56				
PLACE1006373	3.53	2.18	2.19	3.47	4.18	3.83	2.92	2.88	2.88				
PLACE1006382	0.97	0.61	1.44	1.43	2.65	2.53	1.94	2.62	2.62			*	+
PLACE1006385	4.48	1.74	2.64	3.36	3.37	3.94	3.78	4.13	4.13				
PLACE1006391	2.37	0.62	1.55	2.01	1.29	1.94	1.72	2.56	2.56				
PLACE1006412	4.8	2.68	3.85	7.96	8.66	10.16	7.60	4.54	4.54	**	+		
PLACE1006414	1.25	0.89	0.94	1.45	2.86	1.96	0.92	1.08	1.08				
PLACE1006419	17.56	9.39	8.08	6.95	7.32	5.48	8.27	8.11	8.11				
PLACE1006438	8.55	3.61	3.22	5.14	6.25	6.01	5.43	4.95	4.95				
PLACE1006443	13.27	8.13	8.94	9.9	11.09	10.15	9.09	10.58	10.58				
PLACE1006445	4.37	2.38	3.95	6.95	9.30	6.55	3.68	5.38	5.38	*	+		
PLACE1006447	3.95	1.73	1.16	4.37	4.04	4.18	2.52	2.55	2.55				
PLACE1006466	2.16	1.21	1.47	2	2.00	2.12	1.67	2.19	2.19				
PLACE1006469	5.27	2.73	2.42	5.93	3.56	4.11	2.77	4.56	4.56				
PLACE1006470	5.41	1.20	2.14	5.2	5.53	6.27	4.08	3.01	3.01				
PLACE1006472	11.56	7.21	5.05	18.35	19.64	11.78	13.72	15.01	15.01	*	+	*	+
PLACE1006476	5.69	2.73	2.21	5.81	8.49	6.21	4.48	5.62	5.62				
PLACE1006482	2.17	1.70	2.74	3.32	3.51	3.07	2.54	2.44	2.44	*	+		
PLACE1006488	12.25	5.32	6.03	9.43	11.28	10.04	10.74	9.34	9.34				
PLACE1006492	6.49	3.62	3.60	9.32	9.53	11.55	11.09	11.09	11.09	**	+	**	+
PLACE1006506	4.02	1.67	1.46	3.66	1.98	4.89	2.21	2.62	2.62				
PLACE1006515	1.42	1.65	2.04	2.45	1.89	3.92	0.81	1.40	1.4				
PLACE1006516	2.44	0.98	1.54	4.26	3.82	5.07	3.64	3.02	3.02	**	+	*	+
PLACE1006520	3.63	0.73	1.91	3.9	6.61	4.44	1.81	3.39	3.39				
PLACE1006521	6.56	3.47	2.11	9.33	11.45	8.09	6.98	6.31	6.31	*	+		
PLACE1006529	8.21	3.84	3.76	6.99	8.95	8.26	5.00	11.36	11.36				
PLACE1006531	4.94	2.43	2.89	5.42	4.81	4.48	4.13	3.68	3.68				
PLACE1006534	5.02	1.96	2.25	4.42	4.01	5.10	4.71	2.91	2.91				
PLACE1006540	7.85	3.19	3.56	8.91	8.99	10.06	5.53	6.70	6.7	*	+		
PLACE1006549	6.58	4.45	4.11	5.8	5.03	4.33	3.92	6.01	6.01				
PLACE1006550	5.23	2.28	2.45	4.69	4.00	3.88	3.29	3.49	3.49				
PLACE1006552	6.12	1.72	2.67	5.75	4.74	3.07	2.71	2.86	2.86				
PLACE1006557	5.34	2.94	3.14	4.05	3.81	4.16	3.41	4.94	4.94				
PLACE1006563	9.2	2.53	5.98	6.32	8.19	6.80	4.10	7.57	7.57				
PLACE1006579	2.63	1.19	1.62	2.98	3.80	3.82	2.66	2.84	2.84	*	+		
PLACE1006594	2.07	1.44	0.90	5.07	5.06	4.32	1.36	3.33	3.33	**	+		
PLACE1006598	1.81	0.42	0.76	1.91	2.22	2.18	1.31	2.09	2.09				
PLACE1006607	3.34	1.19	1.08	3.9	3.89	4.86	2.07	2.61	2.61	*	+		
PLACE1006610	8.31	5.63	5.00	11.87	9.53	10.14	8.32	7.46	7.46	*	+		
PLACE1006615	14.76	9.42	9.72	14.75	13.78	11.87	9.86	12.58	12.58				
PLACE1006617	3.05	1.29	1.68	3.75	3.86	3.39	2.76	2.76	2.76	*	+		
PLACE1006618	6.92	2.44	3.52	4.27	4.86	5.91	4.69	6.70	6.7				
PLACE1006626	5.11	2.06	2.30	4.94	4.91	4.81	2.78	5.05	5.05				
PLACE1006629	0.66	0.42	0.61	1.08	1.24	1.75	1.19	2.37	2.37	*	+	*	+
PLACE1006637	4.27	1.61	1.80	4.69	6.26	5.06	2.25	2.76	2.76	*	+		
PLACE1006640	0.61	0.64	0.44	0.58	0.66	0.88	0.53	0.93	0.93				
PLACE1006644	4.05	2.79	2.37	3.98	3.74	4.19	3.10	4.40	4.4				
PLACE1006657	2	0.91	0.90	4.27	3.82	3.51	2.62	2.98	2.98	**	+	*	+
PLACE1006673	4.86	2.75	3.39	6.61	5.20	7.30	3.73	3.71	3.71	*	+		
PLACE1006678	2.03	0.79	2.52	1.93	2.13	1.51	1.82	3.83	3.83				
PLACE1006682	12.66	6.71	7.70	9.17	11.56	9.08	12.78	10.93	10.93				
PLACE1006684	0.85	0.40	0.58	0.51	0.62	0.80	0.74	0.98	0.98				
PLACE1006698	2.49	1.60	2.01	2.82	3.08	3.05	2.36	3.97	3.97	*	+		
PLACE1006704	2.61	1.71	2.74	4.42	5.65	7.34	3.32	3.83	3.83	*	+	*	+
PLACE1006708	5.71	3.09	2.56	5.97	10.34	7.12	1.92	5.99	5.99				

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Table 318

PLACE1006711	7.17	2.48	3.66	6.98	7.47	5.78	4.03	4.95	4.95				
PLACE1006714	3.92	2.24	1.78	5.56	4.95	3.81	3.00	4.91	4.91				
PLACE1006716	2.25	1.27	1.41	2.91	2.85	2.05	3.03	4.59	4.59			*	+
PLACE1006731	2.78	1.41	1.10	2.51	2.88	3.14	3.12	3.70	3.7			*	+
PLACE1006754	2.7	1.40	1.42	2.85	1.89	2.31	2.05	2.80	2.8				
PLACE1006760	3.7	1.96	3.99	17.24	15.19	18.35	5.74	7.75	7.75	**	+	*	+
PLACE1006779	0.53	0.60	0.34	1.36	0.57	1.21	0.75	1.01	1.01			*	+
PLACE1006782	3.05	2.67	1.94	3.22	2.17	3.97	2.17	3.27	3.27				
PLACE1006783	2.73	1.09	1.46	2.19	2.99	2.41	1.48	1.96	1.96				
PLACE1006786	2.68	1.84	0.83	3.12	2.79	4.30	2.72	2.69	2.69				
PLACE1006792	5.78	3.42	3.75	8.62	10.09	8.98	4.28	5.86	5.86	**	+		
PLACE1006795	0.68	0.34	0.21	1.2	1.49	1.27	1.37	1.67	1.67	**	+	**	+
PLACE1006800	0.58	0.50	0.45	1.01	1.36	1.09	0.49	1.98	1.98	**	+		
PLACE1006805	1.33	0.93	2.03	1.99	1.23	2.62	4.47	8.37	8.37			*	+
PLACE1006809	3.99	2.53	2.85	4.94	4.18	4.26	2.87	3.81	3.81				
PLACE1006815	2.42	2.62	2.14	3.2	3.02	2.39	2.60	2.42	2.42				
PLACE1006819	0.94	0.46	0.62	1.41	2.34	1.11	0.55	1.74	1.74				
PLACE1006820	4.68	2.07	1.78	6.12	5.69	5.61	3.23	3.27	3.27	*	+		
PLACE1006826	5.96	2.02	3.35	4.28	4.36	3.41	2.91	3.64	3.64				
PLACE1006829	5.22	3.72	3.02	4.2	5.82	4.43	2.98	5.22	5.22				
PLACE1006853	1.92	0.96	0.85	1.93	2.19	2.15	1.79	1.77	1.77				
PLACE1006860	0.52	0.28	0.19	0.7	1.33	1.10	0.18	0.88	0.88	*	+		
PLACE1006867	3.61	1.51	1.29	3.02	3.99	3.62	1.66	1.92	1.92				
PLACE1006875	3.81	2.86	3.20	2.81	3.41	2.95	2.46	3.28	3.28				
PLACE1006878	2.74	2.03	2.05	2.44	3.93	2.25	1.87	2.15	2.15				
PLACE1006883	6.43	2.64	2.47	5.83	6.59	4.26	4.67	3.84	3.84				
PLACE1006898	2.65	0.75	0.60	1.14	1.52	1.02	0.75	1.07	1.07				
PLACE1006901	2.51	0.47	1.17	2.93	3.57	2.34	0.90	1.69	1.69				
PLACE1006904	2.19	1.14	0.97	3.15	2.91	3.59	2.13	2.06	2.06	*	+		
PLACE1006917	6.14	2.79	3.06	4.32	4.29	4.20	3.17	2.44	2.44				
PLACE1006932	5	1.78	2.39	3.19	3.17	4.46	2.94	4.82	4.82				
PLACE1006935	2.14	0.74	0.92	1.51	0.93	2.00	1.13	1.70	1.7				
PLACE1006956	4.8	2.30	2.67	3.82	4.93	3.67	2.67	3.02	3.02				
PLACE1006958	3.3	0.68	0.97	1.15	2.53	1.83	2.18	2.76	2.76				
PLACE1006959	5.12	2.95	4.08	5.45	7.11	5.94	4.25	6.06	6.06				
PLACE1006961	6.24	3.14	3.71	8.87	11.45	12.47	5.75	6.96	6.96	*	+		
PLACE1006962	3.09	1.63	2.08	6.06	7.00	5.67	3.12	4.82	4.82	**	+	*	+
PLACE1006966	3.67	1.18	1.70	1.85	1.83	1.79	1.92	2.51	2.51				
PLACE1006979	2	0.97	1.09	2.59	1.79	2.03	1.44	1.20	1.2				
PLACE1006989	6.78	4.06	4.71	5.85	5.19	8.95	4.33	4.95	4.95				
PLACE1007001	4.54	2.23	1.52	6.32	8.61	5.77	3.73	6.03	6.03	*	+		
PLACE1007014	7.18	3.58	3.26	4.66	5.59	4.03	3.90	5.33	5.33				
PLACE1007021	1.97	0.96	1.13	2.46	2.25	1.64	1.52	0.94	0.94				
PLACE1007026	2.03	0.23	0.75	2.47	2.67	2.53	4.15	4.32	4.32	*	+	**	+
PLACE1007028	3.59	1.48	2.53	3.68	2.34	2.63	3.78	4.37	4.37				
PLACE1007038	9.6	3.28	7.64	12.57	9.19	16.41	73.23	81.92	81.92			**	+
PLACE1007040	3.28	1.64	2.20	3.38	2.82	2.64	2.43	2.13	2.13				
PLACE1007045	2.23	0.95	1.52	6.73	6.04	4.31	5.12	5.62	5.62	**	+	**	+
PLACE1007048	283.34	168.88	128.09	131.34	214.44	117.39	119.27	112.98	113				
PLACE1007053	5.82	1.54	2.58	3.59	4.38	2.76	2.77	4.36	4.36				
PLACE1007068	5.93	3.20	2.64	4.13	5.60	3.12	3.77	3.46	3.46				
PLACE1007070	1.79	1.14	1.74	2.68	3.48	2.65	2.23	3.69	3.69	*	+	*	+
PLACE1007076	49.7	17.82	25.75	20.08	16.26	21.00	15.39	17.24	17.24				
PLACE1007077	2.93	1.23	2.63	2.96	2.01	1.85	3.14	3.21	3.21				
PLACE1007081	1.29	0.25	0.75	1.37	1.15	1.43	0.54	1.23	1.23				
PLACE1007082	8.76	4.12	5.94	5.68	4.75	5.79	2.91	3.11	3.11				

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Table 319

PLACE1007092	13.8	11.82	5.85	6.03	7.76	3.70	4.55	4.38	4.38				
PLACE1007096	3.67	1.72	2.42	3.85	3.61	3.33	2.77	3.95	3.95				
PLACE1007097	2.22	0.99	0.99	1.67	2.32	2.35	2.32	1.09	1.09				
PLACE1007099	3.21	1.35	2.99	3.75	3.60	3.90	2.21	4.60	4.6				
PLACE1007105	3.27	1.47	1.70	2.02	1.66	2.46	3.10	2.81	2.81				
PLACE1007108	1.84	0.54	0.64	1.21	1.32	0.77	1.03	1.13	1.13				
PLACE1007111	1.12	0.75	0.77	2.41	0.87	1.64	1.17	1.43	1.43			*	+
PLACE1007112	2.23	1.33	1.93	1.71	1.54	2.89	1.30	2.04	2.04				
PLACE1007130	1.72	0.36	0.26	1	1.71	0.63	0.85	1.29	1.29				
PLACE1007132	3.87	1.51	1.93	3.65	4.98	3.98	2.58	2.83	2.83				
PLACE1007140	2.78	1.67	1.49	5.51	4.02	1.95	1.59	4.61	4.61				
PLACE1007143	4.57	2.06	2.35	3.69	3.88	3.45	2.67	3.35	3.35				
PLACE1007169	7.86	3.91	6.07	4.6	3.97	4.34	4.66	5.06	5.06				
PLACE1007178	3.63	1.78	2.11	3.46	2.58	2.44	3.58	4.50	4.5				
PLACE1007190	1.52	0.85	1.18	1.02	0.96	1.35	1.62	1.51	1.51				
PLACE1007201	1.85	0.34	1.11	1.37	0.91	2.07	0.93	1.05	1.05				
PLACE1007202	18.73	9.75	12.22	19.49	17.57	13.05	23.70	22.24	22.24			*	+
PLACE1007226	4.6	2.18	1.44	3.72	3.17	3.32	4.10	4.25	4.25				
PLACE1007238	4.59	1.78	4.87	4.05	4.43	2.63	3.54	2.85	2.85				
PLACE1007239	4.19	2.58	2.67	5.05	3.84	2.86	3.07	4.50	4.5				
PLACE1007242	3.6	1.20	1.84	1.27	2.10	2.41	1.99	2.58	2.58				
PLACE1007243	10.2	5.01	6.25	4.24	5.71	6.21	7.36	6.08	6.08				
PLACE1007247	3.28	2.10	1.67	14.75	8.63	15.61	4.03	8.60	8.6	**	+	*	+
PLACE1007257	7.61	5.72	7.16	3.66	3.64	3.79	1.96	3.64	3.64	**	-	**	-
PLACE1007274	4.38	2.42	3.36	7.38	8.79	6.79	3.07	4.64	4.64	**	+		
PLACE1007276	2.97	1.43	1.54	2.93	2.81	2.34	1.57	3.92	3.92				
PLACE1007282	8.6	4.51	8.76	10.51	12.35	10.29	22.66	27.14	27.14			**	+
PLACE1007286	6	1.42	3.35	6.08	8.09	5.91	3.36	4.27	4.27				
PLACE1007296	5.96	3.96	4.56	9.09	9.08	8.48	6.51	8.92	8.92	**	+	*	+
PLACE1007301	1.48	0.84	0.72	0.94	1.65	0.98	0.49	0.96	0.96				
PLACE1007314	7.72	5.09	4.39	7.99	9.50	9.98	8.19	8.10	8.1	*	+		
PLACE1007317	1.71	0.70	0.71	2.11	1.11	1.58	1.38	1.29	1.29				
PLACE1007329	1.19	1.05	0.73	3.19	2.34	1.79	1.73	2.65	2.65	*	+	*	+
PLACE1007338	5.4	1.79	2.69	4.68	5.71	4.16	3.17	5.55	5.55				
PLACE1007342	2.46	2.38	1.37	2.04	2.30	2.39	2.65	5.91	5.91				
PLACE1007345	2.86	1.45	1.69	3.47	3.21	3.18	2.59	3.21	3.21	*	+		
PLACE1007346	5.8	4.00	4.67	8.73	7.57	8.39	4.92	8.73	8.73	**	+		
PLACE1007359	3.11	1.64	2.21	3.58	2.56	2.94	3.24	3.82	3.82			*	+
PLACE1007367	9.92	5.57	5.83	12.43	19.19	16.79	8.33	10.26	10.26	*	+		
PLACE1007375	1.77	1.76	1.63	2.23	2.83	2.75	1.31	0.63	0.63	*	+	*	-
PLACE1007377	4.63	2.52	2.53	3.52	3.56	1.75	2.11	3.18	3.18				
PLACE1007386	1.87	0.97	0.83	6.47	6.90	6.45	4.13	3.04	3.04	**	+	*	+
PLACE1007392	2.72	3.07	3.82	2.83	2.94	3.03	2.89	3.43	3.43				
PLACE1007402	2.84	2.88	1.67	3.44	3.03	2.39	3.94	2.99	2.99				
PLACE1007409	0.93	0.91	1.34	1.36	1.18	1.53	1.35	1.51	1.51				
PLACE1007416	1.46	1.48	1.61	3.34	3.06	3.14	3.57	4.84	4.84	**	+	**	+
PLACE1007420	9.86	15.04	12.94	15.1	14.93	22.60	15.85	14.30	14.3				
PLACE1007431	0.76	1.71	1.22	1.19	2.25	1.99	1.64	1.51	1.51				
PLACE1007450	4.02	1.67	1.64	5.21	4.82	5.24	2.44	2.49	2.49	*	+		
PLACE1007452	2.24	1.00	1.94	2.6	2.82	2.49	1.40	3.18	3.18				
PLACE1007454	10.17	5.34	5.33	10.9	13.21	14.02	9.07	11.14	11.14	*	+		
PLACE1007460	3.51	2.45	2.56	3.47	3.50	3.36	2.34	2.84	2.84				
PLACE1007478	1.85	1.34	0.98	2.14	2.65	2.21	0.62	1.89	1.89	*	+		
PLACE1007484	1.62	2.03	1.82	4.03	4.26	4.32	4.30	4.48	4.48	**	+	**	+
PLACE1007488	2.83	1.13	1.39	2.08	1.66	1.77	1.01	1.64	1.64				
PLACE1007507	4.17	3.85	4.18	3.46	1.91	4.23	1.30	2.17	2.17			**	-

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Table 320

PLACE1007511	1.09	1.11	0.68	1.33	1.45	0.75	0.90	1.48	1.48				
PLACE1007513	4.69	1.71	2.94	3.5	3.66	3.78	3.32	6.37	6.37				
PLACE1007524	6.92	2.48	2.90	3.93	4.08	2.82	1.80	1.66	1.66				
PLACE1007525	4.99	2.20	2.97	4.48	5.31	5.23	2.35	2.30	2.3				
PLACE1007537	3.67	3.75	2.72	3.67	3.58	4.70	2.62	4.19	4.19				
PLACE1007544	1.23	1.96	1.26	3.11	3.23	2.88	3.01	2.55	2.55	**	+	*	+
PLACE1007547	3.83	2.63	2.50	6.49	5.11	5.77	2.96	2.23	2.23	**	+		
PLACE1007557	3.78	2.86	3.01	6.18	5.42	6.26	3.20	3.81	3.81	**	+		
PLACE1007560	7.5	4.33	3.69	5.21	4.40	3.63	6.61	8.29	8.29				
PLACE1007565	1.39	0.57	0.51	1.55	0.69	1.08	1.27	0.93	0.93				
PLACE1007580	0.78	0.25	0.56	1.38	0.71	0.94	1.33	1.46	1.46			**	+
PLACE1007583	1.68	1.21	1.36	3.07	1.74	2.51	1.23	2.34	2.34				
PLACE1007591	2.78	0.84	0.81	2.91	3.12	3.09	1.72	2.45	2.45				
PLACE1007598	4.1	2.36	3.10	8.03	7.01	9.10	4.75	4.36	4.36	**	+		
PLACE1007610	0.9	0.60	0.89	2.28	1.49	1.41	1.23	1.82	1.82	*	+	*	+
PLACE1007618	1.76	1.24	1.15	1.76	2.07	1.52	1.03	1.29	1.29				
PLACE1007621	2.86	1.26	1.24	2.73	3.31	2.18	1.97	2.67	2.67				
PLACE1007626	6.13	3.63	3.43	16.1	18.88	18.33	14.85	19.91	19.91	**	+	**	+
PLACE1007632	4.92	2.23	3.27	3.4	3.01	3.01	4.94	4.29	4.29				
PLACE1007635	3.04	0.96	2.65	2.16	2.56	2.69	1.76	2.94	2.94				
PLACE1007645	4.04	1.20	2.15	4.72	5.27	5.01	4.78	4.87	4.87	*	+	*	+
PLACE1007649	1.28	0.79	0.67	1.29	1.36	2.38	1.28	2.15	2.15				
PLACE1007659	4.23	1.93	2.69	6.75	3.97	6.88	2.94	4.41	4.41				
PLACE1007669	6.2	1.80	2.99	5.47	6.53	4.51	3.57	2.86	2.86				
PLACE1007677	4.22	1.89	1.71	6.84	8.75	7.28	3.90	4.46	4.46	**	+		
PLACE1007688	5.22	1.69	2.55	2.63	3.33	2.71	2.38	2.43	2.43				
PLACE1007690	3.97	2.16	3.39	4.09	4.66	3.97	3.53	4.50	4.5				
PLACE1007697	1.72	0.75	0.98	1.08	0.70	0.98	1.28	0.95	0.95				
PLACE1007702	1.76	0.86	1.32	1.85	1.37	3.00	2.01	1.95	1.95				
PLACE1007705	2.4	0.53	1.89	1.45	2.19	2.67	2.64	2.34	2.34				
PLACE1007706	2.8	1.14	1.84	2.88	2.31	2.20	2.45	2.27	2.27				
PLACE1007725	3.27	2.02	1.52	3.44	3.01	2.26	1.89	1.39	1.39				
PLACE1007729	3.75	0.91	0.48	1.28	1.88	1.09	1.35	1.46	1.46				
PLACE1007730	4.12	1.63	2.33	3.92	2.43	2.55	1.94	4.18	4.18				
PLACE1007737	4.58	2.53	1.58	4.31	5.53	6.14	3.60	3.45	3.45				
PLACE1007743	1.47	0.73	0.61	2.7	2.78	2.53	1.94	2.71	2.71	**	+	*	+
PLACE1007746	3.82	1.81	2.10	5.73	3.58	6.69	6.74	9.08	9.08			**	+
PLACE1007753	2.19	1.29	1.71	1.02	1.20	1.89	1.49	1.55	1.55				
PLACE1007769	0.98	0.53	0.69	1.58	1.14	1.77	1.01	1.04	1.04	*	+		
PLACE1007780	4.5	2.26	1.99	3.89	4.09	2.46	2.36	2.20	2.2				
PLACE1007791	5.12	2.18	2.04	3.75	4.60	3.26	2.31	3.66	3.66				
PLACE1007807	2.35	0.20	1.17	3.74	3.71	3.65	3.45	3.14	3.14	*	+	*	+
PLACE1007810	1.24	0.07	0.47	1.06	0.82	1.32	1.17	1.10	1.1				
PLACE1007814	5.26	2.80	2.95	4.73	4.47	4.22	4.12	5.14	5.14				
PLACE1007828	1.64	1.27	1.04	1.35	1.67	1.95	1.48	2.89	2.89				
PLACE1007829	6.87	2.06	4.61	11.59	10.29	14.12	4.54	6.24	6.24	*	+		
PLACE1007841	2.09	0.69	0.83	1.22	2.33	3.41	1.28	2.06	2.06				
PLACE1007842	2.47	1.09	2.35	2.63	2.75	2.08	1.49	2.36	2.36				
PLACE1007843	1.12	0.63	0.54	0.94	1.58	0.91	0.72	0.88	0.88				
PLACE1007845	3.75	1.17	2.10	1.73	2.80	1.91	2.13	2.52	2.52				
PLACE1007846	4.22	1.07	1.41	5.34	3.41	3.57	3.77	4.73	4.73				
PLACE1007848	1.96	0.65	0.52	1.52	2.21	2.88	2.45	2.38	2.38			*	+
PLACE1007852	2.98	0.96	2.30	2.1	4.32	3.04	2.76	3.44	3.44				
PLACE1007858	1.43	0.68	1.60	6.59	6.03	5.72	3.52	4.91	4.91	**	+	**	+
PLACE1007866	30.58	17.58	17.98	11.58	9.80	8.70	10.80	10.41	10.41				
PLACE1007871	22.99	9.51	12.34	18.55	16.06	17.86	13.04	17.83	17.83				

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Table 321

PLACE1007877	4.54	1.36	1.17	4.16	4.25	2.80	3.39	3.32	3.32				
PLACE1007878	4.4	2.07	2.29	2.41	2.70	2.37	3.13	5.04	5.04				
PLACE1007881	1.27	0.74	0.75	0.94	1.76	0.67	0.87	1.11	1.11				
PLACE1007885	1.23	1.17	1.11	1.97	2.06	1.97	2.46	3.25	3.25	**	+	**	+
PLACE1007897	2.56	0.68	1.11	1.75	1.79	1.50	1.00	2.88	2.88				
PLACE1007908	7.68	3.04	3.27	4.73	4.71	5.04	4.39	4.18	4.18				
PLACE1007922	1.4	0.69	0.89	1.56	0.63	1.43	1.13	0.93	0.93				
PLACE1007946	4.36	3.22	3.12	4.56	4.09	3.11	2.97	3.28	3.28				
PLACE1007950	5.15	1.51	1.60	3.7	3.21	2.35	3.25	8.99	8.99				
PLACE1007954	3.66	2.15	2.27	2.4	2.26	2.19	2.79	1.92	1.92				
PLACE1007955	4.71	1.37	1.67	2.61	3.53	2.54	2.49	4.46	4.46				
PLACE1007956	4.42	1.04	2.64	3.61	3.50	3.32	2.21	3.84	3.84				
PLACE1007958	1.93	0.27	1.12	1.34	1.94	1.66	1.60	1.84	1.84				
PLACE1007965	2.55	1.76	1.99	2.32	2.51	3.02	1.19	2.52	2.52				
PLACE1007969	6.03	2.86	2.43	4.73	5.79	6.79	4.72	3.77	3.77				
PLACE1007971	3.53	1.27	2.02	3.82	4.31	3.71	3.34	3.31	3.31				
PLACE1007990	2.84	1.35	1.80	4.92	3.19	2.61	2.45	2.53	2.53				
PLACE1008000	1.73	0.77	0.35	3.42	1.14	0.76	1.28	1.93	1.93				
PLACE1008002	0.38	0.09	0.23	1.64	0.83	0.73	1.52	1.90	1.9	*	+	**	+
PLACE1008037	0.98	0.19	0.99	1.13	1.05	1.34	1.22	1.68	1.68				
PLACE1008044	4.87	3.62	2.89	3.52	3.76	3.71	2.56	3.52	3.52				
PLACE1008045	1.81	1.03	1.31	1.51	1.59	1.22	1.49	2.12	2.12				
PLACE1008080	4.1	3.05	2.36	3.11	3.91	2.99	2.39	3.89	3.89				
PLACE1008092	2.02	1.71	1.46	1.1	0.88	0.81	1.07	2.15	2.15	*	-		
PLACE1008095	2.93	1.27	1.19	2.55	1.83	2.32	1.34	3.34	3.34				
PLACE1008105	2.48	0.98	1.47	2.27	0.97	1.49	2.91	5.54	5.54			*	+
PLACE1008107	6.58	3.57	3.85	1.29	1.19	1.39	4.33	5.78	5.78	*	-		
PLACE1008111	2.46	1.02	2.41	3.33	2.35	3.47	2.96	3.00	3				
PLACE1008113	25.85	13.24	14.36	22.14	19.88	22.12	9.93	8.27	8.27				
PLACE1008122	1.07	0.36	1.70	1.64	1.18	1.29	1.04	1.29	1.29				
PLACE1008129	1.31	1.01	1.72	3.06	3.91	4.22	1.89	1.53	1.53	**	+		
PLACE1008132	2.89	1.43	1.69	4.85	4.46	4.06	3.75	2.77	2.77	**	+		
PLACE1008137	3.98	1.85	1.77	2.91	2.34	1.96	2.43	2.78	2.78				
PLACE1008174	10.37	5.11	6.06	7.46	7.08	5.83	3.58	4.68	4.68				
PLACE1008177	5.22	2.35	2.42	4.78	5.45	4.55	2.08	2.73	2.73				
PLACE1008181	0.6	0.35	0.59	2.1	1.63	0.83	0.78	0.73	0.73			*	+
PLACE1008195	4.21	3.69	4.41	3.34	3.31	4.29	3.54	5.03	5.03				
PLACE1008198	0.92	1.28	1.62	1.49	2.09	2.17	1.39	2.32	2.32				
PLACE1008201	1.66	0.51	1.49	2.83	2.14	2.43	2.07	1.72	1.72	*	+		
PLACE1008209	5.39	4.27	2.17	7.66	7.83	6.93	6.08	4.07	4.07	*	+		
PLACE1008226	3.09	1.71	1.62	2.88	3.33	2.83	2.61	2.73	2.73				
PLACE1008227	3.17	1.23	2.12	4.9	4.87	5.42	2.16	2.72	2.72	**	+		
PLACE1008231	2.12	0.50	0.70	1.87	1.47	1.28	1.21	0.99	0.99				
PLACE1008238	3.15	3.76	3.38	3.65	4.20	4.83	4.89	4.62	4.62			**	+
PLACE1008244	1.2	0.39	0.55	1.23	1.76	1.25	0.99	1.37	1.37				
PLACE1008249	2.18	0.27	0.99	2.07	1.35	1.47	0.79	1.16	1.16				
PLACE1008266	3.92	3.58	3.56	7.01	10.06	9.34	6.60	6.76	6.76	**	+	**	+
PLACE1008273	2.91	1.72	1.49	4.31	6.22	5.51	5.60	5.70	5.7	**	+	**	+
PLACE1008275	1.29	0.61	1.24	2.1	1.76	1.18	1.34	0.60	0.6				
PLACE1008280	2.51	1.09	1.40	1.61	2.66	1.55	2.19	1.36	1.36				
PLACE1008282	6.02	2.61	4.50	6.93	7.87	7.46	6.98	6.73	6.73	*	+		
PLACE1008297	1.93	0.37	0.80	1.67	1.93	1.78	1.68	1.21	1.21				
PLACE1008303	2.86	2.08	2.50	1.98	2.20	2.57	2.27	1.77	1.77				
PLACE1008309	1	0.36	0.94	1.24	0.57	1.29	1.65	0.87	0.87				
PLACE1008315	12.99	6.08	6.62	5.63	6.15	4.10	5.15	5.08	5.08				
PLACE1008329	5.4	1.64	1.66	3.46	3.09	2.21	1.61	3.12	3.12				

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Table 322

PLACE1008330	3.99	1.02	3.12	3.69	2.72	3.55	2.59	3.30	3.3				
PLACE1008331	3.5	1.58	2.61	2.43	4.87	4.55	2.21	5.77	5.77				
PLACE1008351	3.59	1.91	2.57	5.18	5.19	5.56	3.81	3.50	3.5	**	+		
PLACE1008356	3.92	0.69	2.72	2.64	2.56	2.29	2.42	2.95	2.95				
PLACE1008359	1.48	0.76	0.90	2.22	1.26	2.34	1.68	2.46	2.46			*	+
PLACE1008368	4.18	1.66	2.15	9.15	7.54	8.92	6.11	7.44	7.44	**	+	**	+
PLACE1008369	2.77	0.73	1.19	2.41	7.30	3.35	1.02	1.60	1.6				
PLACE1008392	2.13	0.98	1.09	1.58	3.18	1.77	1.88	2.10	2.1				
PLACE1008394	26.4	13.24	13.94	17.36	15.53	22.06	16.70	19.87	19.87				
PLACE1008398	7.2	3.44	10.45	4.58	8.83	4.91	2.86	4.01	4.01				
PLACE1008401	3.08	0.75	1.07	1.76	1.56	2.79	1.84	3.10	3.1				
PLACE1008402	6.01	1.01	4.48	2.49	3.09	3.48	2.05	3.35	3.35				
PLACE1008405	25.84	13.96	18.38	38.51	28.28	49.12	27.91	33.39	33.39			*	+
PLACE1008409	16.67	9.55	11.29	12.69	10.07	15.56	12.51	11.76	11.76				
PLACE1008420	5.7	4.00	2.86	5.32	4.44	3.71	4.42	4.23	4.23				
PLACE1008424	3.57	2.25	1.23	2.09	2.46	2.00	2.48	2.25	2.25				
PLACE1008426	4.1	1.19	2.55	2.53	2.76	1.73	1.42	1.69	1.69				
PLACE1008429	1.34	0.85	1.46	2	3.50	1.65	1.93	1.52	1.52				
PLACE1008430	1.82	0.58	0.88	2.02	1.64	0.56	0.86	2.26	2.26				
PLACE1008437	2.06	0.49	1.54	1.53	1.27	1.54	1.33	2.88	2.88				
PLACE1008453	3.99	2.14	2.45	2.78	2.86	2.41	2.29	5.19	5.19				
PLACE1008454	4.67	3.03	4.69	8.04	6.50	8.39	3.85	5.65	5.65	*	+		
PLACE1008455	6.35	2.17	1.87	10.14	10.23	5.77	6.05	5.82	5.82				
PLACE1008457	9.43	3.52	3.32	5.83	7.73	6.63	5.24	7.01	7.01				
PLACE1008465	2.14	1.13	1.61	1.55	3.02	1.33	2.20	2.70	2.7				
PLACE1008469	12.37	7.23	7.87	8.96	9.09	12.38	13.17	10.93	10.93				
PLACE1008488	1.94	0.92	1.25	0.9	1.06	1.44	1.44	0.95	0.95				
PLACE1008519	3.83	1.77	1.73	2.4	1.77	1.88	2.77	1.49	1.49				
PLACE1008524	3.06	0.85	1.87	3.33	2.40	3.53	2.10	1.92	1.92				
PLACE1008531	3.02	1.05	2.48	2.83	2.67	2.71	2.79	2.45	2.45				
PLACE1008532	1.95	1.34	1.62	3.81	2.99	2.68	2.83	3.90	3.9	*	+	**	+
PLACE1008533	6.08	2.16	3.15	4.18	5.64	3.25	3.67	5.24	5.24				
PLACE1008542	3.98	1.49	1.76	4.67	6.17	4.59	3.86	6.21	6.21	*	+		
PLACE1008549	2.51	1.53	0.88	1.7	2.81	1.76	1.36	1.66	1.66				
PLACE1008560	1.85	0.72	0.75	0.85	0.84	0.96	2.24	1.41	1.41				
PLACE1008567	2.83	1.62	2.07	2.6	2.14	2.90	2.18	3.74	3.74				
PLACE1008568	1.44	0.85	1.22	4.02	2.55	4.05	2.96	3.07	3.07	*	+	**	+
PLACE1008569	6.68	1.97	2.63	4.52	4.62	4.72	3.58	5.21	5.21				
PLACE1008584	2.8	0.91	1.34	2.88	1.91	1.76	1.37	1.81	1.81				
PLACE1008585	6.05	2.08	1.87	5.97	6.88	5.16	6.30	6.66	6.66				
PLACE1008603	2.79	0.92	1.64	1.88	1.63	1.46	1.46	2.30	2.3				
PLACE1008621	2.19	0.44	1.30	1.02	1.47	0.69	1.47	2.18	2.18				
PLACE1008625	0.9	0.37	0.80	0.8	0.79	0.63	1.51	1.36	1.36			*	+
PLACE1008626	1.01	0.36	0.40	1.03	0.59	0.80	0.60	2.30	2.3				
PLACE1008627	3.31	1.35	1.85	3.04	2.64	2.27	2.82	2.83	2.83				
PLACE1008629	4.46	2.86	3.88	4.95	3.86	3.87	2.66	4.45	4.45				
PLACE1008630	6.49	3.28	4.20	4.75	4.80	4.92	3.62	3.61	3.61				
PLACE1008643	3.94	1.90	2.23	4.63	3.91	2.95	3.01	3.94	3.94				
PLACE1008650	1.04	0.28	0.89	1.14	0.65	0.67	0.98	2.48	2.48				
PLACE1008657	2.91	1.23	0.78	2.05	1.78	1.50	2.02	2.54	2.54				
PLACE1008664	2.55	1.44	2.26	1.59	2.27	1.94	2.31	1.74	1.74				
PLACE1008693	3.83	1.61	1.78	3.36	3.20	3.43	2.03	2.63	2.63				
PLACE1008696	1.57	0.88	1.00	2.25	2.32	2.53	1.82	1.87	1.87	**	+	*	+
PLACE1008715	1.2	1.08	0.38	2.73	1.58	1.58	1.30	1.20	1.2				
PLACE1008716	2.62	1.18	1.33	2.82	3.53	2.15	2.83	1.88	1.88				
PLACE1008722	8.81	3.15	4.14	9.07	11.88	9.16	5.01	7.77	7.77				

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Table 323

PLACE1008738	1.83	2.28	2.00	1.8	1.24	1.00	1.36	3.09	3.09				
PLACE1008742	4.02	1.70	1.54	4.3	5.17	3.46	2.80	3.04	3.04				
PLACE1008744	1.17	0.49	0.67	1.04	1.21	1.19	1.03	1.69	1.69				
PLACE1008748	1.18	0.53	1.02	1.35	1.38	1.66	1.55	1.10	1.1				
PLACE1008757	0.57	0.66	1.64	0.96	1.31	1.19	0.28	1.35	1.35				
PLACE1008766	5.2	1.84	3.38	5.73	6.06	11.79	4.24	3.09	3.09				
PLACE1008785	3.43	1.55	1.67	3.73	3.48	3.51	2.86	2.40	2.4				
PLACE1008790	4.68	2.15	2.15	5.43	4.49	3.61	3.28	3.45	3.45				
PLACE1008798	6.35	0.62	2.86	2.36	3.47	2.89	1.71	2.65	2.65				
PLACE1008807	0.99	1.20	1.36	0.98	1.48	1.58	0.90	2.29	2.29				
PLACE1008808	2.02	1.19	1.16	1.26	1.76	1.00	2.24	1.72	1.72				
PLACE1008813	0.94	0.76	1.96	0.73	1.40	0.71	0.81	2.94	2.94				
PLACE1008836	3.35	2.03	2.82	3.36	3.83	3.93	1.76	4.97	4.97				
PLACE1008851	6.7	2.37	2.20	3.21	3.73	4.45	1.84	2.02	2.02				
PLACE1008854	1.01	0.67	0.67	0.73	1.08	1.01	0.89	0.70	0.7				
PLACE1008864	5.23	2.45	2.26	6.92	5.09	5.19	3.11	3.68	3.68				
PLACE1008867	1.96	1.55	1.26	5.74	4.65	5.92	4.30	4.51	4.51	**	+	**	+
PLACE1008876	51.43	26.54	27.05	38	43.35	42.72	24.30	22.52	22.52				
PLACE1008887	1.78	0.54	1.07	2.31	2.39	2.93	1.78	2.61	2.61	*	+		
PLACE1008902	1.97	0.82	0.85	1.66	1.42	3.56	1.02	2.90	2.9				
PLACE1008911	6.01	5.11	5.63	8.6	8.99	8.79	6.07	6.33	6.33	**	+		
PLACE1008917	3.34	2.37	2.25	2.83	3.74	3.27	2.99	3.43	3.43				
PLACE1008920	1.37	0.52	0.53	1.3	2.33	1.36	0.77	1.37	1.37				
PLACE1008925	1.43	1.01	0.48	2.16	1.60	0.85	1.24	0.93	0.93				
PLACE1008930	8.48	4.04	4.74	5.59	5.27	6.20	2.97	5.51	5.51				
PLACE1008934	2.73	1.83	1.68	2.96	2.07	1.68	2.13	1.92	1.92				
PLACE1008941	2.12	2.49	2.29	2.81	3.70	3.18	1.74	1.69	1.69	*	+	**	-
PLACE1008947	5.3	4.86	3.97	6.01	5.96	5.46	4.91	5.47	5.47				
PLACE1008984	2.32	1.08	1.90	4.47	4.44	4.99	1.56	2.13	2.13	**	+		
PLACE1008985	1.06	1.41	1.57	2.31	2.24	1.90	1.29	3.49	3.49	*	+		
PLACE1008994	1.26	0.32	0.61	1.19	2.34	0.75	0.51	0.61	0.61				
PLACE1009020	2.03	0.83	0.79	1.36	0.98	0.99	0.91	1.17	1.17				
PLACE1009027	2.42	0.29	0.98	17.03	20.58	24.13	13.27	17.48	17.48	**	+	**	+
PLACE1009039	0.66	0.39	0.60	0.97	0.77	0.82	0.81	1.68	1.68	*	+	*	+
PLACE1009045	1.25	0.20	1.18	0.92	1.61	1.30	3.10	3.19	3.19			**	+
PLACE1009048	0.29	0.37	0.55	0.51	0.66	0.96	1.13	0.67	0.67				
PLACE1009050	0.48	(0.04)	0.53	1.13	0.72	1.09	0.42	0.86	0.86	*	+		
PLACE1009060	3.31	1.27	1.72	4.36	1.92	4.74	2.50	4.91	4.91				
PLACE1009067	4.9	1.27	1.78	2.92	1.97	2.26	4.68	4.77	4.77				
PLACE1009071	5.93	4.97	3.58	6.84	4.81	6.47	5.46	4.55	4.55				
PLACE1009090	3.14	0.90	2.12	3.01	2.91	5.24	2.46	1.95	1.95				
PLACE1009091	4.11	1.05	1.26	1.69	2.73	1.26	0.58	1.98	1.98				
PLACE1009094	2.34	2.30	1.26	2.48	1.83	1.50	3.22	2.13	2.13				
PLACE1009099	4.71	2.33	2.35	5.94	5.89	8.61	3.69	5.79	5.79	*	+		
PLACE1009110	1.06	1.13	0.63	4.86	1.21	3.08	2.60	2.41	2.41			**	+
PLACE1009111	1.61	0.55	0.64	2.6	1.26	1.76	1.01	2.06	2.06				
PLACE1009113	5.16	1.93	2.40	3.84	4.61	2.47	1.71	4.56	4.56				
PLACE1009130	2.4	1.03	1.11	1.45	1.93	2.94	1.60	1.65	1.65				
PLACE1009150	1.73	0.66	1.55	2.16	2.01	2.30	1.65	1.47	1.47				
PLACE1009155	3.13	2.31	1.89	4.69	5.44	5.47	2.82	2.95	2.95	**	+		
PLACE1009158	3.54	1.36	1.91	2.88	2.25	2.53	2.92	2.13	2.13				
PLACE1009166	2.58	1.73	2.09	2.03	2.15	2.17	2.50	2.39	2.39				
PLACE1009172	2.84	0.78	1.90	4.25	3.46	3.67	2.50	4.14	4.14	*	+		
PLACE1009174	3.1	1.74	1.40	4.47	5.90	4.15	2.46	2.47	2.47	*	+		
PLACE1009183	6.02	1.51	2.01	3.8	4.98	3.03	2.18	2.53	2.53				
PLACE1009186	3.59	0.98	1.37	2.08	2.13	0.57	1.69	3.99	3.99				

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Table 324

PLACE1009190	2.12	1.27	2.18	1.35	2.00	2.47	0.78	2.21	2.21				
PLACE1009196	1.64	0.69	1.48	2.04	2.57	3.98	1.85	1.52	1.52				
PLACE1009200	4.32	1.99	2.61	4.48	5.35	4.97	2.74	2.68	2.68				
PLACE1009217	2.54	0.82	0.83	0.92	1.24	1.76	2.27	2.78	2.78				
PLACE1009230	3.29	1.25	2.57	3.85	3.86	4.23	1.77	4.02	4.02				
PLACE1009236	3.68	1.44	1.56	2.57	2.82	2.63	1.54	2.09	2.09				
PLACE1009246	9.73	3.62	4.17	6.98	7.72	5.06	6.33	5.96	5.96				
PLACE1009265	21.04	8.85	7.61	12.85	14.86	12.34	4.96	7.60	7.6				
PLACE1009279	1.84	0.86	0.79	1.58	1.52	1.53	1.15	1.01	1.01				
PLACE1009298	3.7	2.72	2.61	7.54	8.77	8.06	7.00	9.82	9.82	**	+	**	+
PLACE1009308	8.08	4.61	4.25	6.42	4.02	4.44	5.48	7.05	7.05				
PLACE1009319	2.03	1.05	1.47	2.87	1.77	3.10	1.90	2.70	2.7				
PLACE1009328	1.59	0.99	1.42	4.54	4.75	5.66	3.66	4.23	4.23	**	+	**	+
PLACE1009335	1.22	0.54	0.61	2.18	1.74	1.92	1.46	0.54	0.54	**	+		
PLACE1009338	3.48	1.35	1.84	5.85	6.71	4.36	2.31	2.98	2.98	*	+		
PLACE1009344	3.01	1.13	2.79	1.83	3.29	2.00	2.97	2.70	2.7				
PLACE1009355	1.86	0.75	0.42	1.64	1.55	1.14	2.65	5.34	5.34			*	+
PLACE1009368	2.14	1.43	1.26	1.31	1.41	1.74	1.22	2.07	2.07				
PLACE1009375	1.44	0.73	1.31	0.98	2.28	1.80	1.47	2.25	2.25				
PLACE1009388	1.69	1.27	1.19	3.96	2.82	3.05	1.65	2.75	2.75	**	+		
PLACE1009398	6.96	2.57	3.77	9	5.66	6.33	4.19	4.18	4.18				
PLACE1009404	4.11	2.25	3.40	3.14	5.18	4.09	2.94	3.62	3.62				
PLACE1009410	1.58	0.66	0.54	0.77	1.47	0.75	1.04	1.03	1.03				
PLACE1009417	1.85	0.80	1.11	2.36	1.87	0.83	1.31	3.04	3.04				
PLACE1009424	10.71	5.65	7.84	8.47	7.50	6.48	8.06	10.17	10.17				
PLACE1009434	3.29	1.53	1.47	2.38	1.85	1.49	1.58	1.71	1.71				
PLACE1009443	2.96	1.10	1.13	1.36	1.62	1.85	0.98	1.60	1.6				
PLACE1009444	3.55	2.71	1.84	4.89	4.13	5.32	3.26	4.47	4.47	*	+		
PLACE1009459	5.23	2.29	2.82	3.92	3.20	3.43	3.08	4.21	4.21				
PLACE1009460	0.43	0.37	0.33	0.44	0.37	1.88	0.42	0.69	0.69				
PLACE1009468	5.92	2.35	2.32	5.44	2.65	2.84	4.15	2.97	2.97				
PLACE1009476	2.6	0.89	1.54	2.02	2.17	1.83	1.69	2.92	2.92				
PLACE1009477	3.84	1.44	1.65	4.37	2.97	3.00	2.09	2.93	2.93				
PLACE1009493	2.08	0.70	1.33	2.12	1.22	1.24	0.82	2.09	2.09				
PLACE1009502	0.95	0.44	0.76	0.93	0.90	0.72	0.86	1.97	1.97				
PLACE1009524	2.21	0.79	1.36	1.49	1.81	1.15	1.58	2.15	2.15				
PLACE1009527	1.81	1.71	1.43	2.21	1.72	1.29	1.43	1.91	1.91				
PLACE1009531	5.24	3.01	2.51	5.69	3.69	5.37	6.78	6.24	6.24			*	+
PLACE1009535	1.5	0.44	0.55	2.44	1.80	1.98	2.38	1.44	1.44	*	+		
PLACE1009539	3.39	1.25	2.38	2.92	3.40	3.47	2.40	3.54	3.54				
PLACE1009540	6	3.37	5.39	4.83	4.41	4.48	4.99	6.08	6.08				
PLACE1009542	2.35	1.42	1.51	1.82	1.71	1.38	1.98	2.97	2.97				
PLACE1009546	1.47	0.53	0.69	0.94	1.26	0.62	1.78	0.85	0.85				
PLACE1009556	1.35	0.95	1.07	1.35	2.21	0.98	2.07	2.20	2.2			**	+
PLACE1009569	2.13	1.30	1.80	2.87	2.82	3.16	1.76	2.07	2.07	*	+		
PLACE1009571	2.72	1.88	1.50	2.08	1.82	2.50	1.30	1.73	1.73				
PLACE1009573	8.32	4.58	4.70	4.98	4.59	3.46	3.53	2.68	2.68				
PLACE1009576	3.44	1.43	2.32	5.25	5.67	4.91	3.85	4.08	4.08	**	+		
PLACE1009580	2.8	1.13	1.78	3.7	3.05	2.82	3.23	3.94	3.94			*	+
PLACE1009581	2.06	1.05	0.67	2.39	2.40	2.16	4.59	3.83	3.83			**	+
PLACE1009587	1.75	1.08	0.69	1.11	1.37	1.41	1.48	2.01	2.01				
PLACE1009593	2.92	1.61	2.66	2.04	2.95	2.35	2.20	2.52	2.52				
PLACE1009595	4.18	2.88	2.05	6.18	7.63	5.15	3.71	4.73	4.73	*	+		
PLACE1009596	1.65	1.09	0.96	1.87	2.16	2.45	1.64	1.48	1.48	*	+		
PLACE1009600	6.27	3.95	2.87	7.95	6.45	4.31	4.05	5.38	5.38				
PLACE1009604	2.52	0.69	0.99	3.24	2.45	1.67	2.85	2.11	2.11				

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Table 325

PLACE1009607	3.67	1.38	1.49	4.1	6.22	4.84	3.49	3.02	3.02	*	+		
PLACE1009613	3.3	1.40	2.05	3.5	4.21	3.44	2.36	3.25	3.25				
PLACE1009621	2.39	1.87	2.42	5.45	5.01	5.43	4.10	6.00	6	**	+	**	+
PLACE1009622	1.78	0.78	1.73	2.06	1.60	1.99	2.28	4.60	4.6			*	+
PLACE1009624	0.78	1.54	0.90	2.28	3.24	1.75	2.30	1.54	1.54				
PLACE1009637	1.33	0.77	0.84	3.69	2.89	3.73	3.44	3.33	3.33	**	+	**	+
PLACE1009639	2.08	0.08	0.65	2.19	1.89	1.62	1.82	1.57	1.57				
PLACE1009654	2.53	0.76	1.11	2.83	1.57	1.39	1.86	2.31	2.31				
PLACE1009659	5.89	3.14	3.71	3.85	5.36	4.32	4.03	5.80	5.8				
PLACE1009665	1.27	1.04	0.92	2.92	2.14	2.54	0.79	2.03	2.03	**	+		
PLACE1009669	3.5	3.60	3.11	3.69	5.37	3.54	3.97	4.99	4.99			*	+
PLACE1009670	2.16	1.80	1.32	3.29	1.88	3.37	1.92	2.64	2.64				
PLACE1009708	2.48	1.90	1.93	4.13	3.31	5.20	2.14	3.90	3.9	*	+		
PLACE1009721	3.15	2.27	2.41	1.67	3.17	2.28	7.20	2.48	2.48				
PLACE1009731	3.26	1.56	1.59	2.49	3.83	1.81	1.89	2.37	2.37				
PLACE1009735	2.96	1.31	2.04	2.52	2.63	2.49	2.46	2.74	2.74				
PLACE1009737	2.94	0.82	1.29	2.21	2.29	2.41	1.51	1.54	1.54				
PLACE1009741	3.13	1.21	2.06	2.99	2.40	4.38	1.51	3.07	3.07				
PLACE1009752	3.23	1.55	1.75	2.3	2.72	2.29	1.86	1.61	1.61				
PLACE1009763	5.82	2.68	2.79	4.62	5.11	4.63	5.66	4.98	4.98				
PLACE1009766	1.66	0.72	1.60	4.14	2.26	2.27	1.82	1.34	1.34				
PLACE1009772	1.8	1.13	2.05	2.49	1.48	2.20	2.00	2.91	2.91				
PLACE1009782	3.79	1.21	0.99	3.99	3.99	2.22	2.25	2.39	2.39				
PLACE1009794	3.98	1.98	2.41	2.73	2.16	1.89	2.44	4.87	4.87				
PLACE1009798	3.03	1.31	2.50	3.63	5.60	4.46	2.46	3.00	3	*	+		
PLACE1009845	0.71	0.31	1.69	2.44	1.45	2.19	0.63	2.13	2.13				
PLACE1009849	2.59	1.40	2.09	2.06	1.75	1.55	1.88	1.44	1.44				
PLACE1009857	2.54	1.21	2.06	1.63	1.90	1.80	2.01	3.22	3.22				
PLACE1009861	3.24	2.05	2.05	5.01	4.66	4.82	3.10	3.89	3.89	**	+		
PLACE1009872	43.66	21.33	23.44	30.54	23.07	32.80	14.91	18.35	18.35				
PLACE1009877	34.76	13.19	14.79	13.63	20.45	13.77	10.79	13.80	13.8				
PLACE1009879	1.98	0.47	1.85	1.36	3.33	1.12	1.96	1.87	1.87				
PLACE1009886	1.09	0.42	0.92	1.49	1.32	1.87	0.94	1.34	1.34	*	+		
PLACE1009888	3.11	1.53	2.24	1.6	2.71	2.32	1.87	2.30	2.3				
PLACE1009908	4.53	2.06	2.64	3.65	2.87	3.85	3.36	4.12	4.12				
PLACE1009919	5.7	2.20	3.89	5.91	4.05	5.41	4.60	6.30	6.3				
PLACE1009921	1.24	0.74	1.00	0.94	2.00	1.75	1.08	0.94	0.94				
PLACE1009923	2.95	1.00	1.09	2.18	1.25	5.57	0.84	2.57	2.57				
PLACE1009924	4.78	1.22	4.05	2.57	4.25	2.76	1.54	3.00	3				
PLACE1009925	1.27	0.73	0.91	0.45	0.87	0.31	1.52	2.61	2.61			*	+
PLACE1009931	11.44	4.02	5.58	10.31	11.46	9.16	5.01	7.71	7.71				
PLACE1009935	0.24	0.55	0.45	0.68	0.48	0.50	1.11	1.18	1.18			**	+
PLACE1009947	4.92	1.59	1.73	2.29	3.03	2.70	3.05	3.68	3.68				
PLACE1009961	1.11	1.73	1.45	1.96	1.63	2.02	1.58	0.96	0.96				
PLACE1009971	2.28	1.16	1.31	3.83	2.51	3.34	2.27	2.89	2.89	*	+		
PLACE1009982	7.21	2.79	4.22	5.07	5.60	7.20	6.47	7.74	7.74				
PLACE1009992	3.36	1.01	0.95	2.29	3.14	1.23	2.29	4.00	4				
PLACE1009995	7.97	4.77	4.17	10.64	14.64	12.97	7.62	12.10	12.1	*	+		
PLACE1009997	3.62	1.37	1.19	4.05	4.29	3.62	2.02	2.74	2.74				
PLACE1010002	3.23	0.90	2.15	1.8	3.62	1.37	1.28	2.45	2.45				
PLACE1010011	3.01	1.89	1.75	1.26	1.49	1.10	1.92	1.85	1.85				
PLACE1010013	1.67	0.86	0.88	1.15	1.55	0.74	1.18	1.56	1.56				
PLACE1010021	2.43	0.87	2.19	2.61	2.46	2.89	3.71	2.58	2.58				
PLACE1010023	4.84	1.80	2.28	2.57	2.67	3.95	1.95	4.34	4.34				
PLACE1010031	5.58	2.99	1.54	4.23	4.90	2.66	3.18	2.93	2.93				
PLACE1010039	1.86	0.50	0.58	0.41	1.70	1.28	1.06	1.35	1.35				

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Table 326

PLACE1010045	6.37	3.18	4.06	5.76	9.98	5.99	3.46	7.87	7.87				
PLACE1010053	7.31	4.10	4.89	8.33	10.67	7.68	5.23	4.89	4.89				
PLACE1010060	5.81	2.55	2.85	4.53	3.83	3.76	4.23	4.25	4.25				
PLACE1010069	1.38	1.53	1.33	0.77	1.42	0.61	0.88	2.96	2.96				
PLACE1010070	1.16	0.11	0.64	0.75	0.45	1.16	2.70	1.27	1.27				
PLACE1010074	9.55	3.59	4.51	8.29	7.15	7.46	5.88	9.16	9.16				
PLACE1010076	32.02	14.06	13.18	16.2	20.29	12.88	25.05	26.03	26.03				
PLACE1010078	5.69	2.44	3.34	4.22	3.97	3.39	4.99	6.24	6.24				
PLACE1010081	3.3	1.78	4.36	4.28	4.59	3.29	2.67	5.51	5.51				
PLACE1010083	2.72	1.96	1.66	0.92	1.44	1.20	2.07	2.63	2.63				
PLACE1010089	2.82	1.29	2.28	4.53	3.47	5.64	3.30	4.44	4.44	*	+	*	+
PLACE1010096	3.39	1.17	2.00	2.56	2.19	2.70	1.45	1.92	1.92				
PLACE1010102	5.26	3.31	3.97	9.27	6.87	8.63	4.86	8.37	8.37	*	+		
PLACE1010105	4.29	0.95	1.09	2.44	2.73	1.94	2.71	4.01	4.01				
PLACE1010106	1.98	0.97	0.87	3.59	2.61	2.19	3.70	3.99	3.99	*	+	**	+
PLACE1010130	2.14	1.13	1.35	4.01	3.52	4.49	5.26	8.14	8.14	**	+	**	+
PLACE1010132	6.25	4.26	5.07	4.52	4.25	5.01	4.63	5.39	5.39				
PLACE1010134	3.87	1.25	2.18	2.61	2.68	1.90	2.26	2.82	2.82				
PLACE1010139	28.44	17.86	18.97	14.51	12.81	13.26	30.01	30.01	30.01				
PLACE1010148	2.71	1.27	1.28	1.81	1.73	1.69	1.33	1.07	1.07				
PLACE1010152	2.7	1.53	1.95	4.96	4.00	5.90	3.04	3.45	3.45	*	+	*	+
PLACE1010155	1.95	0.77	1.06	1.99	1.84	1.65	3.04	2.97	2.97			**	+
PLACE1010156	1.86	1.01	1.72	5.69	7.58	4.30	7.96	8.94	8.94	*	+	**	+
PLACE1010161	2.56	0.74	1.26	2.69	3.12	1.69	2.27	2.44	2.44				
PLACE1010181	1.28	0.65	2.02	2	2.26	1.95	1.65	3.46	3.46				
PLACE1010194	4.75	3.52	3.08	5.35	3.77	3.54	4.56	3.30	3.3				
PLACE1010202	1.47	0.70	0.65	1.46	1.47	1.29	1.34	1.69	1.69				
PLACE1010231	1.3	1.19	0.99	2.11	1.60	1.20	1.89	1.43	1.43				
PLACE1010235	2.55	0.79	1.71	2.65	2.39	3.67	1.07	1.49	1.49				
PLACE1010237	0.84	1.17	0.50	1.96	1.56	2.36	1.09	0.99	0.99	*	+		
PLACE1010251	3.81	2.13	2.41	3.72	3.24	1.88	1.45	3.83	3.83				
PLACE1010261	1.35	0.55	0.65	1.04	1.71	1.55	1.14	1.11	1.11				
PLACE1010270	1.46	0.23	0.71	1.47	1.36	1.19	1.45	1.50	1.5				
PLACE1010273	0.99	0.27	0.37	1.03	1.00	0.75	1.88	1.40	1.4			*	+
PLACE1010274	5.85	2.65	3.07	9.77	6.41	6.98	9.03	7.48	7.48			*	+
PLACE1010277	0.73	0.48	1.84	2.72	1.75	2.20	2.90	4.07	4.07			**	+
PLACE1010293	2.98	2.04	1.13	2.91	3.54	3.25	2.77	2.03	2.03				
PLACE1010297	1.4	1.02	0.95	3.02	1.83	2.84	1.39	2.38	2.38	*	+		
PLACE1010300	2.53	1.14	1.11	3.81	3.04	2.55	5.33	3.77	3.77			*	+
PLACE1010310	32.51	17.93	15.91	30.53	26.14	27.60	23.13	27.43	27.43				
PLACE1010321	4.23	1.98	2.58	2.3	3.07	2.72	3.25	3.30	3.3				
PLACE1010324	1.39	0.54	0.66	1.12	1.26	0.93	0.53	1.22	1.22				
PLACE1010329	2.31	0.98	1.09	3.01	2.16	2.51	0.92	2.83	2.83				
PLACE1010330	5.03	4.25	4.39	4.99	4.21	5.53	4.14	7.36	7.36				
PLACE1010335	15.88	12.79	14.20	8.65	7.50	7.75	5.10	7.02	7.02	**	-	**	-
PLACE1010341	0.29	0.66	0.37	0.99	1.99	0.90	0.42	0.24	0.24				
PLACE1010342	0.95	0.44	0.79	1.64	1.38	0.95	1.00	0.59	0.59				
PLACE1010346	4.09	1.92	1.71	4.43	3.58	3.75	2.92	3.05	3.05				
PLACE1010362	6.71	3.65	3.11	5.41	4.43	4.32	3.93	3.09	3.09				
PLACE1010364	2.59	1.60	1.20	2.85	2.37	2.17	1.17	1.29	1.29				
PLACE1010368	4.89	5.80	6.59	7.12	8.61	9.56	7.27	7.36	7.36	*	+	*	+
PLACE1010373	5.27	3.94	4.28	6.3	5.08	7.04	5.11	6.77	6.77				
PLACE1010383	4.96	2.31	2.06	8.93	6.77	7.08	4.88	5.39	5.39	*	+		
PLACE1010385	0.33	0.37	0.29	0.63	0.70	0.56	0.54	0.63	0.63	**	+	**	+
PLACE1010389	5.32	1.69	2.00	3.34	2.68	4.99	2.13	3.58	3.58				
PLACE1010401	1.04	0.68	0.65	0.51	0.65	1.60	0.87	0.66	0.66				

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Table 327

PLACE1010410	4.61	1.87	2.21	5.83	8.60	7.04	3.70	4.91	4.91	*	+		
PLACE1010418	3.29	1.76	2.41	6.21	6.34	6.33	2.79	3.38	3.38	**	+		
PLACE1010425	1.18	0.35	0.46	1.22	0.78	1.70	0.80	1.37	1.37				
PLACE1010443	5.43	3.03	3.71	5.62	3.76	6.48	4.57	5.05	5.05				
PLACE1010445	4.33	2.64	3.67	5.95	5.86	6.97	4.11	3.20	3.2	*	+		
PLACE1010481	1.37	1.21	1.06	0.8	0.77	1.60	1.13	1.10	1.1				
PLACE1010482	5.16	2.61	3.60	3.41	3.22	3.80	5.36	2.91	2.91				
PLACE1010491	2.88	2.21	3.23	5.03	5.64	4.25	5.35	8.41	8.41	*	+	*	+
PLACE1010492	2.47	1.94	1.90	1.59	2.93	3.57	2.66	2.46	2.46				
PLACE1010509	1.31	0.33	0.65	0.44	1.02	0.95	1.07	1.11	1.11				
PLACE1010518	4.3	2.12	3.06	8.55	9.22	8.31	5.08	9.10	9.1	**	+	*	+
PLACE1010522	4.42	3.30	2.99	4.43	3.15	5.70	4.02	5.51	5.51				
PLACE1010529	4.44	3.27	3.34	4.15	2.17	4.43	2.83	4.60	4.6				
PLACE1010547	1.36	0.46	1.84	1.38	2.57	0.83	0.81	0.68	0.68				
PLACE1010560	3.62	1.42	1.78	3.44	4.11	3.17	1.69	3.25	3.25				
PLACE1010562	2.49	1.56	1.51	2.33	1.85	1.73	1.62	1.70	1.7				
PLACE1010579	1.43	1.21	2.19	1.9	1.92	3.18	1.68	1.93	1.93				
PLACE1010580	6.35	2.50	3.66	4.91	4.74	4.81	3.94	5.30	5.3				
PLACE1010599	2.99	2.56	2.79	4.69	2.68	4.02	2.68	2.87	2.87				
PLACE1010606	0.64	1.41	0.70	0.91	1.32	1.04	0.85	0.75	0.75				
PLACE1010616	1.07	0.75	1.12	3.22	1.83	3.57	1.94	1.36	1.36	*	+		
PLACE1010622	9.24	4.26	4.31	2.37	3.79	2.39	1.80	2.04	2.04				
PLACE1010624	6.73	4.32	4.19	2.38	2.68	1.71	1.73	1.83	1.83	*	-	*	-
PLACE1010628	1.26	1.28	1.00	1.32	2.31	1.21	1.10	0.98	0.98				
PLACE1010629	1.86	1.74	1.96	1.86	4.02	4.33	2.68	2.28	2.28			*	+
PLACE1010630	5.11	3.33	3.71	7.92	7.09	5.39	5.90	7.29	7.29	*	+	*	+
PLACE1010631	1.79	0.95	0.97	2.41	2.47	2.83	1.91	1.86	1.86	*	+		
PLACE1010651	2.68	2.44	2.01	2.53	1.74	2.28	2.68	4.49	4.49				
PLACE1010661	2.42	1.52	2.69	2.28	2.26	4.08	1.65	3.04	3.04				
PLACE1010662	2.49	1.93	2.59	3.46	2.35	2.86	1.94	1.49	1.49				
PLACE1010668	6.55	2.72	2.43	7.07	8.23	6.07	5.21	6.36	6.36				
PLACE1010702	18.26	8.81	10.62	33.41	42.20	27.93	11.82	16.20	16.2	*	+		
PLACE1010709	29.25	14.24	17.35	21.38	21.56	17.73	31.21	41.95	41.95			*	+
PLACE1010713	11.16	4.98	5.23	9.06	10.03	9.81	9.13	15.19	15.19				
PLACE1010714	0.55	0.48	0.52	0.64	0.75	1.34	0.77	0.70	0.7			**	+
PLACE1010716	5.99	2.36	2.79	3.78	2.95	5.02	3.07	3.15	3.15				
PLACE1010717	2.06	1.35	1.59	2.22	1.80	2.83	0.90	1.52	1.52				
PLACE1010720	18.67	8.95	8.08	12.05	17.26	10.51	4.13	4.57	4.57				
PLACE1010739	1.36	1.32	0.50	2.03	2.27	3.00	2.05	1.94	1.94	*	+	*	+
PLACE1010743	1.84	1.21	0.69	1.5	0.87	0.37	0.87	1.50	1.5				
PLACE1010752	5.21	2.95	2.72	2.98	3.08	1.69	2.31	3.98	3.98				
PLACE1010761	9.42	7.63	8.64	20.89	19.08	19.20	8.58	11.68	11.68	**	+		
PLACE1010771	7.47	3.15	3.53	5.95	5.91	7.07	6.15	6.64	6.64				
PLACE1010784	0.87	0.52	1.39	0.62	1.10	1.01	1.14	0.89	0.89				
PLACE1010786	3.62	2.60	1.59	2.95	1.86	4.15	2.62	2.64	2.64				
PLACE1010789	2.47	1.71	1.29	7.34	5.69	4.59	3.94	2.83	2.83	**	+		
PLACE1010800	5.09	2.34	2.77	6.42	5.52	4.71	4.26	4.86	4.86				
PLACE1010802	2.85	0.65	1.48	2.19	2.46	1.85	2.00	3.34	3.34				
PLACE1010811	3.15	1.56	1.75	2.32	2.73	2.52	1.52	3.78	3.78				
PLACE1010813	4.37	2.54	2.23	3.08	2.72	2.68	2.51	3.14	3.14				
PLACE1010827	2.09	0.81	0.76	1.38	1.83	1.70	1.14	4.49	4.49				
PLACE1010833	6.2	2.64	3.19	13.01	9.81	9.59	5.31	5.99	5.99	*	+		
PLACE1010839	3.43	2.31	3.38	7.65	5.31	7.09	3.40	4.37	4.37	*	+		
PLACE1010856	3.15	2.01	1.95	2.4	2.08	1.61	2.50	2.16	2.16				
PLACE1010857	5.31	2.37	3.64	2.66	4.62	2.73	2.23	4.31	4.31				
PLACE1010870	6.19	2.76	3.14	7.02	8.56	7.22	4.56	4.25	4.25	*	+		

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Table 328

PLACE1010877	3.9	0.68	2.81	4.57	8.26	6.30	4.12	5.68	5.68					
PLACE1010882	1.73	0.87	1.34	0.94	1.22	1.41	1.64	2.79	2.79					
PLACE1010891	1.31	1.05	1.38	1.34	2.82	2.67	1.60	1.74	1.74			*	+	
PLACE1010896	2.03	1.93	1.21	5.65	5.89	6.07	2.71	4.67	4.67	**	+	*	+	
PLACE1010900	7.45	5.19	4.52	6.71	10.28	6.75	5.29	6.78	6.78					
PLACE1010916	1.58	1.17	1.07	2.47	2.58	1.67	1.27	2.26	2.26	*	+			
PLACE1010917	1.05	0.96	0.11	1.61	1.38	1.11	1.25	1.13	1.13					
PLACE1010924	2.09	0.79	0.68	3.58	1.12	1.06	1.53	2.87	2.87					
PLACE1010925	6.95	5.48	6.26	14.3	13.92	11.11	10.38	11.87	11.87	**	+	**	+	
PLACE1010926	4.68	2.80	3.56	5.61	3.87	4.95	5.17	4.94	4.94					
PLACE1010942	9.58	6.01	6.54	10.63	11.10	11.71	7.84	8.22	8.22	*	+			
PLACE1010943	34.04	17.63	26.11	27.44	25.58	32.27	17.16	17.20	17.2					
PLACE1010944	4.16	2.44	1.53	4.69	4.52	3.10	3.60	3.71	3.71					
PLACE1010947	3	1.38	1.06	4.09	3.59	3.17	3.08	1.80	1.8					
PLACE1010954	5.64	1.64	2.41	6.89	7.16	7.06	4.57	2.95	2.95	*	+			
PLACE1010960	2.56	1.87	3.84	3.46	4.48	4.07	2.90	5.57	5.57					
PLACE1010965	2.32	1.81	1.90	3.82	3.17	4.63	3.08	3.88	3.88	*	+	**	+	
PLACE1010968	2.01	2.04	1.40	2.48	1.55	2.68	3.26	2.68	2.68			*	+	
PLACE1010978	2.64	1.65	3.12	2.67	4.61	3.98	4.33	3.15	3.15					
PLACE1010982	0.32	0.44	1.17	1.43	1.48	1.69	0.82	1.16	1.16	*	+			
PLACE1010990	1.25	1.65	1.41	1.21	2.03	3.15	1.56	2.02	2.02					
PLACE1011017	4.02	2.33	2.07	4.93	5.02	3.31	2.67	2.53	2.53					
PLACE1011019	4.19	3.51	2.69	3.28	4.24	3.10	3.40	4.43	4.43					
PLACE1011026	0.53	0.56	0.94	1	1.14	1.01	1.44	1.90	1.9			**	+	
PLACE1011032	1.04	1.26	1.14	1.35	3.76	1.41	1.45	1.09	1.09					
PLACE1011041	2.22	2.15	1.83	3.19	3.33	2.65	2.20	2.59	2.59	*	+			
PLACE1011045	4.26	2.55	2.05	3.25	2.44	2.71	2.62	4.66	4.66					
PLACE1011046	2.58	2.74	2.45	7.65	5.20	7.76	2.85	2.98	2.98	**	+	*	+	
PLACE1011054	5.53	5.97	3.21	7.9	9.44	10.30	5.46	7.19	7.19	*	+			
PLACE1011056	12.06	8.95	6.62	12.16	14.46	16.30	10.02	8.27	8.27					
PLACE1011057	1.87	1.37	1.37	4.52	4.54	3.70	1.84	1.48	1.48	**	+			
PLACE1011059	0.6	0.44	0.37	1.23	1.32	1.03	0.88	0.52	0.52	**	+			
PLACE1011066	4.38	2.43	3.65	12.2	18.07	8.10	6.79	9.58	9.58	*	+	**	+	
PLACE1011087	8.25	6.00	13.05	11.16	14.93	13.07	8.67	11.65	11.65					
PLACE1011090	3.34	3.04	3.20	4.44	8.79	7.02	2.18	1.69	1.69	*	+	**	-	
PLACE1011109	4.01	3.02	3.89	8.31	10.21	9.01	3.52	3.74	3.74	**	+			
PLACE1011114	3.2	3.86	3.47	4.71	3.90	4.13	3.10	3.01	3.01					
PLACE1011116	10.05	5.20	4.98	6.55	11.37	7.07	9.74	10.38	10.38					
PLACE1011122	1.51	0.61	0.83	0.61	2.18	1.37	1.66	1.51	1.51					
PLACE1011133	3.84	1.08	1.97	3.52	5.23	3.54	3.50	2.83	2.83					
PLACE1011134	3.94	1.65	2.34	3.61	3.61	3.94	2.95	3.46	3.46					
PLACE1011143	3.34	0.78	1.07	1.6	0.98	1.60	1.65	1.94	1.94					
PLACE1011146	5.79	3.61	4.24	4.94	3.96	4.87	4.89	7.01	7.01					
PLACE1011160	3.37	3.04	1.43	3.14	2.88	3.52	2.47	3.09	3.09					
PLACE1011165	2.82	1.49	1.92	2.09	2.17	1.87	1.17	1.03	1.03					
PLACE1011181	4.06	3.32	2.04	6.31	7.78	3.19	4.22	5.69	5.69					
PLACE1011185	3.65	1.45	1.75	3.91	3.68	3.21	2.20	1.92	1.92					
PLACE1011186	10.21	6.77	9.51	8.05	10.88	9.70	7.96	8.75	8.75					
PLACE1011203	0.72	0.41	0.60	0.86	1.05	1.05	0.76	0.91	0.91	*	+			
PLACE1011214	2.12	1.28	1.87	3.46	4.03	3.52	3.00	2.98	2.98	**	+	**	+	
PLACE1011219	5.09	4.32	4.64	6.07	4.80	4.51	3.57	4.01	4.01			*	-	
PLACE1011221	8.97	5.27	6.20	7.22	3.06	12.50	3.65	4.01	4.01					
PLACE1011229	3.75	1.90	2.65	1.71	3.17	2.00	1.40	2.18	2.18					
PLACE1011231	3.92	2.25	2.28	3.91	4.79	2.77	5.22	2.91	2.91					
PLACE1011236	8.67	4.88	5.11	4.86	4.69	4.64	5.23	5.25	5.25					
PLACE1011247	4.61	2.86	4.14	4.95	3.62	3.74	4.69	6.05	6.05					

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Table 329

PLACE1011263	4.63	1.43	2.06	5.15	3.30	5.05	3.84	4.54	4.54				
PLACE1011273	0.96	0.21	0.03	0.28	0.62	1.29	0.76	0.83	0.83				
PLACE1011278	6.81	4.02	5.42	10.67	8.60	12.25	6.32	6.99	6.99	*	+		
PLACE1011289	5.66	2.33	3.18	4.65	3.12	5.27	3.01	3.39	3.39				
PLACE1011291	16.28	11.06	10.52	7.72	9.80	6.81	14.94	17.29	17.29				
PLACE1011296	3.24	2.37	2.66	4.3	4.86	3.54	3.68	3.04	3.04	*	+		
PLACE1011310	4	1.37	1.23	4.91	7.48	2.45	2.90	2.71	2.71				
PLACE1011311	6.86	4.63	5.58	11.54	13.47	10.02	8.99	6.21	6.21	**	+		
PLACE1011321	2.48	2.00	2.29	4.17	3.53	4.74	3.10	3.06	3.06	**	+	**	+
PLACE1011325	2.45	1.16	0.85	2.15	1.85	2.50	1.87	1.38	1.38				
PLACE1011332	2.06	1.37	1.10	2.9	1.77	3.23	1.54	3.88	3.88				
PLACE1011340	4.71	2.86	3.96	6.93	7.43	10.39	3.26	4.42	4.42	*	+		
PLACE1011353	8.94	8.02	6.47	12.12	12.68	8.45	5.57	6.13	6.13				
PLACE1011360	5.26	2.74	2.31	7.14	13.29	6.66	11.83	17.54	17.54			**	+
PLACE1011364	3.45	2.09	2.62	4.62	3.01	2.44	3.75	3.95	3.95			*	+
PLACE1011365	2.35	1.17	0.95	2.03	1.96	2.41	0.96	2.66	2.66				
PLACE1011371	5.16	2.45	2.43	5.08	2.86	3.23	3.60	3.42	3.42				
PLACE1011375	2.23	1.21	1.56	1.86	1.08	1.78	1.86	1.55	1.55				
PLACE1011386	8.63	5.02	6.24	7.07	6.54	8.61	7.88	10.06	10.06				
PLACE1011399	1.83	1.09	0.89	5.72	1.66	3.52	2.58	2.39	2.39			*	+
PLACE1011406	5.14	2.34	2.53	3.24	3.16	4.75	3.03	4.67	4.67				
PLACE1011407	5.6	2.12	1.49	5.65	6.78	4.60	3.19	4.91	4.91				
PLACE1011419	3.79	1.50	2.18	3.71	3.80	3.26	2.85	4.10	4.1				
PLACE1011433	3.79	3.19	4.12	13.24	18.92	14.07	5.04	9.50	9.5	**	+	*	+
PLACE1011440	3.69	0.88	2.02	3.25	2.87	3.33	3.41	3.73	3.73				
PLACE1011452	3.56	2.32	3.25	5.65	6.92	7.14	3.10	4.52	4.52	**	+		
PLACE1011465	1.9	0.93	1.60	1.74	1.90	2.00	2.17	2.04	2.04				
PLACE1011472	5.01	1.93	2.18	2.83	4.34	2.95	3.24	2.62	2.62				
PLACE1011477	7.19	3.67	4.99	9.17	8.71	7.03	6.34	7.80	7.8				
PLACE1011478	4.7	2.46	2.21	8.34	7.12	6.47	4.52	4.33	4.33	*	+		
PLACE1011492	5.64	3.42	3.03	6.13	7.41	5.44	6.73	7.31	7.31			*	+
PLACE1011498	2.62	0.69	0.77	2.57	1.98	3.73	3.99	6.38	6.38			*	+
PLACE1011501	1.42	0.15	0.63	0.39	1.02	1.21	0.37	2.92	2.92				
PLACE1011503	1.26	0.38	0.38	0.56	0.61	1.28	0.65	1.73	1.73				
PLACE1011509	2.69	1.51	1.96	4.97	3.77	5.32	2.73	3.70	3.7	*	+	*	+
PLACE1011514	3.56	3.02	2.30	6.22	6.65	9.32	5.42	3.34	3.34	*	+		
PLACE1011516	9.2	5.83	6.52	8.39	11.75	7.44	6.58	7.31	7.31				
PLACE1011520	0.67	(0.02)	0.19	0.61	0.97	0.53	0.59	1.82	1.82				
PLACE1011538	2.38	1.78	1.26	2.2	1.67	2.66	4.47	5.04	5.04			**	+
PLACE1011555	2.73	2.02	1.56	3.06	1.29	2.65	3.42	3.23	3.23			*	+
PLACE1011561	0.88	0.17	0.48	1.89	2.38	1.56	4.39	6.30	6.3	*	+	**	+
PLACE1011563	3.61	1.68	1.69	2.85	2.58	2.68	3.94	2.74	2.74				
PLACE1011567	2.71	2.13	1.59	4.37	4.64	3.78	1.76	2.11	2.11	**	+		
PLACE1011569	0.28	1.00	0.40	1.55	1.16	1.18	0.73	0.92	0.92	*	+		
PLACE1011576	30.78	17.05	20.91	58.8	58.74	38.79	22.26	24.68	24.68	*	+		
PLACE1011586	5.24	2.45	1.64	5.28	3.51	3.90	2.49	2.57	2.57				
PLACE1011635	1.82	1.02	0.96	2.22	1.28	1.79	1.86	3.48	3.48				
PLACE1011641	0.55	0.39	0.51	0.79	0.28	0.18	0.89	0.98	0.98			**	+
PLACE1011642	2.33	1.95	2.07	3.44	2.17	2.75	1.72	3.63	3.63				
PLACE1011643	1.74	0.86	1.81	2.9	2.61	2.81	1.78	2.26	2.26	*	+		
PLACE1011646	4.54	1.91	2.30	4.88	5.46	7.17	3.47	4.39	4.39				
PLACE1011649	5.04	2.68	5.39	5.34	8.26	6.45	8.02	7.02	7.02			*	+
PLACE1011650	9.82	9.33	4.23	8.72	9.82	8.25	7.64	7.21	7.21				
PLACE1011661	4.13	2.90	2.81	7.54	8.51	8.47	3.11	3.99	3.99	**	+		
PLACE1011664	2.28	2.16	2.82	2.3	4.01	2.45	1.92	2.20	2.2				
PLACE1011672	1.34	0.43	0.59	1.98	2.38	1.65	1.43	1.75	1.75	*	+	*	+

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Table 330

PLACE1011675	0.49	0.41	0.33	1.54	2.62	1.74	1.03	0.63	0.63	**	+		
PLACE1011682	1.44	1.27	1.77	1.27	1.81	1.50	0.94	2.14	2.14				
PLACE1011708	4.35	4.02	4.14	5.7	7.61	8.08	4.28	4.88	4.88	*	+		
PLACE1011719	1.76	1.55	1.39	2.03	3.35	3.13	2.09	2.66	2.66	*	+	*	+
PLACE1011725	4.47	2.20	1.51	6.52	4.79	5.08	4.70	3.97	3.97				
PLACE1011729	2.26	0.34	1.16	2.9	3.70	2.58	1.88	1.07	1.07	*	+		
PLACE1011741	1.85	1.08	1.46	2.17	2.55	1.44	1.47	2.04	2.04				
PLACE1011749	4.07	1.97	2.35	5.14	5.66	5.55	2.94	2.96	2.96	*	+		
PLACE1011757	7.95	5.78	4.73	28.51	35.97	33.70	18.45	19.91	19.91	**	+	**	+
PLACE1011762	0.6	0.62	0.64	1.51	2.40	1.43	1.31	1.98	1.98	*	+	**	+
PLACE1011778	0.68	0.80	0.85	0.72	1.28	1.91	1.16	0.80	0.8				
PLACE1011783	3.26	3.37	4.33	9.36	8.72	9.68	4.31	3.99	3.99	**	+		
PLACE1011795	2.41	0.78	0.71	3.25	3.16	2.10	1.75	0.51	0.51				
PLACE1011810	1.09	0.35	0.96	0.57	0.96	0.71	1.04	1.41	1.41				
PLACE1011824	1.1	0.61	0.73	1.63	1.19	1.20	1.70	1.61	1.61			**	+
PLACE1011825	19.56	10.93	11.42	10.37	11.28	11.36	8.08	10.44	10.44				
PLACE1011835	2.12	1.20	1.49	1.76	1.50	1.06	1.49	0.95	0.95				
PLACE1011836	32.53	15.61	18.36	27.63	35.75	28.68	27.23	20.95	20.95				
PLACE1011847	0.74	1.05	0.62	0.62	0.87	1.11	1.60	1.10	1.1				
PLACE1011855	1.16	0.16	0.77	0.69	0.71	1.38	0.70	1.13	1.13				
PLACE1011858	2.38	2.07	1.60	2.19	2.08	1.60	2.79	2.84	2.84			*	+
PLACE1011874	3.25	1.54	2.03	4.69	4.12	4.23	2.47	3.11	3.11	*	+		
PLACE1011875	1.26	0.66	0.64	1.26	1.14	1.27	0.79	0.74	0.74				
PLACE1011877	6.46	2.58	3.09	3.53	2.30	3.26	2.14	3.12	3.12				
PLACE1011891	1.77	0.88	0.81	1.69	1.67	1.68	1.49	2.31	2.31				
PLACE1011896	0.86	0.25	0.26	0.37	0.26	0.57	0.67	0.48	0.48				
PLACE1011920	2.91	0.83	1.76	1.44	1.22	2.34	1.43	1.54	1.54				
PLACE1011922	4.71	2.40	2.11	4.92	2.79	4.42	3.68	4.23	4.23				
PLACE1011923	3.63	1.24	1.28	5.32	2.65	2.76	7.49	10.90	10.9			**	+
PLACE1011937	6	2.51	3.82	3.74	4.24	5.24	4.33	4.96	4.96				
PLACE1011939	4.24	2.12	2.87	2.83	3.92	4.33	4.29	5.83	5.83			*	+
PLACE1011940	5.02	1.82	3.30	7.08	7.36	8.48	4.28	5.85	5.85	*	+		
PLACE1011962	13.26	6.64	7.98	11.22	11.07	13.01	8.70	9.69	9.69				
PLACE1011964	2.09	0.16	0.88	0.97	0.96	0.80	0.82	1.29	1.29				
PLACE1011978	6.83	5.17	5.96	14.23	9.13	15.11	5.12	9.01	9.01	*	+		
PLACE1011980	5.54	2.72	4.54	9.74	12.59	11.01	4.66	6.64	6.64	**	+		
PLACE1011981	6.65	3.37	3.46	5.38	6.10	5.01	3.81	4.69	4.69				
PLACE1011982	0.91	0.32	0.06	0.49	1.81	1.02	0.79	1.02	1.02				
PLACE1011995	4.44	2.50	2.12	5.89	6.15	5.90	3.97	3.81	3.81	*	+		
PLACE1012023	1.79	0.70	1.25	1.43	1.61	2.10	1.24	1.17	1.17				
PLACE1012026	1.87	0.19	0.62	1.01	0.13	0.38	0.66	0.81	0.81				
PLACE1012031	2.22	1.02	2.34	1.31	1.21	3.28	1.23	2.49	2.49				
PLACE2000003	10.16	5.53	7.19	14.74	10.74	18.79	8.25	10.16	10.16				
PLACE2000005	4.58	2.43	2.29	4.4	3.89	4.52	3.11	4.04	4.04				
PLACE2000006	6.31	3.28	0.91	2.52	4.28	3.42	2.99	2.00	2				
PLACE2000007	3.33	1.18	1.86	1.87	3.29	3.13	2.74	4.18	4.18				
PLACE2000011	6.03	2.56	4.49	6.77	5.68	6.77	3.61	4.33	4.33				
PLACE2000014	0.21	0.98	0.82	1.07	2.07	1.53	2.21	2.03	2.03			**	+
PLACE2000015	1.83	0.65	1.01	1.76	1.29	2.19	1.52	0.85	0.85				
PLACE2000017	3.21	0.73	1.74	6.58	4.80	4.12	2.77	1.87	1.87	*	+		
PLACE2000021	3.22	1.34	2.09	3.94	3.51	4.88	1.82	2.10	2.1	*	+		
PLACE2000022	7.75	3.64	2.82	8.01	9.76	8.90	3.63	6.09	6.09				
PLACE2000030	8.7	4.13	5.99	6.21	7.35	6.10	5.75	6.25	6.25				
PLACE2000032	4.4	0.93	2.84	5.81	6.65	4.83	2.50	4.03	4.03				
PLACE2000033	1.83	1.13	0.57	2.93	3.15	2.60	1.56	1.76	1.76	*	+		
PLACE2000034	2.2	2.03	1.49	1.47	1.71	2.75	1.92	3.95	3.95				

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Table 331

PLACE2000039	6.48	4.35	4.61	11.87	11.66	13.79	6.80	7.28	7.28	**	+	*	+
PLACE2000043	2.47	1.44	2.20	2.31	3.69	3.32	3.41	4.52	4.52			*	+
PLACE2000044	5.02	3.35	3.46	5.51	3.83	5.89	4.93	7.31	7.31				
PLACE2000047	8.18	4.36	3.83	9.19	11.31	14.75	5.33	7.74	7.74	*	+		
PLACE2000050	12.24	3.78	3.08	8.61	10.29	7.90	7.32	6.64	6.64				
PLACE2000061	2.92	0.96	0.97	1.52	0.96	1.26	1.35	1.85	1.85				
PLACE2000062	4.77	2.50	2.13	5.58	5.65	5.45	2.96	5.42	5.42	*	+		
PLACE2000072	2.7	1.26	2.16	2.17	3.44	2.93	1.74	2.43	2.43				
PLACE2000073	1.69	0.72	0.84	1.41	0.59	1.30	1.70	1.52	1.52				
PLACE2000097	13.16	8.11	9.49	11.41	12.05	13.08	7.86	8.83	8.83				
PLACE2000100	5.14	3.46	2.83	5.96	4.13	5.86	4.27	5.06	5.06				
PLACE2000103	4.64	3.10	3.20	7.22	5.44	6.13	4.03	3.95	3.95	*	+		
PLACE2000106	7.76	2.85	4.06	6.8	7.28	7.13	4.31	4.99	4.99				
PLACE2000111	4.84	2.29	3.47	5	5.26	5.57	4.32	7.27	7.27				
PLACE2000115	2.29	0.90	1.18	1.38	0.91	1.85	2.19	2.02	2.02				
PLACE2000118	40.98	28.15	29.38	32.74	33.08	38.40	30.44	42.97	42.97				
PLACE2000124	16.57	10.11	11.57	19.83	25.65	30.81	16.15	17.74	17.74	*	+		
PLACE2000132	7.64	4.32	5.67	5.55	4.79	4.71	7.51	6.44	6.44				
PLACE2000136	1.78	0.82	1.05	1.68	1.61	1.41	1.31	1.62	1.62				
PLACE2000137	6.66	4.19	3.94	4.2	3.59	5.28	3.96	5.37	5.37				
PLACE2000140	9.31	3.10	5.25	7.95	10.19	7.07	4.50	6.74	6.74				
PLACE2000147	2.32	1.00	0.75	2.39	2.55	2.14	1.33	2.93	2.93				
PLACE2000153	1.79	0.33	0.76	0.89	1.36	1.15	2.17	2.54	2.54			*	+
PLACE2000164	2.92	1.24	1.74	1.97	2.41	1.94	1.21	2.25	2.25				
PLACE2000170	4.49	2.57	2.11	5.8	5.33	5.19	3.14	3.80	3.8	*	+		
PLACE2000172	3.21	1.40	2.70	1.1	3.14	2.28	1.52	1.72	1.72				
PLACE2000173	4.05	3.41	2.95	5.72	7.77	7.43	3.82	4.53	4.53	**	+		
PLACE2000174	2.94	1.68	2.28	3.36	3.27	4.06	2.97	2.61	2.61	*	+		
PLACE2000176	6.55	2.90	2.44	6.47	6.24	4.58	3.30	4.24	4.24				
PLACE2000187	4.34	2.14	1.78	5.63	3.41	5.66	3.80	4.31	4.31				
PLACE2000216	4.17	2.38	2.18	6.97	6.14	5.24	7.33	12.03	12.03	*	+	*	+
PLACE2000219	5.75	2.86	2.79	6.33	5.19	5.66	5.15	5.03	5.03				
PLACE2000221	6	4.55	4.10	13.08	11.16	10.61	6.14	6.36	6.36	**	+		
PLACE2000223	0.66	0.04	0.44	2.56	1.05	0.74	1.35	0.62	0.62				
PLACE2000231	2.73	2.97	1.35	3.88	3.66	2.81	3.23	2.76	2.76				
PLACE2000235	5.15	3.31	3.10	9.33	15.20	9.28	4.35	5.69	5.69	*	+		
PLACE2000246	9.05	5.03	3.92	8.93	10.34	8.27	5.30	6.19	6.19				
PLACE2000264	4.4	2.75	1.21	7.23	5.72	5.03	3.18	4.43	4.43	*	+		
PLACE2000274	8.27	4.14	5.09	4.88	4.54	3.46	4.83	6.06	6.06				
PLACE2000287	14	9.69	10.03	11.98	14.31	14.19	12.42	12.37	12.37				
PLACE2000296	3.51	1.96	2.07	2.61	2.73	3.24	2.29	3.69	3.69				
PLACE2000302	2.31	2.23	2.10	3.57	4.89	5.77	3.81	3.32	3.32	*	+	**	+
PLACE2000305	7.13	5.46	4.88	12.44	18.75	14.01	6.85	6.47	6.47	*	+		
PLACE2000317	1.79	1.81	1.59	2.18	2.88	3.79	2.56	2.49	2.49			**	+
PLACE2000324	1.64	0.45	0.66	1.23	0.90	1.15	1.56	1.03	1.03				
PLACE2000334	4.7	3.19	3.38	3.36	3.85	3.08	3.51	4.53	4.53				
PLACE2000335	6.89	3.67	3.94	9.95	12.98	11.87	4.72	8.12	8.12	**	+		
PLACE2000340	1.92	1.00	1.25	2.13	2.37	2.25	1.13	1.70	1.7	*	+		
PLACE2000341	4.05	3.76	4.37	3.33	6.79	4.35	3.93	3.97	3.97				
PLACE2000342	5.08	6.69	5.71	7.14	7.41	7.08	6.86	8.97	8.97	*	+	*	+
PLACE2000347	4.37	5.20	4.34	7.13	9.07	10.11	6.32	7.54	7.54	*	+	**	+
PLACE2000357	9.87	8.86	7.75	8.78	12.51	9.80	8.70	9.73	9.73				
PLACE2000358	4.58	2.20	2.55	4.28	5.06	2.32	5.59	6.09	6.09			*	+
PLACE2000359	2.5	0.52	0.79	3.39	1.81	2.56	2.27	0.82	0.82				
PLACE2000366	6.64	3.37	2.29	8.44	9.84	6.44	5.08	3.45	3.45				
PLACE2000371	4.65	3.72	1.76	1.73	2.65	2.33	2.69	2.16	2.16				

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Table 332

PLACE2000373	4.09	3.75	3.16	3.93	6.78	5.14	3.59	5.16	5.16					
PLACE2000374	3.8	4.38	3.21	5.4	5.00	4.71	4.60	3.34	3.34	*	+			
PLACE2000379	0.43	0.66	0.58	0.91	0.73	1.09	0.79	0.77	0.77	*	+	*	+	
PLACE2000386	263.51	193.15	186.41	112.96	134.53	97.90	242.44	237.17	237.2	*	-			
PLACE2000388	6.14	2.57	3.20	4.18	4.37	4.11	3.57	5.67	5.67					
PLACE2000392	22.7	12.68	10.22	19.04	26.24	23.82	20.84	18.58	18.58					
PLACE2000394	4.15	2.33	2.30	7.45	7.62	8.22	3.35	4.27	4.27	**	+			
PLACE2000398	5.77	2.40	4.45	3.51	4.25	5.84	4.07	5.00	5					
PLACE2000399	6.61	3.16	3.15	4.97	4.51	4.35	4.73	5.61	5.61					
PLACE2000402	7.01	4.23	4.20	5.54	4.09	5.56	4.44	3.54	3.54					
PLACE2000404	12.23	7.88	7.30	7.71	7.31	9.74	4.74	6.01	6.01					
PLACE2000411	21.27	11.68	11.82	11.14	10.88	25.73	14.78	18.35	18.35					
PLACE2000418	5.51	3.37	3.01	6.69	5.87	6.09	4.87	3.75	3.75					
PLACE2000419	7.28	4.27	3.30	7.57	9.49	8.40	4.83	4.59	4.59					
PLACE2000425	4.32	2.24	3.29	5.08	4.37	6.06	3.45	3.86	3.86					
PLACE2000427	6.26	3.55	3.23	4.54	4.54	5.08	5.10	5.28	5.28					
PLACE2000433	4.59	2.65	3.36	5.7	5.12	6.87	3.87	4.81	4.81	*	+			
PLACE2000435	29.19	15.24	17.32	14.09	10.07	16.26	23.39	24.72	24.72					
PLACE2000438	3.46	1.48	2.18	3.33	2.20	3.83	3.08	2.95	2.95					
PLACE2000450	9.25	3.49	4.71	9.32	13.42	13.35	5.02	6.24	6.24	*	+			
PLACE2000455	4.87	3.05	1.83	4.35	3.25	3.01	3.72	3.76	3.76					
PLACE2000458	7.14	3.76	3.85	4.27	6.42	5.62	5.42	5.04	5.04					
PLACE2000464	10.07	4.31	6.99	6.94	8.11	6.92	5.43	8.55	8.55					
PLACE2000465	5.73	2.78	3.87	8.13	9.58	9.56	5.26	6.47	6.47	**	+			
PLACE2000473	17.94	8.98	12.76	32.72	23.26	29.31	35.66	50.78	50.78	*	+	**	+	
PLACE2000477	1.27	1.02	0.52	1.09	0.78	0.53	1.48	1.22	1.22					
PLACE3000004	7.55	3.19	4.53	8.79	7.24	9.45	5.46	5.75	5.75					
PLACE3000009	61.9	29.47	28.32	32.27	25.30	29.38	45.27	58.28	58.28					
PLACE3000020	9.44	5.05	5.57	6.59	7.39	6.52	4.82	4.55	4.55					
PLACE3000029	9.17	4.67	4.83	9.55	12.07	7.65	6.59	5.44	5.44					
PLACE3000038	3.05	1.65	1.71	3.75	5.45	4.67	2.86	3.09	3.09	*	+			
PLACE3000052	4.37	2.71	2.77	5.23	4.15	6.64	3.13	2.24	2.24					
PLACE3000059	2.05	0.82	1.21	3.28	2.36	2.07	1.89	1.16	1.16					
PLACE3000067	6.3	3.83	5.04	11.45	12.93	15.68	7.26	8.63	8.63	**	+	*	+	
PLACE3000069	5.9	3.04	3.53	5	5.11	8.56	5.67	5.68	5.68					
PLACE3000070	27.81	15.78	20.14	32.22	26.02	53.33	21.90	29.50	29.5					
PLACE3000103	2.43	0.95	1.30	3.54	4.94	4.26	1.89	2.90	2.9	*	+			
PLACE3000119	3.74	2.64	1.89	4.89	6.83	4.96	3.78	3.36	3.36	*	+			
PLACE3000121	1.44	1.22	0.45	2.39	2.51	2.11	1.78	2.32	2.32	*	+	*	+	
PLACE3000124	5.32	4.70	4.50	12.73	13.74	11.54	6.57	8.87	8.87	**	+	*	+	
PLACE3000135	1.71	0.60	0.29	0.53	1.12	0.70	1.32	0.77	0.77					
PLACE3000136	11.16	7.11	7.56	7.93	9.54	12.38	12.19	8.74	8.74					
PLACE3000142	5.52	1.94	3.53	3.47	2.41	3.28	2.84	4.03	4.03					
PLACE3000145	6.76	3.35	3.37	7.36	7.49	6.80	6.17	8.06	8.06					
PLACE3000147	10.95	4.59	5.26	7.55	8.27	7.90	4.11	4.34	4.34					
PLACE3000148	2.39	0.34	0.58	0.98	1.42	1.44	1.27	2.88	2.88					
PLACE3000154	1.15	0.41	0.41	0.66	1.09	1.15	0.77	2.42	2.42					
PLACE3000155	7.02	4.85	4.71	7.95	8.38	9.70	5.71	8.16	8.16	*	+			
PLACE3000156	15.58	8.96	9.94	8.3	7.38	10.26	12.84	18.30	18.3					
PLACE3000157	4.88	2.44	2.98	2.64	3.32	4.31	4.33	4.39	4.39					
PLACE3000158	8.01	3.79	3.91	9.93	12.06	12.18	6.76	6.67	6.67	*	+			
PLACE3000160	0.65	1.38	1.00	1.99	1.58	2.78	2.19	2.27	2.27			**	+	
PLACE3000169	8.16	3.98	2.64	8.16	12.00	9.90	6.56	5.46	5.46					
PLACE3000181	10.19	6.03	5.74	6.99	7.06	6.27	8.77	10.50	10.5					
PLACE3000194	3.17	1.81	1.47	3.38	2.68	2.61	2.86	3.96	3.96					
PLACE3000197	0.71	0.07	1.20	1.17	0.86	1.14	4.41	2.01	2.01					

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Table 333

PLACE3000199	3.29	1.08	1.38	2.04	1.59	1.81	1.36	3.52	3.52				
PLACE3000205	9.93	4.59	5.70	17.83	17.57	18.45	14.66	13.74	13.74	**	+	*	+
PLACE3000207	5.7	3.47	2.72	7.85	6.73	9.27	4.82	3.93	3.93	*	+		
PLACE3000208	5.91	3.83	2.56	4.66	4.50	5.84	3.33	5.31	5.31				
PLACE3000213	3.26	1.41	0.88	1.85	1.88	1.34	1.39	1.20	1.2				
PLACE3000215	5.27	3.36	2.05	2.91	1.77	2.17	4.16	5.65	5.65				
PLACE3000218	0.67	1.20	0.52	0.53	0.72	1.11	0.94	1.60	1.6				
PLACE3000220	4.81	2.27	2.38	5.89	5.17	5.82	4.14	4.16	4.16	*	+		
PLACE3000221	18.58	12.33	11.49	19.49	17.73	21.75	11.62	11.46	11.46				
PLACE3000225	2.26	1.52	1.43	2.24	4.06	3.45	1.47	2.45	2.45				
PLACE3000226	4.27	2.49	2.02	2.27	5.71	4.75	1.91	2.73	2.73				
PLACE3000230	2.53	2.38	1.81	1.66	1.64	1.71	2.48	1.35	1.35				
PLACE3000231	3.29	1.13	0.60	2.47	2.81	2.21	3.05	2.05	2.05				
PLACE3000235	3.68	1.67	2.09	7.18	5.86	5.62	2.96	4.70	4.7	**	+		
PLACE3000242	4.95	3.58	3.28	11.36	12.88	9.51	10.16	9.35	9.35	**	+	**	+
PLACE3000244	1.78	1.29	0.91	1.71	1.41	0.91	1.35	0.85	0.85				
PLACE3000253	1.86	1.24	1.41	3.62	2.97	3.37	3.19	2.28	2.28	**	+	*	+
PLACE3000254	51.54	34.63	40.51	40.03	46.12	56.93	50.43	47.16	47.16				
PLACE3000271	5.35	3.90	4.49	12.52	15.43	16.28	5.75	8.41	8.41	**	+	*	+
PLACE3000276	1.34	1.63	0.94	1.51	1.84	1.69	1.54	1.70	1.7				
PLACE3000304	29.17	18.78	18.07	35.22	34.12	39.27	19.90	28.29	28.29	*	+		
PLACE3000309	5.85	2.02	1.54	4.32	5.65	5.33	3.03	4.10	4.1				
PLACE3000310	2.86	0.49	0.75	1.95	1.51	1.29	0.96	1.26	1.26				
PLACE3000320	2.43	0.72	1.39	2.35	2.67	2.63	2.57	2.39	2.39				
PLACE3000322	3.17	2.14	2.01	4.49	4.42	5.13	3.26	3.42	3.42	**	+		
PLACE3000330	3.98	4.24	5.26	4.75	5.64	8.32	9.28	8.32	8.32			**	+
PLACE3000331	3.82	3.74	4.92	7.37	8.26	9.30	3.96	4.94	4.94	**	+		
PLACE3000336	2.26	2.25	2.90	3.09	4.08	3.48	1.74	3.42	3.42	*	+		
PLACE3000339	1.51	1.25	0.97	2.83	3.03	1.44	3.34	1.37	1.37				
PLACE3000341	4.76	1.28	2.07	6.03	6.07	5.79	3.01	2.61	2.61	*	+		
PLACE3000350	3.67	2.80	1.30	3.28	4.94	3.47	3.39	2.10	2.1				
PLACE3000352	6.03	5.05	2.30	5	5.48	4.50	3.98	4.70	4.7				
PLACE3000353	0.84	1.44	1.91	1.76	2.65	2.70	3.03	3.61	3.61			**	+
PLACE3000362	1.98	1.66	1.84	6.16	5.62	6.95	2.53	2.39	2.39	**	+	**	+
PLACE3000363	0.72	2.27	1.87	2.22	2.71	1.75	1.29	1.32	1.32				
PLACE3000365	2.24	1.70	1.83	4.68	5.39	5.89	3.33	4.21	4.21	**	+	**	+
PLACE3000373	1.03	0.43	0.22	0.96	1.41	0.94	0.42	0.29	0.29				
PLACE3000374	5.08	1.81	1.87	6.16	6.24	4.44	2.12	2.74	2.74				
PLACE3000387	1.31	0.25	0.08	1.67	1.05	0.55	1.33	0.79	0.79				
PLACE3000388	2.58	0.80	0.83	3.55	3.56	3.31	2.70	1.73	1.73	*	+		
PLACE3000399	9.22	8.21	6.43	14.93	15.70	16.79	8.93	10.00	10	**	+		
PLACE3000400	1.92	1.54	0.91	6.92	3.60	4.30	2.99	2.65	2.65	*	+	*	+
PLACE3000401	29	26.24	24.78	59.59	55.01	78.12	29.62	31.31	31.31	**	+	*	+
PLACE3000402	2.02	1.57	1.10	4.22	3.77	2.97	1.86	1.95	1.95	**	+		
PLACE3000405	6.4	2.32	4.16	6.78	5.01	5.58	4.43	5.58	5.58				
PLACE3000406	4.28	1.49	2.84	5.5	4.66	5.13	2.47	2.85	2.85				
PLACE3000413	8.22	3.55	3.63	4.09	5.81	4.91	5.48	4.88	4.88				
PLACE3000416	4.22	2.84	2.70	5.29	3.87	4.91	3.53	2.90	2.9				
PLACE3000425	4.82	2.55	2.93	8.14	7.04	8.00	4.35	5.24	5.24	**	+		
PLACE3000437	6.6	2.18	3.38	8.46	5.80	8.41	4.73	5.68	5.68				
PLACE3000455	10.15	5.78	7.81	11.84	13.57	13.33	7.04	7.08	7.08	*	+		
PLACE3000475	41.33	26.86	19.78	25.89	28.01	22.74	42.53	36.25	36.25				
PLACE3000477	9.34	3.92	3.31	6.31	7.30	5.21	5.44	6.16	6.16				
PLACE4000003	2.47	1.31	0.94	1.5	2.41	1.58	1.49	1.63	1.63				
PLACE4000008	5.72	2.63	3.64	8.57	12.47	10.37	7.46	7.86	7.86	*	+	*	+
PLACE4000009	14.5	7.53	8.72	15.96	13.93	14.92	9.76	11.70	11.7				

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Table 334

PLACE4000014	5.92	2.92	3.44	5.18	6.07	5.84	4.46	4.89	4.89				
PLACE4000029	1.91	1.44	1.35	3.21	1.93	3.26	3.99	3.79	3.79			**	+
PLACE4000034	2.6	1.30	1.44	3.92	3.82	4.60	4.01	3.41	3.41	**	+	*	+
PLACE4000049	10.4	5.48	5.72	12.83	16.95	11.80	9.94	9.10	9.1	*	+		
PLACE4000052	6.49	3.73	2.47	4.77	4.77	5.30	5.23	5.62	5.62				
PLACE4000062	6.59	2.48	4.03	4.7	5.26	5.48	4.59	4.62	4.62				
PLACE4000063	7.7	3.50	3.52	6.91	6.71	9.08	5.77	5.40	5.4				
PLACE4000089	2.96	1.45	2.33	5.97	4.11	5.63	4.54	4.57	4.57	*	+	**	+
PLACE4000093	2.81	1.09	0.89	1.95	1.69	1.17	2.18	1.71	1.71				
PLACE4000100	4.42	2.89	2.49	3.93	4.32	5.21	3.23	2.62	2.62				
PLACE4000103	5.02	1.97	1.98	3.66	2.71	3.95	2.81	2.33	2.33				
PLACE4000106	8.72	4.11	3.74	4.38	5.75	4.55	4.28	4.16	4.16				
PLACE4000128	7.39	4.68	3.31	9.85	9.72	8.43	7.44	6.38	6.38	*	+		
PLACE4000129	6.04	2.07	2.84	4.76	6.70	6.24	4.40	2.79	2.79				
PLACE4000131	8.08	5.12	4.57	12.93	9.62	6.75	8.38	9.08	9.08				
PLACE4000147	1.54	0.95	0.56	0.28	1.32	1.44	1.32	1.12	1.12				
PLACE4000156	10.36	6.90	8.62	23.53	13.89	24.29	10.09	14.64	14.64	*	+		
PLACE4000175	2.77	1.36	1.67	3	2.23	3.75	2.99	2.63	2.63				
PLACE4000190	25.73	14.17	16.07	19.71	16.55	18.77	20.04	22.67	22.67				
PLACE4000192	19.18	10.59	8.86	17.39	19.36	14.48	12.50	10.81	10.81				
PLACE4000206	26.35	11.24	12.17	18.68	19.88	13.96	10.44	9.28	9.28				
PLACE4000211	17.59	9.35	9.22	14.45	14.14	14.09	11.01	11.86	11.86				
PLACE4000214	3.16	2.15	2.41	4.6	3.22	2.93	3.58	2.23	2.23				
PLACE4000222	5.13	3.77	3.41	7.67	6.23	6.64	5.04	5.14	5.14	*	+		
PLACE4000223	5.15	2.40	3.83	4.77	3.40	3.75	4.17	5.28	5.28				
PLACE4000229	2.61	1.29	1.59	3.13	1.82	2.66	3.16	3.28	3.28			*	+
PLACE4000230	10.54	4.47	5.13	3.92	4.50	6.23	2.12	1.74	1.74				
PLACE4000233	7.43	4.11	1.84	9.98	7.86	6.99	4.69	5.82	5.82				
PLACE4000239	10.37	3.20	3.64	8.75	7.61	7.98	4.24	5.32	5.32				
PLACE4000247	3.98	2.15	1.70	4.78	4.11	3.53	4.31	3.20	3.2				
PLACE4000250	6.06	3.58	4.71	8.33	8.43	6.31	5.56	7.08	7.08	*	+		
PLACE4000252	2.91	1.12	1.52	2.79	1.94	3.45	2.33	2.20	2.2				
PLACE4000259	8.04	3.19	7.29	6.61	5.24	7.03	5.35	5.02	5.02				
PLACE4000261	12.86	7.43	11.27	7.94	6.30	11.29	13.49	12.71	12.71				
PLACE4000264	5.07	2.86	1.88	6.35	6.52	5.02	3.87	4.16	4.16				
PLACE4000269	8.57	4.36	5.52	8.01	9.34	7.35	6.12	5.77	5.77				
PLACE4000270	3.13	1.82	0.87	2.42	1.82	3.08	1.61	2.16	2.16				
PLACE4000281	19.68	7.73	9.21	20.75	31.26	26.50	19.08	19.52	19.52	*	+		
PLACE4000300	6.08	3.69	2.60	7.08	6.91	5.29	4.32	5.19	5.19				
PLACE4000320	5.62	3.77	3.47	7.13	6.02	6.80	4.81	4.30	4.3	*	+		
PLACE4000323	8.19	5.61	3.78	9.71	7.40	10.97	6.79	7.01	7.01				
PLACE4000326	4.48	1.87	1.75	4.11	3.23	4.42	3.33	2.91	2.91				
PLACE4000344	2.79	2.15	2.50	2.98	1.69	2.74	1.96	2.31	2.31				
PLACE4000347	20.7	10.82	8.58	19.27	12.61	11.57	8.40	11.08	11.08				
PLACE4000354	4.74	1.02	1.75	4.04	3.76	1.42	1.52	3.10	3.1				
PLACE4000367	2.52	1.53	1.38	2.65	2.91	2.67	2.13	2.39	2.39				
PLACE4000369	4.83	2.57	3.31	5.06	4.32	4.54	4.37	5.39	5.39				
PLACE4000379	5.69	3.46	3.45	6.11	6.24	7.35	4.30	5.61	5.61	*	+		
PLACE4000387	3.69	1.95	1.27	2.17	3.32	3.40	2.28	3.13	3.13				
PLACE4000392	1.14	0.56	0.17	0.91	1.44	1.78	1.07	1.00	1				
PLACE4000399	23.89	17.50	15.29	24.02	23.23	28.14	19.33	22.84	22.84				
PLACE4000401	1.48	0.84	0.45	2.03	4.11	1.07	1.24	1.78	1.78				
PLACE4000403	9.89	5.20	5.81	9.29	8.13	6.25	5.57	7.91	7.91				
PLACE4000411	5.72	2.12	2.75	5.81	4.30	5.15	4.86	3.29	3.29				
PLACE4000415	3.21	2.22	2.69	3.67	4.43	3.44	4.57	6.28	6.28			**	+
PLACE4000416	4.63	3.13	2.08	5.57	4.05	4.56	5.50	4.53	4.53				

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Table 335

PLACE4000424	3.7	2.41	1.28	2.89	2.64	2.63	4.72	2.93	2.93				
PLACE4000431	5.14	3.98	3.86	7.9	6.44	6.77	5.24	3.01	3.01	*	+		
PLACE4000443	1.6	1.50	0.66	1.7	2.14	2.19	1.48	1.16	1.16				
PLACE4000445	9.89	5.81	4.87	15.7	14.02	12.69	8.15	9.68	9.68	*	+		
PLACE4000450	15.76	8.51	6.72	14.02	10.89	10.04	11.01	10.50	10.5				
PLACE4000455	3.87	3.67	2.19	8.55	5.76	6.75	4.27	7.65	7.65	*	+		
PLACE4000465	6.69	5.73	3.42	9.19	8.96	7.57	6.23	7.71	7.71	*	+		
PLACE4000466	31.49	24.03	27.55	30.7	30.16	27.24	58.59	49.41	49.41			**	+
PLACE4000472	17.06	12.16	12.26	19.04	18.92	24.52	24.99	19.96	19.96	*	+	*	+
PLACE4000487	2.64	2.43	1.31	4.42	5.20	4.15	3.23	3.27	3.27	**	+		
PLACE4000489	2.69	2.22	1.81	2.33	3.71	4.57	2.92	1.40	1.4				
PLACE4000494	6.6	3.79	3.88	6.95	7.91	8.87	5.80	5.92	5.92	*	+		
PLACE4000502	21.16	12.73	11.94	19.98	23.69	17.79	12.36	16.13	16.13				
PLACE4000521	6.7	5.05	4.78	4.05	6.11	3.01	4.55	6.40	6.4				
PLACE4000522	4.91	3.07	3.08	7.26	9.24	7.69	9.03	9.77	9.77	**	+	**	+
PLACE4000537	3.84	2.38	2.93	3.81	2.89	3.42	4.63	4.21	4.21			*	+
PLACE4000548	2.58	1.71	3.60	3.4	2.67	4.50	1.35	2.28	2.28				
PLACE4000558	0.39	0.54	0.56	2.25	2.45	2.36	1.46	1.14	1.14	**	+	**	+
PLACE4000581	2.73	1.45	1.75	4.5	4.93	4.59	4.11	3.03	3.03	**	+		
PLACE4000590	0.99	1.06	0.15	1.04	1.17	1.32	1.13	0.97	0.97				
PLACE4000593	4.55	1.55	1.52	5.49	5.70	3.50	2.55	3.08	3.08				
PLACE4000612	14.51	9.28	7.13	10.09	12.95	7.67	9.14	12.79	12.79				
PLACE4000638	3.93	2.21	3.37	3.98	5.06	3.32	3.69	4.06	4.06				
PLACE4000650	1.03	1.91	1.53	2.69	2.70	2.58	3.71	1.90	1.9	*	+		
PLACE4000651	8.37	7.37	5.41	16.13	16.91	20.29	11.75	11.67	11.67	**	+	**	+
PLACE4000654	0.46	0.63	0.26	1.79	1.98	0.98	1.21	0.58	0.58	*	+		
PLACE4000670	1.04	0.70	1.13	2.04	2.89	1.47	0.74	0.43	0.43				
PLACE4000685	23.26	12.26	10.49	28.55	27.61	40.89	20.42	24.20	24.2	*	+		
PLACE4000687	0.45	0.07	0.48	0.48	0.65	1.00	0.21	0.78	0.78				
PLACE5000003	2.7	1.36	1.81	2.51	2.87	2.69	2.63	1.48	1.48				
PLACE5000005	2.1	1.91	0.92	1.98	1.29	2.16	2.69	3.30	3.3			*	+
PLACE5000019	1.64	0.35	0.54	1.85	0.86	1.29	2.04	1.56	1.56				
PLACE5000021	0.69	0.31	0.38	1.1	1.33	1.32	0.87	0.51	0.51	**	+		
PLACE5000022	3.43	2.14	1.68	2.67	2.24	2.05	1.88	2.93	2.93				
PLACE5000024	4.4	3.23	1.21	2.46	4.37	2.88	2.51	2.40	2.4				
PLACE5000036	3.16	1.92	0.93	2.51	3.73	2.77	1.58	2.61	2.61				
PLACE5000059	21.39	11.50	13.49	18.98	12.58	17.80	15.52	22.91	22.91				
PLACE5000076	1.04	0.14	0.59	0.44	1.09	3.27	1.13	0.58	0.58				
PLACE5000117	6.61	3.04	3.55	6.57	7.00	6.53	6.39	6.85	6.85				
PLACE5000143	6.9	3.66	5.74	7.55	3.91	6.50	6.13	5.78	5.78				
PLACE5000152	1.01	0.83	0.51	1.68	1.63	1.58	1.45	0.95	0.95	**	+		
PLACE5000154	2.82	2.00	1.84	2.88	1.96	2.91	1.39	2.76	2.76				
PLACE5000155	24.77	17.51	14.25	20.28	21.63	23.82	15.99	20.71	20.71				
PLACE5000165	32.82	17.87	18.74	27.86	24.93	25.31	22.84	22.39	22.39				
SKNMC1000004	6.53	6.43	3.51	11.48	11.51	13.01	5.92	10.64	10.64	**	+		
SKNMC1000011	4.21	2.51	3.08	4.72	4.77	4.26	3.98	2.83	2.83				
SKNMC1000013	2.24	1.08	1.20	1.57	0.87	2.15	1.79	2.08	2.08				
SKNMC1000014	2.76	2.14	1.24	4.71	2.24	4.37	3.92	1.88	1.88				
SKNMC1000018	3.3	2.08	1.94	2.72	3.17	4.77	4.12	2.92	2.92				
SKNMC1000020	4.56	2.73	1.89	3.66	1.77	4.25	2.81	2.80	2.8				
SKNMC1000046	2.2	1.75	1.00	2.53	2.58	2.02	1.58	2.04	2.04				
SKNMC1000050	2.33	0.87	1.04	1.57	3.28	2.53	3.94	4.06	4.06			**	+
SKNMC1000062	23.15	15.32	13.39	21.75	19.79	22.30	21.79	25.10	25.1				
SKNMC1000075	3.21	1.19	1.16	1.75	2.09	2.04	1.59	1.71	1.71				
SKNMC1000082	5.24	2.03	1.78	3.5	2.07	2.24	2.55	1.68	1.68				
SKNMC1000091	10.17	5.98	5.10	6.85	6.21	8.67	4.99	6.41	6.41				

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Table 336

SKNMC1000099	4.27	1.82	4.32	2.68	2.85	4.25	4.90	2.31	2.31				
SKNMC1000104	2.88	1.34	1.64	2.26	2.75	3.25	1.82	2.06	2.06				
SKNMC1000113	2.91	1.98	1.70	2.53	3.12	2.50	2.17	2.08	2.08				
SKNMC1000119	4.61	2.84	2.09	3.6	4.44	4.19	3.90	3.35	3.35				
SKNMC1000142	2.86	0.96	0.73	2.73	1.96	2.31	2.39	2.51	2.51				
SKNMC1000170	4.02	1.58	1.54	3.23	3.13	3.75	2.53	3.66	3.66				
SKNMC1000178	5.92	3.14	3.92	5.65	4.47	6.23	4.68	4.57	4.57				
SKNMC1000194	3.57	2.37	1.14	2.02	1.84	1.46	1.82	1.68	1.68				
SKNMC1000198	4.86	3.19	3.66	3.95	2.35	5.30	3.50	3.61	3.61				
SKNMC1000225	3.86	1.48	1.25	3.04	2.83	3.41	1.69	1.50	1.5				
SKNMC1000249	2.6	1.16	0.14	2.11	0.98	1.05	0.97	1.03	1.03				
SPLEN1000007	3.1	1.45	1.01	2.61	2.77	3.19	1.50	2.71	2.71				
SPLEN1000012	4.58	1.70	1.35	3.53	2.59	2.41	3.41	4.25	4.25				
SPLEN1000014	6.11	2.53	3.00	5.55	7.51	4.48	3.02	3.02	3.02				
SPLEN1000036	2.67	1.59	1.60	2.81	3.21	2.90	3.30	2.69	2.69				
SPLEN1000059	0.04	0.28	0.35	0.37	0.20	0.93	0.51	0.65	0.65			*	+
SPLEN1000068	2.47	1.01	1.48	3.14	3.20	4.62	4.16	2.46	2.46	*	+		
SPLEN1000072	3.94	2.95	2.34	4.26	4.36	3.28	3.61	3.41	3.41				
SPLEN1000101	41.57	16.82	24.85	23.9	21.81	9.24	15.06	12.84	12.84				
SPLEN1000108	3.06	1.50	1.01	2.01	2.01	1.31	1.57	2.16	2.16				
SPLEN1000113	4.35	2.46	2.67	4.83	2.55	2.28	3.11	3.66	3.66				
SPLEN1000114	2.42	2.37	1.43	3.43	2.78	2.56	2.74	3.97	3.97			*	+
SPLEN1000132	4.91	2.27	3.07	3.65	2.33	4.08	4.07	4.65	4.65				
SPLEN1000135	4.83	1.59	3.15	4.45	2.38	2.83	5.59	5.94	5.94			*	+
SPLEN1000136	4.48	3.01	2.79	7.59	5.71	8.15	9.03	12.90	12.9	*	+	**	+
SPLEN1000141	2.18	1.15	1.72	2.22	2.60	2.27	2.35	1.59	1.59				
SPLEN1000164	4.46	1.47	1.76	5.13	4.33	4.86	3.29	5.58	5.58				
SPLEN1000166	2.49	0.67	1.05	2.36	3.89	2.42	2.08	3.68	3.68				
SPLEN1000175	5.45	3.05	4.54	4.81	4.46	4.23	3.32	5.47	5.47				
SPLEN1000182	2.6	0.65	0.61	1.52	1.41	2.22	1.31	1.69	1.69				
SPLEN1000185	3.66	1.87	1.77	5.3	4.71	4.35	5.29	7.02	7.02	*	+	**	+
THYMU1000004	14.86	7.77	9.02	24.57	18.18	21.23	10.89	18.76	18.76	*	+		
THYMU1000009	8.45	5.32	5.87	7.04	5.33	4.60	6.33	5.23	5.23				
THYMU1000015	26.6	19.78	21.97	16.29	13.38	16.01	9.72	8.42	8.42	*	-	**	-
THYMU1000016	8.26	4.04	3.89	15.26	18.83	11.55	9.39	7.02	7.02	*	+		
THYMU1000023	3.89	1.34	1.23	2.77	2.08	3.06	2.39	2.39	2.39				
THYMU1000034	2.61	1.47	0.66	2.74	1.63	1.39	1.31	3.64	3.64				
THYMU1000035	1.07	0.61	0.61	0.44	0.64	0.76	1.85	2.01	2.01			**	+
THYMU1000037	1.82	1.82	1.19	2.22	2.35	0.98	2.22	2.11	2.11				
THYMU1000042	10.49	6.31	8.55	6.35	4.98	6.18	8.88	5.36	5.36				
THYMU1000047	4.11	2.46	3.11	10.3	9.57	11.11	4.37	4.74	4.74	**	+	*	+
THYMU1000080	3.32	3.11	1.09	3.11	4.52	4.74	2.28	1.83	1.83				
THYMU1000094	32.63	25.01	18.12	54.59	42.21	15.66	23.80	19.03	19.03				
THYMU1000109	8.44	4.34	3.79	6.74	8.15	5.93	7.23	6.42	6.42				
THYMU1000127	6.78	3.40	3.18	8.92	8.62	7.88	6.21	6.83	6.83	*	+		
THYMU1000130	4.13	1.20	1.02	4.32	4.36	3.32	2.41	3.21	3.21				
THYMU1000137	4.62	2.65	2.71	3.35	5.77	3.60	4.29	4.56	4.56				
THYMU1000146	4.71	3.58	4.49	7.3	4.71	6.30	5.63	4.56	4.56				
THYMU1000159	26.83	22.19	24.81	10.37	8.83	13.56	14.02	11.77	11.77	**	-	**	-
THYMU1000163	6.99	6.16	7.74	9.39	10.76	10.43	5.92	8.13	8.13	**	+		
THYMU1000167	2.34	1.29	1.70	2.93	3.51	2.43	1.61	1.52	1.52				
THYMU1000186	5.07	2.17	2.10	3.12	3.14	2.53	2.77	2.94	2.94				
THYRO1000017	5.52	2.12	2.08	4.91	6.19	6.15	4.38	3.34	3.34				
THYRO1000026	3.58	2.32	1.61	2.83	7.78	2.86	6.59	2.67	2.67				
THYRO1000034	3.17	3.08	1.76	3.93	4.73	4.25	3.60	4.07	4.07	*	+		
THYRO1000035	1.48	0.66	0.72	1.53	1.40	2.82	0.67	2.32	2.32				

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Table 337

THYRO1000036	1.47	2.88	1.52	4.59	3.60	4.55	3.37	2.09	2.09	*	+		
THYRO1000040	3.94	3.60	4.34	8.08	4.14	6.42	4.83	5.15	5.15			*	+
THYRO1000061	5.94	3.66	2.97	4.84	6.31	5.19	4.68	3.52	3.52				
THYRO1000067	15.2	9.77	9.78	10.78	13.27	13.10	11.70	12.59	12.59				
THYRO1000070	6	3.76	5.68	6.21	9.32	7.75	5.41	6.34	6.34				
THYRO1000072	2.94	1.82	1.84	5.83	8.39	3.32	2.14	2.54	2.54				
THYRO1000084	4.5	1.85	2.58	3.76	4.67	3.19	3.46	2.16	2.16				
THYRO1000085	10.88	13.54	13.23	14.79	17.02	16.91	12.99	15.14	15.14	*	+		
THYRO1000086	0.12	1.27	1.00	1.39	0.92	1.37	0.61	1.10	1.1				
THYRO1000087	0.56	0.67	0.91	1.37	1.09	0.98	1.47	0.51	0.51	*	+		
THYRO1000092	6	2.56	1.98	8.27	6.56	7.42	3.48	3.45	3.45	*	+		
THYRO1000093	1.44	1.12	0.93	2.32	0.88	2.13	1.21	1.43	1.43				
THYRO1000099	5.17	1.21	1.50	4.31	3.36	5.55	2.12	3.30	3.3				
THYRO1000107	2.2	0.53	1.13	2.82	7.80	4.79	2.15	2.47	2.47				
THYRO1000111	1.83	0.33	0.78	2.31	3.19	3.86	1.66	1.58	1.58	*	+		
THYRO1000121	3.44	1.10	1.03	3.02	3.40	6.52	2.38	1.76	1.76				
THYRO1000124	2.37	0.51	0.78	3.06	2.51	2.25	0.89	1.60	1.6				
THYRO1000129	1.3	0.82	0.51	1.26	1.52	1.53	0.49	1.02	1.02				
THYRO1000130	3.62	2.11	2.49	5.24	10.43	5.75	7.64	2.92	2.92				
THYRO1000132	8.41	1.76	1.74	4.45	6.81	7.03	2.87	3.11	3.11				
THYRO1000134	3.55	1.81	2.95	6.64	4.07	4.40	3.58	4.01	4.01				
THYRO1000144	13.82	5.38	3.94	8.01	7.60	7.93	4.07	4.00	4				
THYRO1000155	2.5	0.51	0.58	1.49	1.11	0.97	0.55	1.08	1.08				
THYRO1000156	1.89	1.44	0.82	2.61	2.67	3.19	1.97	1.97	1.97	*	+		
THYRO1000163	3.98	1.47	3.15	9.1	7.23	11.51	7.86	4.19	4.19	*	+		
THYRO1000173	2.9	2.72	1.68	4.44	4.27	4.08	1.67	3.61	3.61	**	+		
THYRO1000186	9.1	5.19	4.20	10.2	15.51	9.61	7.74	7.44	7.44				
THYRO1000187	5.63	2.01	3.20	6.21	7.01	6.32	5.05	3.18	3.18				
THYRO1000190	2.89	1.46	2.17	5.4	4.76	5.31	4.40	2.66	2.66	**	+		
THYRO1000196	0.92	0.80	1.33	2.19	1.72	1.35	0.94	1.18	1.18				
THYRO1000197	3.18	2.33	2.51	5.88	3.71	6.16	4.77	4.51	4.51	*	+	**	+
THYRO1000199	3.03	1.48	1.85	2.3	1.87	3.05	2.39	2.56	2.56				
THYRO1000206	14.52	5.55	4.65	11.65	9.64	12.12	6.54	6.11	6.11				
THYRO1000221	5.01	1.90	2.05	5.6	6.77	7.34	2.67	3.86	3.86	*	+		
THYRO1000222	7.73	2.24	1.94	3.18	4.68	4.24	4.78	2.83	2.83				
THYRO1000228	1.72	0.91	0.91	5.64	4.49	4.50	3.42	4.40	4.4	**	+	**	+
THYRO1000241	3.26	1.56	2.99	5.29	5.78	7.35	4.01	4.55	4.55	*	+	*	+
THYRO1000242	6.01	2.48	2.81	8.74	10.47	5.58	3.38	6.54	6.54				
THYRO1000246	2.49	0.94	1.13	2.44	2.95	2.72	4.13	4.49	4.49			**	+
THYRO1000253	3.03	2.39	2.12	4	3.56	6.64	2.35	3.27	3.27				
THYRO1000270	0.85	0.93	0.64	2.95	1.36	0.98	0.55	0.45	0.45			*	-
THYRO1000279	2.19	0.22	0.27	0.43	1.67	1.01	0.46	0.46	0.46				
THYRO1000285	6.19	3.69	1.88	4.45	4.41	6.07	8.92	4.83	4.83				
THYRO1000288	7.58	2.67	2.64	4.38	5.78	3.82	4.63	6.75	6.75				
THYRO1000296	3.95	2.07	1.83	3.07	4.49	3.23	3.68	3.54	3.54				
THYRO1000320	4.13	0.95	0.96	3.75	3.95	6.99	3.33	5.20	5.2				
THYRO1000322	38.05	21.86	30.50	21.36	20.13	23.75	18.89	19.42	19.42				
THYRO1000327	1.02	0.47	0.74	3.44	1.87	3.51	2.40	2.03	2.03	*	+	**	+
THYRO1000343	3.18	0.96	1.50	2.27	1.34	2.27	1.96	1.19	1.19				
THYRO1000345	4.6	2.12	2.05	3.98	5.40	3.79	1.33	1.91	1.91				
THYRO1000358	7.71	5.28	3.61	7.26	4.42	4.45	5.44	7.71	7.71				
THYRO1000368	11.25	3.81	3.69	7.91	6.70	6.11	5.37	4.82	4.82				
THYRO1000375	6.52	5.33	3.32	11.74	11.72	9.07	7.23	13.34	13.34	*	+	*	+
THYRO1000381	1.08	0.73	0.85	2.03	1.76	1.73	1.91	1.07	1.07	**	+		
THYRO1000387	2.85	2.46	2.45	4.71	4.58	5.18	3.81	2.92	2.92	**	+		
THYRO1000394	3.11	2.36	2.61	4.86	4.51	5.33	6.21	6.15	6.15	**	+	**	+

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Table 338

THYRO1000395	4.25	2.93	1.91	4.03	3.11	3.93	4.17	2.18	2.18				
THYRO1000400	4.41	1.20	1.12	2.44	2.11	3.30	1.51	2.67	2.67				
THYRO1000401	5.78	2.72	2.22	4.86	5.69	4.69	3.46	3.98	3.98				
THYRO1000407	2.85	1.30	0.87	2.33	1.72	1.87	2.55	3.06	3.06				
THYRO1000420	6.84	3.72	3.92	6.3	4.99	6.57	4.27	4.92	4.92				
THYRO1000438	3.47	2.61	5.10	3.55	4.73	5.14	3.74	2.32	2.32				
THYRO1000452	3.79	2.27	3.32	4.32	3.39	3.80	3.50	2.68	2.68				
THYRO1000455	0.86	0.19	0.08	0.98	0.97	1.02	0.43	0.69	0.69				
THYRO1000471	3.13	0.99	1.71	4.82	2.11	3.45	2.03	2.21	2.21				
THYRO1000481	3.05	2.09	1.78	2.49	2.59	3.24	2.75	3.65	3.65				
THYRO1000484	7.3	2.87	2.29	10.67	15.51	6.38	4.46	3.81	3.81				
THYRO1000488	1.1	0.92	1.15	1.45	1.81	1.35	2.24	2.38	2.38	*	+	**	+
THYRO1000501	2.42	1.63	1.50	2.59	2.38	2.19	2.65	3.01	3.01			*	+
THYRO1000502	1.72	1.26	1.14	1.06	1.74	2.09	1.25	1.88	1.88				
THYRO1000505	1.86	1.15	0.80	1	1.66	1.13	1.93	1.49	1.49				
THYRO1000535	3.34	1.94	2.04	4.99	3.71	3.63	10.07	9.11	9.11			**	+
THYRO1000556	3.48	3.02	2.08	3.02	2.21	3.79	3.38	3.27	3.27				
THYRO1000558	2.31	1.23	1.10	1.93	1.95	2.49	2.30	1.39	1.39				
THYRO1000569	37.42	23.06	26.88	28.52	31.17	30.05	27.41	43.25	43.25				
THYRO1000570	3.86	2.04	1.70	2.58	2.40	4.33	2.86	3.78	3.78				
THYRO1000572	2.15	0.94	1.24	2.2	1.78	1.73	2.48	3.26	3.26			*	+
THYRO1000573	2.15	0.40	1.11	1.23	2.42	1.75	1.79	2.04	2.04				
THYRO1000577	1.28	1.14	0.64	1.15	1.13	1.55	1.85	1.41	1.41				
THYRO1000580	5.42	3.17	3.10	6.46	6.34	9.14	4.00	4.26	4.26	*	+		
THYRO1000584	2.72	2.07	1.38	2.78	3.98	3.94	2.67	3.22	3.22				
THYRO1000585	2.25	1.51	1.61	5.52	5.02	4.69	3.92	4.40	4.4	**	+	**	+
THYRO1000596	0.84	0.25	0.33	0.85	1.98	1.44	1.19	1.17	1.17			*	+
THYRO1000602	5.45	3.58	2.07	8.38	7.15	5.61	4.80	5.98	5.98				
THYRO1000605	3.06	1.73	1.76	2.38	1.83	1.39	2.18	2.05	2.05				
THYRO1000615	1.88	0.80	0.63	1.19	1.72	1.17	1.04	2.25	2.25				
THYRO1000625	3.03	2.54	1.58	4.59	3.95	5.93	3.48	4.60	4.6	*	+	*	+
THYRO1000636	2.66	2.57	2.75	6.51	3.94	8.33	4.69	4.10	4.1	*	+	**	+
THYRO1000637	1.23	0.82	0.65	1.88	1.42	1.92	2.10	1.39	1.39	*	+		
THYRO1000641	1.4	0.60	1.08	0.89	1.31	1.56	1.11	0.84	0.84				
THYRO1000657	3.65	3.07	3.41	3.91	3.79	3.12	1.96	2.62	2.62			*	-
THYRO1000658	7.81	3.42	3.03	11.25	11.55	11.93	5.08	5.90	5.9	*	+		
THYRO1000662	2.88	1.16	0.83	2.17	1.76	1.90	1.97	1.81	1.81				
THYRO1000666	2.42	0.88	1.16	3.25	2.79	4.33	1.98	2.43	2.43	*	+		
THYRO1000676	2.32	1.10	0.52	2.88	3.21	3.68	3.68	2.15	2.15	*	+		
THYRO1000678	-0.09	0.33	0.95	0.54	0.74	1.28	1.19	2.92	2.92			*	+
THYRO1000684	1.03	2.45	1.63	3.34	3.15	3.52	4.80	2.39	2.39	*	+		
THYRO1000694	2.71	3.51	4.23	5.53	5.34	4.52	4.35	3.80	3.8	*	+		
THYRO1000699	15.82	15.18	11.44	15.15	15.90	16.09	15.44	10.86	10.86				
THYRO1000712	3.39	2.96	2.14	8.58	5.42	7.84	3.11	4.20	4.2	*	+		
THYRO1000715	4.02	2.34	2.31	2.86	4.26	2.85	3.39	2.68	2.68				
THYRO1000716	2.32	0.65	1.04	2.97	4.44	2.89	2.03	1.56	1.56	*	+		
THYRO1000717	2.15	0.84	1.30	4.23	5.94	4.84	1.47	3.93	3.93	**	+		
THYRO1000723	0.84	0.47	0.25	0.76	1.49	1.41	0.88	0.44	0.44				
THYRO1000734	0.78	0.54	0.33	1.36	1.43	0.84	0.50	0.83	0.83	*	+		
THYRO1000748	0.59	2.46	1.89	4.51	7.18	3.35	2.76	2.25	2.25				
THYRO1000755	6.84	4.25	3.30	14.94	19.03	9.44	6.39	7.81	7.81	*	+		
THYRO1000756	3.41	1.39	1.44	2.12	2.71	3.18	1.98	2.77	2.77				
THYRO1000776	1.32	1.08	1.00	2.41	2.21	1.88	2.52	1.74	1.74	**	+	*	+
THYRO1000777	2.84	1.43	1.39	4.03	2.36	3.89	2.12	2.28	2.28				
THYRO1000779	0.67	0.56	0.16	1.05	0.79	0.60	0.44	0.25	0.25				
THYRO1000782	3.17	1.32	2.40	4.64	3.68	4.39	4.70	5.63	5.63	*	+	**	+

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Table 339

THYRO1000783	1.63	0.89	1.30	3.1	2.26	1.53	1.80	1.30	1.3				
THYRO1000786	4.89	2.61	2.30	6.28	3.05	5.87	4.15	4.10	4.1				
THYRO1000787	10.6	5.80	4.42	7.07	6.40	5.00	7.52	6.30	6.3				
THYRO1000792	6.58	1.87	1.67	2.34	3.23	1.91	2.22	2.34	2.34				
THYRO1000793	2.04	0.81	0.90	2.24	3.46	2.95	1.63	1.90	1.9	*	+		
THYRO1000795	2.76	1.16	1.46	2.99	2.52	3.49	2.58	3.17	3.17				
THYRO1000796	2.38	0.64	1.44	4.8	3.84	4.16	2.52	2.59	2.59	**	+		
THYRO1000798	3.16	1.83	2.57	4.6	3.74	3.94	2.76	3.06	3.06	*	+		
THYRO1000800	7.44	4.89	4.90	15.05	11.25	16.69	6.56	6.96	6.96	**	+		
THYRO1000805	0.7	1.04	0.84	1.39	1.41	1.19	1.16	1.27	1.27	*	+	*	+
THYRO1000815	7	4.02	3.01	10.69	12.71	10.92	7.46	5.49	5.49	**	+		
THYRO1000829	4.85	1.50	0.99	3.49	4.27	2.08	2.62	2.36	2.36				
THYRO1000835	2.11	1.21	1.15	2.86	3.23	3.63	2.50	4.32	4.32	*	+	*	+
THYRO1000843	5.05	2.38	2.97	4.77	5.02	6.46	4.36	3.37	3.37				
THYRO1000846	2.51	1.06	0.98	2.34	1.74	1.56	2.17	1.43	1.43				
THYRO1000852	2.42	0.77	2.13	2.03	1.40	2.69	3.08	3.10	3.1				
THYRO1000855	4.5	4.43	3.85	5.88	4.56	7.12	5.76	3.18	3.18				
THYRO1000865	3.16	2.10	3.34	4.86	6.09	6.43	5.14	2.65	2.65	**	+		
THYRO1000866	11.62	9.40	6.30	9.67	9.65	5.08	11.39	9.54	9.54				
THYRO1000881	36.03	18.32	15.54	24.61	23.19	29.23	22.14	28.98	28.98				
THYRO1000894	3.99	1.72	1.92	2.01	2.07	2.23	2.83	2.03	2.03				
THYRO1000895	2.03	0.86	1.43	1.55	2.22	2.83	1.11	1.40	1.4				
THYRO1000916	3.35	1.86	1.68	6.43	4.60	5.32	3.15	2.84	2.84	*	+		
THYRO1000917	19.78	13.58	15.27	18.14	13.63	19.91	15.55	24.10	24.1				
THYRO1000926	3.79	1.84	2.71	4.53	2.38	2.98	3.39	2.18	2.18				
THYRO1000934	0.9	1.09	0.59	2.64	2.45	2.04	2.64	2.12	2.12	**	+	**	+
THYRO1000951	4.53	2.89	1.88	3.09	4.97	2.59	3.91	3.92	3.92				
THYRO1000952	3.27	1.18	1.32	2.44	2.17	2.23	1.41	2.31	2.31				
THYRO1000956	2.11	1.50	1.47	2.05	2.05	1.60	2.11	2.25	2.25				
THYRO1000960	5.02	0.63	1.57	3.83	4.64	3.41	3.77	4.16	4.16				
THYRO1000961	1.21	1.05	0.73	2.4	1.40	1.52	2.97	2.62	2.62			**	+
THYRO1000964	2.36	2.00	1.45	3.05	2.41	3.11	3.20	2.63	2.63				
THYRO1000971	6.39	3.74	2.87	7.64	6.60	7.93	4.97	5.58	5.58				
THYRO1000974	8.5	6.07	6.15	9.83	9.20	11.43	9.21	8.90	8.9	*	+		
THYRO1000975	6.08	2.45	2.54	7.25	6.73	7.67	5.66	3.65	3.65	*	+		
THYRO1000983	6.75	2.78	2.84	5.03	3.45	3.63	5.16	7.50	7.5				
THYRO1000984	4.73	2.02	2.56	6.84	6.78	4.19	3.85	4.94	4.94				
THYRO1000988	5.73	4.61	2.66	9.09	5.83	6.82	5.38	4.73	4.73				
THYRO1000991	5.53	2.99	3.68	7.73	4.24	7.53	5.28	4.92	4.92				
THYRO1000999	1.49	2.18	1.52	3.22	3.15	4.39	2.64	2.87	2.87	*	+	*	+
THYRO1001003	3.32	1.87	1.67	2.91	2.45	1.95	2.38	1.98	1.98				
THYRO1001015	6.07	3.22	4.17	6.03	3.39	4.75	4.51	4.29	4.29				
THYRO1001016	5.47	1.00	0.49	0.81	2.15	1.07	3.41	1.14	1.14				
THYRO1001022	4.57	1.75	1.46	2.49	2.37	2.27	3.16	2.69	2.69				
THYRO1001031	7	3.67	3.54	7.94	8.10	9.10	7.42	6.69	6.69	*	+		
THYRO1001033	2.8	0.57	1.23	2.39	2.37	1.06	1.41	2.32	2.32				
THYRO1001062	3.82	2.25	2.08	5.76	5.14	5.15	3.45	3.99	3.99	*	+		
THYRO1001063	2.69	1.60	2.09	4.12	3.13	4.17	2.95	2.51	2.51	*	+		
THYRO1001071	0.69	1.53	1.22	0.98	1.08	0.43	1.16	1.21	1.21				
THYRO1001080	5.05	2.34	2.74	5.3	3.96	5.08	3.55	4.04	4.04				
THYRO1001093	3.71	2.05	1.76	6.8	6.51	4.95	3.07	3.82	3.82	*	+		
THYRO1001100	2.79	1.59	1.28	2.23	2.44	2.67	1.71	3.71	3.71				
THYRO1001102	4.56	2.46	2.61	2.98	3.38	2.67	4.62	4.11	4.11				
THYRO1001104	7.28	6.54	6.58	7.94	7.41	6.48	4.57	5.35	5.35			**	-
THYRO1001109	2.63	2.02	1.30	2.32	2.09	1.60	2.52	1.80	1.8				
THYRO1001113	1.05	0.71	0.52	0.95	1.64	0.74	2.24	3.05	3.05			**	+

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Table 340

THYRO1001120	3.6	3.56	2.97	4.01	3.89	3.81	3.24	4.59	4.59				
THYRO1001121	4.68	3.13	2.03	5.64	4.07	3.90	2.70	4.05	4.05				
THYRO1001128	6.11	5.32	3.34	12.06	12.42	10.51	5.36	6.39	6.39	**	+		
THYRO1001133	6.15	4.73	4.57	9.2	11.55	7.92	6.41	7.28	7.28	*	+	*	+
THYRO1001134	3.36	2.97	3.23	3.78	3.94	5.18	4.36	4.50	4.5			**	+
THYRO1001142	0.74	0.74	1.04	0.72	2.52	2.41	0.96	1.79	1.79				
THYRO1001173	15.19	9.02	12.22	26.91	29.74	31.51	28.83	31.54	31.54	**	+	**	+
THYRO1001175	1.52	0.43	1.46	2.01	0.80	2.13	0.96	1.73	1.73				
THYRO1001177	2.64	2.90	2.12	5.03	6.80	5.41	2.98	4.26	4.26	**	+		
THYRO1001189	11.01	7.39	8.79	19.93	32.38	18.70	9.07	8.97	8.97	*	+		
THYRO1001194	3.46	1.13	2.28	5.96	5.42	5.39	1.82	2.43	2.43	**	+		
THYRO1001204	4.45	2.95	2.30	6.96	6.86	8.50	3.26	4.79	4.79	**	+		
THYRO1001205	24.03	16.88	15.68	32.39	32.90	31.15	22.06	24.66	24.66	**	+		
THYRO1001213	3.76	2.34	2.06	5.73	8.42	6.51	4.19	4.49	4.49	*	+	*	+
THYRO1001224	9.88	5.89	5.95	9.43	12.54	11.82	5.58	6.76	6.76				
THYRO1001237	2.56	2.32	3.39	3.81	2.63	3.98	5.21	5.02	5.02			**	+
THYRO1001242	27.87	23.01	22.93	21.64	25.67	32.15	25.14	28.77	28.77				
THYRO1001258	3.57	5.51	4.92	4.9	6.74	6.73	7.47	5.30	5.3				
THYRO1001262	1.72	1.10	1.83	6.36	5.01	5.41	2.24	3.79	3.79	**	+	*	+
THYRO1001266	1.55	0.64	0.79	1.26	1.48	1.18	1.70	1.12	1.12				
THYRO1001271	3.44	2.05	1.29	2.26	3.55	2.36	3.05	2.35	2.35				
THYRO1001287	3.96	1.21	1.37	3.53	2.40	2.74	3.19	2.91	2.91				
THYRO1001290	1.14	0.69	1.23	1.44	2.26	2.04	2.54	3.09	3.09	*	+	**	+
THYRO1001291	1.66	1.74	1.06	3.35	4.38	3.14	2.28	4.20	4.2	**	+	*	+
THYRO1001297	5.89	5.62	3.44	7.28	6.73	6.27	3.04	3.57	3.57				
THYRO1001302	0.7	1.17	1.36	2.14	3.01	3.14	1.40	2.26	2.26	*	+		
THYRO1001313	4.31	2.12	1.72	3.28	3.86	2.48	2.67	3.67	3.67				
THYRO1001320	4.07	2.24	2.43	7.21	7.25	7.12	3.37	4.30	4.3	**	+		
THYRO1001321	4.3	1.74	1.67	5.83	6.09	3.75	2.97	2.21	2.21				
THYRO1001322	2.79	2.55	2.39	3.89	5.05	3.82	2.48	1.98	1.98	*	+		
THYRO1001327	1.5	1.06	0.78	3.17	2.62	2.46	1.64	1.54	1.54	**	+		
THYRO1001336	5.87	4.46	7.00	13.05	17.27	14.64	6.39	6.28	6.28	**	+		
THYRO1001347	0.03	0.55	0.25	0.69	2.15	0.73	1.35	0.54	0.54				
THYRO1001358	11.06	9.93	9.25	14.71	16.38	14.53	9.85	8.62	8.62	**	+		
THYRO1001363	5.86	3.17	4.11	5.35	3.91	6.10	4.52	5.65	5.65				
THYRO1001365	5.19	2.07	3.95	4.26	3.12	4.83	2.55	3.93	3.93				
THYRO1001374	9.65	2.81	3.50	6.43	5.39	7.37	3.94	7.65	7.65				
THYRO1001401	7.01	3.08	4.71	9.44	10.37	11.91	6.83	6.19	6.19	*	+		
THYRO1001403	5.97	2.05	2.57	7.36	6.46	7.19	3.33	5.45	5.45				
THYRO1001405	5.97	3.44	4.77	7.32	6.00	9.69	6.01	5.53	5.53				
THYRO1001406	18.99	10.90	12.10	23.76	22.00	31.87	17.99	23.95	23.95	*	+		
THYRO1001411	13.78	6.66	6.31	15.64	15.28	13.18	9.35	10.33	10.33				
THYRO1001420	16.57	7.72	7.86	12.67	12.64	10.93	13.35	14.42	14.42				
THYRO1001426	12.94	7.75	6.41	21.71	18.55	24.48	11.12	13.81	13.81	**	+		
THYRO1001430	8.77	5.32	6.79	6.79	9.85	9.38	6.22	8.03	8.03				
THYRO1001434	4.36	1.78	2.26	3.34	4.87	4.04	2.27	4.13	4.13				
THYRO1001456	6.47	2.68	3.34	4.42	3.96	4.89	4.38	4.91	4.91				
THYRO1001457	6.96	3.92	4.84	6.7	6.42	9.36	5.12	7.08	7.08				
THYRO1001458	9.57	4.98	6.73	8.45	4.79	10.94	7.33	10.09	10.09				
THYRO1001459	11.09	4.54	5.24	11.67	15.21	11.24	5.79	8.41	8.41				
THYRO1001471	6.36	3.07	1.95	5.35	3.31	4.14	2.83	4.03	4.03				
THYRO1001478	6.87	2.62	2.63	3.98	3.73	5.94	4.03	6.74	6.74				
THYRO1001480	13.1	8.34	8.71	20.72	21.69	22.38	10.45	33.77	33.77	**	+		
THYRO1001481	5.7	2.94	3.90	7.61	6.97	7.30	4.44	6.00	6	*	+		
THYRO1001487	7.46	5.22	5.93	9.3	8.06	9.99	6.17	7.84	7.84	*	+		
THYRO1001495	11.89	6.81	10.31	8.41	6.19	9.91	4.61	6.76	6.76				

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Table 341

THYRO1001498	9.2	3.54	3.52	8.32	6.23	9.44	6.75	6.00	6				
THYRO1001510	8.51	2.92	3.62	4.12	4.26	4.21	2.96	4.74	4.74				
THYRO1001512	9.32	6.84	5.74	9.67	9.37	8.03	7.58	10.22	10.22				
THYRO1001519	9.13	4.10	4.70	9.27	7.38	9.67	6.98	8.20	8.2				
THYRO1001522	6.26	4.50	5.23	7.93	8.82	7.33	5.58	9.26	9.26	*	+		
THYRO1001523	3.53	2.10	1.99	6.46	5.54	6.24	4.04	4.29	4.29	**	+	*	+
THYRO1001526	6.91	4.84	5.74	14.18	9.51	13.49	12.30	16.11	16.11	*	+	**	+
THYRO1001529	2.41	1.14	1.41	2.28	1.58	4.28	2.24	2.20	2.2				
THYRO1001534	3.65	2.24	1.50	4.38	3.58	6.43	2.88	4.21	4.21				
THYRO1001537	18.2	10.50	9.67	21.59	21.38	19.81	8.19	10.14	10.14	*	+		
THYRO1001541	14.28	6.89	6.76	16.77	16.36	14.76	9.61	10.03	10.03				
THYRO1001545	3.56	2.76	2.72	3.42	3.96	4.48	3.96	4.30	4.3			*	+
THYRO1001559	3.99	2.04	2.13	4.24	3.76	7.51	3.56	3.91	3.91				
THYRO1001563	11.96	7.39	6.70	7.96	5.68	9.41	7.19	8.07	8.07				
THYRO1001570	4.68	4.47	3.76	4.09	3.00	4.87	4.64	6.87	6.87				
THYRO1001573	8.02	5.52	6.21	6.26	3.61	8.28	6.11	6.00	6				
THYRO1001584	8.32	5.29	4.71	9.43	6.63	9.84	5.17	6.12	6.12				
THYRO1001593	2.99	0.93	1.22	3.14	4.86	2.61	2.01	4.21	4.21				
THYRO1001595	5.67	1.96	2.39	7.68	7.67	6.34	3.91	4.14	4.14	*	+		
THYRO1001596	5.89	2.66	3.80	3.78	3.65	3.11	2.98	3.57	3.57				
THYRO1001602	7.81	2.64	3.23	7.32	8.69	7.89	4.74	7.00	7				
THYRO1001605	5.26	2.56	2.24	5.13	5.05	4.87	3.48	3.41	3.41				
THYRO1001608	7.75	3.89	6.86	6.23	6.07	8.04	6.19	6.87	6.87				
THYRO1001617	14.26	9.34	10.47	17.37	15.68	19.92	9.80	12.17	12.17	*	+		
THYRO1001634	4.95	3.06	3.93	4.4	3.84	4.30	4.75	4.39	4.39				
THYRO1001637	10.18	6.14	4.65	17.45	14.38	17.46	8.06	9.17	9.17	**	+		
THYRO1001641	6.38	3.44	3.03	6.59	5.36	5.81	5.90	5.59	5.59				
THYRO1001656	4.52	2.95	2.83	3.81	4.14	7.31	4.33	5.14	5.14				
THYRO1001658	4.29	2.01	1.79	2.18	2.89	2.10	2.16	2.58	2.58				
THYRO1001661	3.1	1.45	1.64	1.96	2.33	1.46	4.01	2.50	2.5				
THYRO1001671	5.77	2.59	2.20	4.22	4.26	4.64	3.03	5.39	5.39				
THYRO1001672	6.81	4.51	5.53	5.21	5.27	6.87	6.28	6.63	6.63				
THYRO1001673	4	1.65	1.66	5.32	3.21	5.73	2.44	2.64	2.64				
THYRO1001677	6.31	4.12	3.30	6.16	7.35	6.56	2.26	3.46	3.46				
THYRO1001683	8.24	4.40	3.37	4.91	4.29	8.77	5.76	11.28	11.28				
THYRO1001700	4.49	4.00	2.73	4.05	4.60	4.19	4.01	4.47	4.47				
THYRO1001702	15.24	5.52	7.38	9.42	10.75	10.20	8.66	10.47	10.47				
THYRO1001703	9.25	6.47	6.51	7.26	6.71	8.49	10.46	8.63	8.63				
THYRO1001706	4.3	2.92	3.16	5.43	6.68	7.52	2.62	4.78	4.78	*	+		
THYRO1001721	5.23	3.35	2.76	6.77	6.22	4.74	5.26	7.04	7.04			*	+
THYRO1001725	4.92	2.94	2.29	5.59	6.33	8.71	2.75	4.72	4.72	*	+		
THYRO1001730	24.29	13.18	13.43	14.02	17.03	13.70	21.66	22.76	22.76				
THYRO1001738	9.75	4.90	4.82	9.04	5.85	7.43	4.92	7.98	7.98				
THYRO1001743	4	3.23	1.86	3.1	3.27	3.05	4.23	2.96	2.96				
THYRO1001745	2.52	1.07	1.25	1.89	1.88	1.53	1.75	2.88	2.88				
THYRO1001746	4.33	2.26	1.61	3.33	3.91	4.02	3.18	3.68	3.68				
THYRO1001770	12.11	9.28	9.48	15.96	14.31	15.08	8.82	12.34	12.34	**	+		
THYRO1001772	5.17	2.74	2.39	6.3	7.93	7.50	3.31	3.90	3.9	*	+		
THYRO1001778	15.04	12.42	11.52	14.35	19.15	15.23	13.02	16.18	16.18				
THYRO1001793	14.69	6.79	7.43	12.47	11.95	9.29	6.11	8.93	8.93				
THYRO1001796	11.97	7.13	5.24	9.74	7.66	8.26	8.13	8.63	8.63				
THYRO1001800	6.25	3.20	2.10	5.72	6.37	4.12	5.27	7.47	7.47				
THYRO1001803	19.67	13.46	12.81	14.42	14.10	16.43	18.72	18.13	18.13				
THYRO1001809	3.63	3.46	2.67	3.26	4.76	4.46	2.91	5.54	5.54				
THYRO1001817	6.44	6.33	5.18	4.47	3.95	4.74	8.83	7.32	7.32	*	-	*	+
THYRO1001819	5.55	5.75	5.06	8.24	5.95	6.83	5.79	6.86	6.86				

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Table 342

THYRO1001828	5.58	5.56	4.00	9.32	9.83	9.03	4.86	6.29	6.29	**	+		
THYRO1001854	20.22	7.97	7.27	24.83	26.41	23.02	14.19	14.50	14.5	*	+		
THYRO1001895	4.5	1.82	1.66	2.69	3.40	3.20	2.51	2.17	2.17				
THYRO1001907	6.37	2.87	2.77	7.43	8.35	6.14	3.08	4.67	4.67				
TRACH1000006	1.82	2.19	1.60	2.9	3.42	2.53	2.58	3.05	3.05	*	+	*	+
TRACH1000013	2.15	1.13	1.31	1.45	1.80	3.25	1.50	1.76	1.76				
TRACH1000074	3.42	3.57	4.39	5.62	7.83	7.88	4.19	10.27	10.27	*	+		
TRACH1000095	2.45	2.91	2.44	3.1	3.04	4.04	2.50	2.45	2.45				
TRACH1000102	7.43	5.84	4.56	10.07	11.80	13.53	5.10	8.65	8.65	*	+		
TRACH1000108	3.15	1.08	0.60	4.55	2.50	3.75	3.10	1.49	1.49				-
TRACH1000126	6.59	4.83	4.15	6.73	6.75	6.24	2.66	4.52	4.52				
TRACH1000146	4.1	2.48	3.17	3.77	4.50	3.73	2.81	3.85	3.85				
TRACH1000160	2.88	1.73	0.69	2.15	3.29	1.84	1.31	2.46	2.46				
TRACH1000184	9.18	5.15	6.68	9.87	12.29	12.18	7.92	7.13	7.13	*	+		
VESEN1000004	1.43	3.20	2.03	4.77	4.23	4.76	2.44	2.90	2.9	*	+		
VESEN1000007	4.67	3.71	3.03	4.92	4.79	4.78	3.45	3.27	3.27				
VESEN1000013	3.8	4.40	3.49	6.08	5.11	8.39	4.08	5.78	5.78				
VESEN1000028	10.32	4.13	4.71	9.23	9.35	9.07	7.29	12.27	12.27				
VESEN1000059	7.75	3.60	4.26	7.63	6.94	7.73	4.60	5.95	5.95				
VESEN1000100	14.3	7.29	8.52	11.77	17.29	16.55	10.06	12.85	12.85				-
VESEN1000107	8.09	2.86	4.55	5.28	4.93	5.96	5.50	6.28	6.28				
VESEN1000117	4.56	2.53	3.13	3.83	3.21	3.98	3.40	4.83	4.83				
VESEN1000122	6	2.68	4.24	3.89	4.52	7.18	4.38	7.65	7.65				
VESEN1000137	2.93	1.73	1.82	1.57	3.65	3.17	2.10	3.43	3.43				
VESEN1000195	14.98	5.35	5.89	8.11	8.22	6.74	10.54	12.97	12.97				
VESEN1000215	2.26	0.13	1.20	1.57	1.68	0.85	0.67	1.63	1.63				
VESEN1000279	26.58	15.13	14.91	21.43	14.13	23.59	19.30	20.07	20.07				
VESEN1000363	15.34	8.73	10.79	17.48	16.61	12.88	9.72	13.31	13.31				
VESEN1000388	9.91	6.40	6.52	7.89	4.01	10.40	6.86	10.14	10.14				
VESEN1000394	12.12	6.72	8.23	12.56	8.96	9.43	5.04	9.23	9.23				
VESEN1000410	10.78	2.59	2.39	6.85	3.24	4.07	5.06	8.94	8.94				
VESEN1000411	6.18	3.27	4.03	5.74	3.11	6.71	4.21	5.31	5.31				
VESEN1000415	9.24	6.34	4.20	8.16	6.27	5.95	4.08	7.14	7.14				
VESEN1000440	9.05	5.57	4.80	8.89	8.64	8.72	5.45	8.25	8.25				
VESEN1000452	7.8	4.72	5.60	4.86	5.38	4.21	6.76	5.77	5.77				
VESEN1000539	346.75	188.95	244.65	158.74	166.73	144.68	64.90	151.18	151.2				
VESEN1000554	4.46	3.39	3.95	4.07	2.23	3.58	2.95	2.93	2.93			*	-
VESEN1000557	6.06	4.00	4.41	6.38	3.08	5.06	6.10	7.77	7.77			*	+
VESEN1000575	7.82	4.18	4.70	6.03	4.15	4.58	5.87	6.64	6.64				
VESEN1000585	9.14	4.16	5.29	6.86	6.14	7.55	4.21	6.93	6.93				
VESEN1000592	1.51	0.34	0.06	1.48	0.81	0.75	1.11	0.98	0.98				
VESEN1000658	9.42	5.35	3.63	6.6	8.13	5.18	7.65	9.88	9.88				
VESEN1000669	30.52	16.02	17.70	27.74	22.51	23.12	18.76	27.04	27.04				
VESEN1000743	12.62	7.52	8.22	9.64	10.40	10.72	6.57	9.41	9.41				
VESEN1000752	31.33	20.56	19.92	44.49	19.58	40.73	21.19	32.70	32.7				
VESEN1000761	23.86	13.01	17.50	12.45	9.94	17.39	8.43	10.21	10.21				
VESEN2000039	77.69	44.95	56.28	57.5	43.19	64.97	60.33	69.54	69.54				
VESEN2000102	7.33	4.99	5.35	6.83	4.25	7.08	6.69	8.37	8.37				
VESEN2000164	5.18	3.46	3.31	9.13	9.21	6.82	3.36	3.89	3.89	*	+		
VESEN2000175	1.73	0.97	0.12	1.01	1.92	1.13	0.88	1.17	1.17				
VESEN2000186	19.39	12.37	11.60	17.79	16.80	18.96	15.99	20.01	20.01				
VESEN2000199	28.49	19.51	19.01	18.68	21.47	33.21	23.58	23.01	23.01				
VESEN2000200	6.32	1.63	3.02	5.06	3.00	3.70	3.04	4.39	4.39				
VESEN2000204	4.52	1.87	3.26	2.47	1.87	2.02	2.17	3.09	3.09				
VESEN2000218	6.43	3.74	5.10	6.59	6.27	8.76	4.84	5.35	5.35				
VESEN2000230	5.26	2.88	3.63	6.04	5.20	6.82	6.20	5.85	5.85			*	+

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Table 343

VESEN2000272	6.36	2.52	3.61	13.68	15.50	9.23	6.37	6.11	6.11	*	+		
VESEN2000299	5.8	3.32	3.03	6.33	5.54	5.31	4.11	3.82	3.82				
VESEN2000323	3.64	2.70	3.46	7.25	6.60	6.83	4.13	6.99	6.99	**	+	*	+
VESEN2000327	16.91	9.24	9.32	14.89	11.98	16.05	16.51	12.53	12.53				
VESEN2000328	3.41	1.69	2.05	2.7	1.99	2.52	3.68	4.21	4.21			*	+
VESEN2000330	9.06	4.94	3.98	4	3.94	4.40	7.56	5.58	5.58				
VESEN2000336	3.29	2.35	2.63	3.19	2.56	2.84	2.06	2.38	2.38				
VESEN2000354	8.7	4.46	4.22	7.46	6.89	5.83	5.63	5.02	5.02				
VESEN2000378	3.42	2.15	2.25	4.13	2.42	1.91	1.92	2.61	2.61				
VESEN2000379	11.63	7.79	4.82	10.74	10.07	12.49	7.29	10.70	10.7				
VESEN2000397	3.37	1.29	1.36	2.39	2.24	1.99	1.18	3.19	3.19				
VESEN2000416	3.83	2.34	1.55	2.15	2.33	2.91	2.47	2.28	2.28				
VESEN2000420	2.88	0.98	1.36	1.52	0.23	0.52	0.64	1.63	1.63				
VESEN2000430	2.62	1.65	1.71	1.89	2.49	1.83	0.78	2.97	2.97				
VESEN2000448	2.86	2.67	1.17	1	2.01	2.37	2.33	2.73	2.73				
VESEN2000449	8.25	5.92	4.67	9.14	8.56	10.89	5.16	6.55	6.55				
VESEN2000456	5.37	3.06	1.86	3.12	2.41	3.57	2.05	2.65	2.65				
VESEN2000562	7.78	4.41	5.30	5.84	5.51	4.92	4.30	6.44	6.44				
VESEN2000573	0.6	0.35	0.41	0.67	0.40	0.67	1.28	2.60	2.6			*	+
VESEN2000604	5.64	1.48	1.85	3.25	2.37	2.19	2.91	4.05	4.05				
VESEN2000614	25.21	13.24	16.03	20.97	19.46	20.96	23.97	21.61	21.61				
VESEN2000638	1.7	1.28	1.62	1.56	1.85	1.20	2.41	1.35	1.35				
VESEN2000641	1.73	2.11	1.08	1.79	1.66	1.77	1.14	1.95	1.95				
VESEN2000645	3.09	2.77	2.30	2.12	2.14	1.71	1.70	3.15	3.15				
Y79AA1000013	10.79	7.40	5.68	11.91	9.74	8.63	7.82	6.74	6.74				
Y79AA1000030	13.95	8.47	8.24	10.96	9.10	13.62	9.47	12.29	12.29				
Y79AA1000033	16.96	12.16	9.55	7.65	10.20	8.44	7.18	10.76	10.76				
Y79AA1000037	2.11	1.49	0.71	2.23	2.21	3.27	2.75	2.51	2.51			*	+
Y79AA1000041	2.2	2.48	1.77	2.69	2.36	2.74	2.02	3.82	3.82				
Y79AA1000059	7.6	6.90	6.65	10.99	11.69	12.90	4.30	7.70	7.7	**	+		
Y79AA1000065	22.39	17.36	15.96	24.43	21.67	25.09	14.43	16.06	16.06				
Y79AA1000081	42.69	41.35	51.24	111.38	113.45	103.25	45.62	16.30	16.3	**	+		
Y79AA1000127	22.29	16.01	11.79	12.57	10.65	7.07	3.98	5.58	5.58			*	-
Y79AA1000130	6.17	3.27	2.80	10.01	8.60	9.63	4.89	5.13	5.13	**	+		
Y79AA1000131	448.19	235.19	299.39	399.75	486.28	438.12	277.73	304.61	304.6				
Y79AA1000134	8.96	7.49	5.25	6.6	6.53	6.62	9.23	10.69	10.69				
Y79AA1000143	9.99	4.29	8.06	7.58	8.06	8.95	6.96	8.30	8.3				
Y79AA1000144	8.55	7.18	6.04	6.31	5.55	6.00	4.05	4.40	4.4			*	-
Y79AA1000150	18.22	14.18	15.26	14.89	15.33	21.06	9.92	9.91	9.91			**	-
Y79AA1000153	201.67	139.66	172.85	190.71	189.25	179.30	103.81	119.17	119.2			*	-
Y79AA1000166	6.51	3.61	2.42	6.7	8.84	4.48	3.56	4.21	4.21				
Y79AA1000179	15.16	9.65	7.92	10.53	9.30	7.94	4.29	5.64	5.64				
Y79AA1000181	10.66	5.30	5.63	7.26	8.22	5.85	3.94	5.98	5.98				
Y79AA1000202	18.5	15.06	12.86	18.25	18.73	23.11	15.84	25.98	25.98				
Y79AA1000207	5.87	4.02	4.27	14.67	14.22	14.10	7.48	5.85	5.85	**	+		
Y79AA1000214	29.22	23.27	20.29	36.32	37.06	45.40	22.86	25.86	25.86	*	+		
Y79AA1000222	12.84	9.84	10.93	9.21	6.89	9.06	5.29	5.66	5.66			**	-
Y79AA1000226	5.63	6.09	5.68	7.41	7.20	8.09	8.84	8.79	8.79	**	+	**	+
Y79AA1000227	17.27	10.05	8.43	12.69	17.80	12.32	9.20	10.19	10.19				
Y79AA1000230	6.42	4.02	2.20	3.72	4.88	2.48	3.03	2.90	2.9				
Y79AA1000231	34.72	21.74	21.36	20.87	19.10	17.13	9.21	15.10	15.1				
Y79AA1000239	15.79	9.79	7.30	10.27	13.40	11.55	12.77	13.82	13.82				
Y79AA1000258	4.05	3.20	3.26	4.22	5.80	4.84	3.99	4.25	4.25				
Y79AA1000268	7.27	4.70	4.79	10.11	6.83	6.96	5.20	6.24	6.24				
Y79AA1000269	3.42	2.81	2.55	4.54	6.08	5.88	5.38	5.60	5.6	**	+	**	+
Y79AA1000270	3.64	4.17	2.51	5.74	6.14	5.66	3.62	4.41	4.41	**	+		

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Table 344

Y79AA1000280	11.25	5.37	6.77	11.8	13.92	12.66	5.46	9.54	9.54					
Y79AA1000285	4.46	1.52	2.70	3.31	1.78	2.60	2.43	3.53	3.53					
Y79AA1000295	3.61	2.65	3.31	10.15	10.34	10.77	4.41	5.66	5.66	**	+	*	+	
Y79AA1000307	12.46	9.65	13.13	11.87	8.54	13.75	5.29	6.68	6.68			**	-	
Y79AA1000313	15.46	6.94	8.62	10.28	12.44	14.87	10.41	13.90	13.9					
Y79AA1000314	14.81	9.18	10.30	22.74	18.92	27.80	24.11	31.46	31.46	*	+	**	+	
Y79AA1000328	3.09	1.87	2.24	2.09	2.55	2.73	1.78	2.96	2.96					
Y79AA1000334	7.09	3.70	2.56	5.55	4.48	4.69	3.41	4.25	4.25					
Y79AA1000342	35.87	15.66	15.62	22.36	17.70	23.91	21.00	29.07	29.07					
Y79AA1000346	17.41	15.57	12.74	9.41	9.10	10.71	4.23	5.49	5.49	*	-	**	-	
Y79AA1000347	23.11	14.24	15.07	23.5	39.38	38.47	19.81	25.73	25.73	*	+			
Y79AA1000349	19.76	10.53	12.68	20.31	16.01	21.05	12.82	17.27	17.27					
Y79AA1000355	4.87	2.42	3.06	7.26	6.44	8.31	4.76	6.17	6.17	*	+			
Y79AA1000368	6.76	2.87	3.15	4.62	3.69	5.41	4.31	4.40	4.4					
Y79AA1000388	25.23	15.44	16.71	26.79	21.25	29.10	12.60	17.85	17.85					
Y79AA1000392	14.91	8.34	9.71	13.34	7.02	19.13	9.61	11.82	11.82					
Y79AA1000405	24.03	14.82	7.15	15.39	22.71	12.76	14.12	17.35	17.35					
Y79AA1000410	24.25	16.23	12.97	37.19	36.14	36.35	20.62	22.06	22.06	**	+			
Y79AA1000420	1.83	1.06	1.88	2.33	1.74	3.81	1.85	2.84	2.84					
Y79AA1000423	7.25	4.11	5.48	9.75	7.86	8.44	5.00	5.45	5.45	*	+			
Y79AA1000426	5.29	3.84	5.55	4.45	2.88	4.33	3.32	3.94	3.94					
Y79AA1000432	3.27	2.71	3.28	1.62	1.68	2.55	1.63	2.22	2.22	*	-	*	-	
Y79AA1000453	141.24	53.68	107.37	81.71	59.38	81.50	30.05	43.77	43.77					
Y79AA1000465	3.59	1.59	2.02	2.43	1.32	2.55	1.95	3.10	3.1					
Y79AA1000469	14.01	11.65	7.90	12.08	10.53	7.10	8.31	7.33	7.33					
Y79AA1000480	4.69	1.58	1.60	4.05	2.82	2.60	2.60	2.44	2.44					
Y79AA1000502	12.81	5.39	8.31	9.83	13.49	9.32	5.96	11.12	11.12					
Y79AA1000521	6.28	4.42	6.32	6.26	4.77	4.40	6.38	6.79	6.79					
Y79AA1000534	17.26	8.63	8.69	10.74	7.23	7.43	4.39	5.56	5.56					
Y79AA1000538	6.63	3.28	4.52	10.32	7.26	8.06	5.36	6.47	6.47	*	+			
Y79AA1000539	19.25	8.27	12.78	24.31	26.47	21.68	9.27	11.72	11.72	*	+			
Y79AA1000540	11.13	5.92	6.15	9.13	9.09	8.44	6.65	9.21	9.21					
Y79AA1000560	173.06	134.34	94.53	202.66	161.69	169.55	95.78	139.04	139					
Y79AA1000574	2.89	2.45	2.28	4.12	2.97	2.60	1.96	2.63	2.63					
Y79AA1000584	3.2	1.68	1.63	1.75	2.10	2.56	2.05	2.41	2.41					
Y79AA1000589	8.66	5.80	5.36	6.79	3.71	6.73	6.49	7.62	7.62					
Y79AA1000598	5.98	2.97	4.18	3.57	3.29	6.10	4.35	4.63	4.63					
Y79AA1000600	6.57	3.44	3.89	3.3	2.25	3.48	2.55	2.77	2.77					
Y79AA1000609	6.92	3.42	2.75	2.76	4.04	6.09	4.13	5.52	5.52					
Y79AA1000618	58.41	30.55	40.08	29.92	37.02	38.12	11.43	14.49	14.49			*	-	
Y79AA1000627	6.08	3.22	3.45	5.69	5.50	4.18	4.40	3.93	3.93					
Y79AA1000636	38.19	23.55	23.75	16.84	22.87	15.14	9.44	11.05	11.05			*	-	
Y79AA1000649	8.69	4.34	4.67	4.61	4.61	4.01	3.93	8.79	8.79					
Y79AA1000656	5.76	3.08	3.22	5.58	4.90	5.16	3.04	4.23	4.23					
Y79AA1000673	5.03	2.72	1.36	3.23	1.94	2.41	3.39	4.06	4.06					
Y79AA1000674	10.61	7.11	11.17	10.18	8.67	10.62	6.76	10.00	10					
Y79AA1000678	7.25	4.89	6.06	10.19	6.81	7.33	5.06	5.92	5.92					
Y79AA1000682	24.87	16.17	18.30	22.46	26.14	12.58	16.87	20.51	20.51					
Y79AA1000683	15.32	7.96	8.21	6.64	7.38	6.63	4.88	6.13	6.13					
Y79AA1000697	54.8	30.85	37.16	42.84	41.24	37.90	36.31	42.61	42.61					
Y79AA1000700	9.78	3.97	5.64	3.6	3.66	3.51	4.90	7.29	7.29					
Y79AA1000702	17.82	9.90	9.05	9.33	10.05	8.49	5.94	9.28	9.28					
Y79AA1000704	2.05	0.88	1.35	0.9	1.80	0.91	1.41	1.66	1.66					
Y79AA1000705	2.45	1.63	1.24	3.99	2.73	3.50	2.26	2.26	2.26	*	+			
Y79AA1000717	11.47	6.51	7.68	14.26	8.53	10.93	5.99	11.28	11.28					
Y79AA1000722	6.59	5.15	4.02	3.83	3.18	4.48	1.26	1.65	1.65			**	-	

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Table 345

Y79AA1000724	28.17	13.18	13.80	13.88	13.98	11.98	3.06	4.28	4.28			*	-
Y79AA1000726	8.11	5.46	4.24	6.09	4.77	4.52	5.43	7.82	7.82				
Y79AA1000734	3.88	2.62	2.34	5.17	3.55	4.31	2.92	6.05	6.05				
Y79AA1000748	3.95	1.81	1.83	2.64	2.02	2.92	1.57	2.24	2.24				
Y79AA1000750	10.39	6.10	4.86	9.81	8.59	9.78	5.43	7.43	7.43				
Y79AA1000752	2.87	0.53	1.08	2.54	2.81	2.11	1.32	1.59	1.59				
Y79AA1000774	5.72	4.59	2.86	2.14	2.79	5.77	3.53	3.76	3.76				
Y79AA1000776	4.35	4.36	2.86	3.71	4.12	5.01	3.48	3.30	3.3				
Y79AA1000777	11.76	6.21	5.54	8.56	11.90	10.17	6.16	6.66	6.66				
Y79AA1000778	13.22	6.87	8.41	14.77	13.90	13.40	7.19	13.72	13.72				
Y79AA1000782	7.86	4.93	5.51	5.52	4.90	5.05	5.46	7.23	7.23				
Y79AA1000784	12.43	9.12	11.59	13	14.52	14.46	11.05	11.31	11.31				
Y79AA1000794	4.35	2.95	2.89	4.43	4.95	3.90	3.24	3.10	3.1				
Y79AA1000800	2.57	2.36	2.08	3	3.32	3.30	2.93	3.69	3.69	**	+	*	+
Y79AA1000802	1.85	1.48	1.65	1	0.76	1.64	0.34	1.23	1.23				
Y79AA1000805	4.24	3.55	2.28	3.22	3.19	3.89	2.71	4.15	4.15				
Y79AA1000814	14.61	9.83	7.28	9.51	9.83	6.77	3.86	4.30	4.3			*	-
Y79AA1000823	12.6	9.53	9.56	15.44	14.21	12.23	9.08	15.12	15.12				
Y79AA1000824	4.44	3.44	2.16	2.49	3.58	2.72	2.72	3.74	3.74				
Y79AA1000827	3.1	1.46	1.84	2.99	1.29	1.77	1.89	2.61	2.61				
Y79AA1000831	5.49	4.85	5.37	3.74	4.89	3.85	3.76	5.38	5.38				
Y79AA1000833	40.22	31.45	37.17	40.96	46.51	50.53	34.20	40.04	40.04				
Y79AA1000850	2.09	2.81	2.57	4.27	3.76	4.02	3.33	2.26	2.26	**	+		
Y79AA1000856	6.74	5.50	6.27	7.85	6.17	10.60	4.73	5.48	5.48				
Y79AA1000862	12.52	7.78	4.39	13.89	9.86	8.13	7.63	7.94	7.94				
Y79AA1000876	8.46	4.16	4.01	6.87	6.89	6.26	3.75	5.07	5.07				
Y79AA1000888	1.47	1.34	1.40	1.56	1.46	1.29	1.98	1.99	1.99			**	+
Y79AA1000902	16.38	10.81	14.11	11.4	9.46	11.97	5.88	7.23	7.23			*	-
Y79AA1000935	16.25	11.98	13.09	25.37	21.17	25.92	23.44	29.28	29.28	**	+	**	+
Y79AA1000959	3.1	2.66	3.26	3.18	3.69	2.84	2.68	4.50	4.5				
Y79AA1000962	1.8	2.34	1.77	4.45	3.80	4.94	2.33	2.34	2.34	**	+		
Y79AA1000963	43.49	20.23	23.14	40.9	40.35	45.98	17.97	19.24	19.24				
Y79AA1000966	8	6.62	3.05	7.53	7.98	4.56	6.48	5.59	5.59				
Y79AA1000967	11.14	8.37	5.21	15.29	15.02	10.80	8.86	10.67	10.67				
Y79AA1000968	11.05	6.63	3.78	6.32	9.03	6.81	4.66	7.08	7.08				
Y79AA1000969	4.13	3.63	3.19	4.09	3.12	3.96	2.88	4.11	4.11				
Y79AA1000976	2.07	1.66	1.63	2.46	2.43	2.76	2.15	3.14	3.14	*	+	*	+
Y79AA1000978	3.15	2.68	2.59	3.19	2.43	2.99	1.56	2.57	2.57				
Y79AA1000985	4.53	6.21	3.11	9.92	6.66	7.93	4.84	4.19	4.19				
Y79AA1000989	27.14	18.46	21.17	22.61	22.40	25.64	17.86	17.83	17.83				
Y79AA1000991	14.41	7.65	8.70	14.5	16.91	8.11	10.68	10.04	10.04				
Y79AA1001013	35.7	19.64	14.11	24.63	29.38	32.01	18.46	27.65	27.65				
Y79AA1001014	8.41	5.13	3.58	6.96	7.27	8.35	6.51	8.47	8.47				
Y79AA1001019	6.41	3.32	4.05	4.98	4.88	5.75	4.58	5.04	5.04				
Y79AA1001020	13.26	4.81	6.74	9.29	9.05	11.19	6.66	10.83	10.83				
Y79AA1001023	3.99	2.27	3.29	3.71	4.41	3.42	4.24	3.90	3.9				
Y79AA1001030	4.36	2.82	3.64	7.73	6.53	9.26	7.69	8.68	8.68	**	+	**	+
Y79AA1001035	-0.01	7.25	7.50	9.11	6.84	10.21	7.88	15.95	15.95				
Y79AA1001041	8.33	4.39	3.51	5.69	4.65	4.21	2.70	5.79	5.79				
Y79AA1001043	18.02	12.74	10.03	8.74	8.44	9.66	9.73	11.39	11.39				
Y79AA1001048	5.98	4.37	5.02	5.57	4.35	5.46	5.24	5.86	5.86				
Y79AA1001056	2.8	1.67	2.69	4.83	3.64	3.93	2.91	3.52	3.52	*	+		
Y79AA1001061	4.66	2.07	2.99	8.42	5.16	8.18	3.38	5.08	5.08	*	+		
Y79AA1001062	4.59	1.72	3.28	8.74	7.23	9.33	3.95	5.55	5.55	**	+		
Y79AA1001068	7.33	4.55	5.57	10.85	9.20	12.48	5.68	6.64	6.64	*	+		
Y79AA1001073	12.4	6.75	7.01	7.75	5.93	9.79	5.80	7.72	7.72				

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Table 346

Y79AA1001077	11.3	7.81	9.27	10.02	10.61	11.75	11.20	11.01	11.01				
Y79AA1001078	2.85	2.15	2.01	4.62	7.48	2.90	4.22	3.26	3.26			*	+
Y79AA1001081	16.61	9.85	12.79	10	10.38	11.30	5.81	7.08	7.08			*	-
Y79AA1001088	26.22	15.63	20.41	21.72	24.28	26.25	25.14	31.31	31.31				
Y79AA1001089	11.17	5.53	8.30	9.49	6.56	8.41	9.43	10.79	10.79				
Y79AA1001090	4.51	2.54	4.20	6.81	5.20	6.61	4.39	5.95	5.95	*	+		
Y79AA1001105	27.01	7.71	19.38	6.68	4.28	6.75	6.37	6.27	6.27				
Y79AA1001142	8.95	5.63	7.03	5.98	7.11	5.88	10.76	13.80	13.8			*	+
Y79AA1001145	11.65	9.12	8.63	15.01	11.35	17.02	8.48	10.99	10.99				
Y79AA1001162	4.06	1.39	1.51	5.09	3.87	3.44	4.59	3.13	3.13				
Y79AA1001167	7.25	3.07	2.49	5.01	3.56	4.46	3.63	5.24	5.24				
Y79AA1001176	4.11	2.23	2.70	4.09	2.43	5.22	2.25	2.60	2.6				
Y79AA1001177	4.68	4.25	4.38	3.59	3.61	5.91	4.61	3.71	3.71				
Y79AA1001179	21.68	16.62	20.48	11.99	9.19	16.21	8.81	11.14	11.14	*	-	**	-
Y79AA1001185	5.31	2.79	3.61	5.39	3.59	5.46	3.84	4.29	4.29				
Y79AA1001201	28.52	17.14	23.93	16.35	22.62	37.53	18.59	26.16	26.16				
Y79AA1001205	10.97	3.75	3.90	5.2	4.84	4.63	3.49	3.72	3.72				
Y79AA1001211	11.99	5.80	6.48	8.33	12.82	9.17	4.23	4.74	4.74				
Y79AA1001212	7.31	3.41	4.24	5.88	4.00	4.88	4.13	6.49	6.49				
Y79AA1001216	55.35	32.24	33.00	52.32	49.82	57.61	27.61	40.72	40.72				
Y79AA1001228	9.47	5.39	6.44	9.83	8.83	13.70	14.26	14.88	14.88			**	+
Y79AA1001233	7.94	5.13	5.27	5.47	5.22	5.58	6.11	7.96	7.96				
Y79AA1001236	9.41	4.91	6.23	8.19	6.64	8.01	4.19	7.99	7.99				
Y79AA1001239	17.51	11.16	12.48	23.85	15.23	20.67	15.26	22.26	22.26				
Y79AA1001240	6.74	4.58	4.53	7.09	6.25	7.67	6.30	7.17	7.17				
Y79AA1001255	11.62	4.94	6.87	6.84	9.34	6.89	3.77	5.35	5.35				
Y79AA1001264	8.92	4.36	4.37	5.15	4.83	5.09	6.25	11.76	11.76				
Y79AA1001272	16.07	9.52	9.48	17.58	13.84	18.59	12.50	13.21	13.21				
Y79AA1001281	2.39	1.46	1.20	2.86	1.50	1.94	1.67	2.71	2.71				
Y79AA1001299	15.84	12.69	13.71	17.01	14.77	25.21	17.79	21.80	21.8			*	+
Y79AA1001312	7.69	3.18	3.48	9.46	10.75	7.56	6.31	5.09	5.09				
Y79AA1001319	9.18	6.58	8.51	11.43	8.41	10.88	8.28	9.95	9.95				
Y79AA1001323	5.8	3.74	3.41	4.67	5.59	4.56	4.04	5.77	5.77				
Y79AA1001328	9.21	5.33	4.01	6.44	6.42	8.24	6.73	9.42	9.42				
Y79AA1001343	862.89	462.45	576.89	529.68	551.94	571.68	1081.07	1529.21	1529			*	+
Y79AA1001351	1.98	0.57	1.69	0.7	1.23	1.95	1.38	2.51	2.51				
Y79AA1001364	13.67	8.79	10.09	17.42	16.54	19.67	6.03	14.83	14.83	*	+		
Y79AA1001367	6.28	4.16	4.34	5.94	4.67	6.56	4.76	4.90	4.9				
Y79AA1001384	1.87	1.73	1.53	1.86	1.16	2.08	1.66	1.46	1.46				
Y79AA1001391	3.6	2.56	1.82	3.57	3.95	4.39	3.23	2.67	2.67				
Y79AA1001394	7.58	3.85	2.91	6.13	4.47	4.34	2.98	3.74	3.74				
Y79AA1001402	14.12	9.28	8.02	15.91	14.24	20.22	15.90	16.49	16.49			*	+
Y79AA1001410	6.61	3.47	3.47	4.7	4.77	5.26	4.23	5.49	5.49				
Y79AA1001414	4.82	2.47	3.52	4.85	3.10	4.46	3.68	4.21	4.21				
Y79AA1001426	6.98	4.46	5.28	4.95	5.72	4.24	5.87	6.84	6.84				
Y79AA1001427	3.95	3.35	3.13	5.95	6.19	3.76	4.11	6.23	6.23				
Y79AA1001430	3.36	4.23	3.56	4.36	4.28	5.52	6.35	7.62	7.62			**	+
Y79AA1001439	4.05	2.77	2.23	5.27	3.53	5.80	5.59	7.03	7.03			**	+
Y79AA1001485	1.52	0.56	1.47	1.8	1.02	1.80	1.03	1.44	1.44				
Y79AA1001493	1.38	0.86	0.94	2.07	2.04	2.30	1.06	3.12	3.12	**	+		
Y79AA1001511	7.88	6.25	4.30	5.78	8.49	6.85	6.79	10.70	10.7				
Y79AA1001523	10.75	7.00	5.10	7.67	3.96	7.11	7.19	5.22	5.22				
Y79AA1001530	6.54	3.62	3.97	4.77	5.40	7.25	5.26	7.92	7.92				
Y79AA1001532	4.4	3.73	3.24	7.17	5.68	6.14	4.71	4.96	4.96	*	+	*	+
Y79AA1001533	5.01	4.00	3.23	3.96	6.97	7.08	2.96	4.09	4.09				
Y79AA1001541	12.19	9.13	10.66	12.21	12.80	16.01	5.59	5.41	5.41			**	-

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Y79AA1001548	10.61	7.08	4.15	16.42	14.68	15.82	9.30	9.38	9.38	*	+		
Y79AA1001555	7.52	5.37	3.80	6.53	5.95	5.70	7.04	7.00	7				
Y79AA1001562	13.12	10.40	12.01	18.73	17.97	15.42	12.97	18.83	18.83	*	+		
Y79AA1001581	2.59	2.12	1.33	2.27	2.33	1.95	1.31	2.40	2.4				
Y79AA1001585	1.89	1.52	2.52	3.13	3.14	3.51	2.68	3.89	3.89	*	+	*	+
Y79AA1001592	8.75	5.76	6.22	9.06	9.03	12.16	6.95	10.71	10.71				
Y79AA1001594	2.44	2.99	2.99	4.89	6.76	6.84	2.08	3.52	3.52	**	+		
Y79AA1001603	41.01	29.22	27.39	35.33	47.15	41.79	19.68	22.24	22.24				
Y79AA1001613	11.06	8.37	6.50	10.25	10.82	7.55	6.69	6.52	6.52				
Y79AA1001630	0.95	0.54	0.85	1.19	0.72	0.95	1.19	0.88	0.88				
Y79AA1001647	6.2	2.96	3.68	2.82	5.76	5.40	3.17	4.07	4.07				
Y79AA1001664	13.85	6.76	7.31	10.57	12.90	8.91	7.51	7.68	7.68				
Y79AA1001665	3.6	3.81	4.37	4.15	4.52	5.51	3.17	4.23	4.23				
Y79AA1001679	14	9.57	9.87	11.81	14.25	13.41	7.94	7.63	7.63				
Y79AA1001692	3.06	2.79	3.66	3.62	3.64	6.60	2.78	2.76	2.76				
Y79AA1001696	0.47	0.94	0.29	1.8	1.18	2.00	1.48	1.81	1.81	*	+	**	+
Y79AA1001705	5.59	4.16	3.52	5.12	5.14	5.00	3.05	4.02	4.02				
Y79AA1001711	17.19	10.51	9.53	37.34	40.06	24.12	26.85	27.39	27.39	*	+	**	+
Y79AA1001717	1.38	0.95	0.69	2.28	1.17	1.95	0.86	2.01	2.01				
Y79AA1001719	3.1	2.90	1.65	4.96	4.48	2.69	2.06	2.48	2.48				
Y79AA1001727	5.47	4.87	4.29	8.17	8.05	7.12	4.94	6.45	6.45	**	+		
Y79AA1001750	20.76	27.54	23.83	38.95	38.37	32.83	22.83	25.62	25.62	*	+		
Y79AA1001760	6.22	6.83	3.78	10.14	8.09	8.51	8.09	4.11	4.11	*	+		
Y79AA1001777	4.19	4.98	4.30	10.69	9.61	8.63	5.89	5.49	5.49	**	+	*	+
Y79AA1001781	1.41	(0.02)	0.49	0.49	0.41	1.88	0.28	0.56	0.56				
Y79AA1001787	6.73	4.26	4.09	6.64	5.23	7.45	4.25	5.24	5.24				
Y79AA1001793	7.3	4.12	4.31	5.83	5.04	3.68	5.12	4.48	4.48				
Y79AA1001795	3	0.80	2.09	2.69	3.85	3.29	1.73	3.18	3.18				
Y79AA1001799	5.26	2.91	2.67	5.21	5.65	6.10	3.13	5.77	5.77				
Y79AA1001800	4.16	2.57	3.82	5.16	2.55	3.90	3.53	6.79	6.79				
Y79AA1001801	6.56	3.89	3.46	8.87	3.49	7.02	3.18	4.68	4.68				
Y79AA1001803	6.72	4.12	3.95	5.51	7.22	5.68	5.48	5.55	5.55				
Y79AA1001805	22.35	9.91	10.35	15.2	27.86	21.20	9.25	13.14	13.14				
Y79AA1001807	6.96	2.99	4.40	6.3	4.51	3.72	4.95	5.25	5.25				
Y79AA1001827	8.38	3.69	5.67	7.55	7.81	11.23	9.11	12.46	12.46			*	+
Y79AA1001846	4.45	2.15	3.75	6.2	4.92	5.41	3.96	7.82	7.82				
Y79AA1001848	2.85	1.48	2.40	3.01	2.43	2.61	2.57	2.46	2.46				
Y79AA1001853	13.89	10.72	11.89	14.4	8.43	13.46	12.95	13.31	13.31				
Y79AA1001863	15.14	7.58	9.41	15.02	11.89	14.02	8.02	12.33	12.33				
Y79AA1001866	9.57	4.75	5.85	11.97	24.49	9.54	5.28	9.21	9.21				
Y79AA1001874	1.66	0.73	0.26	0.48	1.10	0.61	0.67	0.63	0.63				
Y79AA1001875	9	6.56	7.74	8.02	10.17	8.54	9.22	11.36	11.36			*	+
Y79AA1001907	117.42	47.16	76.24	98.59	98.47	94.40	33.03	51.77	51.77				
Y79AA1001908	2.02	0.84	1.62	1.52	1.88	1.08	1.03	1.18	1.18				
Y79AA1001923	4.54	1.74	1.64	1.87	1.96	1.62	3.56	1.90	1.9				
Y79AA1001927	7.1	4.39	6.61	6.81	4.65	6.65	7.02	7.63	7.63				
Y79AA1001930	11.14	5.72	8.19	8.38	8.79	9.40	6.07	5.53	5.53				
Y79AA1001932	4.55	2.74	2.35	3.75	4.07	2.57	2.61	2.55	2.55				
Y79AA1001933	5.44	2.77	4.71	4.94	5.23	2.92	4.54	4.08	4.08				
Y79AA1001942	5.27	2.57	3.54	3.47	2.89	2.27	3.23	4.03	4.03				
Y79AA1001963	16.6	6.83	11.89	12.17	15.10	11.74	8.04	11.18	11.18				
Y79AA1001968	19.06	9.81	14.73	19.14	20.00	14.84	13.89	19.22	19.22				
Y79AA1001983	8.12	2.93	5.67	4.13	3.77	4.79	3.53	4.78	4.78				
Y79AA1002000	8.2	3.32	3.60	7.79	5.70	5.11	5.48	4.05	4.05				
Y79AA1002004	31.21	14.32	20.67	18.62	19.17	22.54	12.67	21.19	21.19				
Y79AA1002008	6.53	5.69	5.73	9.64	7.46	8.70	4.99	6.08	6.08	*	+		

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Table 348

Y79AA1002012	3.88	1.69	1.78	4.4	6.99	4.19	2.25	2.80	2.8				
Y79AA1002017	4.13	2.53	3.93	3.44	3.03	1.90	3.46	3.57	3.57				
Y79AA1002022	14.79	9.29	9.45	11.91	10.49	14.24	13.65	16.25	16.25				
Y79AA1002027	2.08	0.73	0.78	2.44	1.84	1.40	2.55	2.70	2.7			*	+
Y79AA1002050	9.08	4.52	6.60	9.28	6.06	9.49	5.33	7.52	7.52				
Y79AA1002058	11.36	5.78	6.33	12.51	9.30	13.02	7.69	9.93	9.93				
Y79AA1002060	25.88	13.74	19.34	20.14	18.93	22.49	14.01	18.58	18.58				
Y79AA1002062	13.71	6.57	6.87	16.86	16.66	14.29	6.71	8.83	8.83	*	+		
Y79AA1002065	12.17	6.23	5.09	7.95	5.75	3.68	6.63	7.77	7.77				
Y79AA1002067	14.5	8.32	9.44	2.21	3.03	2.42	3.46	4.06	4.06	*	-	*	-
Y79AA1002069	7.51	3.78	4.23	4.94	4.88	2.84	3.88	6.24	6.24				
Y79AA1002070	60.51	38.18	52.01	44.77	31.84	34.13	26.73	37.56	37.56				
Y79AA1002074	151.4	80.88	106.02	132.97	122.53	136.83	70.79	85.36	85.36				
Y79AA1002076	2.73	1.63	2.34	2.2	2.35	2.60	2.59	2.75	2.75				
Y79AA1002083	5	2.28	2.46	3.91	2.83	3.75	3.56	3.71	3.71				
Y79AA1002084	5.09	3.13	3.51	5.26	3.68	3.36	3.65	3.99	3.99				
Y79AA1002086	7.09	2.92	3.98	4.7	3.74	3.75	3.43	4.46	4.46				
Y79AA1002087	17.27	8.44	10.83	14.51	15.32	11.91	7.90	9.56	9.56				
Y79AA1002089	5.98	2.23	2.36	4.43	5.76	5.05	4.46	3.99	3.99				
Y79AA1002093	4.42	1.41	2.73	3.3	2.91	3.64	2.40	3.24	3.24				
Y79AA1002101	7.66	3.43	4.43	3.23	2.81	2.96	1.93	9.08	9.08				
Y79AA1002103	9.64	4.31	6.49	12.68	13.50	19.90	7.83	9.63	9.63	*	+		
Y79AA1002115	6.16	3.44	3.46	8.76	8.88	8.21	5.06	7.31	7.31	*	+		
Y79AA1002121	4.13	1.90	2.75	5.52	3.99	4.66	2.99	2.94	2.94				
Y79AA1002125	12.29	7.02	6.63	8.98	11.00	7.52	5.97	9.22	9.22				
Y79AA1002129	4.01	2.55	2.79	4.98	5.25	5.00	4.03	4.07	4.07	*	+		
Y79AA1002131	3.98	1.83	2.10	2.08	2.08	3.32	2.24	4.89	4.89				
Y79AA1002139	1.73	1.39	1.53	2.67	1.39	3.06	1.75	4.33	4.33				
Y79AA1002144	13.61	9.16	11.69	45.27	42.86	41.51	20.24	31.90	31.9	**	+	*	+
Y79AA1002177	11.17	7.99	8.29	8.46	8.96	11.14	8.89	10.57	10.57				
Y79AA1002183	20.7	16.65	16.79	14.07	13.54	11.10	9.93	9.44	9.44	*	-	**	-
Y79AA1002202	16.44	8.10	6.76	14	14.11	9.08	7.13	7.42	7.42				
Y79AA1002204	6.31	4.49	4.52	4.3	4.77	3.13	5.10	6.00	6				
Y79AA1002206	3.17	2.15	1.77	3.09	3.03	2.45	3.04	3.50	3.5				
Y79AA1002208	5.15	2.57	2.96	5.99	4.60	5.97	4.50	4.63	4.63				
Y79AA1002209	3.58	4.01	5.76	4.15	3.13	3.39	4.99	7.55	7.55				
Y79AA1002210	3.18	1.43	2.37	3.02	2.02	1.71	2.10	2.41	2.41				
Y79AA1002211	4.91	3.46	4.17	4.11	5.81	4.91	5.34	5.38	5.38			*	+
Y79AA1002213	3.71	2.49	1.89	7.09	8.26	4.18	2.61	4.10	4.1	*	+		
Y79AA1002215	12.98	6.72	6.55	11.46	10.70	7.31	10.62	11.29	11.29				
Y79AA1002220	3.6	0.24	1.50	2.1	2.24	1.13	3.21	3.17	3.17				
Y79AA1002226	15.84	9.35	12.55	20.91	22.33	23.57	11.78	20.18	20.18	**	+		
Y79AA1002229	6.49	3.85	3.45	4.63	4.19	3.44	5.38	5.16	5.16				
Y79AA1002234	3.86	2.44	4.84	4.04	4.91	5.32	5.97	5.64	5.64			*	+
Y79AA1002235	1.93	0.75	1.35	1.7	1.20	2.27	2.65	2.05	2.05				
Y79AA1002246	2.63	2.09	2.74	2.5	3.97	3.37	2.34	1.90	1.9				
Y79AA1002258	3.31	3.27	3.40	4.93	5.68	4.75	4.02	4.20	4.2	**	+	**	+
Y79AA1002279	4.56	2.57	2.26	6.13	5.09	3.71	4.81	5.29	5.29				
Y79AA1002292	6.26	3.04	2.73	4.57	5.32	3.62	2.90	5.67	5.67				
Y79AA1002298	1.82	0.51	1.99	1.65	1.57	1.30	1.17	0.87	0.87				
Y79AA1002307	5.23	1.97	1.83	2.94	3.94	2.54	2.69	3.59	3.59				
Y79AA1002309	1.73	1.34	1.76	1.52	3.43	2.98	1.67	1.76	1.76				
Y79AA1002311	4.03	2.76	3.87	5	3.49	3.66	2.61	6.69	6.69				
Y79AA1002334	2.47	4.14	2.46	2.65	3.80	4.63	2.18	3.21	3.21				
Y79AA1002351	3.38	3.58	4.03	5.8	3.67	5.58	3.56	6.63	6.63				
Y79AA1002355	7.23	3.03	2.25	63.68	74.46	52.07	46.06	44.44	44.44	**	+	**	+

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Table 349

Y79AA1002361	5.46	3.35	2.57	6.5	7.83	6.14	2.75	4.60	4.6	*	+		
Y79AA1002365	1.93	1.66	1.86	2.93	2.21	2.54	1.34	2.05	2.05	*	+		
Y79AA1002373	3.38	1.43	1.37	3.37	3.29	2.38	2.95	2.21	2.21				
Y79AA1002376	434.81	300.04	466.40	120.28	171.61	120.00	316.81	454.58	454.6	**	-		
Y79AA1002378	5.45	6.92	5.32	7.99	10.13	8.03	4.87	4.92	4.92	*	+		
Y79AA1002381	11.63	11.08	9.56	16.28	16.98	14.53	7.89	7.01	7.01	**	+	**	-
Y79AA1002388	4.34	4.47	7.01	11.41	12.79	9.45	5.70	6.37	6.37	*	+		
Y79AA1002399	4.43	1.48	1.47	4.2	2.82	2.25	3.39	3.35	3.35				
Y79AA1002407	1.81	1.09	1.32	2.36	2.58	2.43	1.55	2.35	2.35	**	+		
Y79AA1002413	15.88	6.76	10.60	19.95	26.46	17.33	9.58	12.56	12.56				
Y79AA1002416	5.12	2.89	2.97	4.45	4.32	5.10	4.13	4.19	4.19				
Y79AA1002429	2.82	1.17	1.77	2.75	1.85	2.91	4.10	5.62	5.62			*	+
Y79AA1002431	4.04	2.82	3.86	2.55	4.38	4.86	4.06	5.56	5.56	-			
Y79AA1002433	11.76	5.78	6.28	9.49	4.53	7.78	4.34	8.17	8.17				
Y79AA1002445	10.95	9.11	9.11	11.15	8.78	14.80	10.37	11.14	11.14				
Y79AA1002461	10.04	5.58	4.92	9.55	8.99	8.05	5.89	7.75	7.75				
Y79AA1002466	22.18	13.94	11.33	23.59	18.02	25.25	10.79	17.76	17.76				
Y79AA1002471	5.76	3.00	5.65	6.94	8.49	9.26	5.31	7.89	7.89	*	+		
Y79AA1002472	12.12	5.83	9.20	16.86	14.60	20.34	6.74	12.38	12.38	*	+		
Y79AA1002474	3.46	0.84	1.92	1.74	1.49	1.64	2.77	1.35	1.35				
Y79AA1002482	13.92	8.55	11.10	23.82	23.90	29.62	10.40	14.99	14.99	**	+		
Y79AA1002487	1.72	0.87	1.11	1.3	1.59	1.75	1.57	1.93	1.93				
Y79AA1002490	13.58	4.80	6.45	5.13	6.72	3.78	4.31	7.19	7.19				
Y79AA1002493	5.77	2.96	3.11	8.04	10.37	7.90	4.77	5.75	5.75	*	+		
ZRV6C1006278	1.43	0.95	1.01	1.16	2.05	0.47	1.35	2.06	2.06				

[0245] The correspondence of the full-length nucleotide sequences of the present invention and the corresponding deduced amino acid sequences with the clone names are shown below.

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Table 350

clone name	name of full-length nucleotide sequence	SEQ ID of full-length nucleotide sequence	SEQ ID of deduced amino acid sequence
HEMBA1000005	C-HEMBA1000005	10468	10469
HEMBA1000030	C-HEMBA1000030	10470	
HEMBA1000046	C-HEMBA1000046	10471	
HEMBA1000050	C-HEMBA1000050	10472	
HEMBA1000076	C-HEMBA1000076	10473	10474
HEMBA1000156	C-HEMBA1000156	10475	10476
HEMBA1000158	C-HEMBA1000158	10477	10478
HEMBA1000168	C-HEMBA1000168	10479	10480
HEMBA1000185	C-HEMBA1000185	10481	10482
HEMBA1000193	C-HEMBA1000193	10483	10484
HEMBA1000227	C-HEMBA1000227	10485	10486
HEMBA1000288	C-HEMBA1000288	10487	
HEMBA1000302	C-HEMBA1000302	10488	
HEMBA1000304	C-HEMBA1000304	10489	10490
HEMBA1000307	C-HEMBA1000307	10491	10492
HEMBA1000369	C-HEMBA1000369	10493	10494
HEMBA1000387	C-HEMBA1000387	10495	
HEMBA1000392	C-HEMBA1000392	10496	
HEMBA1000460	C-HEMBA1000460	10497	
HEMBA1000488	C-HEMBA1000488	10498	10499
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NT2RM2000624	C-NT2RM2000624	11103	11104
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OVARC1000035	C-OVARC1000035	12402	
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OVARC1000151	C-OVARC1000151	12414	12415
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OVARC1000347	C-OVARC1000347	12435	
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OVARC1000605	C-OVARC1000605	12463	12464
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OVARC1001038	C-OVARC1001038	12477	12478
OVARC1001065	C-OVARC1001065	12479	12480
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OVARC1001381	C-OVARC1001381	12486	12487
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PLACE1000005	C-PLACE1000005	12490	
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PLACE1010102	C-PLACE1010102	13218	
PLACE1010105	C-PLACE1010105	13219	13220
PLACE1010106	C-PLACE1010106	13221	
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PLACE1010148	C-PLACE1010148	13224	13225
PLACE1010194	C-PLACE1010194	13226	13227
PLACE1010202	C-PLACE1010202	13228	13229
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PLACE1010547	C-PLACE1010547	13252	13253
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Table 351

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HEMBA1000545	C-HEMBA1000545	13332	
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HEMBA1000749	C-HEMBA1000749	13344	
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HEMBA1000773	C-HEMBA1000773	13346	
HEMBA1000774	C-HEMBA1000774	13347	
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HEMBA1001330	C-HEMBA1001330	13368	
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HEMBA1001866	C-HEMBA1001866	13391	13392
HEMBA1001910	C-HEMBA1001910	13393	
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HEMBA1001921	C-HEMBA1001921	13396	13397
HEMBA1001939	C-HEMBA1001939	13398	13399
HEMBA1001950	C-HEMBA1001950	13400	13401
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HEMBA1002102	C-HEMBA1002102	13408	13409
HEMBA1002150	C-HEMBA1002150	13410	13411
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HEMBA1002189	C-HEMBA1002189	13414	
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HEMBA1003556	C-HEMBA1003556	13445	13446

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	HEMBA1003692	C-HEMBA1003692	13451	13452
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	HEMBA1003725	C-HEMBA1003725	13454	
	HEMBA1003729	C-HEMBA1003729	13455	13456
	HEMBA1003758	C-HEMBA1003758	13457	
	HEMBA1003773	C-HEMBA1003773	13458	13459
	HEMBA1003783	C-HEMBA1003783	13460	13461
	HEMBA1003799	C-HEMBA1003799	13462	
	HEMBA1003804	C-HEMBA1003804	13463	13464
	HEMBA1003805	C-HEMBA1003805	13465	13466
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	HEMBA1003856	C-HEMBA1003856	13469	
	HEMBA1003866	C-HEMBA1003866	13470	13471
	HEMBA1003879	C-HEMBA1003879	13472	
	HEMBA1003880	C-HEMBA1003880	13473	
	HEMBA1003893	C-HEMBA1003893	13474	13475
	HEMBA1003908	C-HEMBA1003908	13476	
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	HEMBA1003942	C-HEMBA1003942	13478	
	HEMBA1003958	C-HEMBA1003958	13479	
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	HEMBA1004038	C-HEMBA1004038	13486	13487
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	HEMBA1004048	C-HEMBA1004048	13489	13490
	HEMBA1004111	C-HEMBA1004111	13491	
	HEMBA1004131	C-HEMBA1004131	13492	13493
	HEMBA1004138	C-HEMBA1004138	13494	
	HEMBA1004143	C-HEMBA1004143	13495	13496
	HEMBA1004150	C-HEMBA1004150	13497	
	HEMBA1004168	C-HEMBA1004168	13498	13499
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	HEMBA1004202	C-HEMBA1004202	13501	13502

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HEMBA1007319	C-HEMBA1007319	13744	13745
HEMBA1007320	C-HEMBA1007320	13746	13747
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HEMBA1007347	C-HEMBA1007347	13749	

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HEMBB1000556	C-HEMBB1000556	13767	13768
HEMBB1000586	C-HEMBB1000586	13769	
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HEMBB1001302	C-HEMBB1001302	13793	13794
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THYRO1000070	C-THYRO1000070	18212	18213
THYRO1000072	C-THYRO1000072	18214	18215
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THYRO1000197	C-THYRO1000197	18222	18223
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PLACE1011896	C-PLACE1011896	18861	18862
PLACE2000003	C-PLACE2000003	18863	
PLACE2000132	C-PLACE2000132	18864	18865
PLACE2000170	C-PLACE2000170	18866	
PLACE2000335	C-PLACE2000335	18867	18868

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PLACE3000124	C-PLACE3000124	18869	18870
PLACE3000158	C-PLACE3000158	18871	
PLACE3000207	C-PLACE3000207	18872	
PLACE3000221	C-PLACE3000221	18873	18874
PLACE3000271	C-PLACE3000271	18875	18876
PLACE3000304	C-PLACE3000304	18877	
PLACE3000322	C-PLACE3000322	18878	18879
PLACE3000341	C-PLACE3000341	18880	
PLACE3000373	C-PLACE3000373	18881	18882
PLACE3000399	C-PLACE3000399	18883	18884
PLACE3000401	C-PLACE3000401	18885	
PLACE3000402	C-PLACE3000402	18886	
PLACE3000406	C-PLACE3000406	18887	18888
PLACE3000475	C-PLACE3000475	18889	
PLACE4000063	C-PLACE4000063	18890	18891
PLACE4000093	C-PLACE4000093	18892	
PLACE4000100	C-PLACE4000100	18893	18894
PLACE4000247	C-PLACE4000247	18895	18896
PLACE4000250	C-PLACE4000250	18897	18898
PLACE4000252	C-PLACE4000252	18899	18900
PLACE4000259	C-PLACE4000259	18901	18902
PLACE4000320	C-PLACE4000320	18903	
PLACE4000344	C-PLACE4000344	18904	
PLACE4000367	C-PLACE4000367	18905	18906
PLACE4000401	C-PLACE4000401	18907	18908
PLACE4000411	C-PLACE4000411	18909	18910
PLACE4000487	C-PLACE4000487	18911	18912
PLACE4000494	C-PLACE4000494	18913	18914
PLACE4000521	C-PLACE4000521	18915	18916
PLACE4000548	C-PLACE4000548	18917	18918
SKNMC1000013	C-SKNMC1000013	18919	18920
SKNMC1000091	C-SKNMC1000091	18921	18922
THYRO1000343	C-THYRO1000343	18923	18924
THYRO1000569	C-THYRO1000569	18925	18926
THYRO1001142	C-THYRO1001142	18927	
THYRO1001189	C-THYRO1001189	18928	18929
THYRO1001320	C-THYRO1001320	18930	18931
THYRO1001537	C-THYRO1001537	18932	18933
THYRO1001721	C-THYRO1001721	18934	18935

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THYR01001828	C-THYR01001828	18936	18937
Y79AA1000346	C-Y79AA1000346	18938	18939
Y79AA1001167	C-Y79AA1001167	18940	
Y79AA1001384	C-Y79AA1001384	18941	18942
Y79AA1001875	C-Y79AA1001875	18943	
Y79AA1002103	C-Y79AA1002103	18944	18945
HEMBA1000290	C-HEMBA1000290	18946	
HEMBA1001196	C-HEMBA1001196	18947	18948
HEMBA1006650	C-HEMBA1006650	18949	18950
HEMBA1006796	C-HEMBA1006796	18951	18952
HEMBB1000337	C-HEMBB1000337	18953	18954
HEMBB1001619	C-HEMBB1001619	18955	
MAMMA1000270	C-MAMMA1000270	18956	
MAMMA1000559	C-MAMMA1000559	18957	
MAMMA1000940	C-MAMMA1000940	18958	
MAMMA1002545	C-MAMMA1002545	18959	
MAMMA1002972	C-MAMMA1002972	18960	18961
NT2RP2001440	C-NT2RP2001440	18962	18963
NT2RP3002770	C-NT2RP3002770	18964	18965
NT2RP3003138	C-NT2RP3003138	18966	18967
NT2RP3004470	C-NT2RP3004470	18968	
OVARC1000891	C-OVARC1000891	18969	
PLACE1001545	C-PLACE1001545	18970	18971
PLACE1003383	C-PLACE1003383	18972	
PLACE1005549	C-PLACE1005549	18973	18974
PLACE1008455	C-PLACE1008455	18975	
PLACE4000131	C-PLACE4000131	18976	18977
PLACE4000261	C-PLACE4000261	18978	18979
THYR01001602	C-THYR01001602	18980	
HEMBA1006092	C-HEMBA1006092	18981	
HEMBA1006406	C-HEMBA1006406	18982	
HEMBB1000790	C-HEMBB1000790	18983	
HEMBB1000917	C-HEMBB1000917	18984	
HEMBB1002280	C-HEMBB1002280	18985	
MAMMA1000802	C-MAMMA1000802	18986	
MAMMA1001322	C-MAMMA1001322	18987	
MAMMA1002597	C-MAMMA1002597	18988	
MAMMA1002868	C-MAMMA1002868	18989	
NT2RP2003161	C-NT2RP2003161	18990	18991

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NT2RP2003339	C-NT2RP2003339	18992	
NT2RP3001282	C-NT2RP3001282	18993	18994
PLACE1001761	C-PLACE1001761	18995	18996
PLACE1004491	C-PLACE1004491	18997	
PLACE1004686	C-PLACE1004686	18998	
PLACE1005574	C-PLACE1005574	18999	
PLACE1006382	C-PLACE1006382	19000	
PLACE1006792	C-PLACE1006792	19001	
PLACE3000455	C-PLACE3000455	19002	19003
PLACE4000230	C-PLACE4000230	19004	19005
THYR01000916	C-THYR01000916	19006	
HEMBA1000327	C-HEMBA1000327	19007	19008
HEMBB1000637	C-HEMBB1000637	19009	19010
HEMBB1001967	C-HEMBB1001967	19011	
MAMMA1000266	C-MAMMA1000266	19012	
NT2RP2002979	C-NT2RP2002979	19013	
PLACE1007866	C-PLACE1007866	19014	19015
PLACE3000350	C-PLACE3000350	19016	19017
PLACE4000156	C-PLACE4000156	19018	19019
THYR01001637	C-THYR01001637	19020	19021
MAMMA1002215	C-MAMMA1002215	19022	19023
MAMMA1002721	C-MAMMA1002721	19024	
NT2RP2002070	C-NT2RP2002070	19025	

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Table 352

Expression of each cDNA in synovial cells or in the synovial cells in the presence of TNF (This table also contains clones without description in Examples)

In the table, Synoviocyte and Synoviocyte_TNF represent synovial cells and TNF-treated synovial cells, respectively. The assay was performed in triplicate (n=3), and each result is shown in the column of exp.1, exp.2, or exp.3. In addition, "t-test vs TNF" represents a result of test for significance of difference between the untreated synovial cells and the TNF-treated synovial cells. The increase and decrease in the expression level of a particular gene in response to TNF are represented by + and -, respectively. The results of test for significance of difference are shown in the columns of *:p<0.05 and **:p<0.01.

Clone	Synoviocyte			Synoviocute_TNF			t test vs TNF	INC. and DEC.
	exp. 1	exp. 2	exp. 3	exp. 1	exp. 2	exp. 3		

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	GAPDH(Cr1)	0.4	0.8	0.89	0.9	1	1.15	
	βactin(Cr2)	385.94	262.23	582.98	443.28	422.61	573.47	
	ADRGL1000005	2.72	2.97	4.46	7.27	7.45	3.51	
	ADRGL1000007	4.36	5.19	9.58	20.78	19.59	18.29	** +
	ADRGL1000009	0.99	1.25	1.64	2.16	4.08	2.02	
	ADRGL1000011	1.98	3.56	5.24	22.22	23.49	19.81	** +
	ADRGL1000027	0.79	1.22	1.66	2.82	4.99	1.9	
	ADRGL1000058	4.12	7.08	26.9	62.55	67.32	49.15	** +
	ADRGL1000069	1.91	1.68	2.47	14.19	14.54	13.74	** +
	ADRGL1000077	1.98	2	2.54	5.5	2.9	4.16	
	ADRGL1000092	2.99	4.79	12.53	21.46	22.09	26.19	** +
	ADRGL1000099	2.77	4.79	12.85	23.61	24.02	25.56	** +
	ADRGL1000136	20.49	27.18	31.85	62.44	40.69	48.29	* +
	ADRGL1000147	2.09	2.58	5.47	5.69	7.52	3.85	
	ADRGL1000159	1.51	1.77	3.07	3.4	4.71	2.59	
	ADRGL1000160	2.42	4.34	6.89	8.08	7.24	7.06	
	ADRGL1000171	0.95	1.11	1.64	1.89	2.69	1.87	
	ADRGL1000181	0.64	1.37	1.74	3.99	4.27	3.89	** +
	BGGI11000015	2.13	3.89	5.02	10.49	11.35	9.14	** +
	BGGI11000016	27.77	35.71	52.17	57.18	48.51	63.57	
	BGGI11000017	1.29	3.19	3.14	3.24	3.65	2.34	
	BGGI11000022	4.72	4.45	6.75	10.71	5.56	8.27	
	BGGI11000031	4.47	6.58	8.77	14.79	11.63	10.04	* +
	BGGI11000042	9.55	11.29	20.54	23.39	18.75	20.23	
	BGGI11000046	8.56	9.77	17.04	34.24	30.76	25.79	** +
	BNGH41000020	246.16	211.77	380.83	658.32	647.37	559.16	** +
	BNGH41000025	4.31	3.12	6.92	11.4	13.1	15.01	** +
	BNGH41000026	2.71	4.77	7.53	4.45	7.17	6.23	
	BNGH41000027	11.52	13.5	12.69	20.62	12.48	24.91	
	BNGH41000035	23.02	25.91	36.46	51.05	31.83	41.67	
	BNGH41000037	2.7	5.21	6.72	12.95	8.98	8.59	* +
	BNGH41000042	14.55	16.06	22.84	49.62	37.57	36.25	** +
	BNGH41000048	3.92	6.27	25.68	66.19	74.4	66.21	** +
	BNGH41000056	0.74	1.75	3.26	5.28	7.34	3.75	* +
	BNGH41000087	3.36	4.08	5.19	5.59	8.15	3.01	
	BNGH41000091	0.18	1.45	2.47	2.72	3.4	2.14	
	BNGH41000157	6.93	7.99	6.23	13.37	10.28	9.98	* +
	BNGH41000169	1.09	1.53	2.99	2.77	4.23	2.59	
	BNGH41000181	3.5	4.06	7.5	5.71	6.81	6.09	

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BNGH41000198	1.32	2.3	4.35	2.06	2.55	2.22		
BNGH41000219	2.29	3.91	5.61	12.4	13.73	10.76	**	+
BNGH41000229	9.65	9.99	12.99	18.34	18.92	18.94	**	+
BNGH41000237	8.4	12.99	12.61	27.63	11.26	13.45		
BNGH41000238	1.56	2.59	6.77	3.45	4.55	3.32		
BNGH41000243	5.56	8.95	6.71	15.03	12.55	16.36	**	+
BNGH41000270	2.94	2.77	2.88	3.67	3.99	3.74	**	+
BRAWH1000004	1	2.19	6.99	6.45	8.36	6		
BRAWH1000018	1.8	2.24	5.06	4.43	6.95	5.24		
BRAWH1000021	1.33	2.73	4.81	4.16	5.85	5.21		
BRAWH1000027	0.58	1.7	1.62	2.39	3.65	2.63	*	+
BRAWH1000029	2.32	3.63	6.21	6.03	6.73	4.81		
BRAWH1000040	4.68	4.98	8.01	7.28	7.2	8.67		
BRAWH1000050	11.04	10.47	43.79	51.7	73.7	60.92	*	+
BRAWH1000051	2.14	0.63	2.71	2.25	4.43	1.04		
BRAWH1000060	7.84	8.07	48.26	59.16	66.12	63.86	*	+
BRAWH1000075	1.85	1.86	2.98	2.07	4.4	2.34		
BRAWH1000081	1.88	2.78	7.19	5.9	10.82	7.4		
BRAWH1000084	30.23	30.57	65.21	235.81	180.86	211.35	**	+
BRAWH1000095	1.38	2.47	4.51	3	4.78	2.67		
BRAWH1000096	1.37	2.89	4.71	3.7	4.8	5.17		
BRAWH1000097	3.32	3.27	10.74	9.24	10.62	7.75		
BRAWH1000100	4.77	5.19	7.69	6.98	7.06	7.28		
BRAWH1000101	12	12.04	36.52	46.19	41.09	50.21	*	+
BRAWH1000104	1.37	0.92	4.33	1.47	4.47	2.41		
BRAWH1000107	0.62	1.88	2.48	2.43	5.03	3.15		
BRAWH1000110	4.4	4.06	16.81	13.87	11.1	15.74		
BRAWH1000111	3.98	6.14	6.05	8.85	8.95	10.64	*	+
BRAWH1000135	4.95	4.91	7.7	7.37	9.42	9.98		
BRAWH1000190	2.22	3.84	5.07	4.66	7.16	4.99		
HEMBA1000005	5.91	6.44	11.97	17.55	22.88	18.65	*	+
HEMBA1000006	2.61	3.17	4.64	3.08	8.49	4.75		
HEMBA1000012	10.97	11.75	51.07	71.4	106.82	74.8	*	+
HEMBA1000020	50.65	49.12	113.3	197.41	293.79	216.89	*	+
HEMBA1000030	1.93	3.08	4.67	5.72	3.62	6.43		
HEMBA1000034	3.27	3.21	5.35	4.62	10.29	6.85		
HEMBA1000042	1.64	3.17	6	4.72	6.92	8.12		
HEMBA1000045	7.13	9.44	11.07	9.55	14.43	10.44		
HEMBA1000046	1.14	2.24	2.77	3.73	5.3	4.34	*	+

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HEMBA1000047	1.17	1.99	3.83	2.98	4.47	3.78		
HEMBA1000048	3.76	4.75	3.64	8.73	12.38	5.48		
HEMBA1000050	0.48	1.77	1.78	1.4	3.39	1.46		
HEMBA1000053	1.64	1.28	2.57	4.68	4.03	3.99	**	+
HEMBA1000060	1.88	2.71	4.51	7.29	7.94	9.74	**	+
HEMBA1000072	52.79	53.46	135.73	165.97	221.75	230.97	*	+
HEMBA1000073	16.54	11.43	27.32	22.4	36.09	33.78		
HEMBA1000076	5.06	5.33	9.77	12.16	10.46	11.15	*	+
HEMBA1000084	4.75	4.46	20.71	30.15	43.67	33.92	*	+
HEMBA1000087	0.51	1	3.32	0.65	2.82	1.61		
HEMBA1000088	1.98	2.97	4.6	6.2	9.87	8.46	*	+
HEMBA1000091	6.36	5.4	17.56	30.15	44.04	35.43	**	+
HEMBA1000111	1.52	1.77	3.63	5.29	6.65	6.4	**	+
HEMBA1000121	0.86	1.17	3.58	3.52	4.47	5.83		
HEMBA1000128	1.52	2.99	6.04	4.28	6.05	5.93		
HEMBA1000129	2.04	1.81	3.95	2.66	3.26	3.32		
HEMBA1000141	2.31	3.45	5.98	3.56	6.67	5.6		
HEMBA1000146	0.84	1.29	2.96	1.93	4.98	3.52		
HEMBA1000150	3.34	3.29	10.65	8.27	11.97	9.46		
HEMBA1000154	25.17	29.21	82.33	128.3	134.42	139.59	**	+
HEMBA1000156	3.28	4	5.87	8.69	6.19	6.13		
HEMBA1000158	7.98	10.04	12.52	16.99	15.47	12.88		
HEMBA1000168	1.21	2.2	4.11	5.7	7.3	5.21	*	+
HEMBA1000180	0.4	2.04	2.87	2.86	4.06	2.05		
HEMBA1000185	1.65	3.84	4.88	7.5	9.46	9.07	**	+
HEMBA1000188	1.37	1.64	3.31	4.94	4.19	3.35		
HEMBA1000193	1.53	0.66	3.16	2.68	4.33	2.5		
HEMBA1000194	2.18	2.95	5.68	9.11	8.74	8.83	**	+
HEMBA1000201	2.6	4.47	9.74	13.45	14.8	14.65	*	+
HEMBA1000213	1.33	1.95	2.76	2.08	4.49	3.7		
HEMBA1000216	1.26	1.82	3.27	2.92	5.2	3.47		
HEMBA1000227	0.99	2.27	2.38	3.28	4.21	1.83		
HEMBA1000231	1.5	1.97	5	7.56	7.19	6.16	*	+
HEMBA1000237	4.5	6.13	9.14	14.79	18.3	14.71	**	+
HEMBA1000243	0.6	1.89	3.01	4.3	4.34	3.67	*	+
HEMBA1000244	1.54	2.45	3.78	6.08	5.58	3.36		
HEMBA1000251	1.15	1.92	2.97	2.26	4.59	3.22		
HEMBA1000254	0.69	1.8	4.81	3.57	4.97	3.58		
HEMBA1000264	0.84	2.28	3.01	2.84	3.23	3.12		

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HEMBA1000269	1.9	2.34	3.69	4.41	4.09	2.51		
HEMBA1000275	5.31	4.29	8.03	7.96	12.04	8.54		
HEMBA1000280	1.43	0.83	2.19	3.3	4.08	4	**	+
HEMBA1000282	1.15	1.01	4.23	6.29	7.01	5.46	*	+
HEMBA1000287	2.86	3.19	4.45	5.81	6.04	6.37	**	+
HEMBA1000288	1.37	2.23	6.13	3.51	6.02	3.85		
HEMBA1000290	1.01	2.17	4.11	2.46	3.26	2.73		
HEMBA1000296	2.4	3.66	5.49	6.15	6.55	5.84		
HEMBA1000300	1.22	2.73	6.6	7.64	8.88	7.23		
HEMBA1000302	0.93	2.17	2.86	3.04	3.74	1.97		
HEMBA1000303	1.36	2.15	3.57	4.13	4.43	3		
HEMBA1000304	1.06	1.99	4.26	5.51	7.28	4.87	*	+
HEMBA1000307	1.21	1.73	2.65	4.4	5.64	2.99	*	+
HEMBA1000312	6	8.7	10.77	13.2	9.18	9.65		
HEMBA1000318	1.5	4.22	3.25	5.39	6.05	4.49		
HEMBA1000327	2.18	3.7	3.34	10.58	6.06	6.02	*	+
HEMBA1000333	0.68	2.75	4.33	3.12	4.74	2.98		
HEMBA1000338	1.61	2.84	5.33	5.8	5.78	4.32		
HEMBA1000343	1.79	3.5	3.69	5.55	6.7	3.99		
HEMBA1000349	0.97	1.52	3.24	3.9	5.37	4.09	*	+
HEMBA1000351	1.6	2.06	5.75	4.8	6.22	5.24		
HEMBA1000355	1.52	3.09	4.09	3.78	5.14	3.59		
HEMBA1000356	9.3	10.42	14.39	26.93	22.26	24.97	**	+
HEMBA1000357	1.88	2.11	4.76	3.81	5.7	4.62		
HEMBA1000366	1.67	1.94	3.83	3.14	4.75	3.28		
HEMBA1000369	1.87	2.94	5.17	2.82	5.2	4.56		
HEMBA1000370	2.45	3.4	4.63	3.75	5.34	3.6		
HEMBA1000376	3.64	4.55	14.48	26.69	29.98	28.36	**	+
HEMBA1000387	2.95	3.19	6.2	7.85	7.62	8.15	*	+
HEMBA1000389	2.88	3.74	8.83	14.4	10.9	13.61	*	+
HEMBA1000390	1.86	2.27	3.5	4.28	4.98	3.95	*	+
HEMBA1000392	1.49	1.4	3.06	2.58	3.78	1.94		
HEMBA1000396	1.82	2.16	3.45	3.43	4.93	3.34		
HEMBA1000411	1.01	1.41	4.49	1.94	4.41	2.21		
HEMBA1000418	2.85	3.21	4.41	7.75	6.81	5.17	*	+
HEMBA1000422	0.99	1.89	2.14	2.64	4.03	2.89		
HEMBA1000428	0.36	2.43	3.09	2.58	3.31	2.75		
HEMBA1000434	0.54	2.19	2.93	2.11	3.6	2.69		
HEMBA1000442	0.82	2.2	3.37	2.13	3.8	2.28		

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HEMBA1000443	1.19	1.9	3.12	2.99	6.28	3.59		
HEMBA1000446	38.48	43.56	75.05	56.34	60.86	69.87		
HEMBA1000456	5.19	4.41	6.5	7.45	5.62	8.77		
HEMBA1000459	1.95	2.11	4.24	3.46	6.17	5.55		
HEMBA1000460	7.46	7.84	8.87	13.59	12.54	18.45	*	+
HEMBA1000462	2.11	3.51	5.04	6.05	5.16	7.49		
HEMBA1000464	1.33	0.96	1.73	1.69	2.74	2.53		
HEMBA1000468	1.25	1.44	2.43	1.69	3.48	2.22		
HEMBA1000469	2.89	3.37	8.1	5.42	8.81	8.01		
HEMBA1000477	2.87	3.03	7.4	5.41	9.68	6.83		
HEMBA1000481	29.67	31.97	31.95	42.76	52.75	25.82		
HEMBA1000488	1.75	2.43	2.96	3.11	5.9	3		
HEMBA1000490	1.34	2	3.49	4.41	3.7	2.88		
HEMBA1000491	1.21	1.71	2.85	4.24	4.99	5.97	*	+
HEMBA1000498	2.12	3.21	4.55	4.39	7.76	5.94		
HEMBA1000501	2.22	3.36	6.25	6.44	8.93	9.74	*	+
HEMBA1000504	2.93	3.18	4.82	3.63	5.37	3.83		
HEMBA1000505	0.81	1.97	3.33	2.72	5.1	3.58		
HEMBA1000507	1.02	2.24	5.29	4.17	8.62	7		
HEMBA1000508	2.25	2.3	7.65	4.84	8.57	6.64		
HEMBA1000518	1.38	0.96	0.98	1.89	2.97	1.8	*	+
HEMBA1000519	9.5	7.28	15.97	19.28	20.99	19.72	*	+
HEMBA1000520	0.45	1.12	1.18	1.94	4.83	4.3	*	+
HEMBA1000523	2.32	1.88	3.22	3.48	5.33	3.65		
HEMBA1000531	1.39	1.46	2.44	2.67	5.34	4.63	*	+
HEMBA1000534	0.55	0.95	2.97	6.63	11.62	10.39	**	+
HEMBA1000538	0.51	1.08	2.31	12.58	21.02	13.18	**	+
HEMBA1000540	2.8	3.11	6.06	5.82	10.38	6.39		
HEMBA1000542	9.16	7.79	43.94	62.25	95.7	81.15	*	+
HEMBA1000545	1.51	2.31	1.65	3.19	4.29	3.7	**	+
HEMBA1000547	2.99	3.12	4.94	4.94	5.3	4.97		
HEMBA1000551	2.32	1.99	9.54	4.68	7.33	9.81		
HEMBA1000555	3.81	3.23	6.39	5.03	6.43	8.08		
HEMBA1000557	2.16	2.06	6.07	3.98	6.46	5.06		
HEMBA1000561	1.71	2.9	4.9	1.63	4.39	3.67		
HEMBA1000563	1.73	1.85	4.09	2.72	3.94	2.83		
HEMBA1000567	1.02	1.01	1.67	1.21	2.59	1.92		
HEMBA1000568	2.19	2.5	6.09	7.62	6.65	6.84		
HEMBA1000569	1.3	2.8	3.02	2.18	6.47	2.3		

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HEMBA1000575	3.73	4.91	10.84	10.19	15.17	13.08		
HEMBA1000588	1.75	2.49	4.16	3.12	5.5	3.83		
HEMBA1000590	0.59	1.02	2.06	2.24	2.53	1.35		
HEMBA1000591	3.17	3.3	5.18	10.84	12.16	9.8	**	+
HEMBA1000592	4.2	5.19	7.77	13.85	14.94	11.78	**	+
HEMBA1000594	1.95	1.97	3.16	4	5.86	4.94	*	+
HEMBA1000604	1.19	3.37	3.48	5.41	10.91	5.29		
HEMBA1000607	2.83	5.09	12.7	15.52	18.13	20.66	*	+
HEMBA1000608	0.9	2.34	2.46	2.6	5.5	2.31		
HEMBA1000622	0.96	2.19	3.55	3.61	5.24	3.8		
HEMBA1000634	17.56	22.96	30.36	71.62	60.59	51.59	**	+
HEMBA1000636	4.59	3.95	6.78	15.48	12.35	12.73	**	+
HEMBA1000637	0.93	0.48	2.58	2.42	3.19	2.21		
HEMBA1000655	1.33	2.11	4.84	6.91	5.57	6.31	*	+
HEMBA1000657	1.35	1.78	3.24	4.89	5.28	3.26	*	+
HEMBA1000662	1.3	2.42	2.73	2.52	3.78	2.72		
HEMBA1000664	0.94	1.6	2.87	3.11	4.63	2.94		
HEMBA1000671	2.96	3.84	11.68	21.25	18.69	15.76	*	+
HEMBA1000673	1.46	2.23	4.76	7.44	7.49	5.51	*	+
HEMBA1000675	4.18	3.09	4.54	8.18	7.19	8.04	**	+
HEMBA1000678	2.23	2.7	4.47	5.03	7.16	5.16		
HEMBA1000682	3.4	4.64	8.41	13.76	13.69	14.29	**	+
HEMBA1000686	2.73	3.88	4.83	6.23	6.6	5.32	*	+
HEMBA1000702	1.56	2.07	5.25	4.15	5.78	4.32		
HEMBA1000705	0.65	1.71	3.43	2.34	3.21	1.64		
HEMBA1000713	3.31	5.6	6.12	6.94	5.86	5.47		
HEMBA1000718	2.14	2.7	5.25	6.11	5.09	5.95		
HEMBA1000719	9.64	12.27	17.77	16.64	15.52	15.64		
HEMBA1000722	1.97	1.7	3.6	6.55	6.45	5.02	**	+
HEMBA1000726	2.2	2.23	5.12	9.4	8.77	9.36	**	+
HEMBA1000727	4.09	5.35	6.41	5.13	9.08	8.37		
HEMBA1000732	1.22	2.74	4.21	4.93	5.58	4.42		
HEMBA1000736	1.56	2.15	3.24	4.11	5.19	4.62	*	+
HEMBA1000743	1.25	2.72	3.41	5.05	4.88	4.16	*	+
HEMBA1000745	1.59	2.47	3.64	4.88	5.33	3.49		
HEMBA1000747	1.19	1.59	2.56	2.35	3.12	1.49		
HEMBA1000748	1.67	1.51	4.85	5.11	6.08	4.81		
HEMBA1000749	1.14	2.04	5.69	5.98	5.91	5.96		
HEMBA1000752	1.4	2.3	4.38	3.69	4.53	3.85		

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HEMBA1000753	2.56	4.21	6.53	7.98	8.59	4.93		
HEMBA1000757	1.95	2.95	3.27	6.33	6.68	5.94	**	+
HEMBA1000760	3.71	3.81	6.62	6.96	7.03	6.89		
HEMBA1000769	1.99	2.36	5.17	3.48	5.87	2.85		
HEMBA1000773	1	2.32	3.07	2.17	3.18	1.4		
HEMBA1000774	2.69	2.76	6.37	6.29	7.77	5.22		
HEMBA1000780	1.12	2.33	3.66	2.7	4.78	3.29		
HEMBA1000783	1.32	2.39	4.1	2.78	7.73	2.57		
HEMBA1000791	2.07	2.4	6.39	4.97	10.17	7.84		
HEMBA1000793	12.73	12.73	17.88	19.93	17.49	16.69		
HEMBA1000802	1.57	1.65	2.59	2.07	4.41	1.1		
HEMBA1000813	38.24	35.83	34.83	54.63	42.38	53.94	*	+
HEMBA1000817	2.63	3.82	5.44	5.12	7.02	5.49		
HEMBA1000822	1.83	2.89	4.1	4.42	5.76	3.91		
HEMBA1000827	2.26	2.74	6.45	9.31	7.75	6.94	*	+
HEMBA1000833	3.1	4.46	7.31	8.06	4.49	4.85		
HEMBA1000835	12.53	15.55	75.61	94.51	110.02	86.95	*	+
HEMBA1000843	1.21	2.2	4.6	3.32	5.63	4.93		
HEMBA1000851	2.13	1.26	3.5	2.7	5.61	2.74		
HEMBA1000852	1.95	1.83	5.5	3.52	5.49	3.83		
HEMBA1000867	0.85	2.79	4.72	2.77	5.39	3.07		
HEMBA1000869	0.58	1.29	2.51	2.84	3.97	2.38		
HEMBA1000870	2.56	2.97	2.59	3.39	5.16	5.49	*	+
HEMBA1000872	1.44	2.87	4.01	4.31	4.14	4.34		
HEMBA1000875	1.89	3.09	5	3.8	4.38	3.77		
HEMBA1000876	1.75	3.36	4.64	3.9	6.21	4.9		
HEMBA1000907	1.99	2.47	3.81	3.21	7.15	5.53		
HEMBA1000908	0.81	2.06	3.85	2	5.43	1.98		
HEMBA1000910	1.97	1.61	3.71	3.35	5.25	2.98		
HEMBA1000918	0.76	1.34	4.37	4.93	6.54	6.95	*	+
HEMBA1000919	0.86	1.97	2.19	2.49	3.07	3.07		
HEMBA1000934	2.5	2.56	1.16	2.14	3.51	2.5		
HEMBA1000935	1.46	1.62	4.21	2.08	5.15	3.64		
HEMBA1000940	1.98	3.08	3.1	2.52	9.96	5.72		
HEMBA1000942	2.31	2.27	4.77	4.81	7.75	6.69		
HEMBA1000943	0.58	1.25	2.28	1.83	3.38	2.18		
HEMBA1000946	3.63	4.04	4.54	6.87	14.9	8.4		
HEMBA1000960	2.63	3.48	9.97	10.24	12.79	10.7		
HEMBA1000962	1.99	2.18	2.01	4.43	3.83	4.56	**	+

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HEMBA1000968	1.73	1.86	4.7	4.1	4.83	4.66		
HEMBA1000971	1.75	2.51	2.9	4.18	5.27	5.71	**	+
HEMBA1000972	1.45	1.57	3.83	2.63	4.44	3.49		
HEMBA1000974	1.69	2.69	6.33	7.39	9.35	8.82	*	+
HEMBA1000975	0.9	1.83	4.17	3.31	5.54	5.12		
HEMBA1000979	1.45	1.69	3.98	2.55	6.12	3.93		
HEMBA1000981	4.21	6.9	9.5	11.75	13.27	14.72	*	+
HEMBA1000983	1.94	1.45	3.01	3.89	4.53	4.15	*	+
HEMBA1000985	1.58	0.92	2.75	1.73	3.28	2.79		
HEMBA1000986	1.2	1.48	2.47	3.61	4.91	4.26	**	+
HEMBA1000991	1.56	1.86	3.8	3.11	5.05	5.96		
HEMBA1001007	0.89	1.08	4.08	1.84	3.89	2.71		
HEMBA1001008	3.64	3.41	5.86	3.89	7.89	4.95		
HEMBA1001009	0.89	1.3	3.07	1.58	3.83	1.81		
HEMBA1001014	3.54	4.39	9.91	11.82	15.38	14.12	*	+
HEMBA1001017	4.21	2.82	5.6	6.04	5.41	8.55		
HEMBA1001019	1.92	2.81	3.97	8.71	7.74	8.29	**	+
HEMBA1001020	1.23	2.71	2.3	2.84	5.05	3.6		
HEMBA1001021	1.07	1.62	2.89	3.13	5.24	2.63		
HEMBA1001022	2.29	2.25	4.35	6.33	8.57	3.81		
HEMBA1001024	0.31	1.14	2.16	2.87	3.97	1.26		
HEMBA1001026	0.42	1.52	1.86	2	3.22	2		
HEMBA1001043	1.43	2.46	2.38	4.63	5.28	4.25	**	+
HEMBA1001051	3.36	2.79	11.52	13.26	18.17	18.47	*	+
HEMBA1001052	0.86	2.15	2.18	1.75	3.58	2.48		
HEMBA1001059	5.62	9.28	26.25	40.62	56.12	43.49	*	+
HEMBA1001060	2.66	3.67	6.45	10.78	8.35	9.62	*	+
HEMBA1001064	2.12	2.87	3.3	6.04	6.48	4.69	**	+
HEMBA1001071	29.39	41.54	55.57	143.9	102.43	121.71	**	+
HEMBA1001077	2.37	1.77	5.21	5.36	6.66	3.96		
HEMBA1001078	2.18	2.6	5.91	13.3	13.21	11.09	**	+
HEMBA1001080	4.03	3.46	11.86	24.15	26.66	26.65	**	+
HEMBA1001084	1.27	2.37	2.9	5.07	5.88	5.13	**	+
HEMBA1001085	1.24	2.87	4.04	4.34	5.41	4.56		
HEMBA1001088	6.62	6	8.04	3.79	4.34	5.81		
HEMBA1001093	0.61	1.76	2.72	3.09	3.02	2.99		
HEMBA1001094	0.64	0.78	2.07	2.08	2.99	1.99		
HEMBA1001099	1.01	1.72	3	2.5	2.95	2.26		
HEMBA1001104	1.2	1.75	2.63	3.64	8.04	3.3		

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HEMBA1001109	4.87	3.77	8.57	11.32	14.48	11.73	*	+
HEMBA1001114	44.68	41.2	93.35	141.87	145.19	167.76	**	+
HEMBA1001121	2.14	2.03	3.87	2.41	6	3.25		
HEMBA1001122	9.79	10	14.12	7.73	11.5	22.69		
HEMBA1001123	2.79	3.28	5.2	5.81	6.02	4.95		
HEMBA1001133	0.97	1.69	2.54	2.78	3.84	1.21		
HEMBA1001137	0.82	1.73	3.65	3.74	3.36	2.54		
HEMBA1001140	1.23	2.75	2.98	3.62	5.18	4.34	*	+
HEMBA1001144	4.12	3.41	9.06	14.13	14.12	13.96	**	+
HEMBA1001145	47.87	43.87	65.7	98.4	75.15	81.3	*	+
HEMBA1001158	7.55	9.5	11.62	13.02	7.58	12.5		
HEMBA1001172	1.44	2.85	4.37	5.32	5.77	5.17	*	+
HEMBA1001174	0.95	2.06	2.83	3.88	6.31	3.25		
HEMBA1001175	6.93	8.56	10.73	14.17	14.5	10.18		
HEMBA1001182	16.93	19.89	82.44	135.93	145.36	122.22	*	+
HEMBA1001184	1.41	1.24	2.45	1.85	3.03	1.47		
HEMBA1001192	1.72	1.75	4.01	5.65	5.17	3.98		
HEMBA1001196	2.31	3.63	7.61	9.43	10.51	8.97	*	+
HEMBA1001197	31.18	35.89	86.14	95.35	83.09	93.59		
HEMBA1001208	1.83	2.59	3	2.67	5.3	2.61		
HEMBA1001213	12.99	16.12	69.9	102.88	119.96	113.72	*	+
HEMBA1001214	1.39	3.11	4.36	5.14	7.04	4.62		
HEMBA1001221	1.63	1.62	3.66	2.06	4.19	1.89		
HEMBA1001225	1.06	2.66	3.53	1.44	3.43	1.52		
HEMBA1001226	4.76	4.65	11.94	13.58	15.58	14.92	*	+
HEMBA1001228	72.4	75.3	102.4	38.23	64.63	78.89		
HEMBA1001229	18	21.39	82.05	115.91	145.39	128.91	*	+
HEMBA1001235	3.58	4.11	6.48	7.31	6.7	10.2		
HEMBA1001238	2.46	2.49	7.23	4.6	6.94	4.74		
HEMBA1001242	15.36	14.03	91.45	92.81	94.02	90.34		
HEMBA1001247	4.41	4.36	12.46	12.48	14.07	15.62		
HEMBA1001253	8.79	11.4	61.56	77.17	102.24	94.81	*	+
HEMBA1001257	1.98	2.71	3.78	3.52	4.29	3.17		
HEMBA1001261	3.01	3.18	4.56	4.54	3.75	5.59		
HEMBA1001262	1.48	3.79	2.81	2.42	4.34	4.59		
HEMBA1001265	2.76	3.21	6.85	5.5	7.32	5.1		
HEMBA1001266	3.97	3.17	6.31	7.8	10.5	8.38	*	+
HEMBA1001269	15.98	10.36	12.79	22.69	24.71	25.21	**	+
HEMBA1001272	1.31	2.04	4.3	1.62	5.12	2.07		

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HEMBA1001279	2.54	3.52	13.6	18.68	23.45	18.99	*	+
HEMBA1001281	16.58	20.99	40.84	47.71	59.04	45.72	*	+
HEMBA1001286	3.25	4.71	10.71	11.24	10.65	12.38		
HEMBA1001289	0.41	1.57	1.64	1.3	3.57	2.41		
HEMBA1001291	3.52	4.58	9.53	10.91	18.3	18.8	*	+
HEMBA1001294	2.01	1.81	4.6	4.04	7.73	5.12		
HEMBA1001296	3.4	3.52	4.37	3.77	5.94	5.22		
HEMBA1001297	2.88	3.61	5.51	4.81	6.88	5.38		
HEMBA1001299	2.49	2.9	6.21	6.45	8.84	7.74	*	+
HEMBA1001302	9.42	11.94	15.5	23.25	35.12	25.74	*	+
HEMBA1001303	1.8	1.99	2.61	3.57	3.8	3.3	**	+
HEMBA1001306	1.4	1.15	2.85	5.01	4.46	4.82	**	+
HEMBA1001308	3.43	4.37	16.7	16.31	18.28	21.75		
HEMBA1001310	1.93	1.71	4.17	2.38	6.26	3.28		
HEMBA1001312	10.09	10.35	17.42	20.51	24.71	21.67	*	+
HEMBA1001319	1.23	1.41	3.85	2.23	4.27	4.01		
HEMBA1001322	1.81	2.29	4.17	2.83	4.74	3.78		
HEMBA1001323	4.04	3.65	8.44	14.68	23.44	18.68	*	+
HEMBA1001326	8.79	7.35	10.15	12.24	13.62	15.04	*	+
HEMBA1001327	0.94	1.65	3.18	3.55	5.18	4.56	*	+
HEMBA1001330	1.59	2.22	6.96	7.36	9.28	9.64	*	+
HEMBA1001348	1.68	3.99	3.89	6.33	9.84	7.47	*	+
HEMBA1001350	5.28	4.16	6.34	7.24	13.17	10.12		
HEMBA1001351	15.37	14.99	17.64	37.37	49.52	25.96	*	+
HEMBA1001352	3.25	3.62	5.97	8.16	13.65	5.75		
HEMBA1001353	30.24	37.73	49.4	76.74	96.09	96.34	**	+
HEMBA1001358	13.98	9.73	17.96	30.89	27.69	30.6	**	+
HEMBA1001361	1.7	3.24	4.96	4.18	6.08	6.06		
HEMBA1001364	0.8	1.71	2.4	1.47	4.11	2.95		
HEMBA1001375	3.45	2.77	5.75	5.71	5.83	6.32		
HEMBA1001377	2.81	3.16	7.36	5.37	7.98	7.89		
HEMBA1001383	0.25	1.64	2.61	1.26	2.47	1.84		
HEMBA1001387	1.81	2.15	3.66	1.94	5.14	2.47		
HEMBA1001388	1.52	1.78	5.07	2.01	4.61	3.49		
HEMBA1001390	34.61	34.52	66.57	67.03	50	56.4		
HEMBA1001391	1.65	2.77	4.83	4.32	7.98	3.82		
HEMBA1001398	1.98	2.87	7.47	7.24	10.42	8.29		
HEMBA1001405	1.17	2	3.87	2.99	5.3	2.61		
HEMBA1001406	2.01	3.27	3.75	5.35	6.62	4.33	*	+

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HEMBA1001407	1.13	1.78	3.73	6.39	6.64	4.44	*	+
HEMBA1001411	1.44	2.81	4.47	7.2	6.35	6.04	*	+
HEMBA1001413	1.84	1.53	3.31	3.61	3.75	3.76		
HEMBA1001414	1.47	2.34	5.3	5.33	7.22	5.47		
HEMBA1001415	1.91	2.36	4.97	4.4	5.86	4.29		
HEMBA1001416	4.73	4.85	9.54	8.87	11.06	9.4		
HEMBA1001432	1.23	1.27	4.43	4.27	6.64	3.59		
HEMBA1001433	1.96	2.93	4.55	4.33	8.66	3.64		
HEMBA1001435	2.17	2.27	6.39	7.02	10.35	5.88		
HEMBA1001442	0.99	0.68	2.02	2.36	3.12	1.81		
HEMBA1001446	1.87	1.84	5.82	9.71	8.93	11.01	**	+
HEMBA1001450	2.35	2.32	11.22	8.61	10.08	6.34		
HEMBA1001454	3.08	4.25	9.69	13.64	10.73	11.82	*	+
HEMBA1001455	2.28	2.7	3.11	2.69	5.54	2.8		
HEMBA1001459	2.74	3.37	6.03	5.07	7.38	5.52		
HEMBA1001461	3.34	4.47	6.96	6.8	9.85	7.47		
HEMBA1001462	1.07	1.47	2.79	2.67	4.5	2.54		
HEMBA1001463	1.38	1.61	5.25	4.95	5.46	5.51		
HEMBA1001469	3.9	4.51	7.32	10.63	9.83	7.76	*	+
HEMBA1001473	4.56	3.49	8.25	7.52	10.34	6.53		
HEMBA1001477	2.14	1.59	4.64	3.41	5.75	2.59		
HEMBA1001478	2.46	2.8	3.77	2.95	3.73	2.55		
HEMBA1001480	4.15	6.8	8.96	11.64	11.87	8.48		
HEMBA1001483	1.9	1.64	5.71	6.6	8.22	7.23	*	+
HEMBA1001490	1.45	2.09	3.76	5.16	4.52	4.65	*	+
HEMBA1001495	56.8	53.41	123.27	193.11	133.65	132.04		
HEMBA1001497	2.06	1.98	7.47	4.81	8.45	5.85		
HEMBA1001510	3.99	4.23	15.22	11.46	13.7	14.56		
HEMBA1001515	1.45	2.33	4.02	3.73	6.11	3.04		
HEMBA1001517	1.6	2.21	4.6	5.26	5.4	4.6		
HEMBA1001522	1.56	2.72	3.77	3.61	6.37	2.43		
HEMBA1001526	2.19	2.97	4.97	4.05	4.38	3.59		
HEMBA1001533	3.19	2.86	6.23	6.83	7.76	4.64		
HEMBA1001547	7.26	5.37	13.69	5	7.96	6.19		
HEMBA1001552	7.12	4.72	17.79	16.12	16.3	16.05		
HEMBA1001553	41.67	45.48	66.23	57.2	47.01	79.81		
HEMBA1001557	2.24	2.93	5.15	5.81	8.33	4.59		
HEMBA1001563	1.69	2.4	4.56	3.66	6.99	4.76		
HEMBA1001566	1.42	3.27	8.29	5.94	9.04	5.84		

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HEMBA1001569	11.15	11.91	26.6	30.2	31.14	32.61	*	+
HEMBA1001570	3.25	4.61	10.2	9.19	10.25	9.53		
HEMBA1001579	3.63	4.4	7.77	9.26	7.4	9.93		
HEMBA1001581	2.79	3.33	10.95	8.81	12.09	9.08		
HEMBA1001582	3.22	3.18	6.68	6.35	6.84	4.03		
HEMBA1001585	2.7	3.07	4.52	4.4	5.6	3.5		
HEMBA1001589	1.82	2.31	3.63	4.39	6.19	3.78		
HEMBA1001595	13.06	15.57	19.7	13.25	13.29	14.02		
HEMBA1001604	1.96	2.67	3.64	3.76	6.53	2.82		
HEMBA1001608	5.58	7.09	16.17	14.14	16.46	14.43		
HEMBA1001615	113.28	90.33	205.41	240.97	118.65	165.59		
HEMBA1001620	3.71	5.56	10.54	12.22	12.24	11.46		
HEMBA1001621	0.76	2.13	3.42	1.76	3.44	2.97		
HEMBA1001635	2.32	2.13	3.41	3.55	4.9	2.85		
HEMBA1001636	1.9	1.93	4.01	3.34	5.33	2.97		
HEMBA1001640	3.07	3.31	13.65	10.96	15.01	10.74		
HEMBA1001647	8.92	8.44	57.38	88.92	112.42	87.46	*	+
HEMBA1001651	2.53	3.54	7.85	6.62	9.07	8.73		
HEMBA1001655	2.09	2.66	4.78	3.35	6.75	4.09		
HEMBA1001658	4.33	4.5	9.27	7.26	11.15	8.6		
HEMBA1001661	0.75	1.78	2.8	1.98	3.22	1.77		
HEMBA1001665	1.52	1.85	3.47	2.63	6.63	1.73		
HEMBA1001670	5.32	6.54	8.82	12.45	15.21	12.42	**	+
HEMBA1001672	2.49	3.06	5.9	4.28	7.62	3.39		
HEMBA1001673	8.23	10.76	13.22	20.04	19.39	15.65	*	+
HEMBA1001675	2.4	2.01	2.53	3.21	5.79	3.36		
HEMBA1001676	54.19	46.09	107.65	245.72	212.81	275.65	**	+
HEMBA1001678	9.46	10.2	21.87	23.65	19.51	27.88		
HEMBA1001680	4.58	4.89	12.32	9.39	10.95	11.65		
HEMBA1001681	1.71	2.44	5.75	6.25	9.11	6.36		
HEMBA1001684	1.89	2.74	6.26	4.32	7.57	6.98		
HEMBA1001695	1.48	2.08	3.42	2.3	4.76	3.15		
HEMBA1001702	1.54	2.96	3.55	2.36	7.57	3.09		
HEMBA1001709	1.23	1.8	3.51	3.21	4.87	3.5		
HEMBA1001711	1.29	1.98	2.83	2.99	2.45	3.18		
HEMBA1001712	0.92	1.55	2.56	2.13	3.02	2.24		
HEMBA1001714	10.37	10.82	19.06	23.54	22	23.8	*	+
HEMBA1001717	79.4	71.16	124.25	152.62	195.81	173.65	*	+
HEMBA1001718	1.95	2.12	7.32	5.99	6.59	5.26		

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HEMBA1001723	3.43	3	10.19	9.09	12.53	9.64		
HEMBA1001731	1.3	1.36	3.27	1.58	4.8	2.29		
HEMBA1001734	2.37	2.38	4.28	4.78	6.06	4.27		
HEMBA1001736	2.3	2.12	2.87	3.5	4.69	5.33	*	+
HEMBA1001741	1.69	2.19	3.5	4.02	4.74	2.9		
HEMBA1001744	0.86	0.94	2.81	2	3.64	2.64		
HEMBA1001745	0.95	1.56	2.3	2.53	5.28	2.58		
HEMBA1001746	4.02	3.91	8.66	9.21	12.06	7.01		
HEMBA1001761	2.2	2.01	4.69	2.58	3.95	3.37		
HEMBA1001762	1.41	1.6	3.57	1.93	4.38	2.03		
HEMBA1001781	1.56	1.5	4.17	2.15	5.87	3.25		
HEMBA1001784	1.36	1.39	4.5	4.02	3.58	3.75		
HEMBA1001791	2.16	1.74	6.97	6.04	7.62	5.68		
HEMBA1001794	2.15	4.31	12.57	13.54	13.65	12.96		
HEMBA1001800	5.61	9.63	60.44	84.85	100.03	76.26	*	+
HEMBA1001803	2.84	4.25	5.36	4.27	7.02	3.67		
HEMBA1001804	6.2	8.13	20.95	29.84	26.86	24.39	*	+
HEMBA1001808	1.61	1.6	3.87	3.71	3.67	2.89		
HEMBA1001809	8.07	6.27	10.64	14.33	20.56	16.63	*	+
HEMBA1001811	8.32	7.83	16.8	22.75	21.75	17.6	*	+
HEMBA1001815	1.75	2.67	6.56	5.58	6.33	5.03		
HEMBA1001816	1.96	2.67	4.47	3.09	4.6	3.04		
HEMBA1001819	0.98	3.09	6.16	6.19	8.53	6.3		
HEMBA1001820	0.93	1.32	2.22	2.36	3.32	1.21		
HEMBA1001822	1.87	2.06	5.43	6.02	7.7	4.44		
HEMBA1001824	3.21	4.62	14.88	12.81	16.29	12.34		
HEMBA1001835	1.04	1.05	3.05	3.72	5.21	3.14		
HEMBA1001844	7.88	6.55	18.04	17.77	21.36	13.19		
HEMBA1001847	0.93	1.8	5.21	1.96	5.18	3.06		
HEMBA1001849	2.32	2.77	7.58	6.65	8.19	7.62		
HEMBA1001850	2.51	2.71	8.43	8.76	8.88	7.89		
HEMBA1001861	0.95	2.04	1.73	2.64	3.93	2.01		
HEMBA1001862	138.58	133.42	191.61	266.65	221.43	227.58	*	+
HEMBA1001864	1.31	1.16	2.44	4.79	2.88	2.59		
HEMBA1001866	1.49	2.39	7.45	7.67	7.07	4.61		
HEMBA1001869	7.55	6.84	10.82	10.31	7.69	9.02		
HEMBA1001871	29.48	30.98	54.77	63.07	62.43	66.59	*	+
HEMBA1001876	0.96	1.27	4.42	2.08	4.57	2.26		
HEMBA1001878	2.23	3.34	5.7	6.83	8.18	5.5		

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HEMBA1001879	1.89	2.57	5.58	5.99	7.24	5.72		
HEMBA1001884	6.21	6.49	17.14	11.31	12.71	10.87		
HEMBA1001886	2.12	2.21	4.38	4.57	5.67	4.23		
HEMBA1001888	2	2.12	6.6	7.41	10.17	9.46	*	+
HEMBA1001890	4.03	3.67	7.6	6.8	7.01	4.4		
HEMBA1001896	1.34	1.61	2.62	2.27	4.12	3.01		
HEMBA1001899	33.43	39.48	61.77	106.52	41.01	101.91		
HEMBA1001904	76.64	122.45	233.99	299.33	174.47	322.82		
HEMBA1001910	1.4	1.93	3.23	2.53	6.35	2.97		
HEMBA1001911	8.36	8.75	10.86	21.15	16.9	13.23	*	+
HEMBA1001912	8.92	7.97	33.97	57	51.9	48.59	*	+
HEMBA1001913	4.89	6.19	17.29	18.56	14.16	16.85		
HEMBA1001915	1.35	2.61	4.49	3.3	5.63	2.46		
HEMBA1001918	15.23	13.29	21.07	17.07	14.31	12.13		
HEMBA1001921	4	3.5	4.38	5.2	5.35	4.86	*	+
HEMBA1001931	1.19	1.95	2.53	2.14	5.17	2.19		
HEMBA1001939	1.92	1.77	4.72	1.97	5.21	2.57		
HEMBA1001940	2.61	2.99	7.14	3.51	5.86	3.24		
HEMBA1001942	1.18	1.88	3.71	2.33	5.14	1.56		
HEMBA1001944	4.35	5.83	42.16	51.42	66.43	59.75	*	+
HEMBA1001945	0.98	2.3	2.95	2.98	3.4	2.21		
HEMBA1001950	2.56	2.84	7.87	5.72	5.23	3.68		
HEMBA1001951	10.37	11.26	15.33	24.16	18.26	22.94	*	+
HEMBA1001958	1.04	1.28	2.58	3.1	4.83	2.54		
HEMBA1001960	6.87	6.28	13.93	10.02	12.99	12.47		
HEMBA1001962	1.01	1.08	4.19	1.58	4.24	1.67		
HEMBA1001964	1.39	3.45	4.13	2.54	4.45	3.39		
HEMBA1001967	6.06	5.65	9.33	14.45	10.5	13.18	*	+
HEMBA1001979	0.7	2.67	3.31	2.04	3.46	2.4		
HEMBA1001987	1.96	3.92	7.99	6.19	8.35	7.22		
HEMBA1001991	1.61	3.59	9.06	5.06	8.7	7.44		
HEMBA1002003	4.86	4.71	14.56	15.86	16.03	22.9		
HEMBA1002005	2.62	3.39	7.82	4.16	7.48	4.76		
HEMBA1002008	2.64	3.51	7.78	6.07	10.15	6.37		
HEMBA1002018	1.86	2.37	4.23	3.32	5.47	3.87		
HEMBA1002022	0.52	2.3	2.5	2.83	3.53	2.82		
HEMBA1002029	43.82	40.22	73.75	89.27	96.12	122.81	*	+
HEMBA1002030	2.23	2.88	4.32	3.88	4.26	4.67		
HEMBA1002035	1.69	1.75	3.82	5.43	5.14	3.75		

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HEMBA1002037	4.47	4.34	6.69	4.5	6.47	7.94		
HEMBA1002038	4.12	3.13	7.74	6.36	8.8	5.42		
HEMBA1002039	2.46	3.43	7.03	6.74	8.99	6.37		
HEMBA1002042	5.52	5.55	9.8	10.55	13.01	9.94		
HEMBA1002043	3.81	3.79	11.32	12.53	12.64	13.95		
HEMBA1002048	2.76	2.31	3.81	2.03	4.32	3.44		
HEMBA1002049	1.72	2.35	5.55	4.43	5.2	5.2		
HEMBA1002053	7.33	6.91	14.52	11.09	15.25	13.63		
HEMBA1002055	9.81	8.76	10.65	18.44	13.58	17.78	*	+
HEMBA1002056	2.24	2.62	4.26	5.46	8.06	5.67	*	+
HEMBA1002061	2.24	2.51	4.58	4.17	5.34	4.58		
HEMBA1002080	46.55	49.5	54.6	91.78	122.41	83.23	*	+
HEMBA1002084	0.71	1.43	2.36	3.25	3.66	2.64	*	+
HEMBA1002085	0.97	1.47	2.87	3.45	4.52	3.74	*	+
HEMBA1002092	1.79	1.56	3.94	4.01	5.53	4.15		
HEMBA1002098	1.51	1.82	4.12	3.2	5.11	2.83		
HEMBA1002100	9.07	8.18	22.37	25.95	23.04	29.67		
HEMBA1002101	18.26	17.64	27.49	23.44	27.16	23.74		
HEMBA1002102	2.65	1.98	5.99	4.58	7.06	6.99		
HEMBA1002105	6.79	6.2	22.13	24.47	40.8	25.31		
HEMBA1002107	57.97	37.86	84.35	155.21	136.27	136.87	**	+
HEMBA1002113	6.77	4.75	17.24	12.05	12.83	14.78		
HEMBA1002119	3.85	3.28	24.05	24.29	30.66	27.04		
HEMBA1002125	7.03	6.73	10.43	11.38	7.34	11.85		
HEMBA1002131	9.71	9.72	20.58	14.97	19.12	13.71		
HEMBA1002133	3.67	3.52	6.32	6.97	9.51	9.46	*	+
HEMBA1002139	0.75	1.07	3.35	1.52	4.37	1.47		
HEMBA1002141	1.67	1.36	3.23	2.99	3.92	2.14		
HEMBA1002144	2.33	2.44	6.11	5.28	5.68	6.57		
HEMBA1002147	8.84	9.55	17.93	36.22	21.92	21.88		
HEMBA1002150	38.34	38.68	51.42	19.74	26.62	15.85	*	-
HEMBA1002151	3.76	3.36	9.95	11.15	14.23	9.84		
HEMBA1002153	0.57	1.74	3.36	3.39	5.64	2.96		
HEMBA1002156	0.8	1.74	2.33	1.94	4.28	1.26		
HEMBA1002160	2.16	3.17	5.7	6.08	7.26	6.18		
HEMBA1002161	2.13	2.9	6.99	13.53	11.79	9.76	*	+
HEMBA1002162	2.65	2.17	7.76	5.61	6.27	7.81		
HEMBA1002163	12.02	12.04	19.93	34.48	19.96	27.11		
HEMBA1002164	6.58	10.55	59.92	71.46	78.61	67.82		

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HEMBA1002166	21.88	18.32	39.58	57.35	49.05	46.09	*	+
HEMBA1002167	0.89	2.89	3.89	4.96	5.45	3.98		
HEMBA1002173	3.24	3.83	6.22	7.97	7.11	6.28		
HEMBA1002177	1.31	1.78	3.31	5.68	4.97	2.98		
HEMBA1002178	6.91	10.17	14.77	23.33	23.58	17.49	*	+
HEMBA1002179	53.56	46.86	94.4	58.33	85.22	54.47		
HEMBA1002185	2.75	4.07	13.4	11.73	16.23	14.56		
HEMBA1002188	5.76	7.57	10.27	11.86	12.9	9.8		
HEMBA1002189	1.98	2.85	4.96	5.23	4.63	4.71		
HEMBA1002191	0.67	2.16	4.96	3.47	5.44	2.81		
HEMBA1002192	2.98	2.83	4.91	7.53	8.35	4.57		
HEMBA1002195	2.96	3.27	6.6	10.35	10.11	7.27	*	+
HEMBA1002196	3.34	4.33	8.55	8.62	8.85	8.39		
HEMBA1002199	1.33	1.86	4.9	4.62	5.71	3.52		
HEMBA1002204	1.31	1.97	4.08	5.48	11.37	3.73		
HEMBA1002208	24.58	26.61	45.85	49.77	25.48	39.6		
HEMBA1002212	3.73	5.95	9.01	8.9	11.85	17.18		
HEMBA1002215	1.95	2.63	4.27	5.1	3.54	3.78		
HEMBA1002217	15.61	16.71	59.91	78.46	82.88	80.94	*	+
HEMBA1002220	1.11	2.07	4.1	3.58	3.39	2.33		
HEMBA1002226	2.17	3.13	9.18	10.47	12.61	9.58		
HEMBA1002227	39.9	47.13	92.5	109.42	65.74	71.79		
HEMBA1002229	4.5	4.77	13.39	11.16	13.55	12.49		
HEMBA1002237	1.73	3.22	4.08	3.71	5.64	3.41		
HEMBA1002239	9.36	13.83	72.18	100.62	109.3	113.84	*	+
HEMBA1002241	7	7.54	38.36	64.27	68.93	68.72	**	+
HEMBA1002253	1.11	2.44	3.33	2.3	4.42	2.68		
HEMBA1002257	1.83	2.65	4.11	3.18	3.6	1.74		
HEMBA1002259	1.12	2.17	2.69	3.12	3.6	2.67		
HEMBA1002262	6.95	7.37	19.16	14.43	14.78	17.04		
HEMBA1002265	1.35	1.63	3.7	3.75	6.23	2.43		
HEMBA1002267	16.87	20.81	22.76	32.99	16.96	27.5		
HEMBA1002270	3.73	4.79	7.49	8.18	13.43	8.7		
HEMBA1002286	1.03	1.86	5.42	2.85	5.53	0.98		
HEMBA1002290	4.73	3.7	7.52	5.16	8.88	4.38		
HEMBA1002302	6.12	9.63	45.04	45.66	49.69	45.23		
HEMBA1002304	3.28	3.42	6.88	5.57	6.97	4.34		
HEMBA1002307	45.71	53.69	92.31	71.87	55.79	61.03		
HEMBA1002316	2.16	3.29	4.63	3.04	5.32	2.41		

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HEMBA1002319	1.97	2.96	4.46	8.32	9.58	8	**	+
HEMBA1002320	1.99	1.76	3.22	2.51	4.45	1.76		
HEMBA1002321	1.22	2.04	2.84	2.71	4.44	2.77		
HEMBA1002328	2.44	3.04	4.89	2.43	5.73	2.94		
HEMBA1002333	3.88	4.27	7.14	7.37	10.84	7.5		
HEMBA1002337	3.02	3.62	5.5	5.98	7.49	7.48	*	+
HEMBA1002339	15.86	13.92	111.66	135.44	169.95	156.76	*	+
HEMBA1002341	0.8	2.08	3.22	2.71	4.34	2.35		
HEMBA1002348	2.84	2.78	7.14	3.69	6.73	4.49		
HEMBA1002349	1.28	1.44	3.59	2.24	4.64	2.59		
HEMBA1002353	1.83	3.04	4.03	4.61	7.72	5.68		
HEMBA1002356	6.05	6.96	17.53	14.27	16.02	16.1		
HEMBA1002357	114.85	156.08	306.32	300.67	286.5	328.19		
HEMBA1002360	7.18	8.32	8.29	14.57	14.46	13.78	**	+
HEMBA1002363	2.79	3.35	4.84	7.02	8.02	8.72	**	+
HEMBA1002365	1.7	2.7	2.7	1.63	3.12	2.67		
HEMBA1002370	1.43	1.78	2.37	1.53	4.2	1.9		
HEMBA1002374	4.55	4.53	7.79	8.33	10.27	9.11	*	+
HEMBA1002376	46.59	33.18	118.8	101.1	189.18	114.36		
HEMBA1002377	18.02	20.98	25.61	32.58	34.44	32.19	**	+
HEMBA1002380	5.68	6.36	16.28	17.43	21.85	18.83		
HEMBA1002381	1.52	1.8	4.16	4.12	7.16	4.94		
HEMBA1002384	1.79	3.09	3.69	5.67	4.27	5.71	*	+
HEMBA1002389	1.93	2.93	2.88	3.63	5.31	4.7	*	+
HEMBA1002396	21.16	20.01	36.93	14.29	14.94	19.1		
HEMBA1002402	125.09	124.52	168.42	100.85	107.79	164.62		
HEMBA1002417	1.41	1.07	4.27	2.17	3.19	2.6		
HEMBA1002419	1.42	2.38	3.8	1.81	4.59	2.41		
HEMBA1002420	9.55	11.97	14.11	16.34	18.28	16.16	*	+
HEMBA1002421	7.47	10.35	12.5	8.97	10.24	9.6		
HEMBA1002423	2.89	1.3	4.28	3.35	4.29	3.82		
HEMBA1002424	11.91	10.05	25.13	9.11	9.2	10.43		
HEMBA1002426	3.42	3.69	5.56	7.57	8.24	5.6	*	+
HEMBA1002430	0.39	1.41	2.51	1.7	4.19	2.85		
HEMBA1002439	1.59	1.94	4.17	2.69	4.46	6.8		
HEMBA1002441	31.85	29.77	27.79	48.74	52.7	34.64		
HEMBA1002454	0.62	1.48	2.27	1.76	2.43	1.55		
HEMBA1002458	3.17	5	8.09	10.24	10.55	11.71	*	+
HEMBA1002460	2.14	1.59	3.89	5.16	4.63	5.01	*	+

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HEMBA1002462	5.18	3.83	9.52	11.92	9.29	8.58		
HEMBA1002465	0.93	1.96	2.26	1.46	3.13	1.27		
HEMBA1002469	6.88	7.27	45.87	49.02	75.59	67.74	*	+
HEMBA1002475	1.54	2.35	8.01	4.88	7.87	7.66		
HEMBA1002477	1.75	1.59	5.25	3.19	6.99	3.55		
HEMBA1002480	4.46	3.98	8.49	8.76	13	10.54		
HEMBA1002481	1.9	2.02	4.22	2.71	6.25	4.7		
HEMBA1002486	3.62	3.98	10.08	9.98	8.04	9.75		
HEMBA1002490	2.02	3.08	5.7	8.76	9.64	7.65	*	+
HEMBA1002495	2.37	2.29	3.78	3.92	4.79	4.08		
HEMBA1002498	0.95	2.14	2.97	1.83	5.09	2.14		
HEMBA1002501	2.96	4.73	14.13	19.98	23.55	17.54	*	+
HEMBA1002503	1.7	2.52	5.11	4.68	7.06	2.97		
HEMBA1002504	1.95	2.19	5.99	6.68	7.09	4.65		
HEMBA1002508	1.48	2.59	5.99	7.8	7.47	5.65		
HEMBA1002513	1.31	1.7	4.85	3.91	7.67	3.02		
HEMBA1002515	1.17	1.82	3.04	2.67	5.1	2.89		
HEMBA1002524	1.67	2.09	2.53	4.44	4.49	3.82	**	+
HEMBA1002538	4.68	4.14	7.39	9.31	8.91	7.86	*	+
HEMBA1002542	3.31	3.27	6.77	10.11	9.3	7.74	*	+
HEMBA1002544	1.42	2.24	3.33	2.69	6.59	3.24		
HEMBA1002546	31.01	31.64	56.69	95.52	83.15	72.77	*	+
HEMBA1002547	3.13	3.22	8.44	20.11	20.37	17.21	**	+
HEMBA1002550	5.46	3.86	10.87	10.85	11.2	10.23		
HEMBA1002551	2.15	3.09	5.8	3.7	5.08	3.08		
HEMBA1002552	2.21	2.06	8.39	5.66	6.55	5.68		
HEMBA1002555	1.54	1.78	4.56	2.27	4.4	2.97		
HEMBA1002558	2.74	3.26	7.02	8.08	7.47	8.27		
HEMBA1002561	1.01	1.58	5.26	4.42	5.08	3.87		
HEMBA1002562	0.59	0.83	2.34	3.29	3.29	2.36		
HEMBA1002568	1.71	1.16	3.09	3.06	3.26	3.6		
HEMBA1002569	3.8	4.67	10.32	7.29	8.59	5.14		
HEMBA1002570	5.22	4.72	9.84	6.07	10.29	12.99		
HEMBA1002574	24.62	22.75	26.01	44.47	30.74	40.85	*	+
HEMBA1002583	4.07	4.52	8.07	6.64	6.43	8.47		
HEMBA1002587	9.78	10.9	19.23	24.67	18.08	20.4		
HEMBA1002590	2.51	2.58	7.47	5.35	5.6	4.05		
HEMBA1002592	2.51	3.03	6.4	6.34	7.84	5.1		
HEMBA1002595	1.66	2.13	3.1	4.12	4.25	2.68		

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HEMBA1002609	4.47	6.27	51	68.51	85.44	66.33	*	+
HEMBA1002617	6.31	4.76	7.99	7.25	6.84	6.48		
HEMBA1002619	3.33	4.8	5.99	7.86	6.14	7.27		
HEMBA1002621	1.21	2.94	3.09	3.24	4.17	2.03		
HEMBA1002624	4.6	5.19	19.48	22.04	24.39	26.87	*	+
HEMBA1002628	3.37	3.64	6.41	6.08	6.11	4.1		
HEMBA1002629	2.71	2.24	4.66	3.77	7.98	4.48		
HEMBA1002632	1.39	2.23	5.16	4.29	5.49	4.58		
HEMBA1002645	1.77	1.98	6.43	4.68	6.91	5.37		
HEMBA1002651	1.87	2.73	4.73	4.68	4.83	3.74		
HEMBA1002652	3.38	5.27	6.21	6.09	8.66	7.92		
HEMBA1002659	2.84	3.86	4.8	6.32	8.18	9.6	*	+
HEMBA1002661	3	2.71	6.19	4.41	6.93	4.93		
HEMBA1002666	1.74	2.47	4.21	2.95	4.25	1.41		
HEMBA1002667	1.39	2.25	3.91	2.79	5.24	1.94		
HEMBA1002673	16.08	19.36	30.31	32.54	35.18	29.96		
HEMBA1002678	2.11	2.33	7.44	5.39	5.98	4.22		
HEMBA1002679	1.23	2.33	5.25	3.7	7.48	3.81		
HEMBA1002688	1.74	2.98	8.3	8.33	11.41	7.86		
HEMBA1002696	1.7	2.79	2.92	3.48	6.13	3.32		
HEMBA1002703	2.95	3.88	10.15	8.35	9.73	9.21		
HEMBA1002706	4.97	4.24	8.99	5.07	7.16	5.54		
HEMBA1002712	2.39	3.94	8.67	8.4	10.9	10.57		
HEMBA1002715	7.92	9.81	49.65	79.65	93.63	79.61	*	+
HEMBA1002716	3.93	4.26	5.53	4.63	5.02	4.53		
HEMBA1002718	11.79	12.87	17.77	24.16	18.07	24.3	*	+
HEMBA1002728	2.37	3.1	5.01	5.52	5.94	4.42		
HEMBA1002730	1.13	2.48	5.86	3.71	6.19	4.61		
HEMBA1002734	2.89	3.54	8.82	8.6	10.7	10.59		
HEMBA1002742	1.94	2.06	3.96	1.86	4.27	2.74		
HEMBA1002746	1.2	2.86	4.61	2.83	4.43	2.94		
HEMBA1002748	2.19	1.75	4.01	5.36	5.98	3.92		
HEMBA1002750	1.99	2.46	3.45	6.74	6.39	6.27	**	+
HEMBA1002755	1.85	3.1	5.31	5.96	6.62	5.16		
HEMBA1002759	1.93	3.12	7.98	4.65	7.92	7.08		
HEMBA1002763	9.62	12.05	74.52	68.84	88.82	77.22		
HEMBA1002767	4.48	5.85	5.8	8.88	6	6.13		
HEMBA1002768	2.99	3.76	6.2	3.46	8.3	3.04		
HEMBA1002769	1.47	2.35	2.82	3.46	5.21	3.49		

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HEMBA1002770	5.89	5.83	12.41	14.24	22.53	15.53	*	+
HEMBA1002777	1.6	1.9	2.58	2.29	4.74	3.76		
HEMBA1002779	10.92	7.6	16	17.39	19.81	19.36	*	+
HEMBA1002780	2.6	2.77	6.82	6.43	6.89	6.35		
HEMBA1002790	3.14	2.52	10.6	7.26	8.67	9.25		
HEMBA1002794	1.52	2.28	5.49	3.68	6.8	4.45		
HEMBA1002798	1.33	1.59	3.61	2.77	5.12	4		
HEMBA1002801	2.13	2.25	3.64	3.12	6.93	5.24		
HEMBA1002810	4.56	3.99	7.85	10.27	17.31	11.1	*	+
HEMBA1002816	2.24	1.97	2.88	5.34	5.05	4.8	**	+
HEMBA1002818	24.6	23.26	95.11	130.84	121.74	135.78	*	+
HEMBA1002820	1.95	2.63	6.41	6.96	6.99	6.04		
HEMBA1002826	1.96	1.48	2.99	3.21	4.84	3.59		
HEMBA1002833	8.71	7.46	19.84	20.18	21.16	20.04		
HEMBA1002850	1.16	1.94	3.67	3.87	4.96	5.11	*	+
HEMBA1002862	9.06	9.31	17.9	20.11	25.3	13.43		
HEMBA1002863	2.47	2.93	5.28	6.16	8.44	6.52	*	+
HEMBA1002867	1.51	1.17	2.4	2.3	3.28	1.87		
HEMBA1002876	3.9	3.54	5.48	5.61	5.78	6.48		
HEMBA1002886	1.28	1.56	2.45	1.83	3.13	2.71		
HEMBA1002896	5.82	3.82	9.38	7.22	11.23	8.51		
HEMBA1002913	2.37	2.22	4.56	4.19	4.28	3.11		
HEMBA1002921	0.97	0.81	2.36	1.82	2.41	1.41		
HEMBA1002924	1.07	1.2	2.86	2.11	4.41	3.27		
HEMBA1002934	6.01	5.17	10.48	9.93	15.27	13.16		
HEMBA1002935	4.27	2.55	6.59	7.1	5.34	7.14		
HEMBA1002937	4.61	5.71	9.4	10.82	8.36	7.36		
HEMBA1002939	2.21	2.92	5.39	5.51	5.7	3.26		
HEMBA1002944	1.45	1.97	4.66	3.1	5.68	3.21		
HEMBA1002951	5.88	7.88	10.99	6.04	12.17	5.67		
HEMBA1002954	2.4	4.57	6.12	6.09	7.78	4.78		
HEMBA1002962	3.93	6.02	9.14	13.42	15.92	12.44	*	+
HEMBA1002968	1.22	1.71	4.32	5.34	4.07	5.3		
HEMBA1002970	1.13	1.13	3.14	2.5	3.72	3.13		
HEMBA1002971	0.96	2.02	2.75	2.02	3.71	2.43		
HEMBA1002973	1.68	3.36	7.84	6.19	10.81	6.31		
HEMBA1002978	2.09	3.81	4.35	5.49	5.3	4.22		
HEMBA1002981	1.82	2.51	4.01	9.33	7.48	6.53	**	+
HEMBA1002985	0.83	1.92	4.91	4.74	5.59	4.13		

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HEMBA1002986	2.72	4.88	6.67	14.7	14.62	13	**	+
HEMBA1002988	1.77	2.36	4.25	4.2	5.67	3.46		
HEMBA1002992	8.73	11.38	68.65	83.81	96.4	94.02	*	+
HEMBA1002995	6.13	6.97	11.94	8.64	11.47	14.09		
HEMBA1002997	5.77	6.33	9.6	12.88	10.65	8.75		
HEMBA1002999	1.36	2.77	2.84	2.48	3.92	3.31		
HEMBA1003004	0.78	1.39	1.96	1.86	3.32	1.37		
HEMBA1003006	2.03	1.84	4.26	5.44	8.08	5.87	*	+
HEMBA1003008	1.58	1.26	2.83	3.4	5.4	2.28		
HEMBA1003021	1.72	2.09	5.98	8.49	8.58	6.67	*	+
HEMBA1003027	1.79	1.73	4.47	2.11	6.17	3.72		
HEMBA1003029	16.39	17.36	46.06	37.07	42.91	45.58		
HEMBA1003031	33.04	32.41	50.08	48.18	24.56	40.3		
HEMBA1003032	3.42	6.52	7.98	8.81	6.53	9.45		
HEMBA1003033	2.36	4.11	6.85	7.85	8.94	9	*	+
HEMBA1003034	2.43	3.17	7.63	8.24	7.47	8.23		
HEMBA1003035	1.24	2	2.59	2.88	3.46	1.93		
HEMBA1003037	1.74	2.09	6.21	4.13	7.36	3.43		
HEMBA1003041	3.4	4.14	8.51	10.28	10.48	9		
HEMBA1003046	11.44	11.53	28.31	33.77	21.19	36.32		
HEMBA1003047	2.02	2.35	5.11	4.57	5.41	4.03		
HEMBA1003048	1.8	2.96	3.76	7.97	7.47	9.3	**	+
HEMBA1003064	3.7	4.12	15.74	15.78	25.09	19.36		
HEMBA1003067	1.92	2.31	7.09	4.56	7.96	3.23		
HEMBA1003071	5.24	5	8.74	11.32	10.02	8.7		
HEMBA1003072	2.81	3.22	5.7	4.43	3.65	5.17		
HEMBA1003076	20.6	21.34	31.6	41.86	28.3	32.74		
HEMBA1003077	1.41	1.58	4.37	1.68	4.03	2.27		
HEMBA1003078	2.02	1.92	2.4	3.14	4.9	3.38	*	+
HEMBA1003079	2.72	2.66	6.42	5.88	7.13	4.48		
HEMBA1003083	1.56	2.11	3.94	4.42	6.23	4.59		
HEMBA1003086	2.5	2.72	5.27	4.09	5.78	4.68		
HEMBA1003090	5.14	4.79	13.3	11.57	12.88	12.73		
HEMBA1003094	0.82	1.67	2.94	2.51	3.22	2.14		
HEMBA1003096	8.6	8.76	15.55	10.1	13.7	10.97		
HEMBA1003098	3.88	5.66	7.38	9.42	7.11	8.4		
HEMBA1003101	4.73	5.48	7.29	9.04	6.59	6.36		
HEMBA1003109	2.88	3.42	4.72	5.73	6.93	7.22	*	+
HEMBA1003114	2.87	4.67	5.67	6.47	7.94	5.69		

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HEMBA1003117	2.1	3.41	4.4	3.36	4.99	2.44		
HEMBA1003120	3.02	2.65	5.55	3.23	7.38	4.29		
HEMBA1003129	2.47	2.6	6.66	10.28	6.19	7.28		
HEMBA1003133	2.05	4.74	7.61	7.74	7.59	5.59		
HEMBA1003136	2.64	3.59	5.25	5.37	5.88	4.49		
HEMBA1003142	2.01	2.27	6.15	6.62	6.35	5.34		
HEMBA1003148	1.3	1.4	2.82	1.49	4.26	1.6		
HEMBA1003151	1.91	2.08	4.23	2.9	5.34	4.24		
HEMBA1003152	3.27	1.98	5.84	4.74	5.71	2.58		
HEMBA1003157	1.23	1.88	2.58	4.2	5.38	3.21	*	+
HEMBA1003166	6.14	6.06	14.06	22.98	18.03	21.74	*	+
HEMBA1003171	1.3	2.28	2.23	2.62	3.09	2.53		
HEMBA1003175	1.54	2.63	4.2	3.54	4.52	4.11		
HEMBA1003179	4.66	5.95	37.4	36.91	43.86	45.13		
HEMBA1003186	2.58	3.17	7.13	6.71	6.71	5.78		
HEMBA1003196	3.04	3.79	7.33	6.95	8.31	5.18		
HEMBA1003197	0.46	1.51	2.86	1.85	3.97	1.09		
HEMBA1003199	1.26	1	2.32	1.66	3.22	2.47		
HEMBA1003202	2.86	3.49	5.69	9.44	10.48	11.14	**	+
HEMBA1003204	1.67	2.46	3.35	4.99	4.72	4.81	**	+
HEMBA1003210	6.48	7.36	11.66	12.02	12.1	14.78		
HEMBA1003212	1.4	2.87	5.52	7.58	8	5.7		
HEMBA1003218	1.2	1.26	1.71	1.24	4.35	1.36		
HEMBA1003220	34.65	32.6	73.43	78.35	79.82	83.89		
HEMBA1003222	2.37	3.03	3.41	3.04	6.13	4.29		
HEMBA1003225	1.95	2.07	3.34	1.59	3.45	2.05		
HEMBA1003229	2.37	1.91	2.4	5.62	5.1	4.9	**	+
HEMBA1003230	7.83	7.14	12.08	11.08	11.44	10.09		
HEMBA1003235	0.91	1.33	4.32	4.98	5.25	5.44	*	+
HEMBA1003236	5.54	5.43	10.62	11.5	15.4	13.97	*	+
HEMBA1003250	1.41	1.4	2.68	1.76	2.98	2.42		
HEMBA1003252	4.96	7.17	16.59	17.06	18.68	14.37		
HEMBA1003257	2.7	3.33	7.33	8.25	8.83	6.78		
HEMBA1003268	0.95	0.44	1.92	1.92	3.36	1.81		
HEMBA1003273	1.4	1.38	2.96	2.5	3.37	5.1		
HEMBA1003276	1.13	1.99	3.18	4.21	4.42	3.98	*	+
HEMBA1003277	0.95	0.83	1.85	0.56	1.63	1.34		
HEMBA1003278	1.07	1.18	3.49	1	4.56	2.32		
HEMBA1003280	2.37	2.6	4.59	3.08	4.91	4.2		

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HEMBA1003281	1.83	1.29	3.53	1.79	3.85	2.48		
HEMBA1003284	1.24	1.91	3.43	3.03	5.05	3.32		
HEMBA1003286	7.75	6.73	34.23	45.25	71.61	51.97	*	+
HEMBA1003291	1.65	1.91	4.84	3.21	3.32	3.25		
HEMBA1003294	1.89	3.5	7.47	4.86	5.7	5.62		
HEMBA1003296	4.74	8.32	46.61	63.82	70.23	54.45	*	+
HEMBA1003304	0.77	1.44	2.88	2.91	5.37	1.87		
HEMBA1003306	4.37	6.3	10.28	15.7	17.76	11.56	*	+
HEMBA1003309	0.91	1.9	2.85	2.87	4	2.3		
HEMBA1003314	1.43	2.26	3.82	4.48	3.52	4.02		
HEMBA1003315	6.37	4.38	10.14	15.2	16.23	17.88	**	+
HEMBA1003322	4.81	5.92	10.9	8.46	10.83	8.07		
HEMBA1003326	1.94	3.97	5.55	2.93	7.4	3.68		
HEMBA1003327	0.81	1.61	3.63	2.36	4.3	2.28		
HEMBA1003328	0.76	2.43	5.38	4.25	5.51	5.06		
HEMBA1003330	2.27	2.81	4.84	4.66	5.83	6.94		
HEMBA1003348	3.22	2.45	11.3	11.28	13.98	16.37		
HEMBA1003369	2.39	2.6	7	9.64	8.65	5.33		
HEMBA1003370	3.14	3.6	8.85	12.54	10.83	13.98	*	+
HEMBA1003373	1.12	1.3	3.4	2.14	5.05	2.94		
HEMBA1003376	3.75	2.83	7.71	9.83	12.46	10.39	*	+
HEMBA1003380	1.12	2.3	3.63	2.25	3.9	2.57		
HEMBA1003384	0.98	1.71	2.91	2.11	4.78	2.14		
HEMBA1003387	1.3	1.24	2.14	1.83	3.24	1.98		
HEMBA1003392	2.51	2.28	3.43	5.21	5.91	4.44	*	+
HEMBA1003395	1.02	1.45	2.84	4.06	4.29	2.18		
HEMBA1003399	1.03	1.4	3.27	3.21	3.26	2.19		
HEMBA1003400	1.36	2.22	4.64	3.23	7.19	5.22		
HEMBA1003402	1.62	1.74	3.29	2.32	4.22	2.59		
HEMBA1003403	7.13	9.32	50.9	66.1	66.81	77.49	*	+
HEMBA1003408	3.68	4.5	7.27	6.02	5.77	7.71		
HEMBA1003412	5.08	6.79	8.35	10.96	8.79	9.75		
HEMBA1003417	5.71	6.5	10.15	8.18	8.86	7.36		
HEMBA1003418	4.01	5.12	6.53	7.37	11.45	9.3	*	+
HEMBA1003420	16.29	17.91	35.46	33.32	34.37	32.89		
HEMBA1003425	0.76	1.65	3.06	2.33	3.58	2.21		
HEMBA1003433	1.4	2.43	3.34	4.88	4.54	4.09	*	+
HEMBA1003440	11.39	12.08	19.86	24.13	13.99	24.26		
HEMBA1003442	4.37	4.67	4.94	3.54	6.73	5.96		

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HEMBA1003447	7.55	9.08	49.72	65.41	63.46	65.15	*	+
HEMBA1003453	21.03	22.03	42.15	27.85	29.02	27.64		
HEMBA1003461	1.5	2.13	3.49	2.6	3.63	2.2		
HEMBA1003463	2.82	3.68	6.02	5.97	3.84	6.41		
HEMBA1003465	1.77	2.21	6.31	4.75	5.02	3.82		
HEMBA1003480	2.58	3.91	8.62	9.63	9.6	9.42		
HEMBA1003485	7.06	4.84	5.29	6.13	7.26	5.52		
HEMBA1003487	1.8	1.85	3.4	7.12	6.39	6.79	**	+
HEMBA1003492	1.42	1.95	4.11	2.41	5.87	2.1		
HEMBA1003494	9.36	8.61	12.16	18.24	18.69	17.83	**	+
HEMBA1003497	2.19	2.16	3.29	3.35	6.06	2.97		
HEMBA1003503	0.98	1.74	3.37	5.04	3.18	2.13		
HEMBA1003511	0.99	2.19	3.7	2.3	4.42	2.5		
HEMBA1003528	3.33	4	6.51	5.77	5.04	4.46		
HEMBA1003530	1.33	0.85	3.62	1.97	3.15	2.45		
HEMBA1003531	1.14	1.72	5.39	4.74	7.24	4.51		
HEMBA1003532	12.97	14.66	34.3	28.69	25.31	31.26		
HEMBA1003538	2.54	2.4	17.88	14.54	21.58	16.83		
HEMBA1003545	0.68	2.08	3.17	1.85	3.6	2.17		
HEMBA1003546	1.27	2.03	1.68	1.98	2.15	2.42		
HEMBA1003548	1.4	3.18	3.6	1.41	4.15	2.23		
HEMBA1003553	31.29	31.45	47.99	54.36	41.34	45.65		
HEMBA1003555	1.39	2.73	4.81	3.53	4.48	5.19		
HEMBA1003556	1.24	1.76	2.96	3.14	5.75	3.31		
HEMBA1003560	1.89	2.66	7.87	10.08	13.24	9.9	*	+
HEMBA1003565	54.27	66.88	96.28	121.29	139.88	148.68	*	+
HEMBA1003568	1.86	2.27	3.24	2.36	7.41	2.78		
HEMBA1003569	2.93	2.61	2.96	5.07	3.95	4.53	**	+
HEMBA1003571	3.53	2.33	3.8	5.19	5.3	5.83	*	+
HEMBA1003579	3.51	4.29	4.83	3.79	5.68	5.91		
HEMBA1003580	3.82	4.09	4.96	3.11	4.41	3.53		
HEMBA1003581	0.82	2.62	2.07	1.63	3.19	2.4		
HEMBA1003591	10.8	11.44	30.24	33.74	35.7	36.88	*	+
HEMBA1003595	0.93	1.16	2.46	2.98	4.02	2.01		
HEMBA1003597	3.15	3.18	8.74	10.82	11.39	11.59	*	+
HEMBA1003598	0.58	0.93	1.33	2.62	1.83	1.61	*	+
HEMBA1003600	3.71	4.19	13.35	14.77	13.86	16.69		
HEMBA1003602	2.84	2.64	4.89	5.89	6.97	9.14	*	+
HEMBA1003604	2.3	3.35	5.67	6.63	8.29	8.16	*	+

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HEMBA1003610	2.33	3.2	4.48	6.12	5.64	6.81	*	+
HEMBA1003615	1.76	2.61	5.23	4.95	5.21	4.96		
HEMBA1003617	3.59	3.54	8.59	6.92	11.37	8.5		
HEMBA1003620	5.76	6.01	4.98	13.48	17.69	12.58	**	+
HEMBA1003621	1.6	1.66	3.19	4.52	5.42	5.08	**	+
HEMBA1003622	0.96	0.69	1.38	1.47	3.17	2.25		
HEMBA1003630	0.78	1.02	1.95	1.68	2.97	1.55		
HEMBA1003637	0.66	1.93	2.59	2.11	3.11	2.63		
HEMBA1003640	2.33	2.1	5.27	4.16	5.68	5.5		
HEMBA1003645	1.12	1.2	4.41	2.3	3.82	3.06		
HEMBA1003646	0.94	1.21	1.76	1.25	3.25	1.8		
HEMBA1003647	0.49	2.15	3.27	2.46	3.79	2.21		
HEMBA1003656	3.32	3.77	6.96	17.01	10.45	13.78	*	+
HEMBA1003662	1.37	2.08	1.54	5.2	3.81	4.91	**	+
HEMBA1003666	23.84	17.7	51.57	21.97	21.85	24.71		
HEMBA1003667	4.74	3.63	6.03	4.61	6.22	7.09		
HEMBA1003670	0.83	0.65	1.94	1.18	2.61	1.51		
HEMBA1003674	32.16	29.41	63.99	118.95	138.25	123.17	**	+
HEMBA1003677	1.84	2.06	4.28	2.32	5.31	3.78		
HEMBA1003679	1.2	1.68	3.72	2.22	6.19	3.23		
HEMBA1003680	4.55	4.68	20.52	27.26	28.13	28.07	*	+
HEMBA1003684	1.57	1.9	3.98	4	3.65	4.47		
HEMBA1003690	6.22	7.41	8.65	7.94	9.93	7.33		
HEMBA1003692	2.41	3.82	7.23	8	8.28	7.7		
HEMBA1003702	2.64	3.82	4.83	7.11	6.86	6.07	*	+
HEMBA1003711	1.06	1.21	3.39	2.93	3.88	2.37		
HEMBA1003714	1.31	1.26	2.13	1.61	2.45	1.42		
HEMBA1003715	1.46	2.7	6.58	10.21	9.15	6.87	*	+
HEMBA1003717	1.91	2.31	3.91	3.03	3.66	4.38		
HEMBA1003720	0.81	2.6	5.07	4.16	4.16	4.21		
HEMBA1003725	0.83	1.57	2.47	3.22	4.91	3.17	*	+
HEMBA1003728	1.28	2.48	3.4	2.65	4.36	2.72		
HEMBA1003729	0.98	2.35	2.85	3.6	4.36	3.52	*	+
HEMBA1003732	1.11	1.52	3.49	3.01	2.75	1.88		
HEMBA1003733	1.18	1.9	2.94	3.7	4.95	3.92	*	+
HEMBA1003742	5.15	7.3	5.95	21.53	22.58	19.56	**	+
HEMBA1003743	1.37	1.76	3.21	4.13	4.36	3.68	*	+
HEMBA1003758	3.26	3.29	11.72	10.07	16.03	12.24		
HEMBA1003760	0.82	2.43	3.09	1.92	4.19	3.16		

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HEMBA1003764	0.88	2.06	4.9	1.86	4.36	4.24		
HEMBA1003769	6.61	8.95	15.57	22.58	17.05	20.77	*	+
HEMBA1003773	2.16	3.5	4.48	5.8	6.7	5.98	*	+
HEMBA1003783	3.12	3.11	4.95	8.58	8.64	8.27	**	+
HEMBA1003784	0.46	1.37	2.89	2.37	2.45	1.77		
HEMBA1003794	3.48	3.61	13.64	11.98	11.61	15.55		
HEMBA1003799	1.09	1.05	4.29	2.44	5.06	3.76		
HEMBA1003803	7.58	6.67	12.05	11.68	7.64	8.41		
HEMBA1003804	1.08	2.53	4.45	1.86	3.35	2.05		
HEMBA1003805	6.41	7.87	10.45	15.74	7.09	11.93		
HEMBA1003807	1.52	1.53	3.21	2.71	6.32	2.37		
HEMBA1003810	1.72	3.29	6.06	5.98	4.85	4.55		
HEMBA1003827	2.71	4.55	12.08	13.28	10.48	15.35		
HEMBA1003836	3.42	4.84	10.27	11.16	12.81	9.96		
HEMBA1003838	16.58	16.15	31.32	34.24	33.25	35.46		
HEMBA1003843	4.6	6.54	7.01	13.61	6.48	11.42		
HEMBA1003846	19.54	21.94	61.32	72.86	70.58	83.4	*	+
HEMBA1003856	1.41	1.66	2.85	2.07	4.03	2.51		
HEMBA1003857	2.89	3.1	5.85	5.89	8.29	6.88		
HEMBA1003864	1.56	2.61	4.04	3.32	4.03	2.75		
HEMBA1003866	0.89	0.75	2.21	1.66	2.23	0.73		
HEMBA1003868	10.92	10.88	18.59	13.26	7.59	15.72		
HEMBA1003879	0.95	1.33	3.16	3.49	4.42	3.09		
HEMBA1003880	1.81	2.35	2.78	3.53	4.78	2.3		
HEMBA1003884	10.97	11.37	39.03	54.69	62.46	57.8	*	+
HEMBA1003885	4.59	4.82	7.14	9.19	6.32	8.41		
HEMBA1003887	3.58	4.93	7.7	8.65	7.93	8.18		
HEMBA1003890	4.2	4.48	7.18	7.53	9.1	6.26		
HEMBA1003893	4.38	6.39	9.53	8.75	13.24	9.94		
HEMBA1003896	4.15	4.15	10.62	7.4	9.12	6.43		
HEMBA1003902	1.39	3.78	5.09	4.91	6.42	5.1		
HEMBA1003904	0.87	2.16	2.46	2.82	4.32	2.11		
HEMBA1003908	1.18	1.3	2.89	2.12	5.25	1.43		
HEMBA1003926	14.46	12.2	39.79	45.5	34.97	55.56		
HEMBA1003937	2.75	3.31	5.38	4.3	6.85	4.57		
HEMBA1003939	2.43	2.48	6.56	8.3	13.32	8.04		
HEMBA1003940	2.45	3.08	5.01	4.29	6.22	5.55		
HEMBA1003941	1.4	2.26	2.48	3.37	4.57	4.42	*	+
HEMBA1003942	1.63	2.88	3.13	2.01	3.85	2.22		

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HEMBA1003945	12.57	13.75	22.75	20.99	14.77	19.74		
HEMBA1003949	1.4	1.9	3.53	3.29	6.22	4.14		
HEMBA1003950	3.46	4.86	6.49	14.69	17.53	13.02	**	+
HEMBA1003953	1.91	1.6	5.14	0.72	3.97	1.44		
HEMBA1003958	5.16	3.6	7.47	7.54	9.45	6.64		
HEMBA1003959	2.42	2.72	5.72	5.5	5.5	9.02		
HEMBA1003960	3.25	5.81	34.7	24.04	26.4	28.28		
HEMBA1003966	9.63	8.28	16.73	16.75	17.67	19.84		
HEMBA1003967	1.75	3.06	3.47	3.48	3.6	3.27		
HEMBA1003968	0.97	2.14	2.55	2.49	4.56	1.82		
HEMBA1003974	634.2	699.64	821.36	986.231	340.97	1248.21	*	+
HEMBA1003976	1.05	1.84	3.36	1.21	3.27	2.04		
HEMBA1003977	1.48	2.07	1.99	1.41	3.49	2.15		
HEMBA1003978	2.91	3.72	3.54	3.77	6.18	3.53		
HEMBA1003981	9.01	6.77	14.06	12.05	11.49	18.27		
HEMBA1003982	102.64	103.61	302.15	380.08	375.9	466.69	*	+
HEMBA1003985	1.18	1.9	2.43	3.21	3.79	2.18		
HEMBA1003987	3.04	2.23	3.1	2.56	4.34	5.53		
HEMBA1003989	1.62	1.77	4.56	3.79	5.12	3.31		
HEMBA1004000	1.63	2.35	5.05	3.46	5.35	4.18		
HEMBA1004006	2.79	2.88	12.86	16.29	22.13	19.73	*	+
HEMBA1004007	0.7	1.92	5.28	3.03	5.18	4.72		
HEMBA1004010	67.4	61.25	98.24	112.56	96.78	136.86		
HEMBA1004011	0.48	1.74	2.18	2.58	3.29	1.62		
HEMBA1004012	0.79	1.84	2.3	3.11	4.8	3.53	*	+
HEMBA1004015	2.68	4.15	5.38	8.68	10.65	9.21	**	+
HEMBA1004024	1.47	2.73	5.65	5.68	8.26	8.07		
HEMBA1004029	1.93	3.1	3.03	4.6	8.38	13.11		
HEMBA1004038	1.04	1.24	1.55	1.18	3.38	1.59		
HEMBA1004042	0.89	1.42	2.22	1.58	4	2.48		
HEMBA1004045	0.28	0.94	2.42	3.07	3.32	2.53		
HEMBA1004048	4.16	4.16	12.1	19.93	14.84	22.3	*	+
HEMBA1004049	3.56	3.18	4.87	4.92	6.83	5.48		
HEMBA1004051	136.19	118.77	205.49	243.62	283.22	223.29	*	+
HEMBA1004053	5.11	4.64	8.92	25.25	27.24	21	**	+
HEMBA1004055	2.28	3.2	4.24	2.15	5.51	2.86		
HEMBA1004056	3.78	3.07	6.73	5.3	10.99	9.56		
HEMBA1004060	0.86	1	1.7	0.78	3.94	1.65		
HEMBA1004061	4.76	3.94	6.44	7.37	12.64	8.57		

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HEMBA1004067	10.12	14.76	90.67	108.89	125.21	128.6	*	+
HEMBA1004071	7.51	7.77	16.52	17.31	12.23	13.37		
HEMBA1004074	0.78	1.93	3.97	4.48	7.06	5.69	*	+
HEMBA1004078	3.87	2.95	5.22	6.52	6.2	6.87	*	+
HEMBA1004085	1.05	1.19	2.83	3.57	4.57	2.45		
HEMBA1004086	3.38	4.95	6	8.92	8.09	6.51	*	+
HEMBA1004097	1.18	1.13	2.97	3.66	3.28	2.97		
HEMBA1004100	3.85	4.81	8.96	6.9	9.64	9.55		
HEMBA1004103	2	2.91	6.25	6.25	7.24	7.38		
HEMBA1004110	3	3.77	5.43	4.18	4.23	5.02		
HEMBA1004111	3.96	7.64	44.2	53.81	60.1	57.3	*	+
HEMBA1004124	7.14	10.51	60.12	83.27	97.96	83.59	*	+
HEMBA1004130	3.12	3.46	10.29	9.45	6.84	8.43		
HEMBA1004131	2.14	2.12	3.06	4.08	3.73	3.21	*	+
HEMBA1004132	0.77	2.22	4.84	3.94	6.31	4.2		
HEMBA1004133	0.69	1.77	2.56	3.28	5.17	3.22		
HEMBA1004138	0.89	1.19	3.05	2.21	4.11	1.83		
HEMBA1004143	7.1	7.48	17.43	18.83	15	17.6		
HEMBA1004146	0.89	2.03	3.01	2.96	4.21	2.69		
HEMBA1004148	1.85	1.57	2.13	2.25	3.38	1.99		
HEMBA1004149	1.54	1.44	2.77	2.83	2.59	3.32		
HEMBA1004150	0.49	1.06	2.15	2.31	1.58	1.08		
HEMBA1004154	2.24	1.64	5.28	6.28	7.07	4.61		
HEMBA1004164	1.84	2.23	5.63	6.89	7.13	5.81		
HEMBA1004168	2.16	2.24	4.69	3.9	5.32	7.84		
HEMBA1004199	1.37	1.92	2.34	3.17	3.66	1.8		
HEMBA1004200	0.84	1.98	3	1.5	4.05	1.78		
HEMBA1004201	4.87	5.68	17.64	26.94	32.17	25.65	*	+
HEMBA1004202	7.7	10.5	9.9	18.08	16.29	15.77	**	+
HEMBA1004203	1.63	2.31	3.66	4.5	5.3	4.44	*	+
HEMBA1004207	1.9	3.24	3.62	5.73	6.23	6.2	**	+
HEMBA1004210	1.13	1.72	2.67	1.95	4.14	1.87		
HEMBA1004225	1.1	2.47	5.23	5.96	7.12	5.4		
HEMBA1004227	2.17	4.44	3.86	5.14	5.71	5.16		
HEMBA1004235	2.68	2.91	3.74	5.79	5.78	4.44	*	+
HEMBA1004237	3	3.31	5.23	5.95	4.67	5.47		
HEMBA1004238	2.06	3.24	5.93	5.84	7.64	6.52		
HEMBA1004241	2.32	3.09	3.87	2.74	3.74	3.35		
HEMBA1004242	8.66	13.05	20.15	26.83	32.28	26.48	*	+

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HEMBA1004243	1.8	2.09	3.58	2.8	3.03	2.76		
HEMBA1004246	1.6	2.68	5.65	6.18	6.24	6.15		
HEMBA1004247	0.89	2.73	3.74	3.69	4.23	3.37		
HEMBA1004248	4.01	3.54	3.85	5.91	8.31	7.47	**	+
HEMBA1004250	1.55	2.16	2.87	1.91	5.22	1.47		
HEMBA1004252	3.57	3.27	4.8	4.64	5.79	4.28		
HEMBA1004260	2.56	3.08	6.87	7.32	8.16	7.61		
HEMBA1004264	1.26	2.11	2.59	2.16	2.86	1.37		
HEMBA1004267	5.5	5.81	14.29	14.22	12.19	11.57		
HEMBA1004272	1.75	2.31	3.31	2.26	3.84	2.04		
HEMBA1004274	5.83	8.13	58.69	77.19	87.61	76.22	*	+
HEMBA1004275	1	5.4	3.34	1.49	4.49	2.42		
HEMBA1004276	2.27	2.2	3.42	3.45	4.2	3.06		
HEMBA1004279	2.13	2.33	4.37	3.29	5.2	3.88		
HEMBA1004284	1.78	2.56	6.03	4.16	4.9	5.23		
HEMBA1004286	1.41	1.35	2.44	1.65	3.55	2.1		
HEMBA1004289	2.58	4.17	5.59	5.16	7.18	8.44		
HEMBA1004293	20.24	18.64	51.03	77.3	52.39	74.25	*	+
HEMBA1004295	1.08	2.65	3.08	2.73	4.02	2.05		
HEMBA1004302	0.72	1.84	2.29	1.21	3.39	1.49		
HEMBA1004306	2.11	3.01	5.96	3.99	5.74	6.01		
HEMBA1004312	1.3	1.58	4.98	3.57	3.56	3.56		
HEMBA1004314	1.78	1.86	4.1	3.35	6.23	4.38		
HEMBA1004321	0.88	1.66	2.56	4.05	4.15	4.82	**	+
HEMBA1004323	2.4	3.16	4.7	4.77	5.29	5.1		
HEMBA1004327	1.18	1.78	3.23	3.51	4.46	3.1		
HEMBA1004329	5.57	6.73	15.22	16.29	15.33	15.14		
HEMBA1004330	3.93	3.54	4.06	5.87	7.54	5.36	*	+
HEMBA1004334	2.92	3.63	4.69	4.18	4.74	6.06		
HEMBA1004335	1.15	1.77	5.1	3.04	4.75	3.14		
HEMBA1004341	1.01	1.1	1.25	1.13	3.34	1.14		
HEMBA1004344	29.93	34.05	68.18	74.25	94.77	82.54	*	+
HEMBA1004347	0.67	1.65	2.21	2.31	2.25	2.78		
HEMBA1004349	12.07	11.55	22.26	19.39	22.71	24.41		
HEMBA1004352	2.06	2.56	6.96	6.05	6.92	6.58		
HEMBA1004353	10.21	14.95	25.3	19.64	26.63	25.83		
HEMBA1004354	1.9	2.56	6.29	5.42	6.94	5.83		
HEMBA1004356	5.75	6.89	9.43	20.06	19.7	20.1	**	+
HEMBA1004360	1.35	1.16	2.73	1.23	4.23	2.26		

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HEMBA1004366	1.97	1.91	3.57	4.53	6.9	4.73	*	+
HEMBA1004372	0.3	0.67	1.03	2.04	1.85	0.96		
HEMBA1004377	6.57	5.58	10.48	16.45	11.58	13.72	*	+
HEMBA1004389	8.39	7.87	13.69	16.87	19.3	11.15		
HEMBA1004391	1.18	0.88	1.37	1.27	4.23	2.34		
HEMBA1004393	65.85	84.9	114.17	77.61	53.19	85.8		
HEMBA1004394	0.84	1.14	1.88	1.68	3.9	2.59		
HEMBA1004396	1.62	0.82	3.24	2.43	5.44	2.15		
HEMBA1004401	4.33	4.37	5.25	8.95	14.42	11.05	*	+
HEMBA1004405	3.86	2.57	5.7	7.45	7.46	9.38	*	+
HEMBA1004408	4.27	2.66	5.34	7.19	8.8	9.85	*	+
HEMBA1004414	1.72	1.74	5.93	9.48	8.98	13.19	*	+
HEMBA1004429	2.95	3.96	4.23	4.68	6.9	6.8	*	+
HEMBA1004433	1.27	1.43	2.98	2.55	2.65	3.47		
HEMBA1004440	1.33	1.33	2.62	2.3	2.63	1.79		
HEMBA1004444	2.73	1.9	4.47	4.64	5.38	4.66		
HEMBA1004446	1.37	0.95	2.26	1.84	2.94	3.19		
HEMBA1004451	3.79	7.37	7.66	12.15	9.81	9.87	*	+
HEMBA1004452	0.71	1.96	2.89	3.53	8.91	2.36		
HEMBA1004454	1.56	1.71	3.06	2.81	4.83	4.1		
HEMBA1004460	1.91	3.49	7.49	4.39	6.91	5.19		
HEMBA1004461	1	1.87	1.43	1.09	3.95	1.99		
HEMBA1004468	3.22	4.71	7.36	9.92	12.73	8.79	*	+
HEMBA1004479	1.02	1.38	2.44	2.59	5.99	3.42		
HEMBA1004482	2.77	1.93	5.5	5.62	5.83	5.6		
HEMBA1004491	6.18	5.55	13	12.32	15.5	15.72		
HEMBA1004499	9.09	12.56	65.85	86.22	91.62	102.95	*	+
HEMBA1004502	1.81	1.9	4.82	3.14	4.83	2.49		
HEMBA1004505	1.57	2.42	4.6	4.78	7.66	4.09		
HEMBA1004506	0.96	2.32	3.48	3.28	5.58	2.73		
HEMBA1004507	29.33	30.94	74.36	85.26	112.08	83.25	*	+
HEMBA1004509	1.62	2.92	3.8	5.09	5.19	4.5	*	+
HEMBA1004523	1.04	1.68	1.65	1.82	3.64	3.02		
HEMBA1004528	9.41	10.46	59.94	86.06	89.35	98.27	*	+
HEMBA1004534	6.43	9.06	20.99	14.78	16.24	20.46		
HEMBA1004536	1.91	1.91	4.04	2.58	5.65	4.53		
HEMBA1004538	10.84	12.11	16.22	14.06	12.69	14.98		
HEMBA1004542	4.37	3.88	23.08	31.45	41.94	35.14	*	+
HEMBA1004552	2.98	1.35	4.27	9.89	9.44	7.1	**	+

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HEMBA1004554	1.21	1.05	2.53	1.91	7.29	2.16		
HEMBA1004558	2.98	4.6	12.99	21.19	21.7	23.66	**	+
HEMBA1004560	1.74	2.06	4.16	3.47	6.18	4.25		
HEMBA1004564	4.31	3.3	8.73	7.27	9.96	8.65		
HEMBA1004566	50.51	49.26	83.43	126.94	55.59	138.13		
HEMBA1004573	1.07	1.97	3.91	2.91	4.11	2.3		
HEMBA1004576	3.68	3.22	10.49	4.73	5.64	3.11		
HEMBA1004577	6.11	7.2	14	11.74	13.04	10.71		
HEMBA1004586	1.56	1.32	5.09	5.01	6.65	4.67		
HEMBA1004596	3.97	3.19	19.1	27.4	39.04	32.16	*	+
HEMBA1004604	9.04	8.14	40.08	64.86	69.99	62.02	*	+
HEMBA1004607	0.96	1.97	4.17	3.02	4.39	3.96		
HEMBA1004610	1.16	1.89	3.19	2.91	4.8	2.64		
HEMBA1004617	0.78	0.89	3.29	2.77	4.53	2.51		
HEMBA1004622	1.05	2.39	5.1	4.07	5.84	5.04		
HEMBA1004626	1.56	2.36	4.75	4.06	4.93	2.33		
HEMBA1004629	1.5	1.34	3.95	3.17	4.58	2.74		
HEMBA1004631	1.57	1.73	4.41	3.3	5.73	4.97		
HEMBA1004632	1.02	1.3	3.43	2.38	3.64	2.36		
HEMBA1004633	3.2	3.98	8.84	9.3	9.04	10.74		
HEMBA1004636	1.29	2.07	3.22	3.23	3.61	6.58		
HEMBA1004637	1.57	2.12	4.19	3.97	4.85	2.39		
HEMBA1004638	1.31	1.67	3.26	1.8	4.24	1.52		
HEMBA1004645	3.04	2.88	6.5	5.07	6.21	5.08		
HEMBA1004656	4.38	2.76	4.96	4.13	4.58	3.39		
HEMBA1004657	16.78	17.12	35.48	31.85	17.55	22.74		
HEMBA1004666	1.27	2.2	3.32	2.78	4.52	1.44		
HEMBA1004669	2.49	3.6	6.16	7.32	8.34	5.55		
HEMBA1004670	3.1	2.74	6.27	5.11	6.96	3.3		
HEMBA1004672	1.29	2.33	4.85	2.58	7.25	3.63		
HEMBA1004689	23.54	21.34	82.29	90.21	98.37	106.84		
HEMBA1004690	4.74	5.24	15.26	19.89	22.39	20.76	*	+
HEMBA1004693	3.16	5.98	25.39	24.92	35.74	32.68		
HEMBA1004697	1.64	1.96	4.88	7.14	9.69	4.03		
HEMBA1004702	8.73	11.47	19.57	19.47	14.63	11.2		
HEMBA1004704	1.9	3.35	9.01	3.41	5.17	5.36		
HEMBA1004705	1.13	1.93	3.32	1.8	4.34	1.54		
HEMBA1004706	1.34	2.4	3.89	4.31	6.23	4.7		
HEMBA1004709	2.96	2.9	10.14	6.81	8.65	6.93		

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HEMBA1004711	1.22	1.44	5.01	1.19	3.14	3.28		
HEMBA1004723	4.91	5.18	10.06	11.37	16.92	12.96	*	+
HEMBA1004725	4.14	4.9	7.68	5.67	8.62	8.54		
HEMBA1004730	3.57	2.83	4.74	3.64	8.59	4.41		
HEMBA1004733	1.07	2.64	2.62	1.06	3.54	2.45		
HEMBA1004734	2.57	3.22	4.46	2.68	5.28	5.32		
HEMBA1004736	1.1	1.89	7.12	3.87	12.1	5.09		
HEMBA1004748	2.24	0.94	5.6	3.02	5.22	2.83		
HEMBA1004749	6.88	8.33	19.68	16.49	19.03	23.29		
HEMBA1004751	1.96	1.76	5.55	3.99	9.86	5.04		
HEMBA1004752	1.51	1.6	4.23	4.56	4.11	3.32		
HEMBA1004753	29.15	25.19	85.53	59.89	62.5	95.58		
HEMBA1004755	7.02	6.32	12.37	9.73	12.72	14.63		
HEMBA1004756	1.45	1.76	3.86	2.34	5.21	2.17		
HEMBA1004758	1.18	1.64	4.53	3.92	5.65	3.17		
HEMBA1004763	1.79	2.39	5.56	5.45	6.53	6.09		
HEMBA1004768	0.83	1.64	2.89	1.69	4.26	1.38		
HEMBA1004770	1.09	1.36	2.43	1.47	3.53	1.94		
HEMBA1004771	0.99	1.02	2.44	2.18	3.26	2.57		
HEMBA1004775	4.07	3.84	7.29	8.61	9.62	13.74	*	+
HEMBA1004776	1.86	3.21	3.33	3.95	6.83	6.04	*	+
HEMBA1004778	1.75	2.24	6.11	3.21	7.64	5.74		
HEMBA1004784	1.51	1.59	3.11	2.36	4.18	3.62		
HEMBA1004785	1	1.78	4.15	2.18	6.54	4.48		
HEMBA1004789	2.34	2.07	4.42	1.87	5.64	2.87		
HEMBA1004795	0.62	1.89	3.13	2.45	4.23	1.42		
HEMBA1004797	1.06	0.84	1.85	2.31	2.85	2.76	*	+
HEMBA1004803	4.98	1.72	5.31	4.62	9.79	4.82		
HEMBA1004806	1.23	1.78	3.22	2.36	3.83	2.33		
HEMBA1004807	3.05	1.95	3.86	5.58	7.44	4.14		
HEMBA1004816	4.73	2.61	3.59	3.78	7.97	9.34		
HEMBA1004820	1.73	2.33	4.6	2.97	8.74	3.71		
HEMBA1004833	1.22	1.23	5.54	2.71	6.95	4.37		
HEMBA1004847	4.73	2.8	9.84	8	11.83	9.15		
HEMBA1004850	1.01	1.78	6.15	6.56	13.54	6.38		
HEMBA1004863	1.75	2.3	4.92	3.34	4.45	5.17		
HEMBA1004864	2.66	3.91	6.68	4.19	9.03	6.51		
HEMBA1004865	1.13	2.61	4.06	3.86	6.64	3.38		
HEMBA1004880	2.22	3.32	9.22	9.9	10.38	9.48		

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HEMBA1004882	5.8	7.1	10.16	15.5	15.77	12.03	*	+
HEMBA1004885	2.34	6	8.67	8.58	8.67	9.27		
HEMBA1004889	3.25	3.24	6.5	7.67	10.74	9.8	*	+
HEMBA1004900	1.51	1.59	3.71	3.21	5.14	2.84		
HEMBA1004909	0.71	1.96	3.59	3.21	4.47	4.97		
HEMBA1004918	1.46	1.7	4.93	4.03	7.19	5.77		
HEMBA1004923	1.1	1.83	3.72	3.98	7.3	4.27		
HEMBA1004929	1.01	1.7	2.68	1.66	3.59	1.38		
HEMBA1004930	1.4	2.06	4.31	3.91	5.87	4.72		
HEMBA1004933	2.41	1.5	5.32	5.59	5.43	3.38		
HEMBA1004934	8.61	8.61	17.67	26.2	27.77	26.83	**	+
HEMBA1004937	1.36	2.42	3.57	2.79	7.51	2.54		
HEMBA1004943	1.11	1.75	3.63	2.56	4.88	3.68		
HEMBA1004944	0.95	2.51	4.73	3.85	4.79	3.58		
HEMBA1004946	4.78	4.38	12.5	12.69	14.08	12.8		
HEMBA1004952	0.9	1.83	4.04	2.76	4.41	2		
HEMBA1004954	3.55	3.21	7.92	6.02	6.4	6.12		
HEMBA1004956	1.37	1.11	2.78	2.12	3.66	1.81		
HEMBA1004960	0.86	0.75	3.27	4.17	6.72	3.06		
HEMBA1004971	2.41	2.49	6.81	6.45	8.05	6.92		
HEMBA1004972	2.57	2.31	3.63	2.07	5.66	5.84		
HEMBA1004973	1.16	1.78	3.46	2.53	3.27	3.18		
HEMBA1004977	3.04	3.08	5.36	5.34	6.29	6.36		
HEMBA1004978	4.53	5.08	14.93	21.43	19.01	25.37	*	+
HEMBA1004980	1.92	2.36	7.92	6.55	6.55	7.29		
HEMBA1004982	0.83	1.36	2.92	2.8	4.45	2.65		
HEMBA1004983	1.73	1.88	4.29	3.92	5.5	4.21		
HEMBA1004995	2.76	3.99	6.53	7.5	7.46	7.41		
HEMBA1005004	1.63	3.57	5.12	3.45	5.72	4.07		
HEMBA1005008	1.61	3.52	4.9	4.61	6.42	5.97		
HEMBA1005009	4.55	3.9	8.37	11.95	6.96	9.22		
HEMBA1005019	3.1	2.57	5.78	6.6	8.07	7.19	*	+
HEMBA1005021	16.12	17.89	30.44	29.81	23.38	23.26		
HEMBA1005029	3.13	3.42	7.98	7.23	8.66	6.52		
HEMBA1005035	6.53	6.29	19.38	18.59	17.77	20.38		
HEMBA1005036	19.87	20.39	37.72	23.12	19.26	26.98		
HEMBA1005039	1.7	3.19	4.59	4.36	6.81	3.69		
HEMBA1005047	4.31	4.06	5.6	7.01	8.54	7.83	**	+
HEMBA1005050	2	2.93	5.07	4.33	6.76	4.39		

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HEMBA1005062	2.48	3.06	5.62	2.85	5.13	2.03		
HEMBA1005066	2.28	2.55	5.72	4.81	8.94	6.89		
HEMBA1005067	5.81	10.37	17.44	25.77	30.77	26.84	*	+
HEMBA1005070	3.33	3.01	8.9	8.51	8.13	6.59		
HEMBA1005075	1.29	2.45	6.51	3.97	5.38	4.49		
HEMBA1005078	7.47	6.74	14.34	14.89	9.95	11.01		
HEMBA1005079	5.52	5.68	13.65	14.98	16.02	21.42		
HEMBA1005083	0.94	0.97	2.69	2.17	4.96	1.25		
HEMBA1005084	5.36	4.49	8.84	7.48	10.38	9.99		
HEMBA1005088	1.63	1.64	7.16	3.48	6.18	4.54		
HEMBA1005089	3.12	3.47	5.53	5.04	9	5.52		
HEMBA1005090	5.92	5.56	11.7	17.14	12.91	21.06	*	+
HEMBA1005096	0.88	2.47	3.98	3.35	3.94	2.88		
HEMBA1005101	2.29	2.08	4.54	3.23	5.6	4.54		
HEMBA1005107	1.2	1.92	3.2	2.25	4.48	2.3		
HEMBA1005113	0.96	2.18	3.35	2.12	5.53	2.72		
HEMBA1005123	3.35	3.46	10.83	9.05	10.41	8.28		
HEMBA1005133	2.6	2.26	7.59	5.11	4.58	7.09		
HEMBA1005135	1.19	2.77	3.35	1.47	5.28	3.69		
HEMBA1005145	5.84	6.38	12.56	13.06	14.71	17.84		
HEMBA1005149	4.21	3.2	7.92	6.51	8.54	8.47		
HEMBA1005152	1.81	3.06	3.59	3.31	5.05	3.39		
HEMBA1005159	1.76	1.96	3.62	2.2	8.12	2.2		
HEMBA1005172	120.6	113.48	240.76	174.65	194.57	222.24		
HEMBA1005185	3.16	2.05	4.47	3.54	6.7	4.15		
HEMBA1005186	1.55	2.65	3.96	3.52	8.39	2.03		
HEMBA1005195	2.15	1.08	3.76	1.93	6.73	2.24		
HEMBA1005201	3.27	3.45	8.02	5.52	7.17	8.91		
HEMBA1005202	5.93	4.58	9.4	8.29	9.76	12.83		
HEMBA1005204	86.99	67.86	141.56	134.68	133.57	172.39		
HEMBA1005206	6.39	5.08	66.26	72.89	92.07	89.66	*	+
HEMBA1005219	4.62	6.56	14.55	15.66	21.85	17.87	*	+
HEMBA1005223	2.4	1.91	4.92	1.7	3.83	3.86		
HEMBA1005229	1.18	2.32	3.12	1.57	4.88	2.32		
HEMBA1005230	1.22	1.56	4.24	2.71	5.92	4.32		
HEMBA1005232	0.86	1.13	1.6	0.91	3.81	2.17		
HEMBA1005238	0.84	1.77	2.67	2.16	3.27	2.29		
HEMBA1005241	2.77	2.68	7.42	7.63	11.38	7.62		
HEMBA1005244	0.87	1.97	5.63	2.57	8.33	6.19		

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HEMBA1005246	8.84	7.84	17.94	12.96	18.21	14.79		
HEMBA1005251	3.06	2.57	6.81	6.6	8.47	7.24		
HEMBA1005252	2.3	2.7	5.31	4.73	11.4	5.01		
HEMBA1005267	2.77	3.31	7.25	6.77	12.66	9.89		
HEMBA1005274	1.75	1.53	3.28	4.8	6.38	6.51	**	+
HEMBA1005275	0.62	1.27	1.59	1.63	3.44	2.12		
HEMBA1005288	3.03	1.16	6.1	6.49	6.35	6.68		
HEMBA1005293	1.46	1.37	2.53	1.5	4.09	1.78		
HEMBA1005296	440.88	422.67	780.14	598.1	568.79	483.77		
HEMBA1005301	3.93	3.26	29.41	28.17	47.57	44.12		
HEMBA1005304	1.75	2.3	7	3.36	7.29	7.62		
HEMBA1005305	0.77	1.18	2.57	0.74	3.99	1.71		
HEMBA1005311	0.97	1.05	2.08	0.81	1.97	2.13		
HEMBA1005313	20.35	21.96	39.64	29.02	19.54	26.39		
HEMBA1005314	1	1.36	2.6	2.2	4.08	1.99		
HEMBA1005315	0.81	2.41	4.27	1.95	5.32	3.59		
HEMBA1005317	0.8	1.48	2.93	1.9	3.68	2.43		
HEMBA1005318	1.42	0.95	2.68	1.48	4.54	2.21		
HEMBA1005324	6.24	8.79	28.39	48.36	52.86	57.05	**	+
HEMBA1005331	2.77	5.64	15.05	21.73	18.68	21.33	*	+
HEMBA1005337	12.1	12.25	61.94	98.25	113.65	125.54	*	+
HEMBA1005338	4.53	4.54	27.15	34.04	35.53	42.4	*	+
HEMBA1005344	2.75	2.57	5.08	4.17	4.16	3.3		
HEMBA1005353	1.15	2.78	6.52	4.66	7.21	6.44		
HEMBA1005359	2.6	2.82	7.48	6.59	8.03	7.68		
HEMBA1005362	1.06	2.73	4.93	7.3	11.27	8.37	*	+
HEMBA1005364	0.96	1.48	3	2.55	3.78	2.75		
HEMBA1005367	0.96	1.53	4.19	3.3	4.21	2.99		
HEMBA1005372	1	2.24	4.18	2.3	5.1	3		
HEMBA1005374	2.29	3.31	7.83	6.4	6.45	8.09		
HEMBA1005379	3.19	3.61	7.65	29.57	25.57	24.46	**	+
HEMBA1005382	9.85	11.52	79.62	88.72	86.53	120.52		
HEMBA1005384	1.44	1.76	3.4	2.78	3.74	2.78		
HEMBA1005386	1.52	2.67	4.54	4.17	4.66	4.84		
HEMBA1005389	1.1	0.8	3.01	2.51	4.09	3.75		
HEMBA1005394	1.64	2.32	5	8.09	10.03	6.99	*	+
HEMBA1005403	4.19	4.24	8.81	8.46	11.37	8.87		
HEMBA1005408	1.43	1.71	5.3	4.52	7.12	6.96		
HEMBA1005410	1.06	1.74	3.22	1.78	4.97	2.42		

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HEMBA1005411	1.38	2.58	4.54	2.84	4.09	2.74		
HEMBA1005423	4.14	5.87	4.72	12.75	8.59	11.04	*	+
HEMBA1005426	0.71	1.79	2.35	2.08	3.25	4.15		
HEMBA1005427	9.12	12.47	24.08	37.26	33.57	35.43	*	+
HEMBA1005430	1.71	1.43	3.23	3.26	4.07	4.78		
HEMBA1005438	1.42	2.33	4.26	4.01	5.41	2.66		
HEMBA1005443	15.57	16.88	35.83	20.61	27.42	29.93		
HEMBA1005447	1.55	1.95	3.42	2.25	5.9	3		
HEMBA1005449	1.5	1.36	3.29	1.82	5.83	3.21		
HEMBA1005452	8.96	10.79	63.65	107.56	94.42	105.84	*	+
HEMBA1005454	4.73	4.51	7.91	6.37	8.12	5.33		
HEMBA1005468	2.49	3.19	4	3.6	4.93	4.86		
HEMBA1005469	1.39	1.89	5.38	3.44	5.94	4.04		
HEMBA1005472	4.04	4.76	7.81	6.79	6.75	8.2		
HEMBA1005474	4.91	5.42	11.67	7.77	9.4	9.23		
HEMBA1005475	7.8	7.09	11.75	15.34	10.75	13.59		
HEMBA1005489	2.47	3.48	4.94	6.34	7	6.54	*	+
HEMBA1005497	0.65	1.97	3.47	2.86	4.42	2.14		
HEMBA1005500	4.64	4.25	11.48	9.17	13.98	10.59		
HEMBA1005506	3.88	2.15	4.02	2.71	3.57	1.29		
HEMBA1005508	5.79	7.67	13.3	11.65	14.52	10.99		
HEMBA1005511	2.97	2.29	9	4.36	6.36	6.14		
HEMBA1005513	6.3	9.05	55.46	50.46	60.73	57.45		
HEMBA1005517	1.8	2.89	3.88	4.37	6.41	3.74		
HEMBA1005518	1.48	2.49	3.94	2.94	5.22	2.3		
HEMBA1005520	1.89	3.19	8.8	8.37	10.13	9.32		
HEMBA1005522	1.78	2.29	3.37	2.52	4.72	1.45		
HEMBA1005526	3.24	2.8	6.25	4.37	7.26	4.58		
HEMBA1005528	8.59	16.13	16.28	20.24	22.18	20.01		
HEMBA1005530	2.28	3.62	5.13	4.91	7.75	4.51		
HEMBA1005538	11.07	10.7	15.34	8.46	4.44	5.89	*	-
HEMBA1005539	30.73	31.96	63.32	50.52	49.29	34.26		
HEMBA1005545	1.2	1.08	3	4.28	6.22	2.25		
HEMBA1005548	2.38	2.88	11.1	11.04	12.72	9.21		
HEMBA1005552	2.76	4.58	12.05	9.13	12.8	10.25		
HEMBA1005558	1.59	2	5.86	2.18	6.97	4.17		
HEMBA1005568	3.11	2.96	8.24	6.28	8.45	7.5		
HEMBA1005570	1.87	2.75	3	1.96	4.49	7.13		
HEMBA1005576	1.74	2.8	2.4	3.03	3.55	3.57	*	+

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HEMBA1005577	1.14	2.02	2.78	0.95	3.08	0.87		
HEMBA1005581	4.29	4.22	6.85	14.27	18.37	8.15		
HEMBA1005582	2.74	2.57	5.35	3.25	7.91	3.21		
HEMBA1005583	2.47	3.31	5.86	3.32	6.43	3.44		
HEMBA1005588	2.51	2.85	6.27	5	6.54	6.14		
HEMBA1005593	1.5	1.4	2.85	1.83	4.57	2.89		
HEMBA1005595	2.62	2.82	4.15	3.31	4.65	4.76		
HEMBA1005597	4.77	5.18	8.13	9.39	10.34	8.64	*	+
HEMBA1005606	2.29	2.76	5.79	3.96	6.91	5.83		
HEMBA1005609	2.84	2.64	6.61	4.19	5.77	6.81		
HEMBA1005616	2.01	1.66	8.03	5.44	8.75	7.03		
HEMBA1005621	2.43	1.91	4.42	4.13	6.24	2.7		
HEMBA1005627	3.84	3.92	11.61	9.73	15.14	14.89		
HEMBA1005628	12.1	12.91	20.55	17.92	23.35	18.08		
HEMBA1005631	13.47	11.94	26.82	22.77	22.87	29.03		
HEMBA1005632	1.33	2.33	5.06	3.14	3.68	4.47		
HEMBA1005634	3.06	3.42	5.15	2.81	7.68	5.18		
HEMBA1005662	1.18	1.27	3.17	1.06	4.57	3.03		
HEMBA1005666	5.89	4.51	10.09	10.5	9.01	10.25		
HEMBA1005670	1	1.08	4.06	2.87	4.35	3.19		
HEMBA1005671	2.11	3.38	5.07	5.36	9	5.9		
HEMBA1005679	2.33	4.64	7.39	6.5	10.44	10.19		
HEMBA1005680	2.63	2.14	5.9	5.51	7.59	7.72		
HEMBA1005685	2	1.89	7.27	3.8	6.73	1.97		
HEMBA1005698	5.96	4.75	12.88	11.78	14.17	9.93		
HEMBA1005699	1.4	1	2.45	2.17	3.66	2.96		
HEMBA1005703	1.22	1.27	3.57	1.79	3.56	1.88		
HEMBA1005705	2.39	2.78	6.45	3.41	6.27	3.89		
HEMBA1005712	1.23	1.34	4.52	2.18	4.84	2.37		
HEMBA1005717	1.55	1.89	4.7	1.34	5.36	2.16		
HEMBA1005718	5.27	4.35	7.8	10.09	10	15.72	*	+
HEMBA1005721	15.93	20.34	26.12	37.74	25.37	32.79		
HEMBA1005722	18	19.32	35.72	25.36	30.28	26.91		
HEMBA1005724	2.17	2.05	4.6	2.47	6.56	2.98		
HEMBA1005732	1.33	1.54	4.89	7.22	8.38	5.67	*	+
HEMBA1005737	1.49	1.19	2.95	2.44	4.57	1.75		
HEMBA1005742	3.4	4.65	5.7	4.43	6.35	4.22		
HEMBA1005746	1.2	1.61	3.23	5.69	4.42	4.85	*	+
HEMBA1005747	3.8	3.51	7.52	6.08	6.55	6.67		

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HEMBA1005749	9.64	9.37	17.99	21.62	19.82	18.15		
HEMBA1005755	0.49	2.5	3.35	1.66	4.41	2.9		
HEMBA1005760	1.59	2.1	5.37	3.7	4.86	4.14		
HEMBA1005765	1.47	2.89	5.97	5.91	7.42	7.21		
HEMBA1005766	8.52	10.49	61.64	93.4	112.09	106.28	*	+
HEMBA1005780	4.98	5.15	14.49	13.93	16.26	12		
HEMBA1005795	1.15	1.8	3.71	4.28	5.45	4.26	*	+
HEMBA1005809	9.13	9.7	20.95	14.79	29.83	22.75		
HEMBA1005813	1.76	2.74	6.74	5.39	9	7.08		
HEMBA1005815	0.62	1.86	2.75	2.74	4.78	2.13		
HEMBA1005822	1.34	2.83	5.82	3.77	6.65	5.12		
HEMBA1005829	1.49	2.66	4.94	5.11	4.53	5.52		
HEMBA1005833	1.83	1.28	4.41	3.89	5.17	4.57		
HEMBA1005834	2.53	1.87	4.84	5.48	11.84	6.81		
HEMBA1005844	27.89	31.06	52.5	62.42	59.49	58.73	*	+
HEMBA1005852	5.75	4.18	10.12	10.15	12.34	11.51		
HEMBA1005853	2.81	3.05	9.32	5.68	13.84	9.26		
HEMBA1005878	4.42	4.52	10.14	8.84	10.05	11.01		
HEMBA1005883	1.67	2.81	4.56	2.81	5.43	4.01		
HEMBA1005884	1.87	2	3.21	2.27	5.9	2.28		
HEMBA1005891	2.39	3.04	3.59	4.34	5.46	3.95		
HEMBA1005894	2.12	2.41	8.68	8.23	9.08	6.9		
HEMBA1005898	4.52	3.75	7.4	10.51	10.74	9.53	*	+
HEMBA1005902	2.57	3.14	8.63	5.36	6.75	5.82		
HEMBA1005907	1.15	2.28	2.2	2.28	4.2	1.74		
HEMBA1005909	0.93	2.68	2.97	2.96	4.55	2.6		
HEMBA1005911	1.66	3.12	4.9	3.96	9.5	3.41		
HEMBA1005912	8.83	7.86	13.57	16.44	8.16	15.58		
HEMBA1005913	5.05	5.39	10.39	9.57	7.71	7.06		
HEMBA1005921	2.36	3.86	6.29	5.25	10.06	7.64		
HEMBA1005922	5.49	5.47	6.99	8.51	10.1	8.74	*	+
HEMBA1005929	1.91	2.53	7.53	5.05	5.68	6.47		
HEMBA1005931	3.32	2.95	6.04	5.31	9.49	6.09		
HEMBA1005934	2.9	4.69	8.2	8.17	10.14	9.73		
HEMBA1005945	3.1	4.12	7.73	6.36	9.39	6.65		
HEMBA1005962	1.72	1.81	3.16	1.93	3.96	1.72		
HEMBA1005963	1.86	1.67	3.91	2.26	3.95	2.05		
HEMBA1005990	6.04	7.39	17.86	14.14	16.18	17.02		
HEMBA1005991	2.39	3.35	8.55	7.2	7.64	6.94		

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HEMBA1005999	2.34	4.39	8.84	6.52	8.18	8.75		
HEMBA1006002	3.53	5	7.73	5.96	10.24	8.99		
HEMBA1006005	0.96	2.31	3.93	2.87	5.65	3.27		
HEMBA1006011	26.27	24.03	34.08	62.88	44.8	64.92	*	+
HEMBA1006013	2.43	2.57	6.31	4.17	6.87	3.74		
HEMBA1006016	1.65	1.98	5.64	3.22	5.34	2.16		
HEMBA1006019	2.97	3.23	6.91	4.46	7.22	5.44		
HEMBA1006021	5.06	6.45	9.21	10.29	12.48	8.77		
HEMBA1006022	3.19	4.34	6.89	6.52	6.1	5.94		
HEMBA1006031	1.32	2.46	4.38	3.72	5.57	5.34		
HEMBA1006035	3.05	3.72	7.96	4.99	6.37	4.54		
HEMBA1006036	2.02	2.3	7	4.27	10.14	7.22		
HEMBA1006042	3.36	3.1	8.51	5.76	9.59	8.31		
HEMBA1006044	1.44	1.99	3.61	2.8	3.4	1.67		
HEMBA1006045	1.98	1.99	5.08	4.3	8.55	5.64		
HEMBA1006048	2.42	4.18	5.41	6.84	7.96	8.18	*	+
HEMBA1006053	1.51	2.72	3.55	3.09	3.3	3.93		
HEMBA1006055	1.84	1.91	2.46	3.04	4.92	3.67	*	+
HEMBA1006058	4.04	4.62	11.59	7.42	10.66	12.41		
HEMBA1006063	9.2	9.36	32.62	26.37	33.39	27.19		
HEMBA1006067	4.14	3.27	5.81	5.8	8.4	7.17		
HEMBA1006081	0.84	2.59	4.77	2.54	7.08	2.49		
HEMBA1006089	2.58	4.48	6.82	8.28	10.12	9.66	*	+
HEMBA1006090	1.66	2.31	2.28	1.66	5.26	1.84		
HEMBA1006091	1.1	1.35	1.75	3.15	4.31	2.95	*	+
HEMBA1006093	1.65	1.77	4.21	2.27	6.67	4.26		
HEMBA1006099	11.9	9.88	23.12	21.57	16.43	20.57		
HEMBA1006100	2.78	3.18	13.25	8.38	15.71	13.52		
HEMBA1006108	2.69	2.08	4.22	3.42	5.24	3.75		
HEMBA1006114	7.21	8.76	39.36	34.51	62.97	50.98		
HEMBA1006121	1.18	1.8	3.13	2.43	5.83	2.91		
HEMBA1006124	1.79	1.74	4.47	3.11	4.89	4.13		
HEMBA1006125	18.52	14.19	23.44	25.23	22.56	34.45		
HEMBA1006130	5.15	3.1	7.57	6.89	7.84	9.51		
HEMBA1006138	2.43	2.41	5.55	5.27	9.2	8.12		
HEMBA1006142	2.62	1.87	6.23	6.67	9.36	8.91	*	+
HEMBA1006150	8.32	7.44	21.06	20.42	21.82	24.68		
HEMBA1006151	567.67	524.4	796.07	915.23	875.11	682.15		
HEMBA1006155	0.93	1.33	2.92	1.44	5.54	1.94		

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HEMBA1006158	3.06	4.95	7.5	5.7	9.04	6.31		
HEMBA1006164	2.61	1.96	5.89	5.26	4.54	5.82		
HEMBA1006171	29.76	24.08	54.44	32.3	33.25	34		
HEMBA1006173	5.15	3.15	30.41	36.16	55.46	57.62	*	+
HEMBA1006176	315.12	232.27	427.53	476.77	458.01	381.49		
HEMBA1006182	1.47	1.71	6.13	3.02	5.84	5.82		
HEMBA1006197	6.14	5.09	9.26	9.53	12.1	10.41		
HEMBA1006198	10.07	6.46	26.71	35.03	45.64	55.68	*	+
HEMBA1006213	1.98	1.78	2.4	2.33	2.69	2.3		
HEMBA1006217	44.9	41.62	72.62	94.44	74.92	78.25		
HEMBA1006226	40.86	36.82	63.27	77.37	79.96	57.39		
HEMBA1006235	2.13	1.96	4.34	2.6	5.85	2.32		
HEMBA1006248	1.74	2.03	4.04	3.37	6.4	2.95		
HEMBA1006251	5.41	7.29	7.88	11.96	12.95	9.22	*	+
HEMBA1006252	0.72	1.28	3.67	2.25	3.56	2.92		
HEMBA1006253	2.13	2.26	4.1	5.93	5.38	5.76	*	+
HEMBA1006259	1.96	2.29	6.02	5.7	3.9	5.32		
HEMBA1006261	12.25	7.27	18.84	14.23	14.08	13.61		
HEMBA1006268	2.05	2.56	3.86	4.83	5.09	4.06	*	+
HEMBA1006271	2.04	3.99	10.58	7.13	9.33	8.51		
HEMBA1006272	0.97	2.26	2.84	2.38	6.01	1.93		
HEMBA1006273	1.53	2.09	4.55	3.58	4.52	2.46		
HEMBA1006276	2.8	1.26	3.62	4.45	5.84	2.82		
HEMBA1006278	1.57	2.03	3.19	4.08	4.51	2.72		
HEMBA1006283	3.09	3	6.08	7.34	11.13	7.09		
HEMBA1006284	2.47	1.57	3.14	4.75	6.96	2.82		
HEMBA1006291	1.42	2.56	4.41	4.6	6.16	2.57		
HEMBA1006292	3.36	5.12	17.34	19.95	23.83	21.11	*	+
HEMBA1006293	1.83	1.46	3.19	2.92	4.02	1.36		
HEMBA1006299	1.92	2.26	7.03	5.02	6.39	4.74		
HEMBA1006309	2.26	1.43	3.53	4.47	4.69	3.73	*	+
HEMBA1006310	4.14	4.32	7.72	9.51	8.34	5.7		
HEMBA1006311	1.4	2.33	6.68	5.59	5.85	5.72		
HEMBA1006313	1.2	1.6	2.74	4.29	4.68	2.26		
HEMBA1006316	2.16	3.08	6.72	6.63	6.28	5.59		
HEMBA1006328	2.78	4.28	13.48	15.14	17	16.56		
HEMBA1006334	1.46	3.1	2.77	2.79	3.95	2.05		
HEMBA1006335	10.42	13.98	21.66	20.81	18.03	16.77		
HEMBA1006344	2.86	3.55	6.9	7.18	6.88	5.75		

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HEMBA1006347	2.04	1.83	4.2	2.94	2.76	1.68		
HEMBA1006349	2.47	2.79	6.73	3.62	5.65	3.5		
HEMBA1006352	1.65	1.65	3.27	2.63	5.64	1.32		
HEMBA1006357	4.99	4.26	8.6	8.36	7.8	7.74		
HEMBA1006358	1.67	2.57	4.95	4.7	5.11	5.63		
HEMBA1006359	1.56	2.17	4.02	3.67	5.48	3.3		
HEMBA1006360	2.53	2.12	5.1	9.73	10.02	8.61	**	+
HEMBA1006364	1.71	2.76	4.82	4.02	5.55	3.51		
HEMBA1006377	5.8	8.03	13.25	20.48	16.19	15.31	*	+
HEMBA1006380	1.31	1.57	8.75	6.78	7.01	6.9		
HEMBA1006381	2.38	3.07	12.65	6.18	7.97	6.66		
HEMBA1006385	3.21	3.33	8.65	5.41	8.17	5.32		
HEMBA1006390	9.49	7.85	14.66	22.01	20.52	22.7	**	+
HEMBA1006391	6.58	6.85	6.73	12.83	10.12	13.15	**	+
HEMBA1006398	1.32	1.67	4.19	2.57	4.12	1.69		
HEMBA1006405	23.81	23.5	38.82	23.85	22.13	24.92		
HEMBA1006410	8.26	4.16	6.14	5.74	11.61	6.06		
HEMBA1006416	2.14	2.62	5.93	5.3	6.98	4.23		
HEMBA1006418	5.06	5.49	11.76	8.17	8.09	5.92		
HEMBA1006419	2.67	3.93	8	6.89	7.77	5.2		
HEMBA1006421	2.03	3.28	3.09	3.44	4.19	2.27		
HEMBA1006424	1.48	1.92	3.59	1.94	5.42	1.84		
HEMBA1006426	3.03	3.99	7.91	7.23	7.87	5.51		
HEMBA1006430	2.31	2.64	6.29	5.89	7.43	5.08		
HEMBA1006438	2.06	2.22	6.35	4.37	6.53	2.92		
HEMBA1006445	1.98	2.68	5.72	6.11	5.6	4.16		
HEMBA1006446	1.32	2.61	5.59	2	6.51	2.43		
HEMBA1006456	3.51	5.07	8.64	14.9	21.76	15.91	*	+
HEMBA1006461	1.54	2.18	5.35	4.35	5.49	4.07		
HEMBA1006467	1.52	1.78	3.61	2.82	7.24	3.2		
HEMBA1006470	4.06	4.03	22.46	18.72	29.54	19.52		
HEMBA1006471	1.58	1.6	6.6	6.45	6.78	6.26		
HEMBA1006474	7.35	6.37	43.12	55.87	62.01	52.31	*	+
HEMBA1006476	9.48	10.05	66.66	94.3	119.21	92.71	*	+
HEMBA1006482	71.42	71.44	219.31	199.96	180.73	192.88		
HEMBA1006483	2.03	2.96	7.22	3.36	4.88	3.24		
HEMBA1006485	2.24	1.72	6.31	4.09	6.53	5.51		
HEMBA1006486	5.08	5.55	13.73	18.4	16	15.46	*	+
HEMBA1006489	1.21	2.18	4.1	3.18	5.4	2.17		

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HEMBA1006492	5.34	7.71	10.69	15.16	24.33	15.92	*	+
HEMBA1006494	1.27	1.18	2.67	2.44	3.88	1.86		
HEMBA1006497	1.67	2.33	4.75	4.3	3.79	4.49		
HEMBA1006501	7.61	7.52	62.05	58.03	78.37	58.59		
HEMBA1006502	4.73	3.55	15.72	18.66	22.55	21.66	*	+
HEMBA1006507	8.7	6.8	51	49.69	71.2	48.41		
HEMBA1006517	1.51	1.99	5.07	3.43	5.9	4.64		
HEMBA1006521	1.79	1.8	4	2.41	4.55	3.02		
HEMBA1006529	4.77	3.74	3.86	5.97	5.83	2.78		
HEMBA1006530	1.8	1.39	2.06	1.62	3.53	2.42		
HEMBA1006535	1.66	1.43	2.01	2.66	2.81	2.43	**	+
HEMBA1006536	0.59	2.22	3.96	3.04	3.23	2.33		
HEMBA1006540	1.61	1.68	3.33	3.05	4.1	3.56		
HEMBA1006544	1.39	1.63	8	3.54	5.85	4.35		
HEMBA1006546	2.06	2.56	6.98	4.25	5.77	4.51		
HEMBA1006549	1.74	2.13	5.93	4.57	4.63	4.61		
HEMBA1006559	2.55	1.45	4.63	2.99	5.76	3.32		
HEMBA1006562	0.74	1.32	4.07	2.39	5.24	2.72		
HEMBA1006566	0.67	1.28	0.97	1.34	1.69	0.99		
HEMBA1006569	2.33	1.36	3.97	3.25	3.89	4.02		
HEMBA1006572	1.02	2.38	2.94	2.68	3.92	2.01		
HEMBA1006579	20.44	16.82	51.93	59.14	66.28	72.54	*	+
HEMBA1006583	3.17	2.85	5.59	5.83	5.94	6.45		
HEMBA1006595	1.82	1.63	4.29	2.83	5.22	3.68		
HEMBA1006597	1.65	2.1	5.34	3.81	6.75	3.77		
HEMBA1006606	1.75	2.31	4.96	3.72	5.71	2.8		
HEMBA1006612	2.63	3.54	7.11	7.32	5.31	7.07		
HEMBA1006617	1.93	2.58	6.24	4.62	4.6	5.41		
HEMBA1006624	6.37	8.61	16.93	12.84	15.78	10.91		
HEMBA1006631	3.24	3.13	8.01	8.11	11.54	6.97		
HEMBA1006635	1.7	2.57	5.7	4.27	6.27	3.8		
HEMBA1006639	1.12	1.98	4.52	4.14	5.3	3.06		
HEMBA1006643	1.88	1.23	1.85	2.12	3.81	2.17		
HEMBA1006648	7.69	6.84	16.92	17.63	23.57	23.73	*	+
HEMBA1006652	5.96	7.86	16.11	16.41	16.83	17.34		
HEMBA1006653	2.21	3.66	7.23	6.92	5.18	5.17		
HEMBA1006658	5.04	6.58	12.68	14.07	13.59	12.01		
HEMBA1006659	6.8	10.14	48.92	66.47	78.17	67.44	*	+
HEMBA1006665	1.44	0.89	3.32	2.77	2.91	1.82		

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HEMBA1006666	1.83	1.25	3.23	3.24	4.14	2.45		
HEMBA1006671	8.69	6.74	11.66	17.25	16.13	15.21	**	+
HEMBA1006674	1.64	1.99	7.42	6.71	9.73	7.34		
HEMBA1006676	1.46	2.36	5.19	4.28	6.75	3.19		
HEMBA1006682	2.17	1.64	3.43	2.2	4.98	1.88		
HEMBA1006688	1.48	2.46	4.74	3.31	4.38	3.54		
HEMBA1006695	1.58	2.41	4.85	3.54	5.79	2.46		
HEMBA1006696	2.84	3.93	6.29	5.95	6.74	5.82		
HEMBA1006702	3.31	1.83	13.28	4.13	5.58	4.87		
HEMBA1006707	2.89	2.62	5.9	5.04	7.54	5.5		
HEMBA1006708	2.21	1.52	5.71	4.42	4.57	2.63		
HEMBA1006709	1.64	1.97	4.6	4.29	5	4.74		
HEMBA1006717	1.58	2.28	3.58	2.5	4.93	2.28		
HEMBA1006724	2.68	3.42	4.55	4.45	4.5	5.47		
HEMBA1006731	1.83	2.95	3.95	4.12	5.51	3.1		
HEMBA1006737	1.82	3.5	6.59	3.89	5.09	4.45		
HEMBA1006742	1.78	2.44	4.16	3.32	4.14	3.61		
HEMBA1006743	4	4.02	11.48	14.16	17.25	11.88		
HEMBA1006744	1.84	1.79	7.74	6.6	8.29	5.72		
HEMBA1006749	1.14	1.27	3.72	1.88	3.8	1.71		
HEMBA1006752	16.53	16.28	26.81	35.31	18.85	33.99		
HEMBA1006754	1.44	2.6	3.63	5.55	4.33	2.49		
HEMBA1006758	1.38	2.83	4.25	6.89	4.68	4.02		
HEMBA1006767	3	4.14	7.88	6.81	7.89	5.51		
HEMBA1006770	5.05	2.61	7.12	7.89	8.1	5.05		
HEMBA1006779	4.44	4.1	10.99	9.57	10.28	8.42		
HEMBA1006780	3.28	3.19	10.27	7.6	8.33	8.38		
HEMBA1006789	2.83	1.87	11.34	4.55	5.42	5.51		
HEMBA1006795	2.13	2.45	7.58	4.56	7.87	3.29		
HEMBA1006796	4.31	3.15	5.37	5.85	7.06	4.72		
HEMBA1006805	2.72	2.73	5.9	12.77	17.38	12.96	**	+
HEMBA1006807	30.32	28.07	75.38	54.22	54.72	67.82		
HEMBA1006813	0.93	1.73	2.81	1.93	4.17	0.97		
HEMBA1006819	3.73	4.53	8.5	7.02	8.09	5.29		
HEMBA1006821	1.56	2.37	6.09	5.05	4.24	4.36		
HEMBA1006824	2.13	3.13	7.39	5.69	6.04	5.75		
HEMBA1006832	19.84	18.63	56.97	59.26	61.56	53.28		
HEMBA1006834	13.23	12.47	20.38	29.88	28.37	21.62	*	+
HEMBA1006835	1.11	1.49	3.88	5.08	7.25	4.6	*	+

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HEMBA1006843	19.27	17.89	35.47	55.34	39.67	68.17	*	+
HEMBA1006849	5.64	4.37	11.23	10.07	11.23	10.83		
HEMBA1006850	31.45	33.76	60.2	44.62	53.25	45.59		
HEMBA1006861	12.19	11.3	24.61	22.49	16.43	17.99		
HEMBA1006865	5.42	8.35	31	33.77	33.36	34.49		
HEMBA1006867	4.32	5.03	6.41	6.27	7.76	6.15		
HEMBA1006873	3.14	3.59	8.87	6.5	9.26	7.75		
HEMBA1006877	2.52	4.03	5.87	4.03	6.26	3.68		
HEMBA1006878	2.52	2.36	6.79	3.82	7.86	3.51		
HEMBA1006879	6.19	5.68	8.83	11.06	15.86	17.33	*	+
HEMBA1006884	10.11	3.17	6.59	6.15	8.42	8.78		
HEMBA1006885	7.02	6.82	14.16	20.86	19.11	21.73	*	+
HEMBA1006886	20.38	17.25	26.55	29.45	29.15	40.93		
HEMBA1006889	2.61	4.02	4.85	4.48	5.99	6.09		
HEMBA1006896	19.11	24.76	31.7	33.67	39.11	40.41	*	+
HEMBA1006900	6.19	5.93	20.76	16.81	23.73	18.45		
HEMBA1006902	1.43	2.45	3.86	4.03	6	3.98		
HEMBA1006912	1.24	1.74	6.86	4.12	5.8	5.3		
HEMBA1006914	6.64	6.11	18.27	14.81	18.62	15.03		
HEMBA1006916	3.11	2.71	5.78	10.29	7.48	9.36	*	+
HEMBA1006921	3.03	3.5	9.63	9.77	11.26	13.59		
HEMBA1006926	2.65	2.61	5.68	5.01	6.53	6.98		
HEMBA1006927	3.06	2.2	5.17	3.57	5.26	5.89		
HEMBA1006929	2.94	2.69	4.02	4.31	6.36	5.25	*	+
HEMBA1006936	3.72	3.21	6.51	4.67	6.25	5.45		
HEMBA1006938	1.21	2.11	6.57	2.37	3.76	3.44		
HEMBA1006941	9.52	8.15	12	19.26	28.62	23.74	**	+
HEMBA1006942	5.2	2.63	6.65	10.7	10.65	11.4	**	+
HEMBA1006945	10.07	5.91	16.81	23.73	17.09	19.91		
HEMBA1006949	1.6	1.43	3.88	2.48	5.34	2.81		
HEMBA1006952	1.16	1.66	2.98	3.02	5.04	2.22		
HEMBA1006960	2.53	2.78	7.66	5.9	8.28	8.68		
HEMBA1006973	1.74	2.27	5.91	4.7	7.84	5.54		
HEMBA1006974	2.49	3.44	6.76	6.09	11.01	8.14		
HEMBA1006976	1.39	1.5	4.12	3.18	4.96	4.36		
HEMBA1006989	1.85	1.66	6.51	2.05	3.01	1.81		
HEMBA1006993	2.71	2.39	6.49	6.11	7.69	8.79		
HEMBA1006996	0.74	1.15	2.98	2.52	3.13	3.58		
HEMBA1007001	1.91	2.47	5.12	3.98	6.37	4.76		

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HEMBA1007002	7.02	4.12	31.4	26.92	38.45	42.11		
HEMBA1007013	1.02	0.94	3.04	1.44	4.39	2.27		
HEMBA1007016	2.02	1.43	5.06	3.27	5.97	5.28		
HEMBA1007017	0.69	1.24	2.55	1.42	3.33	1.83		
HEMBA1007018	4.02	4.52	6.54	7.65	6.1	7.07		
HEMBA1007044	8.13	8.41	17.4	15.48	11.97	12.27		
HEMBA1007045	1.64	2.15	4.42	2.61	5.08	3.47		
HEMBA1007051	2.26	2.56	4.71	3.42	4.42	3.28		
HEMBA1007052	2.23	1.25	3.47	2.37	4.62	1.83		
HEMBA1007053	1.83	3.14	4.03	2.64	4	2.5		
HEMBA1007057	0.92	2.56	3.21	3.52	4.03	3.41		
HEMBA1007062	0.91	0.82	2.73	2.34	2.87	1.82		
HEMBA1007063	3.87	2.7	8.87	8.56	8.02	7.58		
HEMBA1007066	1.72	2.03	3.62	2.2	4.39	2.71		
HEMBA1007069	1.36	2.29	3.87	3.84	3.48	3.66		
HEMBA1007073	1.93	2.16	6.12	2.96	9.57	3.6		
HEMBA1007076	1.48	2.6	5.56	4.66	7.6	3.4		
HEMBA1007078	6.5	6.83	18.61	26.96	27.47	23.78	*	+
HEMBA1007080	7.6	9.46	38.27	61.02	68.15	51.34	*	+
HEMBA1007084	1.28	1.42	4.76	3.68	6.27	4.76		
HEMBA1007085	3.28	2.89	8.21	5.76	7.21	5.42		
HEMBA1007087	2.6	2.88	6.31	3.96	6.92	5.63		
HEMBA1007089	26.17	28.1	43.8	46.11	34.41	29.42		
HEMBA1007095	75.81	62.79	111.43	134.53	48.47	121.4		
HEMBA1007101	2.78	3.27	8	26.73	21.52	19.57	**	+
HEMBA1007104	1.87	1.92	3.52	2.46	4.53	2.57		
HEMBA1007106	4.77	4.8	9.03	16.42	12.5	9.49		
HEMBA1007112	3.01	3.07	5.16	6.39	6	4.77		
HEMBA1007113	1.53	2.29	9.04	6.03	6.1	5.97		
HEMBA1007121	13.76	14	92.08	116.14	111.53	129.12	*	+
HEMBA1007129	1.54	2.44	2.87	2.66	4.37	1.89		
HEMBA1007147	1.68	2.88	4.4	3.96	4.76	4.06		
HEMBA1007149	5.3	7.24	8.38	10.48	6.82	9.73		
HEMBA1007151	0.85	1.87	3.38	3.32	3.88	2.54		
HEMBA1007172	1.26	1.91	4.13	2.96	4.81	3.51		
HEMBA1007174	1.4	1.43	2.75	3.96	3.65	2.5		
HEMBA1007176	2.58	3.95	11.7	6.7	6.78	4.52		
HEMBA1007178	4.77	4.71	9.32	10.94	13.03	8.12		
HEMBA1007185	9.38	10.32	9.59	19.5	7.83	15.16		

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HEMBA1007186	1.71	2.76	4.49	4.95	5.47	3.86		
HEMBA1007194	4.81	3.43	5.58	7.83	9.34	8.67	**	+
HEMBA1007200	1.18	2.33	2.9	3.25	4.6	1.66		
HEMBA1007203	1.54	3.5	5.38	6.03	6.87	5.05		
HEMBA1007206	1.92	2.46	5.72	7.07	7.91	5.94		
HEMBA1007224	5.4	6.5	9.06	9.23	5.85	8.06		
HEMBA1007226	7.19	8.07	40.61	59.31	70.51	62.19	*	+
HEMBA1007240	10	10.96	13.45	15.35	7.71	11		
HEMBA1007241	3.59	2.88	4.56	4.61	6.81	3.63		
HEMBA1007242	2.52	2.86	5.01	6.29	6.87	4.23		
HEMBA1007243	10.23	10.91	69.57	70.17	95.69	82.75		
HEMBA1007251	1.32	1.8	4.14	3.02	3.67	2.01		
HEMBA1007256	1.39	1.91	3.36	3.93	5.74	3.44		
HEMBA1007267	3.19	3.71	8.75	8.73	9.18	8.1		
HEMBA1007273	0.98	2.66	3.84	3.56	5.82	2.25		
HEMBA1007279	1.55	2.25	3.52	2.95	4.35	2.02		
HEMBA1007281	1.73	1.54	2.12	2.95	4.43	1.01		
HEMBA1007283	2.45	3.15	6.78	6.37	6.58	5.96		
HEMBA1007288	2.12	2.77	5.54	4.35	6.74	5.48		
HEMBA1007291	1.59	1.8	4.29	2.14	4.4	0.98		
HEMBA1007299	20.39	22.25	39.67	40.95	47.97	40.26		
HEMBA1007300	2.08	2.75	3.59	4.17	4.45	4.07	*	+
HEMBA1007301	1.97	2.82	3.15	3.73	3.99	3.44	*	+
HEMBA1007319	2.84	3.61	6.73	5.21	6.12	3.32		
HEMBA1007320	1.29	1.22	3.12	4.19	3.45	2.42		
HEMBA1007322	19.97	17.81	27.74	45.24	39.42	37.31	**	+
HEMBA1007323	4.54	6.69	11.47	6	6.36	6.21		
HEMBA1007326	4.58	3.85	13.34	8.29	8.07	9		
HEMBA1007327	3.37	3.98	8.91	6.14	9.31	8.98		
HEMBA1007332	3.12	3.47	5.42	5.27	7.56	5.33		
HEMBA1007341	1.4	2.51	3.24	2.93	3.38	3.36		
HEMBA1007342	1.06	2.05	3.02	1.52	3.23	1.98		
HEMBA1007347	3.39	3.24	6.34	4.55	7.34	6.32		
HEMBA1007353	2.43	2.22	4.99	2.68	6.9	3.01		
HEMBB1000005	1.57	2.54	5.35	2.68	4.65	3.64		
HEMBB1000008	2.19	2.53	5.99	3.51	6.31	3.71		
HEMBB1000018	2.21	2.16	7.13	9.9	9.79	7.24		
HEMBB1000024	3.71	2.15	5.4	5.13	5.77	6.39		
HEMBB1000025	2.11	2.09	3.55	1.68	5.13	2.62		

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HEMBB1000030	3.12	3.53	6.58	6.62	7.77	6		
HEMBB1000036	5.3	4.76	5.04	6.95	8.19	5.93	*	+
HEMBB1000037	4.43	3.64	4.73	4.63	8.38	5.32		
HEMBB1000039	1.17	0.96	3.98	2.61	4.11	2.95		
HEMBB1000044	1.22	2.35	4.26	5.28	5.58	5.36	*	+
HEMBB1000048	3.2	1.7	3.48	3.99	5.4	3.96		
HEMBB1000050	2.32	1.55	3.33	2.97	3.98	2.85		
HEMBB1000054	2.03	2.08	7.07	4.49	5.09	3.98		
HEMBB1000055	42.59	36.75	92.41	100.33	86.52	89.35		
HEMBB1000059	2.5	2.65	11.34	10.96	11.52	14.73		
HEMBB1000072	6.84	7.77	58.85	73.22	97.61	76.22	*	+
HEMBB1000081	2.85	3.56	10.79	5.69	6.19	7.23		
HEMBB1000083	1.13	1.95	5.38	4.88	5.89	5.33		
HEMBB1000089	1.14	2.53	4.54	6.03	6.73	5.43	*	+
HEMBB1000094	4.12	4.3	8.4	4.24	5.04	6.62		
HEMBB1000097	2.48	1.71	7.91	4.75	4.55	4.3		
HEMBB1000099	2.69	2.07	6.27	5.18	6.75	5.64		
HEMBB1000103	7.19	5.28	18.55	13.99	19.26	16.16		
HEMBB1000106	3.91	3.75	8.15	4.24	6.4	5.9		
HEMBB1000113	1.25	1.54	3.33	1.39	4.14	2.31		
HEMBB1000119	2.19	2.17	5.66	3.34	6.12	4.05		
HEMBB1000133	21.01	22.21	30.57	43.5	66.13	60.69	*	+
HEMBB1000134	4.92	2.95	8.69	13.39	9.79	9.8		
HEMBB1000136	7.14	8.81	29.63	23.11	26.28	28.23		
HEMBB1000141	1.98	2.85	6.18	4.95	5.75	6.16		
HEMBB1000144	2.05	2.59	4.85	3.09	5.36	1.38		
HEMBB1000147	3.77	2.08	4.51	4.55	7.39	3.07		
HEMBB1000152	0.79	1.45	3.42	5.13	5.15	3.45		
HEMBB1000154	0.98	1.11	3.43	2.59	2.89	2.47		
HEMBB1000155	0.88	0.54	3.15	3.33	4.15	1.92		
HEMBB1000173	3.35	3.72	12.14	10.1	10.89	7.51		
HEMBB1000175	1.85	1.32	3.39	6.06	4.09	3.86		
HEMBB1000176	1.48	4.03	6.12	3.43	9.75	5.03		
HEMBB1000198	0.88	1.72	3.64	2.6	3.59	3.22		
HEMBB1000208	1.12	1.52	3.04	1.74	3.23	2.69		
HEMBB1000209	1.62	1.54	3.76	3.32	3.94	3.28		
HEMBB1000212	1.88	1.03	3.26	4.37	3.93	1.98		
HEMBB1000215	1.61	2.13	3.8	4.67	5.49	5.32	*	+
HEMBB1000217	5.67	4.97	11.23	15.21	18.81	11.78	*	+

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HEMBB1000218	2.13	2.28	11.05	7.47	10.07	7.05		
HEMBB1000226	2.63	3.26	6.02	4.02	5.86	3.41		
HEMBB1000230	1.39	1.83	3.73	1.95	4.31	2.58		
HEMBB1000240	6.04	8.26	10.01	3.97	2.7	1.75	*	-
HEMBB1000244	1.39	1.64	3.51	2.51	2.63	1.68		
HEMBB1000250	1.17	0.99	1.12	1.94	1.25	1.12		
HEMBB1000258	1.71	1.94	5.8	4.38	5.63	3.27		
HEMBB1000264	2.49	3.12	11.01	8.64	8.34	8.1		
HEMBB1000266	2.81	2.65	5.52	3.38	5.95	3.71		
HEMBB1000272	4.76	4.16	6.06	8.38	6.88	7.45	*	+
HEMBB1000274	1.51	1.15	3.17	2.54	3.18	1.88		
HEMBB1000276	1.12	1.84	4.72	3.1	4.01	2.43		
HEMBB1000284	0.94	1.81	2.89	2.83	3.11	1.65		
HEMBB1000307	1.52	1.7	4.78	2.8	5.31	3.27		
HEMBB1000309	1.43	2.73	3.07	3.09	3.56	2.19		
HEMBB1000312	1.99	1.38	5.18	7.03	7.2	4.35		
HEMBB1000317	0.17	1.62	3.32	2.6	4.73	2.14		
HEMBB1000318	1.11	2.69	3.85	2.28	4.46	1.68		
HEMBB1000332	3.12	3.84	4.37	3.75	3.95	2.72		
HEMBB1000335	0.77	2.35	4.66	6.16	4.66	3.44		
HEMBB1000336	0.99	1.11	3.59	2.09	3.52	2.29		
HEMBB1000337	4.3	5.06	20.22	22.86	24.84	22.82		
HEMBB1000338	2.11	1.92	5.86	7.13	8.92	4.71		
HEMBB1000339	1.66	1.76	5.84	3.75	4.99	3.84		
HEMBB1000341	1.4	1.91	3.68	3.06	4.77	2.83		
HEMBB1000343	2.51	3.15	6.96	7.24	8.68	7.46		
HEMBB1000354	3.26	3.5	10.36	7	8.93	8.07		
HEMBB1000358	1.09	2.11	3.82	3.43	2.83	1.93		
HEMBB1000369	1.93	2.33	3.87	5.96	6.54	2.89		
HEMBB1000373	1.77	2.73	3.91	2.26	6.2	2.94		
HEMBB1000374	3.27	4.06	9.34	9.58	13.36	6.95		
HEMBB1000376	2.71	3.92	12.28	10.03	6.99	7.71		
HEMBB1000383	60.87	62.14	104.01	69.28	57.52	83.25		
HEMBB1000391	1.8	2.66	4.57	4.89	6.18	4.29		
HEMBB1000399	2.51	3.79	3.69	3.93	5.72	3.71		
HEMBB1000402	1.61	2.06	3.33	2.67	5.3	1.72		
HEMBB1000404	1.34	1.15	5.18	2.56	5.29	1.81		
HEMBB1000407	2.2	3.36	6.76	5.57	5.75	4.66		
HEMBB1000420	1.93	1.46	3.86	4.33	4.76	4.54	*	+

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HEMBB1000430	38.77	36.24	61.06	51.76	34.69	50.02		
HEMBB1000434	3.05	4.73	9.02	6.54	6.59	6.63		
HEMBB1000438	1.13	1.83	4.16	2.23	4	1.39		
HEMBB1000441	2.26	3	7.35	5.44	8	4.78		
HEMBB1000447	29.84	32.01	39.91	35.88	44.02	33.55		
HEMBB1000449	1.3	1.31	3.72	1.51	3.04	1.54		
HEMBB1000453	8.61	8.04	13.39	14.23	18.78	13.74		
HEMBB1000455	1.29	1.97	3.19	3.13	5.46	3.54		
HEMBB1000472	2.3	2.28	4.22	4.07	4.35	3.52		
HEMBB1000480	1.9	3.59	7.03	5.71	6.63	5.87		
HEMBB1000486	2.15	2.98	6.93	4.82	7.86	5.9		
HEMBB1000487	1.21	1.79	4.48	2.66	4.8	2.57		
HEMBB1000490	3.67	4.13	12.61	7.92	8.7	6.55		
HEMBB1000491	1.36	2.91	5	3.83	4.78	4.42		
HEMBB1000492	3.02	4.04	6.84	5.63	6.94	5.34		
HEMBB1000493	1.57	1.71	3.26	2.41	5.38	3.27		
HEMBB1000510	1.32	1.71	4.94	4.4	5.61	4.21		
HEMBB1000516	5.64	7.71	36.22	16.62	18.58	17.09		
HEMBB1000518	0.88	1.22	2.63	2.21	4.27	1.73		
HEMBB1000523	1.32	2.78	7.41	3.33	7.74	4.1		
HEMBB1000530	2.83	2.51	9.72	6.06	7.81	6.64		
HEMBB1000542	3.08	4.55	9.39	8.48	14.07	9.82		
HEMBB1000550	4.84	2.87	4.77	10.48	5.74	5.33		
HEMBB1000554	2.14	2.26	8.65	6.43	11.59	7.19		
HEMBB1000556	2.64	2.68	4.48	3.1	4.67	4.6		
HEMBB1000564	1.81	1.4	5.87	4.26	5.34	6.18		
HEMBB1000567	1.39	1.71	3.7	2.1	3.87	3.3		
HEMBB1000569	3.78	2.72	8.76	4.88	7.13	5.65		
HEMBB1000573	3.48	3.44	11.31	7.33	9.55	7.56		
HEMBB1000575	12.42	2.7	10.57	7.16	8.38	12.35		
HEMBB1000579	2.12	3.75	4.84	3.01	8.61	4.04		
HEMBB1000585	0.83	1.19	3.19	2	4.1	3.35		
HEMBB1000586	2.18	1.41	4.28	4.07	4.23	4.11		
HEMBB1000589	2.98	1.58	3.62	3.38	3.75	3.69		
HEMBB1000591	2.62	2.15	3.96	4.44	5.26	4.64	*	+
HEMBB1000592	2.05	1.2	3.18	3.87	3.39	2.15		
HEMBB1000593	10.25	5.67	51.69	53.87	82.75	77.88	*	+
HEMBB1000595	6.42	5.2	11.24	12.51	17.1	9.55		
HEMBB1000598	1.57	1.69	5.91	2.94	6.76	4.77		

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HEMBB1000611	0.94	1.16	2.08	1.15	2.79	1.66		
HEMBB1000617	2.01	3.04	9.31	6.14	8.79	6.97		
HEMBB1000623	2.51	3.08	4.64	5.58	5.83	3.9		
HEMBB1000630	3.23	2.5	3.78	2.42	5.54	2.51		
HEMBB1000631	8.91	10.69	18.75	22.52	23.76	22.55	*	+
HEMBB1000632	6.77	8.77	20.85	27.2	18.4	23.31		
HEMBB1000636	9.52	15.91	22.42	25.26	21.65	19.96		
HEMBB1000637	6.63	9.77	19.44	17.77	24.39	20.28		
HEMBB1000638	1.44	1.41	3.23	3.6	5.29	3.34		
HEMBB1000642	3.47	2.31	7.58	7.65	9.33	9.93		
HEMBB1000643	0.71	1.87	2.71	1.62	3.54	2.12		
HEMBB1000649	2.25	2.22	6.45	4.94	7.61	5.72		
HEMBB1000652	1.8	2.21	5.33	5.13	5.14	4.93		
HEMBB1000655	1.07	1.17	3.24	1.64	4.74	2.01		
HEMBB1000665	0.52	1.08	2.23	1.69	2.92	2.01		
HEMBB1000668	1.85	1.46	2.76	5.07	5.42	4.1	**	+
HEMBB1000671	2.36	2.01	6.77	7.03	7.81	6.94		
HEMBB1000673	0.75	1.27	2.92	2.84	4.63	2.43		
HEMBB1000679	3.26	2.84	5.59	4.42	7.19	5.76		
HEMBB1000684	1.83	2.53	6.6	5.01	6.92	5.6		
HEMBB1000692	0.93	2	2.46	1.77	2.5	1.09		
HEMBB1000693	0.96	1.29	2.47	1.6	2.79	1.34		
HEMBB1000705	2.61	2.52	4.85	4.97	8.2	6.53		
HEMBB1000706	0.78	1.07	2.18	2.56	2.93	1.06		
HEMBB1000709	3.53	2.92	8.39	8.16	7.99	10.26		
HEMBB1000714	1.41	2.85	9.32	5.31	10.37	8.79		
HEMBB1000725	1.61	2.22	4.35	3.04	6.22	4.72		
HEMBB1000726	1.88	2.34	8.76	5.63	7.1	4.83		
HEMBB1000729	1.82	3.28	4.3	3.3	5.21	2.79		
HEMBB1000738	1.94	2.6	5.55	3.99	5.53	6.15		
HEMBB1000749	4.06	4.15	7.47	7.48	9.56	8.27		
HEMBB1000763	5.81	5.56	6.21	6.65	9.9	6.61		
HEMBB1000770	2.76	2.06	8.8	7.73	9.62	8.83		
HEMBB1000774	1.62	2.75	3.7	3.07	4.39	2.34		
HEMBB1000777	5.17	5.49	7.42	6.86	4.9	7.37		
HEMBB1000781	3.7	4.19	6.89	7.64	5.28	6.83		
HEMBB1000788	0.87	1.79	2.45	2.65	4.88	1.35		
HEMBB1000789	1.91	2.22	3.01	3.1	6.55	1.86		
HEMBB1000790	1.97	2.15	4.48	4.59	4.21	2.53		

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HEMBB1000794	1.46	1.8	2.85	2.97	3.84	2.06		
HEMBB1000807	2.55	2.72	5.18	3.57	4	4.26		
HEMBB1000809	30.31	26.87	132.99	158.22	156.74	195.14	*	+
HEMBB1000810	1.98	2.67	4.51	3.76	6.08	4.12		
HEMBB1000821	1.98	1.93	2.98	2.05	4.45	1.79		
HEMBB1000822	1.08	1.97	2.31	1.65	5.31	1.46		
HEMBB1000826	1.36	1.99	3.57	3.77	6.11	3.6		
HEMBB1000827	2.48	2.89	5.83	2.67	5.05	2.99		
HEMBB1000831	3.4	2.31	5.67	3.84	7.74	2.95		
HEMBB1000835	1.76	1.94	6.2	7.59	7.62	7.47	*	+
HEMBB1000840	1.27	2.95	6.89	4.48	7.19	3.01		
HEMBB1000848	2.08	3.45	5.63	5.39	6.45	5.3		
HEMBB1000852	1.26	2.16	2.8	1.07	4.51	1.55		
HEMBB1000857	7.65	6.49	8.13	7.01	10.69	11.53		
HEMBB1000858	3.7	3.13	7.3	7.07	9.38	7.31		
HEMBB1000867	2.21	1.84	4.9	3.02	5.55	4.04		
HEMBB1000870	1.64	2.37	4.56	2.84	5.31	3.63		
HEMBB1000876	1.48	2.86	3.91	4.54	3.22	3.93		
HEMBB1000881	3.35	5.56	10.5	6.12	5.88	3.85		
HEMBB1000883	1.02	2.68	2.2	3.03	3.32	2.58		
HEMBB1000887	16.9	14.54	43.41	67.39	61.26	59.84	*	+
HEMBB1000888	1.03	1.67	2.39	1.63	3.92	1.86		
HEMBB1000890	2.93	3.36	10.85	6.01	8.62	7.68		
HEMBB1000893	3.28	2.54	5.46	4.5	6.14	5.57		
HEMBB1000900	1.27	1.53	2.98	2.06	2.54	1.58		
HEMBB1000905	5.09	3.75	6.6	10.05	9.45	8.77	**	+
HEMBB1000908	3.34	2.79	3.01	4.48	4.71	5.7	**	+
HEMBB1000910	1.74	2.91	2.55	2.09	3.56	2.24		
HEMBB1000913	1.41	1.51	2.22	2.8	3.41	1.91		
HEMBB1000915	32.08	25.6	50.05	48	58.92	51.07		
HEMBB1000917	2.1	2.78	5.72	2.99	4.52	3.44		
HEMBB1000927	1.45	1.24	1.82	1.49	3.25	1.88		
HEMBB1000932	0.66	2.06	2.74	1.81	3.41	1.61		
HEMBB1000933	7.47	7.12	10.71	12.88	12.78	19.19		
HEMBB1000936	1.44	1.96	2.87	3.75	6.44	3.55		
HEMBB1000939	7.86	7.14	9.02	15.98	15.3	18.25	**	+
HEMBB1000941	1.53	1.86	3.17	3.99	4.46	3.52	*	+
HEMBB1000947	3.53	3.34	4.61	4.67	6.8	5.72		
HEMBB1000954	1.08	1.82	2.54	1.62	4.01	3.08		

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HEMBB1000959	0.77	1.41	3.11	2.23	4.42	1.87		
HEMBB1000973	1.21	1.12	2.6	2.07	4.47	3.2		
HEMBB1000975	0.9	1.28	1.55	2.48	2.86	1.7	*	+
HEMBB1000981	1.54	0.66	1.99	1.84	3.47	2.03		
HEMBB1000985	1.67	1.82	2.71	3.59	3.99	3.24	*	+
HEMBB1000991	0.99	1.35	2.83	1.46	3.75	2.43		
HEMBB1000996	4.89	3.12	6.78	6.75	6.64	11.18		
HEMBB1001000	1.86	1.39	4.06	3.07	5.46	3.88		
HEMBB1001004	1.15	1.32	2.57	2.56	4.55	2.42		
HEMBB1001008	1.48	1.79	2.75	2.44	4.6	2.88		
HEMBB1001011	1.34	1.15	1.53	2.47	2.24	2.9	**	+
HEMBB1001014	1.31	1.43	2.3	2.73	4.84	4.1	*	+
HEMBB1001020	1.17	0.75	2.77	1.77	2.67	2.26		
HEMBB1001024	3.31	1.72	6.27	5.47	7.56	6.82		
HEMBB1001026	5.14	4.03	5.16	5.46	7.67	5.44		
HEMBB1001037	2	1.45	4.73	3.52	5.69	6.67		
HEMBB1001042	0.52	1.15	2.69	1.29	3.61	0.87		
HEMBB1001046	1.18	1.28	2.16	1.67	3.82	0.96		
HEMBB1001047	1.01	1.7	3.79	2.2	3.83	3.83		
HEMBB1001048	2.5	2.34	7.02	4.34	11.02	6.93		
HEMBB1001051	1.44	2.62	3.23	3.95	6.26	3.9		
HEMBB1001056	1.61	2.67	4.89	3.75	5.7	3.78		
HEMBB1001058	1.3	1.92	4.72	2.64	6.92	2.63		
HEMBB1001060	0.69	0.68	1.75	2.05	4.61	1.85		
HEMBB1001063	1.23	1.83	3.52	2.43	4.21	2.9		
HEMBB1001068	1.84	3.62	3.59	3.46	7.14	5.2		
HEMBB1001082	2.24	2.57	5.98	5.38	6.93	6.36		
HEMBB1001095	6.39	7.45	11.76	14.04	14.61	13.16	*	+
HEMBB1001096	1.3	1.91	3.05	3.21	4.12	3.49		
HEMBB1001101	7.41	8.19	9.74	19.33	13.1	16.69	*	+
HEMBB1001102	1.04	1.47	4.57	3.6	6.07	4.46		
HEMBB1001104	1.66	1.89	3.98	3.1	4.87	4.25		
HEMBB1001105	1.57	1.59	2.13	3.11	4.82	2.71		
HEMBB1001112	9.44	8.91	73.3	100.88	136.14	131.28	*	+
HEMBB1001113	2.11	1.94	9.1	5.65	8.02	6.81		
HEMBB1001114	1.88	2.27	5.18	4.16	7.06	4.82		
HEMBB1001115	5.78	7.88	14.52	16.77	9.5	14.78		
HEMBB1001117	1.7	1.52	2.92	1.85	2.79	1.79		
HEMBB1001119	1.69	1.57	4	2.29	3.74	2.28		

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HEMBB1001126	1.85	1.88	3.63	2.69	4.96	2.9		
HEMBB1001133	3.15	2.42	4.24	6.56	6.15	6.44	**	+
HEMBB1001137	1.97	2.2	4.4	3.28	6.56	5.42		
HEMBB1001142	2.96	2.68	10.51	9.2	11.69	10.38		
HEMBB1001145	3.25	3.56	7.39	6.11	7.7	6.59		
HEMBB1001151	5.67	6.58	9.21	12.85	7.67	7.84		
HEMBB1001153	2	1.89	4.57	3.79	5.37	2.9		
HEMBB1001158	6.96	6.74	12.17	12.04	9.95	11.16		
HEMBB1001169	1.71	2.45	4.42	2.89	4.21	2.86		
HEMBB1001170	1	1.85	3.27	1.26	2.5	1.61		
HEMBB1001175	1.43	1.54	5.16	3.39	6.36	4.14		
HEMBB1001177	3.63	2.4	7.54	5.8	6.94	6.69		
HEMBB1001182	2.6	3.69	4.89	3.89	6.54	3.87		
HEMBB1001192	3.3	3.09	16.1	15.27	20.06	15.75		
HEMBB1001199	1.16	2.27	1.91	1.43	3.96	1.15		
HEMBB1001200	1.86	1.66	3.14	2.43	5.38	2.29		
HEMBB1001208	2.02	2.04	4.56	2.96	6.19	2.74		
HEMBB1001209	2.98	2.28	5.75	5.22	6.56	4.92		
HEMBB1001210	5.14	4.28	7.8	11.05	6.08	10.33		
HEMBB1001215	9.57	10.46	17.69	17.91	15.75	16.96		
HEMBB1001217	1.78	2.13	4.39	2.04	3.69	1.89		
HEMBB1001218	4.28	3.37	5.47	4.52	5.98	4.6		
HEMBB1001221	1.72	1.65	2.75	1.54	4.29	1.34		
HEMBB1001224	2.2	2.46	3.81	2.98	6.08	3.7		
HEMBB1001230	1.51	2.09	4.36	2.55	4.95	2.22		
HEMBB1001234	5.24	6.05	29.26	31	44.04	30.75		
HEMBB1001235	12.72	10.54	21.49	13.27	8.47	10.71		
HEMBB1001237	11	10.54	21.03	32.1	26.16	36.86	*	+
HEMBB1001242	4.82	5.68	8.63	6.92	6.97	4.51		
HEMBB1001244	1.08	1.1	3.9	1.47	4.36	1.36		
HEMBB1001249	1.26	1.63	2.99	1.84	5.52	1.98		
HEMBB1001253	1.53	1.92	5.68	1.96	4.89	2.39		
HEMBB1001254	1.27	1.19	3.73	1.22	5.09	2.45		
HEMBB1001266	2	4.32	4.75	4.49	6.09	4.63		
HEMBB1001267	3.51	2.92	9.98	8.43	7.63	8.01		
HEMBB1001271	2.25	2.93	3.89	2.59	5.85	3.91		
HEMBB1001282	2.27	2.68	3.9	2.77	4.86	2.99		
HEMBB1001287	54.06	45.71	83.21	72.79	57.33	77.51		
HEMBB1001288	2.45	2.58	3.64	4.57	6.08	3.31		

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HEMBB1001289	4.64	5.82	12.2	6.93	9.11	6.88		
HEMBB1001290	2.82	1.27	4.55	2.89	4.14	1.96		
HEMBB1001294	1.03	1.91	3.2	2.93	3.95	2.51		
HEMBB1001299	7.06	7.64	12.49	16.26	14.41	17.87	*	+
HEMBB1001302	2.16	2.34	2.41	1.75	3.39	1.64		
HEMBB1001304	1.73	1.34	2.6	1.81	5.2	1.67		
HEMBB1001314	1.16	1.07	2.47	1.3	3.63	1.25		
HEMBB1001315	1.25	1.62	1.46	0.87	4	0.9		
HEMBB1001317	2.1	3.38	6.51	4.12	8.01	4.41		
HEMBB1001326	0.88	1.54	2.36	1.51	3	1.69		
HEMBB1001331	2.11	2.79	2.81	3.78	6.14	4.55	*	+
HEMBB1001335	1.39	0.9	1.44	1.4	2.81	1.92		
HEMBB1001337	1.86	1.7	3.15	3.34	4.72	4.51	*	+
HEMBB1001339	4.17	3.87	5.91	5.83	7.91	5.25		
HEMBB1001344	1.27	1.36	2.25	1.62	3.44	1.29		
HEMBB1001346	2.17	2.32	7.45	5.89	6.23	5.7		
HEMBB1001348	0.68	1.37	4.05	1.38	3.68	2.82		
HEMBB1001350	2.06	2.09	4.17	2.07	7.74	2.57		
HEMBB1001356	1.4	1.9	2.33	1.74	5.54	2.29		
HEMBB1001364	0.53	1.28	1.25	1.49	2.47	1.43		
HEMBB1001366	1.61	1.71	3.46	4.17	4.27	3.82	*	+
HEMBB1001367	1.11	2.19	3.79	5.05	6.25	5.75	*	+
HEMBB1001369	0.56	1.29	2.54	1.95	3.39	2.82		
HEMBB1001380	3.13	3.56	6.65	5.43	7.36	7.75		
HEMBB1001381	8.45	6.07	9.53	10.2	14.39	11.86		
HEMBB1001384	3.48	4.92	5.66	9.52	13.27	11.91	**	+
HEMBB1001387	1.19	1.57	3.1	2.36	4.34	1.33		
HEMBB1001394	1.53	1.3	1.68	2.7	2.82	1.89	*	+
HEMBB1001407	0.68	0.83	0.99	0.62	1.33	0.97		
HEMBB1001410	1.35	1.04	1.78	2.44	2.63	1.74		
HEMBB1001413	1.68	1.84	3.32	3.48	3.27	4.04		
HEMBB1001419	2.56	2.24	4.42	3.61	5.47	4.6		
HEMBB1001421	2.29	1.66	2.18	1.31	3.16	0.95		
HEMBB1001424	0.51	1.2	1.67	-0.1	1.58	0.41		
HEMBB1001426	2.04	1.51	3.7	2.66	5.67	4.21		
HEMBB1001429	7.11	5.76	9.83	22.69	19.97	19.53	**	+
HEMBB1001436	3.13	2.51	6.8	7.5	6.44	7.24		
HEMBB1001443	5.61	6.48	20.67	20.46	27.07	22.15		
HEMBB1001449	2.02	2	4.92	4.26	6.35	4.27		

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HEMBB1001454	1.2	1.96	3.77	3.74	5.13	2.99		
HEMBB1001458	4.72	6.48	12.41	7.88	9.04	6.89		
HEMBB1001461	0.55	1.38	2.01	2.11	2.65	1.07		
HEMBB1001463	2.28	2.1	3.7	3.95	5.03	4.66	*	+
HEMBB1001464	1.73	1.29	3.62	2.66	3.92	2.27		
HEMBB1001466	1.15	1.84	2.75	1.88	3.77	2.73		
HEMBB1001482	1.76	2.21	4.36	2.94	5.36	3.97		
HEMBB1001500	1.01	1.08	1.77	1.96	4.39	1.97		
HEMBB1001505	3	3.32	5.87	9.35	14.06	11.17	*	+
HEMBB1001521	2.06	2.43	5.4	5.15	5.78	7.14		
HEMBB1001527	2.63	4.74	11.16	8.69	9.66	9.6		
HEMBB1001530	4.15	3.51	6.57	9.43	12.39	7.05		
HEMBB1001531	1.11	1.34	4.62	2.99	5.16	4.17		
HEMBB1001532	0.63	1.86	2.77	1.86	4.41	2.15		
HEMBB1001535	1.99	2.01	4.22	3.34	4.32	5.75		
HEMBB1001536	2.18	2.65	6.37	4.62	6.87	5.45		
HEMBB1001537	1.31	2.24	3.7	3.21	6.12	2.75		
HEMBB1001542	4.39	4.72	6.28	5.26	7.83	5.7		
HEMBB1001543	7.84	3.58	8.49	8.13	7.08	5.38		
HEMBB1001547	2.02	2.25	2.65	4.2	4.27	2.79	*	+
HEMBB1001548	2.53	2.62	11.82	17.73	29.92	23.34	*	+
HEMBB1001551	0.89	1.7	4.47	2.93	5.96	2.65		
HEMBB1001555	2.13	2.79	4.78	3.73	5.8	4.64		
HEMBB1001562	1.9	2.64	4.27	2.23	3.46	3		
HEMBB1001564	132.08	140.08	310.28	333.18	233.12	279.03		
HEMBB1001565	1.72	1.97	3.9	3.77	4.68	2.07		
HEMBB1001569	0.79	0.8	3.04	2.49	3.68	1.44		
HEMBB1001573	1.9	1.04	3.58	4.18	5.53	4.12	*	+
HEMBB1001585	1.5	1.96	10.91	3.75	7.14	4.87		
HEMBB1001586	1.53	2.27	3.22	4.27	5.45	1.95		
HEMBB1001588	1.33	2.9	5.74	4.72	6.32	5.06		
HEMBB1001595	2.68	3.33	6.92	3.78	4.84	4.7		
HEMBB1001596	3.4	2.57	3.74	2.67	5.36	2.54		
HEMBB1001599	1.45	1.57	3.21	3.07	3.47	2.06		
HEMBB1001603	1.99	2.45	4.17	5.7	8.16	4.04		
HEMBB1001606	1.35	2.28	2.42	2	2.39	1.53		
HEMBB1001612	4.31	3.07	9.25	8.81	8.09	8.9		
HEMBB1001618	1.53	1.62	3.86	2.84	4.48	2.31		
HEMBB1001619	2.11	3.03	3.92	5.71	5.1	4.37	*	+

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HEMBB1001623	2.21	2.38	3.16	2.16	5.5	3.37		
HEMBB1001625	3.73	3.04	4.33	2.93	4.81	3.79		
HEMBB1001630	1.31	2.36	3.54	1.84	4.3	1.23		
HEMBB1001635	1.78	1.64	3.76	2.08	3.32	1.34		
HEMBB1001637	1.76	1.14	3.98	2.09	4.4	3.58		
HEMBB1001641	1.43	1.68	2.78	3.17	3.73	2		
HEMBB1001653	2.18	3.17	5.61	3.96	6.63	3.5		
HEMBB1001665	1.08	2.17	2.04	2.5	4.43	0.88		
HEMBB1001666	2.14	1.95	3.52	2.45	4.88	1.79		
HEMBB1001667	2.37	2.25	3.26	2.94	5.13	3.17		
HEMBB1001668	3.19	2.11	5.15	2.45	6.42	2.69		
HEMBB1001669	0.98	2.02	3.19	1.04	4.53	1.38		
HEMBB1001670	4.02	4.82	6.88	10.7	9.71	8.65	*	+
HEMBB1001673	1.48	2.97	3.61	3.51	4.52	4.43		
HEMBB1001675	1.83	3.27	4.65	4.68	5.78	4.88		
HEMBB1001679	2.52	2.34	5.06	2.19	3.87	1.88		
HEMBB1001684	2.13	1.55	3.89	5.17	6.77	5.05	*	+
HEMBB1001685	3.41	1.61	4.43	2.91	6.24	2.49		
HEMBB1001695	1.9	2.22	4.43	1.38	3.88	2.12		
HEMBB1001703	1.25	2.3	5.74	3.58	3.79	4.1		
HEMBB1001704	1.39	2.16	4.58	4.23	5.02	3.94		
HEMBB1001706	2.76	2.6	3.58	5.6	6.26	4.87	**	+
HEMBB1001707	1.35	2.01	2.87	2.25	3.67	2.8		
HEMBB1001717	1.68	2.21	3.23	2.61	3.34	2.83		
HEMBB1001731	13.81	13.48	24.03	11.02	23.09	25		
HEMBB1001734	3.47	3.35	7.62	6.88	9.22	4.18		
HEMBB1001735	1.35	1.4	3.4	1.58	3.52	2.03		
HEMBB1001736	5.01	6.14	7.87	7.15	10.91	8.11		
HEMBB1001747	0.92	1	3.23	1.87	3.67	2.82		
HEMBB1001749	4.71	2.99	9.39	7.29	5.99	8.16		
HEMBB1001753	3.79	3.3	5.5	7.4	8.97	9.3	**	+
HEMBB1001756	0.53	2.05	1.89	2.31	3.91	2.73		
HEMBB1001757	1.08	1.8	2.64	3.04	4.86	4.54	*	+
HEMBB1001760	1.32	0.98	3.74	1.49	3.56	2.13		
HEMBB1001762	0.9	0.61	2.62	1.57	2.95	2.07		
HEMBB1001780	9.82	12.28	11.34	16.64	26.06	22.06	*	+
HEMBB1001785	0.89	1.24	1.02	0.62	2.88	1.64		
HEMBB1001788	3.22	1.26	5.17	5.76	6.13	5.3		
HEMBB1001793	5.6	4.73	18.12	22.08	20.38	22.86	*	+

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HEMBB1001797	1.61	1.82	2.28	2.94	4.97	5.54	*	+
HEMBB1001802	13.28	9.91	67.77	85.35	82.8	81.27	*	+
HEMBB1001812	2.32	2.58	6.49	7.68	8.28	9.74	*	+
HEMBB1001815	128.22	114.78	102.97	87.37	89.21	62.14	*	-
HEMBB1001816	1.95	2.19	3.97	3.73	6.31	5.73		
HEMBB1001831	0.69	0.98	1.54	0.72	3.28	1.16		
HEMBB1001834	16.15	9.68	133.91	102.49	173.48	141.04		
HEMBB1001836	4.07	1.99	11.4	5.89	6.97	6.7		
HEMBB1001839	0.89	0.86	1.43	1.08	1.95	1.21		
HEMBB1001841	80.32	59.68	120.73	35.74	39.04	23.13	*	-
HEMBB1001844	5.26	4.72	9.73	10.15	10.68	8.11		
HEMBB1001847	6.93	4.24	8.6	9.06	14.77	10.3		
HEMBB1001848	25.33	21.68	40.92	49.73	73.94	62.17	*	+
HEMBB1001850	3.07	2.93	5.25	3.75	7.19	3.95		
HEMBB1001859	13.4	8.82	20.85	39.61	27.01	40.75	*	+
HEMBB1001863	1.7	3.65	7.66	6.89	8.88	7.5		
HEMBB1001867	1.69	1.93	3.16	3.16	4.14	3		
HEMBB1001868	2.15	1.53	2.56	1.31	3.57	1.28		
HEMBB1001869	1.5	2.3	4.23	4.62	8.15	3.58		
HEMBB1001872	1.21	0.79	2.23	1.77	4.17	1.75		
HEMBB1001874	1.92	1.2	2.07	2.58	2.47	3.03	*	+
HEMBB1001875	0.83	1.96	1.7	2.05	3.53	1.37		
HEMBB1001880	2.68	2.17	6.79	4.41	8.91	8.35		
HEMBB1001899	0.6	1.62	2.15	2.26	4.68	1.91		
HEMBB1001903	5.56	5.68	9.61	6.06	6.65	6.7		
HEMBB1001905	2.04	2.82	5.49	4.98	6.07	7.14		
HEMBB1001906	0.67	1.65	2.64	2.22	5.14	2.62		
HEMBB1001908	1.82	1.63	5.26	3.31	6.56	3.59		
HEMBB1001910	1.92	1.16	2.64	3.2	4.41	4.61	*	+
HEMBB1001911	2.06	1.11	4.2	5.73	4.81	4.33		
HEMBB1001915	2.53	3.01	5.61	7.13	7.84	9.4	*	+
HEMBB1001921	2.19	2.21	7.12	6.56	8.47	8.25		
HEMBB1001922	1.74	1.77	3.66	4.91	5.85	3.7		
HEMBB1001925	1.48	2.24	4.57	3.07	4.73	3.39		
HEMBB1001930	0.46	0.94	1.67	0.91	3.18	1.01		
HEMBB1001944	1.72	1.88	5.45	4.83	4.6	4.49		
HEMBB1001945	2.15	1.05	3.58	2.25	3.97	2.12		
HEMBB1001947	2.28	1.13	3.23	5.35	5.98	3.15		
HEMBB1001950	3.49	1.95	5.38	5.15	5.46	3.3		

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HEMBB1001952	1.41	2.05	4.72	2.31	4.73	3.1		
HEMBB1001953	1.62	2.09	3.45	3.63	5.78	3.75		
HEMBB1001957	1.16	2.02	4.28	2.68	4.19	2.19		
HEMBB1001959	2.05	3.31	4.07	4.22	5.75	3.68		
HEMBB1001962	5.54	2.61	5.11	3.34	6.28	2.54		
HEMBB1001967	2.59	2.46	5.62	6.11	8.49	6.15		
HEMBB1001973	2.25	2.4	6.14	7.62	10	7.28	*	+
HEMBB1001978	2.08	1.71	6.29	7.2	7.57	5.83		
HEMBB1001983	9.23	8.69	24.64	38.93	34.91	36.79	*	+
HEMBB1001987	1.78	2.34	3.64	1.66	4.75	2.38		
HEMBB1001988	2.02	1.92	3.42	2.92	5.17	1.85		
HEMBB1001990	7.65	7.72	9.18	12.44	11.53	15.42	*	+
HEMBB1001996	1.54	1.47	3.89	1.61	3.51	1.22		
HEMBB1001997	1.46	2.25	6.1	4.2	5.98	4.23		
HEMBB1001999	10.91	11.08	16.84	24.47	26.58	22.28	**	+
HEMBB1002002	1.08	1.58	3.52	1.91	2.76	2.39		
HEMBB1002005	1.88	2.91	4.8	4.82	7.6	4.22		
HEMBB1002009	2.32	2.48	3.03	2.24	6.23	2.7		
HEMBB1002013	0.96	2.07	3.78	1.95	4.26	1.41		
HEMBB1002015	3.95	4.25	9.47	5.82	8.92	6.73		
HEMBB1002024	45.16	34.47	111.32	113.31	106.76	120.55		
HEMBB1002035	2.15	1.91	2.87	2.11	4.5	2.68		
HEMBB1002039	1.18	2.29	5.1	3.28	5.9	2.98		
HEMBB1002041	3.31	4.13	8.49	15.49	14.42	13.38	**	+
HEMBB1002042	3.97	4.66	9.49	8.09	10.63	9.94		
HEMBB1002043	1.34	2.21	4.61	5.97	5.24	3.36		
HEMBB1002044	0.4	1.19	2.68	1.25	4.19	1.92		
HEMBB1002045	2.83	2.5	10.03	6.34	7.63	4.56		
HEMBB1002049	1.31	1.4	3.77	1.71	4.36	1.73		
HEMBB1002050	1.62	1.61	4.5	3.31	4.53	2.94		
HEMBB1002051	1.17	1.13	2.9	2.59	5.05	4.37		
HEMBB1002068	1.69	2.44	2.43	2.3	4.42	2.07		
HEMBB1002069	3.39	3.94	7.83	6.86	7.55	5		
HEMBB1002075	0.72	1.94	3.33	2.99	3.52	2.37		
HEMBB1002079	1.2	1.8	1.89	1.22	2.84	1.3		
HEMBB1002080	1.74	1.85	4.78	1.55	6.02	2.41		
HEMBB1002082	1.03	1.85	4.59	2.38	4.38	1.96		
HEMBB1002084	25.86	22.68	51.44	33.52	35.54	38.37		
HEMBB1002088	13.92	15.78	22.14	29.46	37.25	35.66	**	+

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HEMBB1002092	2.51	2.24	4.48	5.34	3.65	6.27		
HEMBB1002094	3.21	2.62	8.2	5.72	7.27	6.04		
HEMBB1002103	2.42	2.97	3.51	3.74	5.58	4.47		
HEMBB1002109	4.27	3.47	4.84	5.72	7.83	6.36	*	+
HEMBB1002115	42.37	37.4	91.88	95.86	101.94	101.65		
HEMBB1002120	0.89	1.22	2.91	0.86	2.94	2.41		
HEMBB1002121	0.75	1.56	1.63	1.5	4.66	2.53		
HEMBB1002134	11.99	11.22	112.59	98.93	166.1	133.77		
HEMBB1002136	1.29	1.65	2.9	2.59	3.26	2.58		
HEMBB1002138	10.48	9.64	20.72	18.78	23.06	19.4		
HEMBB1002139	1.84	1.6	5.46	4.69	6	5.84		
HEMBB1002141	1.53	0.83	3.44	1.48	4.64	2.54		
HEMBB1002142	1.85	2	4.95	3.22	5.98	6.03		
HEMBB1002145	1.62	0.83	2.96	1.49	3.07	2.42		
HEMBB1002152	1.27	1.19	3.15	2.32	6.36	3.41		
HEMBB1002162	1.25	1.55	3.92	3.42	5.14	3.61		
HEMBB1002173	4.18	1.09	5.58	2.77	4.48	3.84		
HEMBB1002189	2.78	1.95	6.14	7.01	8.25	5.93		
HEMBB1002190	1.81	2.2	6.36	8.01	6.93	8.36	*	+
HEMBB1002193	1.84	1.06	2.06	4.53	4.37	5.48	**	+
HEMBB1002217	3.82	2.26	6.02	3.61	6.06	3.23		
HEMBB1002218	3.91	3.3	7.58	4.94	6.15	5.68		
HEMBB1002228	2.28	2.9	6.17	6.68	7.94	6.97		
HEMBB1002232	1.15	1.4	2.24	2.14	5.79	3.03		
HEMBB1002245	0.86	0.84	2.34	1.53	2.47	1.05		
HEMBB1002247	1.72	0.59	2.44	1.38	2.24	1.03		
HEMBB1002249	2.65	1.64	3.1	3.39	4.08	4.01	*	+
HEMBB1002254	1.35	1.35	3.83	2.64	3.27	2.86		
HEMBB1002255	0.99	1.37	2.6	1.19	2.93	1.4		
HEMBB1002266	1.33	0.83	2.07	0.73	1.99	0.54		
HEMBB1002271	14.89	9.5	29.42	32.9	41.53	37.28	*	+
HEMBB1002280	1.62	0.78	1.6	1.55	2.93	1.12		
HEMBB1002296	11.83	12.31	18.29	31.87	21.06	23.09	*	+
HEMBB1002300	0.78	2.31	3.48	1.49	4.63	3.12		
HEMBB1002302	1.17	2.17	3.26	2.49	4.76	3.04		
HEMBB1002306	1.83	1.96	4.28	2.91	4.34	2.6		
HEMBB1002316	0.66	1.38	2.36	1.19	2.9	0.97		
HEMBB1002326	0.93	1.68	4.52	4.35	4.41	3.9		
HEMBB1002327	0.99	0.99	2.66	1.46	2.95	2.06		

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HEMBB1002329	2.89	3	3.81	6.39	5.88	5.53	**	+
HEMBB1002340	0.6	1.8	2.05	2.29	3.38	2.22		
HEMBB1002342	8.12	9.23	14.09	21.68	18.15	18.03	*	+
HEMBB1002358	1.09	3.22	6.37	6.52	7.91	9.2		
HEMBB1002359	1.09	2.55	4.29	4.66	5.4	3.54		
HEMBB1002364	1.28	1.82	2.33	3.17	5.15	3.11		
HEMBB1002366	13.63	21.17	32.35	56.28	57.48	53.09	**	+
HEMBB1002371	0.83	0.63	1.72	2.32	2.82	2.1	*	+
HEMBB1002381	0.97	1.16	1.74	2.83	3.16	6.26		
HEMBB1002383	1.07	3.17	4.18	3.1	4.5	4.37		
HEMBB1002387	0.98	2.36	2.68	2.09	3.68	2.96		
HEMBB1002409	6.85	7.27	46.98	69.94	70.04	64.2	*	+
HEMBB1002413	3.92	2.99	8.34	9.46	8.16	10.16		
HEMBB1002415	0.84	1.28	2.79	2.36	3.49	2.11		
HEMBB1002424	1.04	1.17	1.63	2.89	3.04	2.66	**	+
HEMBB1002425	1.12	1.69	5.86	6.46	10.1	5.26		
HEMBB1002427	1.5	1.59	2.32	3.72	7.82	3.65		
HEMBB1002442	2.29	1.57	4.33	4.99	8.58	8.89	*	+
HEMBB1002447	2.61	2.7	5.56	6.1	6.6	5.63		
HEMBB1002453	2.5	2.48	6.56	6.31	7.55	5.25		
HEMBB1002457	1.54	2.08	4.77	3.69	4.61	4.8		
HEMBB1002458	0.48	1.53	2.5	2.2	2.35	1.66		
HEMBB1002463	1.36	1.84	6.55	6.24	6.11	8.87		
HEMBB1002465	1.12	1.18	2.4	2.86	2.25	1.59		
HEMBB1002477	0.71	0.66	4.43	3	4.39	4.86		
HEMBB1002479	22.08	21.58	27.54	16.12	19.41	17.27	*	-
HEMBB1002489	0.86	3.02	3.9	5.73	5.51	7.68	*	+
HEMBB1002492	1.27	1.23	3.07	3.53	4.08	3.39	*	+
HEMBB1002495	1.85	1.85	3.2	2.61	5.02	3.98		
HEMBB1002502	0.94	2.52	2.81	1.77	4.83	3.27		
HEMBB1002509	0.73	1.8	2.65	2.03	2.43	1.27		
HEMBB1002510	0.49	1.68	3.06	1.78	2.5	0.81		
HEMBB1002520	1.46	2.47	5.44	6.62	7.57	8.61	*	+
HEMBB1002522	0.82	1.88	4.42	2.31	6.8	2.07		
HEMBB1002527	11.47	13.79	12.46	24.19	10.37	17.52		
HEMBB1002530	1.43	2.15	3.44	2.93	4.92	2.26		
HEMBB1002531	0.46	1.32	2.04	1.23	2.99	0.35		
HEMBB1002534	1.35	2.27	2.73	4.54	4.08	3.92	**	+
HEMBB1002536	6.58	5.93	46.38	45.93	63.71	42.88		

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HEMBB1002544	3.91	3.45	6.89	6.79	7.87	7.99		
HEMBB1002545	0.92	2.76	2.83	3.21	4.15	4.29		
HEMBB1002550	1.32	1.69	1.86	2.99	4.68	2.42		
HEMBB1002556	2.9	3.54	9.69	8.73	8.12	10.62		
HEMBB1002571	17.25	14.03	19.8	21.91	16.59	24.61		
HEMBB1002579	3.32	2.05	4.87	4.38	6.6	6.39		
HEMBB1002582	1.79	2.11	5.59	5.77	6.47	5.63		
HEMBB1002584	2.82	1.94	6.09	3.94	4.67	3.62		
HEMBB1002587	6.39	5.82	10.63	11.3	9.04	9.94		
HEMBB1002590	1.6	3.07	7.46	5.86	7.3	5.84		
HEMBB1002596	1.5	2.01	3.17	5.59	4.94	4.21	*	+
HEMBB1002600	1.55	2.72	3.81	5.02	7.18	3.93		
HEMBB1002601	1.28	2.23	3.9	2.51	5.59	2.99		
HEMBB1002603	2.37	1.64	5.48	3.53	6.59	5.6		
HEMBB1002607	1.48	1.15	4.34	2.59	4.26	2.99		
HEMBB1002610	1.2	0.96	3.48	1.95	3.79	3.45		
HEMBB1002613	0.96	2.41	4.31	3.98	5.39	3.72		
HEMBB1002614	3.18	3.34	5.35	3.87	6.08	9.76		
HEMBB1002615	1.47	3.29	4.63	2.45	3.83	2.67		
HEMBB1002617	0.67	3.09	2.88	2.1	3.34	3.4		
HEMBB1002623	2.31	3.63	4.36	3.96	6.28	5.91		
HEMBB1002624	2.7	1.56	7.52	7.96	8.72	8.3		
HEMBB1002631	1.65	2	4.28	2.14	3.72	1.74		
HEMBB1002635	1.84	1.74	3.55	3.31	3.64	3.56		
HEMBB1002644	7.22	9.04	15.98	18.52	23.94	22.55	*	+
HEMBB1002654	5.22	4.21	7.77	7.92	7.33	11.74		
HEMBB1002661	1.93	2.16	3.96	1.99	4.13	5.33		
HEMBB1002663	1.59	1.8	3.85	5.45	5.58	5.17	*	+
HEMBB1002664	1.28	2.4	4.43	5.05	9.22	6.76	*	+
HEMBB1002677	1.88	1.83	1.86	1.81	4.79	2.34		
HEMBB1002683	2.68	2.21	9.21	5.67	5.9	8.45		
HEMBB1002684	1.71	0.81	2.53	1.92	2.74	2.63		
HEMBB1002686	1.23	1.39	2.88	1.45	3.37	1.64		
HEMBB1002692	0.99	1.4	1.87	2.5	2.53	2.98	*	+
HEMBB1002693	1.75	1.75	4.12	5.03	5.74	3.46		
HEMBB1002697	1.09	2.8	2.73	4.17	5.58	5.34	*	+
HEMBB1002699	1.59	2.27	4.93	4.72	6.74	6.97		
HEMBB1002702	1.63	1.5	2.54	1.76	3.25	3.33		
HEMBB1002705	4.2	2.84	6.79	8.83	8.26	7.92	*	+

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HEMBB1002712	8.55	1.32	2.38	2.92	4.06	1.4		
IMR321000028	1.03	1.71	2.88	1.63	2.76	1.63		
IMR321000031	1.71	2.59	3.51	5.86	4.35	5.31	*	+
IMR321000034	21.95	15.41	30.37	33.73	19.59	34.65		
IMR321000039	5.81	7.11	14.41	14.72	15.71	13.99		
IMR321000044	0.81	2.37	1.44	1.01	3.26	2.06		
IMR321000063	79.52	80.12	127.61	224.23	199.69	128.8		
IMR321000085	21.02	18.07	26.38	30.28	48.13	47.89	*	+
IMR321000089	1.51	1.42	3.86	3	6.7	5.84		
IMR321000091	4.79	2.91	6.5	8.35	11.38	8.55	*	+
LIVER1000004	8.04	9.67	34.15	55.9	56.53	48.86	*	+
LIVER1000008	1.13	1.36	3.06	1.68	4	2.17		
LIVER1000011	3.03	5.9	26.65	37.8	54.37	45.77	*	+
LIVER1000022	2.75	3.66	7.75	9.39	9.82	9.17	*	+
LIVER1000025	1.78	2.77	5.47	9.83	10.83	7.7	*	+
LIVER1000030	1.05	0.96	2.12	2.04	2.56	1.23		
LIVER1000045	1.33	1.37	3.11	5.11	5.12	5.89	**	+
LIVER1000046	1.01	1.53	3.86	4.14	7.82	5.34		
LIVER1000072	1.61	1.26	5.23	12.42	9.54	12.21	**	+
LIVER1000077	0.33	1.79	1.97	1.87	2.84	3.14		
LIVER1000080	1.53	3	5.81	5.96	4.24	5.41		
LIVER1000086	6.38	7.69	47.4	69.84	79.87	70.57	*	+
LIVER1000092	1.6	1.46	3.09	3.85	3.83	2.41		
LIVER1000095	0.91	2.31	2.56	2.16	2.46	1.55		
LIVER1000097	1.26	0.74	2.49	2.18	2.84	2.25		
LIVER1000098	0.43	1.37	2.57	2.76	3.95	2.29		
LIVER1000100	3.3	2.82	5.82	4.99	7.44	3.74		
LIVER1000101	0.36	1.81	2.4	1.69	4.25	2.74		
LIVER1000106	0.83	1.95	1.79	0.97	2.8	1.29		
LIVER1000108	1.36	2.93	4.31	4.35	4.12	3.43		
LIVER1000115	1.12	1.57	4.32	6.38	6.13	6.9	*	+
LIVER1000120	1.45	0.95	2.23	1.39	1.46	0.73		
LIVER1000138	0.6	1.27	1.86	2.11	2.36	1.6		
LIVER1000146	1.38	2.69	6.24	7.17	7.01	7.02		
LIVER1000148	0.88	1.24	2.65	1.68	5.68	3.51		
LIVER1000157	30.11	26.71	67.66	123.41	85.61	124.96	*	+
LIVER1000161	1.3	1.59	2.3	1.73	3.37	1.84		
LIVER1000167	3.07	3.63	14.08	20.36	22.31	21.82	*	+
LIVER1000174	1.53	1.68	1.84	2.1	3.43	1.29		

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LIVER1000185	2.42	2.55	5.16	4.37	4.72	4.23		
LIVER1000187	0.96	1.55	4.84	6.64	4.17	3.5		
LIVER1000190	3.77	3.48	5.95	4.71	6.24	4.47		
LIVER1000192	2.37	2.92	3.93	4.1	5.23	4.04		
MAMMA1000009	1.39	2.55	5.12	3.62	4.72	3.46		
MAMMA1000015	1.72	1.59	4.78	5.23	4.42	6.42		
MAMMA1000019	0.69	2.48	3.4	4.27	4.81	3.1		
MAMMA1000020	2.79	2.35	5.63	6	7.86	5.75		
MAMMA1000024	0.65	1.76	3.79	2.42	2.91	1.61		
MAMMA1000025	1.92	2.56	6.92	4.96	6.72	5.6		
MAMMA1000043	1.06	2.36	6.43	6.93	8.22	6.6		
MAMMA1000045	1.38	2.01	4.84	2.68	3.96	2.89		
MAMMA1000046	1.74	2.44	3.18	2.88	4.5	2.37		
MAMMA1000055	8.51	8.71	9.57	9.38	10.74	9.36		
MAMMA1000057	4.4	3.29	7.56	8.38	9.78	8.16		
MAMMA1000060	26.78	24.33	45.25	48.69	33.84	48.6		
MAMMA1000069	2.13	1.65	4.1	3.43	3.14	2.41		
MAMMA1000084	2.88	3	5.81	5.64	8.15	7.51		
MAMMA1000085	2.75	3.74	7.02	6.45	5.82	6.97		
MAMMA1000092	1.45	2.97	3.8	4.64	5.15	4.55	*	+
MAMMA1000096	4.45	4.96	9.29	8.15	9.11	6.09		
MAMMA1000097	2.4	2.96	3.86	5.93	6.01	6.97	**	+
MAMMA1000102	1.94	1.59	4.27	4.25	6.16	4.44		
MAMMA1000103	1.52	1.65	5	2.39	4.56	2.83		
MAMMA1000106	1.25	2.15	5.1	2.3	4.48	3.27		
MAMMA1000117	1.19	2.12	3.72	1.84	3.32	2.77		
MAMMA1000118	1.03	2.06	3.08	3.38	3.21	4.56		
MAMMA1000129	1.06	2.1	2.97	1.73	2.7	1.31		
MAMMA1000133	1.09	1.96	3.67	2.8	3.87	2.02		
MAMMA1000134	1.23	2.08	4.28	2.27	4.61	1.93		
MAMMA1000139	1.45	1.91	2.69	2.13	3.98	1.85		
MAMMA1000141	1.97	2.27	5.47	3.67	3.61	3.42		
MAMMA1000143	1.66	1.1	2.55	3.83	3.52	1.74		
MAMMA1000150	4.11	4.95	8.99	6.49	6.4	8.66		
MAMMA1000155	1.87	2.71	4.35	5.46	5.69	6.41	*	+
MAMMA1000163	1.65	2.82	2.62	3.45	4.54	4.97	*	+
MAMMA1000171	1.96	2.43	5.53	4.12	6.52	4.97		
MAMMA1000173	3.5	5.27	10.33	17.47	17.44	18.26	**	+
MAMMA1000175	1.58	1.8	2.89	4.06	5.14	3.7	*	+

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MAMMA1000183	1.14	2.12	5.29	3.92	4.7	4.91		
MAMMA1000191	3.25	3.34	14.68	12.56	14.7	18.23		
MAMMA1000192	5.76	8.53	9.67	16.66	19.91	17.65	**	+
MAMMA1000193	1.68	1.54	0.86	1.33	2.25	1.94		
MAMMA1000198	1.88	1.99	5.53	4.44	6.49	5.57		
MAMMA1000204	1.75	2.25	3.39	3.56	4.13	2.85		
MAMMA1000207	1	3.2	3.41	2.86	4.96	3.47		
MAMMA1000214	1.76	2.08	3.68	2.84	4.42	4.74		
MAMMA1000220	6.19	6.12	11.61	12.49	18.06	16.72	*	+
MAMMA1000221	0.57	1.04	1.68	1.14	4.51	0.87		
MAMMA1000226	0.48	1.06	2.07	1.49	3.19	1.88		
MAMMA1000227	0.93	1.23	1.6	2.73	3.67	3.46	**	+
MAMMA1000230	1	1.23	1.77	2.38	3.04	2.94	**	+
MAMMA1000241	2.9	2.2	4.19	7.24	5.8	7.61	**	+
MAMMA1000245	76.63	70.15	118.95	141.45	166.09	104.88		
MAMMA1000248	6.79	4.17	13.48	13.18	13.44	18.8		
MAMMA1000251	1.68	1.72	4.7	5.55	5.39	5.29		
MAMMA1000254	1.24	1.22	3.59	2.14	5.61	5.02		
MAMMA1000257	5.39	2.62	25.06	32.2	43.78	35.79	*	+
MAMMA1000262	15.48	9.75	18.2	40.81	33.23	34.89	**	+
MAMMA1000264	0.99	1.2	2.3	4.43	2.57	3.4	*	+
MAMMA1000266	1.25	0.79	2.73	4.21	5.33	4.03	*	+
MAMMA1000270	2.43	1.94	4.57	6.16	7.16	7.58	*	+
MAMMA1000271	6.01	3.26	8.54	8.94	6.17	8.1		
MAMMA1000277	0.89	0.93	2.56	2.46	2.75	2.09		
MAMMA1000278	1.84	2.01	4.29	2.18	5.06	3.51		
MAMMA1000279	1.82	1.74	4.33	3.51	5.72	4.35		
MAMMA1000283	0.99	1.51	2.36	1.37	2.66	2.71		
MAMMA1000284	2.65	2.51	8.31	6.28	8.49	8.01		
MAMMA1000287	1.58	2.13	6.27	5.55	6.94	7.1		
MAMMA1000294	4.72	5.45	9.44	3.84	8.21	4.74		
MAMMA1000298	0.87	1.36	2.51	1.55	3.1	0.95		
MAMMA1000302	0.9	1.18	4.73	2.22	4.9	2.56		
MAMMA1000303	0.92	1.62	2.63	4.16	4.06	3.22	*	+
MAMMA1000305	1.07	1.28	2.73	2.47	2.74	2.1		
MAMMA1000307	2.29	3.03	9.61	15.85	14.04	14.38	*	+
MAMMA1000309	0.57	1.61	3.69	4.6	3.65	4.61		
MAMMA1000312	3.55	4.99	8.08	6.19	5.18	6.55		
MAMMA1000313	1.06	2.31	2.34	1.79	3.98	3.43		

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MAMMA1000331	1.08	1.65	3	3.33	6.01	3.21		
MAMMA1000335	7.38	9.1	14.27	19.49	16.28	16.92	*	+
MAMMA1000339	0.33	0.39	2.17	1.46	2.09	0.66		
MAMMA1000340	1.43	1.33	4.12	4.37	2.72	2.15		
MAMMA1000348	1.2	1.27	4.6	3.14	4.82	6.11		
MAMMA1000356	1.93	2.21	4.93	3.08	5.42	6.29		
MAMMA1000358	2.93	3.97	5.02	7.42	7.47	4.9		
MAMMA1000360	1.41	1.92	4.6	3.76	5.2	4.63		
MAMMA1000361	2.2	3.45	8.9	8.94	10.67	8.93		
MAMMA1000363	1.09	1.69	3.86	1.87	4.37	4.1		
MAMMA1000370	0.92	0.71	1.76	2.02	2.62	2.57	*	+
MAMMA1000371	2.09	1.73	6.35	10.02	12.1	10.1	*	+
MAMMA1000372	4.45	4.1	12.88	12.01	12.92	11.97		
MAMMA1000385	1.79	2.36	6.41	6.41	7.66	8.72		
MAMMA1000388	1.93	3.02	6.03	4.7	4.53	5.06		
MAMMA1000395	1.3	2.46	3.12	1.69	3.49	0.8		
MAMMA1000402	1.69	1.68	5.62	3.33	4.35	4.63		
MAMMA1000403	1.7	2.36	5.05	5.45	5.81	3.96		
MAMMA1000410	0.87	1.25	2.71	3.23	3.35	3.25	*	+
MAMMA1000413	1.52	0.47	2.48	3.51	3.76	3.61	*	+
MAMMA1000414	1.08	1.53	3.03	2.94	4.91	1.81		
MAMMA1000416	3.3	4.01	10.2	15.8	23.14	20.47	*	+
MAMMA1000421	2.61	2.83	6.11	7.7	7.42	7.09	*	+
MAMMA1000422	2.83	2.53	7.46	9.18	6.64	12.05		
MAMMA1000423	1.7	1.26	6	5.9	6.62	5.89		
MAMMA1000424	0.88	1.7	3.17	1.91	2.38	1.07		
MAMMA1000429	8.73	10.07	13.78	14.98	16.3	11.17		
MAMMA1000431	1.6	1.27	4.27	5.22	6.32	4.26		
MAMMA1000432	1.05	2.33	2.85	2.63	2.82	1.41		
MAMMA1000437	4.61	4.75	8.44	10.54	11.52	8.12		
MAMMA1000444	2.53	4.15	8.55	7.55	10.17	10.13		
MAMMA1000446	1.19	2.07	3.87	2.03	3.63	2.49		
MAMMA1000449	1.77	1.59	3.54	3.37	4.31	3.22		
MAMMA1000457	4.44	4.82	7.12	7.2	6.88	6.22		
MAMMA1000458	1.27	2.22	4.83	2.52	4.03	1.94		
MAMMA1000468	0.55	1.12	2.2	0.51	2.25	1.16		
MAMMA1000472	1.15	2.3	4.42	4.77	6.36	5.79	*	+
MAMMA1000473	1.95	1.72	3.59	3.45	5.46	3.17		
MAMMA1000477	3.86	3.29	5.67	8.71	9.92	7.97	**	+

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MAMMA1000478	2.85	3.26	7.41	5.76	9.1	7.57		
MAMMA1000483	4.16	3.16	8.3	8.09	6.5	8.63		
MAMMA1000490	1.65	2.61	3.68	2.66	4.96	2.14		
MAMMA1000496	1.18	1.7	3.44	1.3	3.79	2.01		
MAMMA1000500	0.68	1.79	3.22	1.41	3.2	2.86		
MAMMA1000501	3.04	3.89	7.86	13.71	15.02	12.51	**	+
MAMMA1000503	0.84	2.08	2.21	3.52	3.52	2.27		
MAMMA1000506	10.14	8.79	32.66	34.77	26.7	18.31		
MAMMA1000510	3.24	3.5	4.59	10.97	10.76	13.61	**	+
MAMMA1000515	2.12	1.54	4.56	5.97	7.55	6.2	*	+
MAMMA1000516	2.18	2.4	6.29	3.89	3.85	5.07		
MAMMA1000522	1.04	1.47	4.39	2.4	3.68	1.85		
MAMMA1000524	2.04	2.09	3.53	3.82	6.18	3.96		
MAMMA1000528	3.74	2.72	2.05	2.7	4.09	2.88		
MAMMA1000534	0.91	2.35	2.11	1.86	2.91	2.04		
MAMMA1000541	2.85	3.16	11.29	11.22	8.81	12.04		
MAMMA1000550	1.21	2.73	1.86	2.46	6.65	4.64		
MAMMA1000556	1.78	1.32	4.25	2.66	3.37	1.4		
MAMMA1000559	1.32	1.49	5.56	2.92	4.2	3.46		
MAMMA1000565	1.82	2.74	3.93	2.13	4.18	4.22		
MAMMA1000567	0.99	2.16	3.77	2.3	4.07	3.64		
MAMMA1000576	3.72	3.12	13.12	10.45	9.76	10.02		
MAMMA1000582	2.07	2.7	5.64	4.13	4.81	6.31		
MAMMA1000583	1.16	2.33	2.45	2.19	4.47	2.93		
MAMMA1000585	1.66	2.04	4.19	3.82	5.38	3.23		
MAMMA1000587	1.64	1.51	3.73	3.12	5.07	3.49		
MAMMA1000591	0.96	1.34	3.11	1.45	3.74	1.72		
MAMMA1000594	2.3	1.76	4.92	3.55	7.68	5.16		
MAMMA1000597	4.42	3.09	9.64	9.46	9.63	10.35		
MAMMA1000605	2.84	3.94	11.44	18.34	15.85	17.89	*	+
MAMMA1000612	1.91	2.15	5.22	3.85	4.33	4.95		
MAMMA1000614	3.11	2.71	9.4	7.48	6.07	6.34		
MAMMA1000616	1.66	1.79	2.44	2.1	5.09	3.45		
MAMMA1000621	1.39	1.67	3.36	3.15	6.31	7.02		
MAMMA1000623	1.08	1.04	3.83	0.92	2.66	2.3		
MAMMA1000625	7.39	6.32	23.76	19.68	25.39	29.8		
MAMMA1000635	0.89	0.68	1.61	0.76	1.75	0.64		
MAMMA1000643	1.47	1.11	1.94	4.21	3.77	6.82	*	+
MAMMA1000646	4.68	3.61	9.55	17.22	16.4	16.44	**	+

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MAMMA1000652	1.98	1.61	3.56	4.21	5.34	5.24	*	+
MAMMA1000657	2.28	1.78	4.51	2.18	4.48	3.26		
MAMMA1000664	1.78	1.49	5.35	2.9	6.43	6.85		
MAMMA1000667	1.24	1.68	2.17	1.96	5.64	2.41		
MAMMA1000668	0.71	1.11	3.23	2.44	3.76	1.74		
MAMMA1000669	0.76	0.97	2.01	0.9	3.94	2.06		
MAMMA1000670	3.27	2.78	4.47	10.4	6.73	9.28	*	+
MAMMA1000672	1.71	3.23	6.88	5.43	5.63	6.03		
MAMMA1000681	0.98	1.19	2.53	1.98	3.73	2.45		
MAMMA1000684	6.87	11.61	18.54	30.76	32.53	30.62	**	+
MAMMA1000696	1.64	3.39	4.99	7.89	14.39	8.69	*	+
MAMMA1000702	3.12	3.07	5.9	7.47	10.05	7.55	*	+
MAMMA1000706	0.63	1.07	1.79	1.08	1.52	0.66		
MAMMA1000707	0.74	1.26	1.76	0.83	1.87	0.63		
MAMMA1000713	1.53	2.14	5.33	5.43	5.8	6.96		
MAMMA1000714	1.19	1.84	4.31	2.64	4.96	4.94		
MAMMA1000718	1.32	2.79	4.84	5.53	7.12	4.37		
MAMMA1000720	1.33	2.19	5.14	4.95	8.51	5.44		
MAMMA1000723	1.22	1.65	4.17	3.26	4.81	3.68		
MAMMA1000731	1.24	1.17	3.11	3.04	4.99	3.26		
MAMMA1000732	1.37	1.59	3.02	4.86	6.5	6.05	**	+
MAMMA1000733	0.58	0.82	1.54	2.31	2.41	1.22		
MAMMA1000734	12.22	11.56	22.62	21.95	22.19	13.18		
MAMMA1000736	4.26	4.34	11.96	4.92	5.77	6.14		
MAMMA1000738	0.8	2.06	3.82	2.52	4.15	1.95		
MAMMA1000744	1.12	2	5.52	3.27	3.97	4.67		
MAMMA1000746	1	2.03	2.24	2.38	4.27	2.48		
MAMMA1000748	8.23	8.93	13.13	15.53	16.06	15.05	*	+
MAMMA1000751	10.46	7.63	32.43	45.16	40.03	54.65	*	+
MAMMA1000752	1.5	2.37	8.68	11.52	14.2	12.68	*	+
MAMMA1000757	1.89	2.48	5.54	7.9	8.53	10.86	*	+
MAMMA1000760	3	2.99	6.77	4.65	8.01	7.12		
MAMMA1000761	1.86	2.58	5.73	4.87	6.29	4.99		
MAMMA1000775	1.37	1.83	4.43	3.23	4.29	2.64		
MAMMA1000776	2.37	2.36	6.3	6.57	7	6.12		
MAMMA1000778	2.14	2.28	5.19	4.95	3.99	3.84		
MAMMA1000781	1.33	1.33	3.06	2.82	2.86	1.23		
MAMMA1000782	1.94	2.36	3.88	2.93	3.11	3.01		
MAMMA1000784	1.28	1.58	3.94	2.22	7.2	3.64		

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MAMMA1000788	3.05	4.31	4.38	4.16	5.12	2.21		
MAMMA1000798	1.01	2.86	2.77	2.03	3.56	2.1		
MAMMA1000802	4.36	3.71	8.23	17.49	15.39	19.2	**	+
MAMMA1000810	3.91	4.98	14.15	17.58	19.04	16.15	*	+
MAMMA1000813	1.63	2.11	3.73	2.82	3.15	2.06		
MAMMA1000814	2.56	2.97	7.82	7.28	7.26	6.61		
MAMMA1000824	12.58	11.27	34.16	62.44	72.28	50.62	*	+
MAMMA1000827	1.83	2.04	5.05	3.3	4.77	4.31		
MAMMA1000831	1.45	2.81	2.84	2.55	5.43	1.85		
MAMMA1000838	6.85	9.27	7.86	13.01	8.43	14.52		
MAMMA1000839	4.89	4.41	9	9.02	8.66	14.04		
MAMMA1000841	1.33	2.02	3.11	2.23	4.44	2.29		
MAMMA1000842	2.48	1.88	3.59	3.03	3.74	1.82		
MAMMA1000843	1.26	2.19	3.88	2.26	4.43	2.35		
MAMMA1000845	0.83	1.01	2.4	2.35	3.88	1.24		
MAMMA1000851	1.3	3.42	5.35	7.83	5.9	6.65		
MAMMA1000854	2.77	3.7	6.33	5.08	5.68	5.13		
MAMMA1000855	0.37	2.97	2.62	2.51	3.74	1.78		
MAMMA1000856	0.87	1.39	3.11	2.05	6.37	3.19		
MAMMA1000859	9.88	8.56	20.5	19.52	18.47	24.31		
MAMMA1000862	1.13	1.55	3.53	1.17	3.18	0.79		
MAMMA1000863	2.62	2.08	4.72	2.59	5.24	4.91		
MAMMA1000865	0.35	0.82	2.48	0.4	1.84	0.35		
MAMMA1000867	1.08	2.83	2.87	1.95	3.68	4.76		
MAMMA1000875	0.89	2.72	2.34	3.31	3.57	2.59		
MAMMA1000876	1.23	1.64	4.59	2.4	3.37	3.22		
MAMMA1000877	3.15	2.89	9.22	8.39	10.32	10.07		
MAMMA1000878	3.05	3.61	8.94	6.33	8.52	9.62		
MAMMA1000880	1.46	1.15	4.77	2.45	3.96	3.01		
MAMMA1000881	1.81	2.09	4.52	3.77	6.07	4.73		
MAMMA1000883	0.57	0.79	2.1	1.37	2.14	2.11		
MAMMA1000897	0.76	2.39	0.36	1.19	2.99	6.19		
MAMMA1000898	1.06	1.99	1.75	1.41	2.49	3.7		
MAMMA1000905	1.8	2.75	4.68	8.32	6.86	10.64	*	+
MAMMA1000906	1.17	2.49	2.63	2.45	4.27	4.08		
MAMMA1000908	1.59	1.63	4.3	1.77	3.05	1.43		
MAMMA1000911	4.97	6.25	8.37	21.77	20.01	20.98	**	+
MAMMA1000914	1.14	0.85	2.41	1.1	2.23	1.61		
MAMMA1000920	1.99	2.17	4.41	10.82	10.67	9.11	**	+

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MAMMA1000921	1.03	1.02	2.41	3.47	3.84	3.17	*	+
MAMMA1000931	2.68	3.44	3.95	6.78	7.66	7.32	**	+
MAMMA1000940	1.67	1.84	6.05	5.78	6.84	6.3		
MAMMA1000941	3.74	2.55	8.61	9.01	10.11	9.46		
MAMMA1000942	2.75	1.85	7.46	8.27	8.47	7.2		
MAMMA1000943	2.16	2.84	10.49	9.04	11.08	8.74		
MAMMA1000952	2.6	1.93	8.65	9.03	7.47	6.75		
MAMMA1000956	0.93	1.24	3.11	3.64	3.1	3.47		
MAMMA1000957	2.5	1.41	2.62	4.81	5.73	6.85	**	+
MAMMA1000962	3.25	3.57	10.48	13.62	11.18	16.85	*	+
MAMMA1000966	1.85	2.19	6.04	6.34	6.23	7.04		
MAMMA1000968	1.6	1.46	5.49	4.79	5.62	4.97		
MAMMA1000972	2.4	1.41	3.83	3.34	3.91	4.32		
MAMMA1000973	5.14	3.37	12.58	7.02	8.56	10.31		
MAMMA1000975	1.44	1.99	3.34	2.37	4.9	5.05		
MAMMA1000976	2.46	2.71	8.57	9.22	11.17	8.92		
MAMMA1000979	1.46	2.62	3.06	4.34	4.41	7.71		
MAMMA1000986	5.75	5.32	10.24	8.83	11.32	13.95		
MAMMA1000987	1.44	1.36	3.99	2.43	3.74	5.66		
MAMMA1000988	3.76	4.86	8.88	10.18	11.34	10.5	*	+
MAMMA1000994	9.82	7.58	15.88	12.02	11.56	9.25		
MAMMA1000998	1.51	1.07	3.13	4.21	5.42	4.04	*	+
MAMMA1001003	1.98	1.83	5.97	4.2	6.86	4.39		
MAMMA1001007	0.38	1.03	1.77	0.14	1.38	0.32		
MAMMA1001008	11.76	11.09	40.52	56.73	50.93	45.37	*	+
MAMMA1001013	3.62	4.16	12.14	8.42	11.54	10.08		
MAMMA1001014	1.4	1.79	5.49	4.36	5.16	4.26		
MAMMA1001021	0.49	2.08	7.85	6.46	5.47	4.26		
MAMMA1001024	0.85	1.59	3.14	2.55	3.92	1.96		
MAMMA1001025	1.03	1.47	2.94	1.27	2.95	1.41		
MAMMA1001028	1.3	1.09	2.23	3.07	4.73	3.28	*	+
MAMMA1001030	1.63	0.48	2.22	3.06	3.24	2.08		
MAMMA1001035	2.48	2.92	10.31	9.29	11.92	11.54		
MAMMA1001036	4.69	4.01	10.7	11.23	8.22	11.33		
MAMMA1001037	1.91	2.88	6.49	5.28	7.53	4.69		
MAMMA1001038	1.18	1.59	4.28	4.12	3.85	4.45		
MAMMA1001041	1.64	1.87	3.18	3.75	4.04	2.64		
MAMMA1001043	1.09	1.24	3.67	3.44	3.35	3.18		
MAMMA1001050	1.52	1.55	5.94	8.4	8.28	6.51	*	+

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MAMMA1001054	2.04	2.58	6.99	9.29	11.07	8.36	*	+
MAMMA1001059	2.66	4.71	9.73	8.85	9.72	8.46		
MAMMA1001066	3.64	2.97	12.26	14.08	12.09	8.96		
MAMMA1001067	1.26	2	4.77	3.53	5.33	3.29		
MAMMA1001072	1.44	2.06	7.76	6.38	7.13	7.2		
MAMMA1001073	1.17	0.79	1.47	1.49	2.74	1.34		
MAMMA1001074	0.78	1.47	3.97	6.24	5.4	4.9	*	+
MAMMA1001075	4.87	4.41	10.48	11.24	9.82	8.21		
MAMMA1001078	1.7	1.83	7.96	9.69	9.99	9.37	*	+
MAMMA1001080	3.77	3.93	6.97	8.71	10.33	5.57		
MAMMA1001082	1.51	2.03	4.03	1.73	5.23	1.6		
MAMMA1001091	1.17	1.36	2.02	1.81	3.03	1.47		
MAMMA1001092	1.93	2.09	4.81	3.17	3.57	1.89		
MAMMA1001094	1.73	4.28	4.65	4	5.62	4.7		
MAMMA1001105	2.45	2.62	7.7	6.99	7.57	6.06		
MAMMA1001110	0.4	1.01	2.74	1.42	2.53	0.47		
MAMMA1001126	1.96	3.09	10.92	8.39	9.27	6.08		
MAMMA1001133	2.5	3.44	10.94	9.48	10.83	10.68		
MAMMA1001139	87.88	86.18	214.31	193.19	47.2	160.92		
MAMMA1001141	1.33	2.89	3.65	3.69	5.25	5.46		
MAMMA1001143	2.02	1.79	4.23	3.95	6.69	4.34		
MAMMA1001145	3.1	2.22	3.39	6.37	7.13	2.84		
MAMMA1001150	1.34	2.48	3.95	3.06	3.31	2.11		
MAMMA1001154	2.16	2.8	5.57	5.44	7.13	5.22		
MAMMA1001159	4.19	4.01	11.06	11.31	5.89	9.45		
MAMMA1001161	4.3	5.27	19.53	18.34	10.8	14.8		
MAMMA1001162	1.98	1.77	3.16	5.25	5.13	2.25		
MAMMA1001181	2.44	2.28	4.87	5.06	4.74	3.62		
MAMMA1001186	2	2.66	4.66	5.38	5.48	3.9		
MAMMA1001189	2.23	3.68	7.17	11	11.17	9.9	*	+
MAMMA1001191	2.54	2.07	5.49	4.37	3.89	2.97		
MAMMA1001198	368.47	416.05	784.82	647.17	738.61	605.52		
MAMMA1001202	11.78	11.85	30.06	34.39	28.74	25.16		
MAMMA1001203	2.57	3.01	7.15	8.72	6.26	5.56		
MAMMA1001206	1.91	3.28	4.5	3.69	6.66	2.65		
MAMMA1001208	2.66	2.93	3.31	3.82	4.95	3.19		
MAMMA1001215	2.9	3.08	6.55	3.49	8.09	4.74		
MAMMA1001220	2.63	3.03	7.25	7.16	7.17	6.03		
MAMMA1001222	1.25	1.18	4.18	2.18	5.85	0.53		

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MAMMA1001223	2.48	3.32	6.53	4.95	6.51	4.1		
MAMMA1001232	2.82	4.27	8.08	12.22	8.82	9.57		
MAMMA1001234	1.25	3.27	3.17	5.05	3.91	3.26		
MAMMA1001237	1.22	1.56	4.21	1.94	3.66	2.09		
MAMMA1001243	2.18	2.28	4.06	4.05	4.89	1.99		
MAMMA1001244	1.22	1.16	2.86	2.96	4.79	2.22		
MAMMA1001249	2.3	1.89	5.93	5.19	5.8	3.75		
MAMMA1001256	3	3.09	8.29	5.89	7.83	8.01		
MAMMA1001259	4.38	3.25	7.15	7.94	9.24	6.63		
MAMMA1001260	1.76	2.71	5.42	6.51	5.33	7.33		
MAMMA1001262	2.1	4.11	5.28	7.86	8.04	6.25	*	+
MAMMA1001268	2	2.16	4.59	2.56	4.23	2.48		
MAMMA1001271	4.84	5.78	17.37	18.29	14.24	15.67		
MAMMA1001274	2.88	3.06	6.17	6.22	8.55	7.93		
MAMMA1001280	2.09	1.48	4.36	1.84	3.78	1.73		
MAMMA1001283	1.63	1.71	6.34	6.88	5.63	4.83		
MAMMA1001284	2.27	2	8.67	5.08	9.09	9.51		
MAMMA1001286	13.83	9.72	17.39	12.15	11.83	14.63		
MAMMA1001289	17.63	13.49	23.32	21.02	26.39	36.8		
MAMMA1001292	3	3.01	5.94	7.26	6.31	6.85	*	+
MAMMA1001296	3.55	3.76	12.61	14.11	12.37	12.8		
MAMMA1001298	1.26	1.7	6.26	4.25	6.78	4.07		
MAMMA1001305	0.86	1.59	4.43	2.49	4.07	2.63		
MAMMA1001309	0.61	0.9	2.7	1.84	3	1.49		
MAMMA1001310	1.72	2.17	3.64	4.81	7.38	4.42		
MAMMA1001322	0.99	1.54	1.83	2.83	1.77	2.13		
MAMMA1001324	1.3	1.12	3.16	2.03	2.83	1.94		
MAMMA1001330	3.35	2.65	9.53	7.93	9.75	5.36		
MAMMA1001333	3.1	3.74	10.23	9.88	11.4	9.07		
MAMMA1001334	5.53	4.17	4.83	10.97	8.23	10.16	**	+
MAMMA1001337	2.49	3.54	6.6	6.99	9.16	8.05	*	+
MAMMA1001341	1.21	1.14	3.48	1.54	5.66	1.41		
MAMMA1001343	2.37	1.89	8.07	8.17	9.75	10.95		
MAMMA1001344	9.59	9.07	11.75	13.63	11.67	15.98		
MAMMA1001346	1.34	1.25	3.9	2.05	3.9	2.94		
MAMMA1001383	3.07	3.61	8.52	8.3	9.02	9.38		
MAMMA1001388	1.62	1.93	5.34	3.38	6.11	4.58		
MAMMA1001396	4.2	2.12	8.12	11.39	10.42	8.68		
MAMMA1001397	2.59	2.27	5.79	8.33	8.96	7.78	*	+

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MAMMA1001401	26.87	16.48	32.72	43.47	57.55	45.66	*	+
MAMMA1001408	1.06	1.06	2.57	0.65	4.22	1.19		
MAMMA1001411	1.65	1.26	3.84	4.38	3.33	3.51		
MAMMA1001414	3.12	3.85	5.74	12.58	10.67	15.28	**	+
MAMMA1001415	2.45	3.16	11.93	14.57	20.15	13.69	*	+
MAMMA1001418	0.66	2.2	5.36	3.57	6.04	4.46		
MAMMA1001419	0.8	2.43	4.93	6.03	7.01	3.92		
MAMMA1001420	0.96	3.09	4.5	3.23	4.11	3.41		
MAMMA1001426	20.24	32.21	42.42	44.31	39.63	38.75		
MAMMA1001428	1.94	2.83	6.35	3.8	6.93	4.33		
MAMMA1001432	1.19	2.33	8.19	5.62	6.19	6.68		
MAMMA1001435	1.43	0.78	3.32	3.48	3.67	2.64		
MAMMA1001442	1.96	3.94	7.41	8.18	8.6	6.63		
MAMMA1001446	2.17	2.57	6.71	6.9	7.34	7.97		
MAMMA1001450	1.22	2.05	3.58	2.81	4.18	2.39		
MAMMA1001452	1.99	1.78	5.92	8.38	6.19	4.83		
MAMMA1001465	3.93	3.25	13.61	16.65	14.6	13.82		
MAMMA1001476	1.63	1.09	4.25	5.87	5.95	4.64	*	+
MAMMA1001478	2.28	2.12	5.98	3.55	6.27	4.19		
MAMMA1001479	3.11	4.71	8.32	5.58	6.74	6.21		
MAMMA1001487	1.1	1.14	3.84	4.73	3.26	2.08		
MAMMA1001498	1.93	3.41	7.78	6.17	7.45	5.64		
MAMMA1001501	0.88	1.97	4.49	2.8	4.77	2.36		
MAMMA1001502	1.82	1.91	6.48	3.29	6.29	6.26		
MAMMA1001510	0.48	0.78	2.92	0.54	3.04	1.19		
MAMMA1001522	1.03	1.29	3.94	5.05	4.9	3.39		
MAMMA1001529	0.72	2.06	3.22	3.74	4.07	2.57		
MAMMA1001532	1.74	1.86	4.27	3.79	5.71	3.12		
MAMMA1001533	0.61	1.31	2.9	1.52	3.06	1.64		
MAMMA1001534	0.44	2.59	2.4	1.48	3.64	1.14		
MAMMA1001535	1.38	1.91	3.99	2.12	3.98	2.38		
MAMMA1001547	2.8	2.89	7.77	9.23	8.22	6.22		
MAMMA1001551	1.1	1.48	4.46	2.23	2.88	2.99		
MAMMA1001569	1.27	1.68	3.41	2.03	3.41	1.94		
MAMMA1001575	1.48	2.41	3.42	4.01	4.43	2.81		
MAMMA1001576	4.79	8.23	9.65	14.75	9.39	17.03		
MAMMA1001584	0.89	2.48	3.33	3.11	4	3.09		
MAMMA1001586	1.43	2.41	3.34	3.78	3.31	1.84		
MAMMA1001590	2.96	2.53	5.55	5.44	6.47	6.04		

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MAMMA1001599	4.64	7.15	16.79	15.8	15.18	15.06		
MAMMA1001600	1.45	2.22	4.73	2.98	4.68	2.11		
MAMMA1001604	1.03	1.76	3.62	2.35	4.01	1.64		
MAMMA1001606	1.64	2.04	5.15	3.58	5.45	4.27		
MAMMA1001609	1.31	2.37	4.36	3.05	5.43	1.59		
MAMMA1001614	2.91	3.57	6.15	5.94	6.11	4.14		
MAMMA1001615	3.98	2.61	10.12	8.87	8.29	8.41		
MAMMA1001619	7.73	7.8	14.29	16.33	12.93	14.61		
MAMMA1001620	2.53	2.41	7.98	5.77	7.13	4.54		
MAMMA1001623	4.11	4.58	9.3	7.34	9.28	6.75		
MAMMA1001626	0.83	1.98	2.52	3.24	3.93	1.93		
MAMMA1001627	1.11	1.98	3.57	2.63	3.68	1.63		
MAMMA1001630	2.02	3.08	7.83	7.49	7.53	4.29		
MAMMA1001633	2.64	3.12	8.8	12.09	9.59	6.16		
MAMMA1001634	2.83	2.7	6.11	8.69	8.27	6.9	*	+
MAMMA1001635	5.65	2.39	9.52	7.92	8.3	8.37		
MAMMA1001649	1.61	1.63	4.71	2.95	4.62	2.53		
MAMMA1001654	8.14	9.45	39	43.4	55	46.79		
MAMMA1001660	19.61	17.92	37.43	40.94	27.03	34		
MAMMA1001663	1.9	4.73	9.42	9.59	9.56	6.58		
MAMMA1001670	1.12	2.66	3.97	3.65	4.09	2.62		
MAMMA1001671	1.08	1.42	3.56	1.37	4.64	1.77		
MAMMA1001679	6.85	6.37	13.89	11.48	17.04	13.91		
MAMMA1001683	2.15	3.29	9.6	6.58	6.53	6.96		
MAMMA1001686	1.25	1.34	3.77	1.39	2.97	3.06		
MAMMA1001688	113.39	113.61	245.56	392.2	458.41	413	**	+
MAMMA1001689	1.01	3.76	4.1	5.04	3.79	4.44		
MAMMA1001692	1.97	2.59	5.37	3.66	5.3	3.88		
MAMMA1001711	1.99	3.64	8.65	4.35	5.51	6.1		
MAMMA1001715	1.31	1.64	3.95	4.64	4.87	4.13		
MAMMA1001730	2.01	2.15	2.5	2.8	4.42	2.83		
MAMMA1001735	44.73	48.32	102.35	94.99	156.23	119.88		
MAMMA1001740	0.64	1.6	4.59	2.06	3.91	1.95		
MAMMA1001743	9.84	11.15	33.16	41.97	51.62	49.6	*	+
MAMMA1001744	0.63	0.72	0.86	1.1	1.72	1.71	*	+
MAMMA1001745	1.41	2.15	6.15	3.27	4.46	3.93		
MAMMA1001751	1.38	2.41	3.24	2.85	4.51	4.32		
MAMMA1001752	4.7	4.78	9.75	6.12	9.61	8.4		
MAMMA1001754	7.25	7.89	7.34	11.04	9.63	9.39	*	+

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MAMMA1001757	1.21	1.1	2.32	2.21	3.25	2.43		
MAMMA1001760	3.87	4.52	20.01	22.91	24.2	27.59	*	+
MAMMA1001764	2.62	2.36	5.97	7.13	10.17	6.51		
MAMMA1001767	1.22	1.55	2.13	1.61	2.96	1.55		
MAMMA1001768	0.57	1.18	4.25	4.74	4.72	4.37		
MAMMA1001769	2.48	2.83	9.22	9.3	9.81	8.94		
MAMMA1001771	2.66	1.58	3.74	2.86	5.85	6.77		
MAMMA1001773	2.7	3.53	3.87	4	6.29	7.61		
MAMMA1001778	0.88	1.92	3.14	3.13	4.21	3.61		
MAMMA1001783	2.01	2.1	11.25	11.63	18.46	13.04		
MAMMA1001785	3	3.52	8.85	10.56	13.38	11	*	+
MAMMA1001788	0.49	0.86	1.21	0.72	1.72	1.11		
MAMMA1001790	1.68	1.67	5.1	2.37	3.73	3.93		
MAMMA1001800	0.83	0.99	1.47	1.5	2.24	3.25		
MAMMA1001804	1.02	1.41	3.18	2.37	4.16	2.4		
MAMMA1001806	2.13	2.78	6.4	3.15	5.5	4.72		
MAMMA1001812	1.46	1.33	5.52	4.21	5.86	5.05		
MAMMA1001815	0.33	1.76	3.07	1.22	3.67	1.24		
MAMMA1001817	3.19	3.38	9.5	6.78	10.89	13.3		
MAMMA1001818	1.68	2.08	3.41	3.94	8.52	3.41		
MAMMA1001819	2.57	4.12	5.82	8.7	10.29	7.87	*	+
MAMMA1001820	2.68	4.51	8.27	7.51	10.98	6.07		
MAMMA1001824	1.66	2.83	8.36	7.55	9.8	7.11		
MAMMA1001832	6.72	7.99	11.85	20.17	21.28	17.21	**	+
MAMMA1001836	1.74	1.66	5.08	4.79	8.19	4.88		
MAMMA1001837	2.61	2	5.84	7.1	9.19	5.37		
MAMMA1001848	1.02	1.61	3.3	2.81	5.33	3.18		
MAMMA1001850	3.79	4.51	9.31	9.98	9.93	14.19		
MAMMA1001851	1.49	2.33	4.98	4.97	4.12	4.02		
MAMMA1001852	2.98	4	9.68	6.4	7.56	6.8		
MAMMA1001854	2.56	3.11	9.16	10.59	10.64	9.98		
MAMMA1001858	3.11	2.22	5.28	9.93	7.91	8.87	**	+
MAMMA1001864	1.69	1.91	4.09	8.91	6.18	4.37		
MAMMA1001868	0.71	0.92	2.64	1.68	2.58	0.91		
MAMMA1001874	1.2	0.87	2.52	1.06	3.48	1.17		
MAMMA1001878	3.1	3.46	10.86	7.7	13.37	6.77		
MAMMA1001880	2.67	2.99	7.24	5.58	7.17	8.12		
MAMMA1001885	1.14	1.93	6.19	4.7	5.54	4.58		
MAMMA1001890	3.54	3.95	12.93	13.59	13.29	12.2		

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MAMMA1001893	3.74	3.42	6.25	6.59	5.49	5.58		
MAMMA1001901	1.13	1.5	5.4	4.53	5.72	2.67		
MAMMA1001907	2.57	1.62	6.43	4.15	7.36	6.34		
MAMMA1001908	3.2	3.36	8.35	11.83	12.96	12.46	*	+
MAMMA1001919	0.23	0.97	3.3	2.24	3.9	2.07		
MAMMA1001931	0.76	1.65	4.04	3.36	5.89	3.25		
MAMMA1001937	2.27	3.15	5.5	6.44	5.06	3.78		
MAMMA1001951	1.74	2.57	6.47	6.48	6.15	4.83		
MAMMA1001956	3.02	3.48	9.72	8.52	7.66	6.76		
MAMMA1001957	3.39	3.51	9.15	7.88	9.47	7.66		
MAMMA1001960	3.1	3.34	7.24	12.06	9.14	6.1		
MAMMA1001963	0.57	0.78	2.14	1.3	2.36	1.06		
MAMMA1001969	1.7	3.43	10.86	8.54	11.14	8.74		
MAMMA1001970	2.86	3.04	8.48	13.11	6.59	6.64		
MAMMA1001978	0.57	1.85	1.76	2.42	3.87	1.53		
MAMMA1001992	2.07	2.04	5.65	6.79	6.75	5.09		
MAMMA1001994	7.97	3.65	11	18.83	13.23	17.17	*	+
MAMMA1002008	3.28	3.77	6.42	3.43	4.06	1.24		
MAMMA1002009	1.46	2.94	5.17	5.73	7.57	4.06		
MAMMA1002011	1.77	1.71	4.26	6.5	6.45	3.37		
MAMMA1002022	1.51	2.1	5.92	6.64	7.42	5.2		
MAMMA1002024	9.79	9.67	19.03	17.61	16.96	22.43		
MAMMA1002032	2.78	2.41	7.25	5.29	6.16	8.07		
MAMMA1002033	3.23	3.95	7.73	11.24	7.23	6.62		
MAMMA1002041	2.87	2.25	3.18	4.74	5.39	1.71		
MAMMA1002042	2.54	2.34	5.66	5.65	5.78	3.76		
MAMMA1002045	2.33	3.51	7.28	8.39	5.05	4.44		
MAMMA1002047	2.58	2.98	8.83	8.7	8.9	6.89		
MAMMA1002056	2.01	5.78	11.14	11.35	10.64	9.14		
MAMMA1002058	1.67	2.61	8.19	4.84	4.66	4.27		
MAMMA1002060	1.08	2.08	1.41	2.5	4.09	1.2		
MAMMA1002065	1.81	2.75	6.04	7.19	5.19	3.26		
MAMMA1002068	2.43	1.84	5.29	4.98	5.6	4.47		
MAMMA1002070	4.5	2.92	4.15	2.58	5.23	2.81		
MAMMA1002078	1.32	1.43	2.94	1.12	4.4	1.07		
MAMMA1002080	7.98	9.71	13.38	14.92	20.84	14.26		
MAMMA1002082	2.54	4.96	13.04	9.67	8.15	7.78		
MAMMA1002084	1.78	3.47	3.38	4.68	4.48	3.6		
MAMMA1002087	1.12	2.15	5.37	3.6	4.67	2.36		

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MAMMA1002091	3.79	3.22	4.32	7.18	6.76	6.41	**	+
MAMMA1002093	0.72	1.4	4.31	2.74	4.39	2.33		
MAMMA1002095	2.4	3.22	7.5	4.73	7.52	4.54		
MAMMA1002108	1.84	1.02	2.63	1.87	3.24	1.31		
MAMMA1002112	2.94	3.4	7.03	12.79	16.02	11.28	**	+
MAMMA1002118	1.02	1.61	2.24	1.41	3.18	2.01		
MAMMA1002119	0.76	2.15	3.61	1.51	3.12	2.54		
MAMMA1002125	1.79	2.61	6.95	4.52	4.19	4.11		
MAMMA1002126	3.72	4.25	9.79	10.08	9.02	11.03		
MAMMA1002128	0.9	2.36	3.07	2.7	3.49	2.88		
MAMMA1002132	3.78	3.24	11.42	6.18	9.05	6.81		
MAMMA1002140	1.46	1.87	3.68	2.18	3.24	2.33		
MAMMA1002142	3.13	3.43	7.06	5.18	7.62	5.46		
MAMMA1002143	5.42	2.27	7.96	7.98	9.87	13.23		
MAMMA1002145	1.47	1.34	3.3	2.9	4.02	2.64		
MAMMA1002147	0.81	1.59	2.9	2.71	4.4	3		
MAMMA1002153	0.99	1.92	5.55	3.52	6.41	4.75		
MAMMA1002155	2.11	1.93	6.76	4.4	6.46	4.46		
MAMMA1002156	0.81	0.8	1.94	0.67	2.63	0.78		
MAMMA1002158	1.38	1.83	5.12	4.09	7.73	5.2		
MAMMA1002164	2.01	2.09	5.86	3.17	3.18	4.04		
MAMMA1002165	4.04	4.29	7.25	8.65	8.1	6.81		
MAMMA1002170	1.01	1.48	154.53	2.65	3.24	4.11		
MAMMA1002174	1.66	2.9	5.88	4.55	7.78	8.58		
MAMMA1002175	3.27	3.3	7.02	6.95	6.64	7.22		
MAMMA1002180	8.59	6.53	35.97	55.49	48.49	51.08	*	+
MAMMA1002198	3.11	2.3	9.33	7.6	11.22	7.13		
MAMMA1002205	2.93	1.66	6.15	6.3	8.04	7.54		
MAMMA1002206	4.6	3.59	8.14	12.4	13.97	11.74	**	+
MAMMA1002209	1.7	1.93	4.03	4.43	4.23	4.57		
MAMMA1002215	4.17	2.72	15.2	11.05	12.43	17.14		
MAMMA1002219	1.57	1.96	4.99	4.84	6.34	5.96		
MAMMA1002224	3.18	2.9	8.18	5.49	7.25	5.86		
MAMMA1002229	3.74	2.21	8.83	8.48	9.26	6.82		
MAMMA1002230	2.02	2.21	6.63	5.31	8.91	6.58		
MAMMA1002233	3.01	1.6	6.08	4.21	7.91	6.14		
MAMMA1002234	3.05	3.06	6.7	8.6	10.45	10.76	*	+
MAMMA1002236	4.13	3.68	14.08	26.56	20.38	24.71	*	+
MAMMA1002243	0.97	2.48	3.48	3.28	3.43	2.96		

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MAMMA1002250	1.06	2.09	5.2	3.95	6.82	6.01		
MAMMA1002253	2.77	2.39	3.45	4.84	6.18	3.37		
MAMMA1002267	17.17	19.95	51.7	130.02	108.53	115.75	**	+
MAMMA1002268	1.72	2.28	5.82	6.92	11.3	6.52		
MAMMA1002269	0.89	0.73	2.25	2.32	2.58	1.67		
MAMMA1002282	0.86	1.09	4.95	5.87	5.31	6.81		
MAMMA1002292	2.71	2.25	7.77	10.57	10.52	11.53	*	+
MAMMA1002293	3.71	3.31	12.81	8.54	10.47	12.05		
MAMMA1002294	0.9	1.71	4.61	3.68	6.03	4.2		
MAMMA1002297	1.53	3.25	7.45	5.77	7.8	6.91		
MAMMA1002298	1.48	1.4	3.98	3.85	3.11	2.46		
MAMMA1002299	1.5	1.69	3.16	3.91	2.97	2.2		
MAMMA1002308	1.39	1.35	6.55	4.5	3.11	2.54		
MAMMA1002310	3.56	3.84	12.73	9.92	12.66	11.48		
MAMMA1002311	2.52	2.13	6.82	9.61	9.66	6.9	*	+
MAMMA1002312	1.63	2.22	5.19	3.51	8.45	2.55		
MAMMA1002317	2.08	2.55	4.89	4.08	3.85	4.09		
MAMMA1002319	0.8	2.78	3.51	2.68	3.97	2.85		
MAMMA1002322	2.48	3.23	7.84	12.21	10.02	8.55	*	+
MAMMA1002329	1.64	1.67	2.93	2.9	3.3	2.76		
MAMMA1002332	2.17	2.38	4.58	5.98	4.14	3.05		
MAMMA1002333	1.7	1.74	4.19	5.35	5.07	3.54		
MAMMA1002335	1.75	2.72	8.53	6.93	11.32	4.23		
MAMMA1002339	2.09	2.42	7.34	5.21	7.5	5.14		
MAMMA1002347	1.7	2.3	6.39	5.5	5.32	4.64		
MAMMA1002351	2.08	2.68	5.74	3.03	4.48	4.84		
MAMMA1002352	1.27	2.28	3.66	3.53	4.63	2.8		
MAMMA1002353	4.46	2.5	5.84	5.95	4.19	4		
MAMMA1002355	3.97	3.38	8.37	7.98	7.31	8.57		
MAMMA1002356	2.18	1.49	4.36	5.43	4.13	3.75		
MAMMA1002359	3.95	3.35	16.09	23.81	24.53	19	*	+
MAMMA1002360	0.93	1.73	3.77	2.48	3.2	1.67		
MAMMA1002361	2.01	2.64	4.53	4.17	4.95	4.03		
MAMMA1002362	2.33	2.33	3.36	5.31	5.51	3.99	*	+
MAMMA1002367	2.97	3.64	14.63	18.34	21.06	21.56	*	+
MAMMA1002371	2.28	3.75	8.3	6.15	6.74	5.88		
MAMMA1002380	1.81	2.26	4.9	4.71	5.76	3.55		
MAMMA1002384	2.14	1.53	4.73	4.48	5.36	4.05		
MAMMA1002385	1.19	2.05	5.63	3.34	4.8	2.47		

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MAMMA1002390	1.41	2.04	3.75	5.48	5.4	3.43		
MAMMA1002392	1.94	3.1	6.1	4.06	5.95	3.32		
MAMMA1002396	4.87	3.49	12.87	10.79	12.9	8.08		
MAMMA1002399	4.42	5.13	10.69	10.95	8.66	4.57		
MAMMA1002400	3	2.22	4.69	3.11	4.36	3.53		
MAMMA1002409	51.57	55.16	63.3	77.54	80.62	77.88	**	+
MAMMA1002411	1.08	1.88	4.13	3.43	5.49	1.92		
MAMMA1002413	2.02	3.01	9.19	5.93	7.17	6.75		
MAMMA1002417	1.83	2.24	4.87	3.45	4.25	2.63		
MAMMA1002427	1.5	2.38	4.54	4.78	5.56	3.41		
MAMMA1002428	2.47	2.26	5.38	4.46	5.11	4.28		
MAMMA1002433	1.74	2.18	6.84	6.72	6.96	6.22		
MAMMA1002434	2.94	2.4	7.38	5.34	4.65	5.03		
MAMMA1002446	1.39	2.34	5.62	3.98	5.84	5.96		
MAMMA1002447	2.51	1.38	6.4	5.11	6.26	5.45		
MAMMA1002454	7.77	9.16	18.07	21.71	17.12	18.35		
MAMMA1002461	2.06	4.11	7.7	4.92	5.41	6.47		
MAMMA1002463	3.28	3.32	8.09	6.98	7.82	5.39		
MAMMA1002464	16.58	16.77	20.05	19.41	20.41	18.09		
MAMMA1002466	9.48	9.89	14.22	14.58	15.75	13.93		
MAMMA1002470	1.39	1.51	5.13	3.54	5.01	3.73		
MAMMA1002475	0.72	1.85	5.03	3.86	5.17	4.65		
MAMMA1002480	0.66	1.21	2.31	1.68	2.84	2.03		
MAMMA1002485	29.98	27.24	46.09	64.83	74.9	80.68	**	+
MAMMA1002494	2	2	4.11	4.48	5.12	5.13	*	+
MAMMA1002498	0.97	2.57	3.16	2.07	3.18	1.55		
MAMMA1002524	3.04	2.96	6.43	5.18	7.34	6.1		
MAMMA1002530	2.5	3.24	4.88	3.17	4.41	2.55		
MAMMA1002538	2.34	2.38	5.62	5.46	5.13	4.91		
MAMMA1002545	2.37	2.64	6.26	4.56	6.49	4.56		
MAMMA1002554	1.96	1.42	5.43	5.3	6.01	7.81		
MAMMA1002556	1.3	1.9	3.6	3.73	5.75	3.89		
MAMMA1002561	2.3	2.99	7.19	8.13	10.46	7.98		
MAMMA1002565	1.22	2.15	3.52	2.57	4.51	2.55		
MAMMA1002566	0.98	1.87	6.21	1.65	4.7	3.9		
MAMMA1002571	0.53	1.8	3.06	1.43	3.1	4.3		
MAMMA1002573	2.14	1.86	7.06	4.54	5.66	5.97		
MAMMA1002576	118.77	131.84	363.97	348.62	471.73	358.66		
MAMMA1002584	3.52	2.27	11.91	12.86	17.82	13.46		

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MAMMA1002585	0.76	1.86	4.38	1.85	3.6	5.26		
MAMMA1002586	1.98	2.55	3.85	4.12	5.02	3.3		
MAMMA1002589	1.08	1.26	2.44	2.36	5.06	3.19		
MAMMA1002590	1.01	1.57	5.87	2.58	6.75	4.57		
MAMMA1002593	2.48	2.48	4.89	4.18	4.07	3.04		
MAMMA1002597	2.47	2.52	7.25	8.06	9.48	8.78	*	+
MAMMA1002598	12.12	13.52	30.83	37.28	48.14	38.91	*	+
MAMMA1002603	1.2	1.39	3.69	3.25	6.24	4.35		
MAMMA1002612	3.51	3.39	12.6	7.66	7.78	9.76		
MAMMA1002617	4.3	3.41	10.15	6.3	7.29	10.05		
MAMMA1002618	1.68	2.27	4.02	2.76	3.59	3.91		
MAMMA1002619	2.96	2.8	5.24	3.22	5.88	3.49		
MAMMA1002622	2.51	2.12	8.02	7.1	7.18	7.15		
MAMMA1002623	2.31	2.21	6.27	5.89	6.17	6.19		
MAMMA1002625	1.32	1.3	3.23	2.3	6.42	2.6		
MAMMA1002627	0.98	0.82	2.93	0.6	1.29	0.21		
MAMMA1002629	1.8	2.23	6.09	5.03	6.74	7.02		
MAMMA1002631	1	1.86	3.61	3.07	4.55	2.97		
MAMMA1002633	6.61	7.44	21.47	19.33	24.55	21.53		
MAMMA1002636	1.02	2.46	6.97	6.79	8.77	9.25		
MAMMA1002637	1.05	1.4	4.66	3.39	4.85	4.28		
MAMMA1002646	1.69	0.8	3.32	2.33	2.86	1.53		
MAMMA1002648	10.51	14.07	21.18	42.29	31.45	39.76	**	+
MAMMA1002650	1.33	0.56	1.62	1.76	2.08	0.57		
MAMMA1002652	1.76	2.82	7.31	7.5	7.41	9.79		
MAMMA1002655	1.7	2.11	3.65	2.54	4.23	3.78		
MAMMA1002662	0.84	2.24	4.33	3.57	5.68	4.13		
MAMMA1002665	3.61	3.57	10.05	13.42	17.97	19.59	*	+
MAMMA1002671	2.84	3.63	10.17	17.04	16.47	19.3	**	+
MAMMA1002673	1.32	2.14	4.93	4.07	5.03	2.82		
MAMMA1002684	2.95	3.11	3.84	6.61	8.19	7.54	**	+
MAMMA1002685	0.68	1.49	2.57	2.05	3.74	2.97		
MAMMA1002692	1.28	1.96	5.45	2.46	4.14	3.62		
MAMMA1002693	1.84	4.18	8	4.63	7.68	6.61		
MAMMA1002698	0.99	1.91	4.05	2.92	4.42	3.3		
MAMMA1002699	2	2.35	4.43	4.05	5.22	3.64		
MAMMA1002701	2.41	2.56	8.46	6.72	8.94	8.93		
MAMMA1002708	1.51	1.55	5.38	4.08	6.16	6.18		
MAMMA1002711	1.58	2.08	7.04	4.37	7.35	5.81		

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MAMMA1002712	3.05	3.13	6.98	4.88	7.12	7.39		
MAMMA1002716	0.56	1.75	3.39	2.38	6.29	2.9		
MAMMA1002721	2.11	2.01	6.57	3.72	6.34	4.59		
MAMMA1002723	2.43	2.46	4.91	3.85	5.98	4.88		
MAMMA1002727	3.85	5.55	5.78	5.29	4.45	6.22		
MAMMA1002728	21.35	22.03	57.81	49.09	54.73	65.13		
MAMMA1002742	4.12	4.39	10.35	7.92	8.63	7.61		
MAMMA1002743	4.12	3.89	6.17	13.81	14.09	13.46	**	+
MAMMA1002744	2.07	3.15	9.18	9.33	12.98	13.16		
MAMMA1002746	0.93	1.28	3.09	2.29	4.31	1.68		
MAMMA1002748	2.71	2.65	4.52	7.15	5.86	4.72	*	+
MAMMA1002754	1.12	2.41	5.56	5.05	5.65	6.26		
MAMMA1002758	0.71	1.66	2.55	1.57	4.41	1.69		
MAMMA1002762	11.3	11.14	36.64	38.42	34.23	48.71		
MAMMA1002764	1.83	3.2	5.95	5.11	6.06	4.26		
MAMMA1002765	1.19	1.63	4.29	4.63	5.26	2.67		
MAMMA1002769	7.4	6.44	13.04	13.78	8.03	12.41		
MAMMA1002771	1.41	2.41	3.31	3.54	5.39	4.39		
MAMMA1002775	4.56	4.48	19.79	22.54	29.77	24.29	*	+
MAMMA1002780	2.59	1.83	3.03	2.11	4.89	3.78		
MAMMA1002782	1.43	2.49	3.85	2.51	4.79	4.11		
MAMMA1002795	1.89	2.03	3.46	6.45	7.68	5.35	**	+
MAMMA1002796	4.35	3.97	7.51	7.2	8.09	8.17		
MAMMA1002805	6.61	11.12	16.52	15.95	24.7	16.5		
MAMMA1002806	1.47	2.02	3.51	2.28	4.62	2.17		
MAMMA1002807	1.63	2.4	6.77	6.78	9.66	6.4		
MAMMA1002814	3.43	3.52	7.92	9.58	12.39	10.66	*	+
MAMMA1002817	1.28	1.56	2.87	2.89	5.43	2.91		
MAMMA1002820	1.66	1.93	2.61	2.52	4.77	2.21		
MAMMA1002830	67.67	70.46	130.59	165.92	139.33	187.18	*	+
MAMMA1002833	4.16	2.88	9.4	8.22	10.68	10.58		
MAMMA1002835	0.77	1.87	4.03	1.73	3.97	2.79		
MAMMA1002838	1.85	2.66	5.31	2.91	4.44	3.93		
MAMMA1002842	1	3.83	3.84	3.32	4.63	5.15		
MAMMA1002843	1.72	2.92	2.33	4.09	4.81	3		
MAMMA1002844	3.05	3.64	6.52	5.26	7.3	4.09		
MAMMA1002845	1.25	1.57	2.45	3.59	3.55	4.67	*	+
MAMMA1002857	92.1	106.97	208.17	209.17	202.29	249.13		
MAMMA1002858	317.94	188.78	378.89	560.7	620.76	724.33	**	+

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MAMMA1002863	2.17	2.83	6.91	3.51	5.12	3.96		
MAMMA1002868	2.73	3.7	6.26	6.35	9.53	10.25	*	+
MAMMA1002869	5.43	6.83	26.64	22.68	30.03	29.85		
MAMMA1002871	0.61	1.7	1.78	1.9	3.8	1.97		
MAMMA1002875	1.9	2.59	3.99	4.48	6.35	4.06		
MAMMA1002879	8.42	9.2	14.19	22.55	23.63	27.96	**	+
MAMMA1002880	1.23	2.02	2.12	1.48	5.42	2.03		
MAMMA1002881	1.21	1.43	1.84	3.01	5.43	2.46		
MAMMA1002885	0.96	1.59	2.71	2.6	3.26	1.59		
MAMMA1002886	2.63	2.52	3.9	6.01	5.37	7.05	**	+
MAMMA1002887	1.28	1.83	2.78	2.98	5.14	4.32	*	+
MAMMA1002890	0.79	1.7	4.05	4.39	4.8	4.01		
MAMMA1002892	1.35	2.45	4.98	6.64	6.24	5.84	*	+
MAMMA1002893	4.52	3.58	5.4	7.6	8.03	8.43	**	+
MAMMA1002895	1.43	1.31	3.28	1.81	3.89	1.64		
MAMMA1002898	0.53	1.67	4.15	2.69	4.72	1.42		
MAMMA1002905	1.32	1.58	2.51	4.1	5.01	3.87	**	+
MAMMA1002906	15.12	10.76	15.42	19.47	13.76	15.58		
MAMMA1002908	0.99	1.24	4.28	3.53	4.24	4.07		
MAMMA1002909	1.92	2.64	5.67	6.82	8.18	6.57	*	+
MAMMA1002918	2.75	2.69	5.42	5.27	7.26	6.58		
MAMMA1002925	92.88	85.77	163.7	127.31	122.97	178.98		
MAMMA1002926	6.08	6.31	16.25	16.64	19.48	19.9		
MAMMA1002930	1.21	1.59	5.67	4.88	8.91	4.21		
MAMMA1002937	4.91	3.87	30.71	40.45	75.17	61.59	*	+
MAMMA1002938	1.67	1.86	2.42	2.35	3.2	3.56		
MAMMA1002941	0.49	1.48	2.78	2.53	3.59	2.24		
MAMMA1002947	2.24	2.59	4.55	6	6.8	7.94	*	+
MAMMA1002964	1.73	2.9	5.91	6.91	7.24	7.16	*	+
MAMMA1002967	1.94	1.59	2.28	2.9	4.19	2.79		
MAMMA1002970	2.72	1.77	6	7.59	7.28	8.96	*	+
MAMMA1002971	1.52	1.6	2.9	2.51	7.27	3.93		
MAMMA1002972	1	1.32	2.95	1.74	4.56	2.12		
MAMMA1002973	1.38	2.45	6.73	4.36	6.72	6.78		
MAMMA1002979	55.6	60.16	121.72	134.02	101.19	107.19		
MAMMA1002982	0.53	1.98	2.28	2.04	3.28	1.9		
MAMMA1002987	1.56	2.11	5.56	3.14	5.55	4.14		
MAMMA1003003	0.77	2.18	4.78	4.46	6.47	5.08		
MAMMA1003004	1.65	1.86	3.7	3.64	3.59	3.16		

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MAMMA1003007	0.69	1.16	2.73	1.88	3.7	2.32		
MAMMA1003011	1.56	1.8	3.67	3.77	5.41	3.94		
MAMMA1003013	3.67	5.57	39.41	47.56	59.11	54.29	*	+
MAMMA1003015	1.16	1.8	2.21	2.54	2.9	2.19		
MAMMA1003019	0.6	1.61	2.1	3.12	4.61	2.63		
MAMMA1003020	2.96	4.19	5.34	11.31	10.33	10.09	**	+
MAMMA1003026	1.29	1.56	2.95	2.66	4.25	2.25		
MAMMA1003031	0.61	1.71	5.64	4.13	5.85	5.89		
MAMMA1003033	1.34	1.65	4.13	2.84	5.11	3.64		
MAMMA1003035	1.66	2.5	5.44	5.12	7.03	4.9		
MAMMA1003039	0.95	0.75	3.31	2.15	4.73	2.48		
MAMMA1003040	1.38	2.54	5.32	4.57	7.47	7.43		
MAMMA1003044	2.36	2.96	6.52	4.29	6.41	5.99		
MAMMA1003047	1.82	3.67	7.61	5.74	7.05	7.13		
MAMMA1003049	0.47	1.72	2.03	1.08	1.56	1.45		
MAMMA1003055	1.24	1.67	4.92	3.77	5.14	3.44		
MAMMA1003056	0.9	0.91	1.85	1.22	2.26	1.02		
MAMMA1003057	2.53	3.34	6.76	7.25	9.2	5.01		
MAMMA1003066	1.65	2.06	4.73	4.1	7.08	5.07		
MAMMA1003075	1.11	1.71	3.16	1.85	4.37	2.32		
MAMMA1003089	1.69	2.11	7.13	7.85	8.66	7.43		
MAMMA1003092	1.25	1.79	3.21	2.62	4.08	1.76		
MAMMA1003095	2.27	3.33	5.4	7.24	8.57	5.34		
MAMMA1003099	1.88	2.51	4.95	4.09	6.45	4.35		
MAMMA1003102	1.33	2.04	2.88	3.2	3.27	2.39		
MAMMA1003104	0.64	1.07	3.17	2.15	3.25	1.56		
MAMMA1003113	4.22	4.21	6.98	9.22	7.02	7.07		
MAMMA1003126	12.93	14.72	20.89	19.28	12	15.63		
MAMMA1003127	2.95	3.14	5.91	3.88	6.12	5.19		
MAMMA1003131	2.82	3.51	4.86	3.82	5.91	5.88		
MAMMA1003135	3.66	4.65	7.61	2.33	4.04	2.64		
MAMMA1003140	0.73	2.01	3.59	2.3	3.32	1.89		
MAMMA1003146	2.08	2.24	3.89	3.17	5.09	3.3		
MAMMA1003150	1.18	1.8	3.01	3.37	4.29	3.45	*	+
MAMMA1003154	0.54	1.41	2.29	2.21	3.57	2.34		
MAMMA1003155	8.08	9.18	20.88	21.41	17.68	20.56		
MAMMA1003157	5.94	4.82	6.07	5.18	7.05	7.89		
MAMMA1003163	1.74	1.69	4.23	2.55	5.46	3.08		
MAMMA1003164	2.94	4.56	6.23	4.08	9.9	8.18		

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MAMMA1003166	3.62	3.5	5.77	6.24	8.66	6.12		
NB9N31000010	2.5	3.88	7.58	9.63	12.26	9.5	*	+
NB9N31000016	0.73	2.8	5.21	4.04	4.41	3.15		
NB9N31000043	8.1	8.88	19.71	12.51	12.3	12.64		
NB9N31000045	167.24	153.32	255.96	401.78	320.53	296.06	*	+
NB9N31000054	7.29	4.42	11.75	11.15	11.87	13.43		
NB9N31000076	2.31	1.94	3.51	4.5	6.35	4.44	*	+
NB9N31000086	2.62	2.65	6.23	3.61	9.71	7.69		
NT2RM1000001	2.56	2.45	6.24	5.7	7.05	6.32		
NT2RM1000018	3.84	4.69	10.6	6.58	9.09	6.92		
NT2RM1000032	1.12	2.64	3.88	2.28	4.92	3.21		
NT2RM1000035	1.72	3.68	5.53	5.44	5.21	5.98		
NT2RM1000037	1.38	2.98	2.75	2.41	4.15	2.11		
NT2RM1000039	3.45	5.13	5.9	6.51	7.26	8.4	*	+
NT2RM1000042	33.96	32.7	65.25	57.46	67.15	64.39		
NT2RM1000055	0.85	1.74	3.34	1.16	3.55	1.16		
NT2RM1000059	3.26	3.16	7.66	4.69	5.97	5.78		
NT2RM1000062	1.13	1.21	1.9	3.47	4.33	2.46	*	+
NT2RM1000065	23.8	16.41	34.06	36.15	35.1	51.38		
NT2RM1000066	4.13	4.31	8.98	7.23	10.95	9.81		
NT2RM1000071	49.63	37.81	86.71	73.04	63.32	84.05		
NT2RM1000080	1.37	2.04	3.8	5.1	5.94	4.5	*	+
NT2RM1000086	4.04	4.65	4.08	5.01	6.23	5.58	*	+
NT2RM1000092	6.17	6.93	15.76	14.48	25.91	15.13		
NT2RM1000118	0.63	1.12	1.22	0.63	1.7	0.44		
NT2RM1000119	1.32	2.27	1.96	1.84	3.38	2.99		
NT2RM1000121	1.13	1.84	1.76	2.92	3.84	2.78	*	+
NT2RM1000122	3.5	3.78	7.34	5.5	8.86	9.57		
NT2RM1000127	0.69	1.34	1.47	2.14	3.36	3.32	*	+
NT2RM1000131	0.71	1.7	1.47	1.36	3.02	2.53		
NT2RM1000132	3.2	4.88	4.83	6.86	6.46	6.31	*	+
NT2RM1000153	1.75	1.9	3.68	2.38	4.45	4.84		
NT2RM1000184	72.82	77.46	151.91	106.39	163.07	125.55		
NT2RM1000186	1.55	1.46	4.32	2.67	4.72	3.94		
NT2RM1000187	3.11	1.96	5.16	10.09	9.1	8.78	**	+
NT2RM1000199	1.12	1.37	2.11	2.41	3.51	2.72	*	+
NT2RM1000213	1.32	1.75	2.38	2.66	2.71	2.22		
NT2RM1000215	10.95	11.07	17.21	19.51	22.84	15.14		
NT2RM1000218	9.72	9.95	23.71	26.94	24.74	29.21		

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NT2RM1000224	8.8	8.63	15.2	15.51	21.29	17.61		
NT2RM1000236	30.38	24.19	61.14	72.86	82.44	71.5	*	+
NT2RM1000242	0.23	1.17	1.32	0.39	2.27	0.12		
NT2RM1000244	1.41	1.48	3.43	6.9	3.69	6.7	*	+
NT2RM1000252	1.75	1.5	3.4	3.4	3.06	3.18		
NT2RM1000256	7.88	5.89	9.46	26.12	29.45	36.8	**	+
NT2RM1000257	1.98	3.01	5.09	4.64	6.83	6.65		
NT2RM1000260	7.9	7.01	13.32	9.18	12.49	11.77		
NT2RM1000269	3.87	2.87	5.12	6.63	9.78	3.87		
NT2RM1000271	0.71	0.8	1.87	0.46	2.47	0.51		
NT2RM1000272	117.67	92.26	202.95	249.32	333.98	356.74	*	+
NT2RM1000273	10.03	9.45	20.12	22.32	16.68	15.76		
NT2RM1000274	63.11	66.41	123.01	137.14	91.97	104.48		
NT2RM1000280	3.95	4.18	8.18	6.71	8.72	7.93		
NT2RM1000295	0.49	1	2.2	1.12	3.16	0.87		
NT2RM1000300	1.51	1.87	2.78	3.63	5.75	3.09		
NT2RM1000304	58.38	98.72	161.87	187.58	185.55	204.78	*	+
NT2RM1000314	1.8	2.12	3.6	3.84	4.07	4.33		
NT2RM1000318	12.6	14.04	20.81	35.01	29.96	29.8	**	+
NT2RM1000335	2.76	2.57	4.34	6.29	5.41	4.09		
NT2RM1000341	0.46	1.27	1.95	1.41	2.33	0.99		
NT2RM1000350	3.04	3.47	5.52	7.32	5.63	6.44		
NT2RM1000354	0.55	1.31	1.31	5.43	7.2	5.72	**	+
NT2RM1000355	30.24	31.5	56.85	74.62	50.25	61.33		
NT2RM1000361	3.63	3.87	7.23	14.39	20.29	18.78	**	+
NT2RM1000365	0.58	1.08	1.71	1.27	1.82	0.52		
NT2RM1000372	14.99	19.56	30.06	42.71	46.67	45.44	**	+
NT2RM1000377	2.04	2.18	9.66	13.38	14.74	13.48	*	+
NT2RM1000388	0.35	1.57	3.01	2.2	3.8	2.42		
NT2RM1000394	0.45	1.31	1.87	1.43	2.72	0.69		
NT2RM1000399	0.53	1.57	3.25	1.98	3.2	1.81		
NT2RM1000407	1.13	1.52	2.17	1.02	2.7	1.51		
NT2RM1000421	0.84	0.57	2.78	1.06	1.77	1.13		
NT2RM1000422	20.65	23.31	54.69	87.5	82.91	79.47	*	+
NT2RM1000430	1.22	1.57	2.01	3.2	3.67	2.95	**	+
NT2RM1000462	1.55	2.33	7.32	5.59	7.28	8.16		
NT2RM1000499	1.36	2.09	4.74	5	6.16	6.37	*	+
NT2RM1000512	12.49	13.22	19.22	10.54	14.15	19.84		
NT2RM1000519	33.96	37.54	55.78	31.14	29.25	47.55		

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NT2RM1000527	7.97	8.92	37.68	55.15	60.19	46.68	*	+
NT2RM1000539	3.45	3.59	12.93	15.52	17.01	18.1	*	+
NT2RM1000542	0.85	1.05	2.99	1.17	2.35	1.02		
NT2RM1000553	3.7	2.42	22.32	42.83	42.96	34.5	*	+
NT2RM1000555	11.3	11.6	23.97	34.11	29.67	22.76		
NT2RM1000558	2.09	5.34	9.74	9.56	16.24	14.29		
NT2RM1000563	1.47	2.42	3.36	4.07	5.58	3.95	*	+
NT2RM1000566	0.88	1.57	3.5	3.62	6.01	2.79		
NT2RM1000570	96.92	77.32	137.63	167.35	105.47	174.1		
NT2RM1000571	13.21	11.87	22.51	43.87	40.18	28.45	*	+
NT2RM1000574	0.84	2.15	2.55	2.15	3.07	1.67		
NT2RM1000580	1.37	2.18	4.07	5.15	7.98	2.96		
NT2RM1000620	2.61	2.95	8.2	8.35	9.58	7.26		
NT2RM1000623	1.25	1.2	2.38	1.75	2.81	0.62		
NT2RM1000630	0.79	2.28	2.39	1.68	3.51	1.67		
NT2RM1000633	30.97	39.36	36.34	54.43	44.6	43.59	*	+
NT2RM1000634	1.91	4.16	8.12	2.56	7.05	5.57		
NT2RM1000642	3.85	5.37	8.13	8.21	8.56	8.52		
NT2RM1000647	41.3	39.09	62.11	57.72	68.29	62.69		
NT2RM1000648	2.49	2.65	4.61	6.14	5.63	4.51		
NT2RM1000650	2.46	3.05	7.6	5.4	6.07	6		
NT2RM1000661	4.48	5.7	15.82	15.48	13.45	13.18		
NT2RM1000666	1	1.77	1.99	1.37	2.8	0.71		
NT2RM1000669	3.51	2.76	4.67	3.63	5.42	3.28		
NT2RM1000672	2.23	3.95	7.81	3.98	8.47	7.22		
NT2RM1000681	99.53	86.09	118.7	105.41	90.59	124.14		
NT2RM1000691	2.02	2.61	5.74	3.61	7.69	3.76		
NT2RM1000698	1.11	1.43	4	6.42	6.29	4.11	*	+
NT2RM1000699	1.85	2.86	3.17	3.67	4.35	4.15	*	+
NT2RM1000702	3.71	4.64	9.47	9.31	9.72	11.4		
NT2RM1000703	11.56	12.36	25.24	26.72	20.42	21.06		
NT2RM1000704	24.48	23	32.91	46.54	24.13	40.82		
NT2RM1000725	60.92	59.45	88.28	94.89	82.36	105.67		
NT2RM1000726	1.85	2.02	5.75	1.97	4.8	4		
NT2RM1000731	1.11	2.24	4.98	2.45	3.47	3.43		
NT2RM1000741	1.38	1.87	3.16	2.69	4.15	2.9		
NT2RM1000742	2.61	4.6	7.41	9.55	10.94	9.84	*	+
NT2RM1000744	2.1	3.61	7.14	4.05	5.24	5.05		
NT2RM1000746	2.25	2.47	2.95	2.22	4.01	3.89		

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NT2RM1000747	23.34	23.92	46.23	44.66	50.12	55.15		
NT2RM1000752	3.83	2.36	4.62	3.95	4.88	3.46		
NT2RM1000767	4.14	7.27	35.27	25.27	38.02	28.81		
NT2RM1000770	2.97	3.08	6.36	4.71	6.71	5.67		
NT2RM1000772	0.76	0.7	1.07	1.34	1.69	0.44		
NT2RM1000779	13.03	12.11	42.22	53.91	45.61	66.73	*	+
NT2RM1000780	1.16	2.9	3.74	3.09	4.32	3.01		
NT2RM1000781	1.07	0.98	1.71	2.58	4.4	1.93		
NT2RM1000789	5.28	5.15	29.74	29.63	46.72	36.53		
NT2RM1000800	2.87	2.63	6.37	5.66	9.57	6.96		
NT2RM1000802	2.44	2.99	7.5	4.34	5.47	4.82		
NT2RM1000811	1.78	1.6	2.13	2.26	4.96	2.76		
NT2RM1000826	6.06	6.36	13.34	14.42	20.73	20.98	*	+
NT2RM1000829	3.91	2.87	6.39	6.73	8.48	8.41	*	+
NT2RM1000831	81.54	64.45	185.14	182.43	179.79	197.27		
NT2RM1000833	14.58	13.33	42.25	76.74	73.25	67.48	**	+
NT2RM1000834	4.06	3.09	6.2	8.49	9.42	10.49	**	+
NT2RM1000841	12.34	10.01	21.15	34.98	36.63	30.81	**	+
NT2RM1000848	4.79	4.42	6.44	9.36	12.74	10.45	**	+
NT2RM1000850	2.66	3.42	13.41	8.55	11.79	9.74		
NT2RM1000852	1.34	1.94	3.23	3.01	5.76	2.61		
NT2RM1000853	1.19	2.85	2.15	3.11	3.26	3.23		
NT2RM1000855	29.27	24.82	45.19	52.48	45.32	58.45		
NT2RM1000857	4.63	5	10.67	8.76	11.3	10.76		
NT2RM1000858	7.3	7.6	15.86	9.09	11.56	10.93		
NT2RM1000867	19.42	15.85	28.1	32.52	35.03	24.06		
NT2RM1000874	3.15	2.65	7.03	5.17	9.62	5.31		
NT2RM1000882	2.36	1.37	3.71	5.39	9.31	5.45	*	+
NT2RM1000883	5.21	3.34	7.42	5.18	11.3	7.9		
NT2RM1000885	3.86	4.43	9.4	7.59	8.15	9.8		
NT2RM1000893	3.15	3.41	8.14	7.73	6.17	8.39		
NT2RM1000894	3.29	4.4	6.18	8.14	6.11	6.61		
NT2RM1000898	3.72	7.33	10.02	13.4	17.51	12.41	*	+
NT2RM1000899	1.02	2.22	3.07	3.68	7.49	4.69		
NT2RM1000905	11.92	17.41	30.36	37.19	45.16	37.3	*	+
NT2RM1000910	7.5	8.78	20.16	36.37	36.98	37.5	**	+
NT2RM1000914	6.46	7.69	19.74	14.28	17.33	17.77		
NT2RM1000919	6.1	3.92	9.91	14.61	17.49	15.37	**	+
NT2RM1000921	0.72	1.9	3.69	2.79	4.27	3.32		

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NT2RM1000922	4.7	6.11	8.09	9.03	5.21	6.36		
NT2RM1000924	0.89	3.03	3.04	3.08	2.89	3		
NT2RM1000927	1.35	1.78	2.85	3.07	4.72	3.46		
NT2RM1000951	7.95	11.33	26.73	32.33	34.46	31.18	*	+
NT2RM1000956	7.91	6.36	13.35	23.61	27.46	21.91	**	+
NT2RM1000960	12.48	10.27	29.06	34.95	37.47	38.96	*	+
NT2RM1000961	3.28	3.61	7.45	9.44	13.18	8.11		
NT2RM1000962	4.14	3.5	8.18	7.59	10.15	9.86		
NT2RM1000973	16.71	15.79	29.32	31.15	11.56	27.73		
NT2RM1000978	0.57	1.46	1.58	0.95	2.64	0.44		
NT2RM1000982	2.34	2.29	3.52	3.57	4.94	4.54	*	+
NT2RM1000991	1.61	1.78	4.25	3.88	5.56	5.23		
NT2RM1000994	6.36	6.16	12.57	16.52	16.64	14.53	*	+
NT2RM1001002	5.11	6.69	15.34	21.78	22.69	22.28	*	+
NT2RM1001003	5.42	5.15	11.98	16.24	9.06	8.46		
NT2RM1001008	1.4	2.22	2.48	1.83	4.34	4.33		
NT2RM1001011	6.29	5.43	7.86	14.4	10.46	14.72	*	+
NT2RM1001013	2.9	2.75	4.75	8.29	7.96	5.81	*	+
NT2RM1001017	1	1.82	3.44	3.28	4.86	3.92		
NT2RM1001018	65.15	74.45	146.86	134.65	125.46	113.93		
NT2RM1001026	1.37	2.64	3.17	2.99	4.61	3.31		
NT2RM1001028	0.98	1.73	2.91	1.74	1.89	0.76		
NT2RM1001043	4.47	3.64	8.42	11.43	12.7	8.01		
NT2RM1001044	2.23	3.17	4.92	5.03	5.51	3.93		
NT2RM1001059	1.47	3.72	4.12	4.05	6.11	3.02		
NT2RM1001063	4.11	3.29	6.1	4.22	5.64	5.6		
NT2RM1001066	0.86	1.85	2.44	2.23	3.99	2.85		
NT2RM1001072	1.8	2.8	4.33	1.94	3.74	1.52		
NT2RM1001074	1.66	2.38	5.18	5.18	4.19	2.67		
NT2RM1001076	1.39	2.2	4.94	3.43	4.42	1.72		
NT2RM1001082	1.79	2.6	5.23	5.31	5.92	4.57		
NT2RM1001085	1.25	1.65	2.81	1.16	3.27	1.17		
NT2RM1001092	3.82	4.2	5.57	9.34	7.94	9.82	**	+
NT2RM1001102	1.7	2.3	4.4	2.49	5.94	4.64		
NT2RM1001103	4.37	3.88	7.18	6.25	10.28	8.08		
NT2RM1001105	1.77	2.02	4.63	2.49	5.11	3.51		
NT2RM1001112	2.68	2.66	3.69	3.85	4.75	2.43		
NT2RM1001115	1.44	1.57	4.72	3	6.46	3.73		
NT2RM1001122	2.84	3.35	7.3	9.43	9.75	9.54	*	+

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NT2RM1001136	0.88	1.41	2.71	2.31	3.87	1.59		
NT2RM1001139	3.9	3.7	5.38	5.33	11.18	6.77		
NT2RM2000003	2.45	3.33	2.4	4.5	6.29	4.88	*	+
NT2RM2000006	2.34	2.95	7.25	5.12	7.11	6.24		
NT2RM2000010	12.79	13.03	22.58	20.2	17.11	21.83		
NT2RM2000013	8.1	9.44	50.36	68.75	95.32	74.36	*	+
NT2RM2000030	4.8	2.21	23.41	26.33	32.15	28.69		
NT2RM2000032	2.76	2.92	8.53	10.01	12.19	10.67	*	+
NT2RM2000039	3.94	4.67	4.75	6.42	5.78	4.99		
NT2RM2000042	3.5	4.9	11.69	17.71	17.4	15.02	*	+
NT2RM2000092	1	2.38	1.98	1.29	4.69	2.25		
NT2RM2000093	8.37	6.63	11.41	9.02	12.23	10.18		
NT2RM2000101	9.2	9.94	40	61.09	76.38	69.62	*	+
NT2RM2000104	6.82	8.02	46.75	51.34	68.83	43.48		
NT2RM2000124	1.54	2.23	6.33	7.73	8.84	8.47	*	+
NT2RM2000155	5.08	3.77	5.8	9.45	11.58	12.51	**	+
NT2RM2000191	3.33	5.68	28.62	26.54	34.38	31.6		
NT2RM2000192	1.03	1.29	2.45	6.3	4.75	3.83	*	+
NT2RM2000239	1.92	2.79	3.09	2.85	5.02	3.1		
NT2RM2000240	32.78	29.59	74.35	61.15	60.54	61.71		
NT2RM2000241	4.49	5.9	6.35	8.24	11.72	6.78		
NT2RM2000250	1.29	1.54	4.16	2.09	5.05	2.54		
NT2RM2000259	3.06	3.42	3.59	6.38	8.44	6.74	**	+
NT2RM2000260	2.53	2.05	3.12	4.23	4.07	5.79	*	+
NT2RM2000265	0.91	1.55	0.99	1.43	2.4	1.09		
NT2RM2000287	4.7	4.23	10.82	10.69	11.54	14.73		
NT2RM2000306	12.24	9.36	10.48	23.63	14	20.79	*	+
NT2RM2000312	19.4	17.81	25.01	38.39	31.27	24.8		
NT2RM2000322	1.93	1.82	4.48	3.79	7.05	3.32		
NT2RM2000343	7.74	8.38	41.34	63.81	79.6	71.12	*	+
NT2RM2000359	3.67	2.86	4.95	4.93	9.55	4.72		
NT2RM2000362	20.09	18.2	62.29	94.88	111.25	95.66	*	+
NT2RM2000363	1.08	1.89	2.97	4.2	4.32	3.33	*	+
NT2RM2000368	2.84	2.4	4.74	6.15	5.98	5.29	*	+
NT2RM2000371	76.64	65.68	119.32	135.82	125	44.64		
NT2RM2000374	1.68	1.92	5.75	3.34	4.8	3.58		
NT2RM2000387	8.98	9.83	11.92	20.02	25.18	17.11	*	+
NT2RM2000393	1.7	1.63	3.75	3.31	7.65	3.28		
NT2RM2000395	1.07	1.51	1.98	1.72	4.34	2.23		

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NT2RM2000402	12.38	11	15.78	25.15	18.31	22.51	*	+
NT2RM2000405	1.33	1.25	2.2	1.52	3.08	3.16		
NT2RM2000407	0.76	1.78	2.49	1.89	2.72	2.89		
NT2RM2000410	0.79	1.94	2.23	1.98	2.84	2.09		
NT2RM2000420	3.09	2.52	4.43	4.24	4.5	3.26		
NT2RM2000422	3.22	2.44	5.81	3.61	6.17	2.87		
NT2RM2000423	1.91	1.96	5.69	3.89	7.64	4.18		
NT2RM2000452	3.46	3.18	4.31	7.35	8.65	9.57	**	+
NT2RM2000469	3.28	3.28	4.44	1.87	2.33	2.46	*	-
NT2RM2000490	6.03	6.03	9.18	5.55	6.16	6.9		
NT2RM2000497	3.29	3.29	4.59	3.15	5.48	2.43		
NT2RM2000502	4.69	4.69	10.24	5.87	7.08	7.02		
NT2RM2000504	7.37	7.37	12.93	10.83	4.49	11.2		
NT2RM2000514	2.75	2.75	6.23	3.11	3.32	3.8		
NT2RM2000522	1.9	1.9	3.27	1.94	1.18	1.13		
NT2RM2000540	6.02	6.02	9.53	9.12	8.96	8.14		
NT2RM2000556	2.09	2.09	2.8	1.24	2.33	0.93		
NT2RM2000565	3.35	3.35	6.02	3.27	4.14	3.72		
NT2RM2000566	6.59	6.59	15.8	9.09	9.21	9.57		
NT2RM2000567	2.16	2.16	5.64	2	5.67	3.82		
NT2RM2000569	4.69	4.69	7.93	5.77	8.18	4.7		
NT2RM2000577	11.08	11.08	15.39	11.79	14.95	14.48		
NT2RM2000581	4.64	4.64	6.49	5.98	7.97	6.85		
NT2RM2000582	5.23	5.23	10.34	8.34	9.14	7.19		
NT2RM2000588	21.84	21.84	65.91	40.15	44.01	45.21		
NT2RM2000589	3.98	3.98	11.35	7.96	7.6	8.64		
NT2RM2000594	1.87	1.87	4.38	1.62	2.71	1.92		
NT2RM2000599	6.34	6.34	16.12	17.82	14.5	15.44		
NT2RM2000609	4.61	4.61	6.77	3.76	5.81	5.48		
NT2RM2000612	3.52	3.52	6.4	5.93	7.47	4.55		
NT2RM2000622	16.6	16.6	56.24	53.07	75.02	55.48		
NT2RM2000623	2.66	2.66	7.1	7.92	6.03	5.58		
NT2RM2000624	4.18	4.18	10.6	7.33	14.39	7.56		
NT2RM2000632	2.8	2.8	6.73	4.1	6.4	4.73		
NT2RM2000635	3.42	3.42	8.09	5.41	6.29	5.31		
NT2RM2000636	2.61	2.61	6.28	3.99	4.39	3.72		
NT2RM2000639	3.73	3.73	8.26	5.42	7.79	5.99		
NT2RM2000649	6.03	6.03	9.69	9.4	9.17	8.05		
NT2RM2000658	6.49	6.49	13.18	15.17	14.66	15.83	*	+

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NT2RM2000660	11.45	11.45	18.34	17.03	7.1	20.16		
NT2RM2000669	3.6	3.6	6.51	5.28	4.28	6.69		
NT2RM2000689	31.07	31.07	59.7	37.03	16.51	70.9		
NT2RM2000691	2.09	2.09	5.73	4.83	7.13	4.27		
NT2RM2000714	3.41	3.41	10.97	11.46	14.54	11.3		
NT2RM2000718	4.08	4.08	7.15	2.88	5.42	4.33		
NT2RM2000732	5.38	5.38	14.81	9.49	14.18	8.25		
NT2RM2000735	3.72	3.72	6.16	4.27	6.55	6.49		
NT2RM2000740	2.26	2.26	6.2	4.27	3.01	3.71		
NT2RM2000743	2.26	2.26	7.89	5.65	3.24	3.89		
NT2RM2000772	6.43	6.43	8.48	5.24	6.72	9.47		
NT2RM2000773	8.17	8.17	19.56	19.18	17.96	18.29		
NT2RM2000776	13.96	13.96	17.16	24.24	9.95	26.76		
NT2RM2000784	6.64	6.64	8.8	8.74	9.02	10.5		
NT2RM2000795	4.35	4.35	13.56	7.44	8.66	10.45		
NT2RM2000796	2.27	2.27	4.64	1.71	2.31	1.38		
NT2RM2000798	25.81	25.81	160.08	158.19	136.83	188.99		
NT2RM2000801	45.09	45.09	161.29	160.44	152.13	189.56		
NT2RM2000821	7.53	7.53	12.33	7.37	7.77	11.87		
NT2RM2000829	5.76	5.76	13.01	8.05	10.13	11.75		
NT2RM2000837	3.29	3.29	7.28	4.27	6.08	4.18		
NT2RM2000924	9.96	9.96	36.74	43.24	57.8	35.84		
NT2RM2000930	10.64	10.64	18.29	24.45	27.78	28.34	**	+
NT2RM2000937	4.35	4.35	8.62	5.08	6.66	6.56		
NT2RM2000939	1.12	1.12	2.37	2.67	1.84	1.82		
NT2RM2000942	124.8	124.8	253.61	161.4	118.61	210.11		
NT2RM2000951	1.01	1.01	2.6	2.13	3.12	1.6		
NT2RM2000952	2.53	2.53	5.31	5.98	6.41	6.86	*	+
NT2RM2000966	19.69	19.69	111.88	95.61	137.32	135.9		
NT2RM2000973	23.45	23.45	16.81	39.12	39.51	33.8	**	+
NT2RM2000983	10.07	10.07	18.59	30.68	39.13	27.52	*	+
NT2RM2000984	6.48	6.48	7.71	4.88	5.64	5.26	*	-
NT2RM2000994	8.27	8.27	16.47	13.2	8.36	21.81		
NT2RM2001004	6.01	6.01	48.58	47.51	54.15	46.8		
NT2RM2001022	101.09	101.09	350.92	239.63	304.37	490.04		
NT2RM2001035	10.75	10.75	24.98	24.17	24.54	34.51		
NT2RM2001038	5.77	5.77	9.86	10.48	11.75	7.9		
NT2RM2001043	4.45	4.45	10.02	5.1	7.41	6.74		
NT2RM2001050	2.71	2.71	6.89	4.72	5.83	4.03		

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NT2RM2001055	3.78	3.78	5.89	4.24	6.31	4.7		
NT2RM2001065	6.17	6.17	15.91	8.51	12.12	14.21		
NT2RM2001075	39.81	39.81	188.21	154.65	156.72	168.68		
NT2RM2001083	2.23	2.23	5.57	4.01	5.8	3.01		
NT2RM2001100	10.38	10.38	93.67	95.8	113.9	97.52		
NT2RM2001105	6.34	6.34	8.27	11.35	5.34	11.8		
NT2RM2001109	6.81	6.81	9.4	11.88	12.47	14.53	*	+
NT2RM2001110	7.67	7.67	21.63	21.2	30.71	23.29		
NT2RM2001126	6.1	6.1	6.53	5.32	6.44	7.27		
NT2RM2001131	5.52	5.52	40.22	21.93	29.37	20.14		
NT2RM2001141	1.64	1.64	6.84	7.09	6.4	5.45		
NT2RM2001152	1.63	1.63	3.27	4.42	5.77	3.02		
NT2RM2001177	3.42	3.42	7.23	10.28	7.25	8.24		
NT2RM2001194	2.74	2.74	7.51	6.68	5.77	8.17		
NT2RM2001195	3.7	3.7	8.8	6.37	7.13	6.89		
NT2RM2001196	5.24	5.24	6.35	5.19	6.46	4.64		
NT2RM2001201	14.45	14.45	25.36	20.02	21.68	22.38		
NT2RM2001221	4.22	4.22	8.61	11.69	13.61	16.63	*	+
NT2RM2001238	2.87	2.87	5.65	3.91	3.88	1.96		
NT2RM2001243	5.39	5.39	8.98	9.81	6.13	6.53		
NT2RM2001244	3.91	3.91	10.63	6.58	9.24	6.41		
NT2RM2001247	14.94	14.94	121.59	110.47	140.27	118.79		
NT2RM2001256	3.84	3.84	5.23	3.15	3.26	2.96		
NT2RM2001269	4.4	4.4	5.98	4.8	5.63	4.74		
NT2RM2001278	5.28	5.28	7.37	8.45	8.56	5.35		
NT2RM2001291	3.05	3.05	5.18	3.24	4.62	2.9		
NT2RM2001294	12.47	12.47	24.39	20.08	15.43	17.81		
NT2RM2001295	2.56	2.56	8.82	4.54	4.43	4.99		
NT2RM2001302	2.38	2.38	4.55	2.3	4.5	2.81		
NT2RM2001306	3.51	3.51	7.62	4.1	4.46	5.14		
NT2RM2001312	2.34	2.34	3.72	1.92	2.84	1.68		
NT2RM2001319	2.76	2.76	3.93	3.61	5.29	4.11		
NT2RM2001324	3.73	3.73	8.29	5.48	4.9	5.71		
NT2RM2001345	8.53	8.53	10.01	6.83	11.12	14.14		
NT2RM2001360	4.02	4.02	6.36	5.67	5.9	5.46		
NT2RM2001370	5.75	5.75	14.53	8.56	9.86	11.69		
NT2RM2001391	1.79	1.79	6.07	1.85	5.04	1.65		
NT2RM2001393	4.49	4.49	6.39	5.12	7.91	7.14		
NT2RM2001420	2.94	2.94	4.61	2.61	3.62	3.14		

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NT2RM2001423	5.44	5.44	9.53	8.64	11.95	11.36		
NT2RM2001424	5.88	5.88	15.09	11.77	10.31	11.63		
NT2RM2001482	2.24	2.24	6.48	3.5	6.06	3.63		
NT2RM2001499	1.4	1.4	5.81	2.84	4.3	2.17		
NT2RM2001504	3.63	3.63	6.99	3.2	4.54	1.68		
NT2RM2001524	2.51	2.51	5.81	2.34	2.22	3.51		
NT2RM2001530	2.56	2.56	4.42	2.68	4.35	3.52		
NT2RM2001533	5.06	5.06	9.09	8.2	9.18	7.84		
NT2RM2001540	5.77	5.77	8.36	14.57	17.99	27.1	*	+
NT2RM2001544	2.4	2.4	6.12	3.7	3.72	2.31		
NT2RM2001547	6.6	6.6	15.29	8.44	7.61	8.24		
NT2RM2001558	1.53	1.53	3.44	1.76	4.87	1.71		
NT2RM2001575	2.45	2.45	4.57	3.36	4.38	2.29		
NT2RM2001582	2.99	2.99	4.98	2.2	5.16	3.06		
NT2RM2001588	3.69	3.69	8.8	6.39	9.14	6.6		
NT2RM2001592	2.66	2.66	6.2	3.1	5.24	4.64		
NT2RM2001603	4.74	4.74	8.7	10.42	12.03	11.77	*	+
NT2RM2001605	1.74	1.74	4.52	3.08	1.51	2.39		
NT2RM2001611	2.28	2.28	8.63	3.74	3.34	3.51		
NT2RM2001613	14.91	14.91	32.53	21.51	13.13	27.42		
NT2RM2001626	2.45	2.45	3.08	2.1	4.28	2.06		
NT2RM2001632	4.93	4.93	7.07	4.67	4.88	5.42		
NT2RM2001633	4.45	4.45	10.39	3.74	5.15	5.43		
NT2RM2001635	4.33	4.33	9.54	4.3	5.81	4.7		
NT2RM2001636	4.88	4.88	7.35	12.75	18.11	13.34	**	+
NT2RM2001637	1.25	1.25	6.48	4.18	3.68	2.51		
NT2RM2001639	3.98	3.98	9.32	4.67	4.33	3.29		
NT2RM2001641	1.63	1.63	4.69	4.84	6.02	2.71		
NT2RM2001643	2.78	2.78	7.46	4.79	4.4	2.83		
NT2RM2001648	12.97	12.97	18.91	20.13	17.07	25.5		
NT2RM2001652	6.32	6.32	5.65	4.29	8.13	4.46		
NT2RM2001659	5.78	5.78	9.17	5.73	5.28	6.95		
NT2RM2001660	3.44	3.44	3.86	2.08	2.29	2.63	**	-
NT2RM2001664	1.24	1.24	6.12	4.51	4.89	4.8		
NT2RM2001668	3.72	3.72	8.16	7.66	5.72	7.02		
NT2RM2001670	1.62	1.62	4.11	2.88	3.96	3.56		
NT2RM2001671	2.67	2.67	5.57	3.9	6.46	4.85		
NT2RM2001675	1.94	1.94	4.28	1.97	3.73	0.64		
NT2RM2001681	2.47	2.47	5.91	3.13	4.64	3.39		

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NT2RM2001685	4.58	4.58	5.68	1.29	2.72	1.14	**	-
NT2RM2001688	5.46	5.46	4.14	3.11	3.82	2.46	*	-
NT2RM2001695	15.09	15.09	35.18	17.41	19.26	34.51		
NT2RM2001696	2.74	2.74	6.64	7.15	6.7	6.8		
NT2RM2001698	1.44	1.44	3	4.06	3.49	1.65		
NT2RM2001699	1.63	1.63	5.03	4.19	3.75	5.48		
NT2RM2001700	1.65	1.65	4.13	2.56	3.37	3.91		
NT2RM2001704	2.68	2.68	5.46	3.89	3.85	3.99		
NT2RM2001706	4.29	4.29	6.77	3.33	3.13	3.32		
NT2RM2001714	6.48	6.48	6.64	5.62	7.33	5.18		
NT2RM2001716	0.97	0.97	3.7	3.03	5.49	2.92		
NT2RM2001718	1.91	1.91	3.47	5	3.5	3		
NT2RM2001723	2.09	2.09	5.48	5.1	5.21	5.71		
NT2RM2001727	3.08	3.08	6.25	7.51	7.28	5.7		
NT2RM2001730	3.52	3.52	7.15	5.04	5.43	3.85		
NT2RM2001738	4.56	4.56	6.2	6.71	10.25	9.08	*	+
NT2RM2001743	2.95	2.95	5.81	4.39	5.02	4.46		
NT2RM2001753	5.98	5.98	7.55	5.72	6.09	4.54		
NT2RM2001755	0.89	0.89	2.82	2.4	2.83	2.67		
NT2RM2001760	14.77	14.77	33.17	27.49	25.48	36.23		
NT2RM2001765	1.35	1.35	1.71	2.45	3.12	2.03	*	+
NT2RM2001767	12.04	12.04	120.66	148.84	168.4	146.29	*	+
NT2RM2001768	2.1	2.1	3.59	3.41	4.21	3.05		
NT2RM2001771	4.82	4.82	5.65	7.15	5.97	5.05		
NT2RM2001778	2.89	2.89	4.09	2.34	3.24	1.48		
NT2RM2001782	5.32	5.32	7.32	4.96	7.71	7.57		
NT2RM2001784	0.84	0.84	2.19	2.81	2.5	1.41		
NT2RM2001785	1.35	1.35	4.11	5.5	5.02	2.76		
NT2RM2001792	6.03	6.03	8.53	5.49	5.54	5.76		
NT2RM2001795	3.97	3.97	6.15	7.62	5.96	8.9		
NT2RM2001797	2.82	2.82	3.78	5	5.94	2.71		
NT2RM2001800	3.46	3.46	4.26	5.01	4.03	5.24		
NT2RM2001803	3.5	3.5	6.61	4.46	7.34	2.44		
NT2RM2001805	3.65	3.65	3.21	2.53	4.2	1.71		
NT2RM2001806	7.34	7.34	17.96	15.62	15.23	21.11		
NT2RM2001813	1.54	1.54	2.05	2.54	1.88	2.32		
NT2RM2001814	2.46	2.46	4.71	3.52	2.89	4.42		
NT2RM2001818	1.21	1.21	2.66	0.97	1.48	0.27		
NT2RM2001823	1.4	1.4	3.24	1.87	2.46	1.37		

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NT2RM2001825	14.79	14.79	36.08	34.68	34.2	35.81		
NT2RM2001832	5.93	5.93	6.1	5.19	5.48	2.93		
NT2RM2001839	67.48	67.48	123.46	152.63	157.11	121.35		
NT2RM2001840	3.04	3.04	7.13	4.61	5.11	5.37		
NT2RM2001851	3.92	3.92	7.61	3.78	4.74	6.49		
NT2RM2001855	8.21	8.21	11.51	10.22	12.06	15.41		
NT2RM2001867	2.82	2.82	5.01	2.83	5.62	3.74		
NT2RM2001869	60.8	60.8	90.58	101.19	79.67	105.32		
NT2RM2001879	3.01	3.01	6.99	2.55	3.19	2.66		
NT2RM2001883	1.52	1.52	3.26	0.98	2.28	0.73		
NT2RM2001886	1.57	1.57	4.56	2.48	3.51	2.42		
NT2RM2001887	3.78	3.78	7.66	4.48	4.97	5.73		
NT2RM2001896	274.2	274.2	378.57	325.68	216.52	497.31		
NT2RM2001902	1.92	1.92	4.28	1.31	2.92	2.14		
NT2RM2001903	16.25	16.25	42.55	35.47	31.71	37.22		
NT2RM2001930	2.11	2.11	6.3	2.3	5.86	5.44		
NT2RM2001935	4.16	4.16	5.04	3.16	4.42	5.87		
NT2RM2001936	2.81	2.81	4.9	2.99	3.44	4		
NT2RM2001939	3.56	3.56	3.34	1.82	3.01	3.16		
NT2RM2001941	1.84	1.84	4.29	2.84	2.82	2.72		
NT2RM2001950	4.66	4.66	10	6.01	6	8.69		
NT2RM2001952	2.67	2.67	4.78	2.49	4.55	5.37		
NT2RM2001976	11.48	11.48	18.2	14.58	11.46	35.27		
NT2RM2001982	1.85	1.85	3.91	2.04	2.47	1.88		
NT2RM2001983	4.45	4.45	8.36	4.18	6.49	7.54		
NT2RM2001984	7.74	7.74	8.88	20.06	27.05	22.95	**	+
NT2RM2001989	2.72	2.72	3.68	2.99	4.26	3.7		
NT2RM2001996	7.51	7.51	8.09	4.8	8.01	5.29		
NT2RM2001997	3.65	3.65	7.29	3.18	5.09	6.78		
NT2RM2001998	2.24	2.24	5.07	3.33	6.53	3.96		
NT2RM2001999	4.86	4.86	7.69	6.88	6.02	4.01		
NT2RM2002003	11.33	11.33	18.17	10.15	11	14.9		
NT2RM2002004	1.99	1.99	5.79	2.51	2.09	1.9		
NT2RM2002009	5.35	5.35	9.03	9.85	11.04	11.09	*	+
NT2RM2002014	2.62	2.62	3	3.65	4.47	4.03	**	+
NT2RM2002019	25.1	25.1	38.52	19.47	14.2	16.35		
NT2RM2002029	12.92	12.92	19.01	10.82	4.88	14.74		
NT2RM2002030	4.15	4.15	5.8	13.54	9.71	21.98	*	+
NT2RM2002034	22.05	22.05	31.76	24.83	20.89	21.04		

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NT2RM2002049	7.4	7.4	12.12	9.76	10.42	13.22		
NT2RM2002055	2.8	2.8	8.01	1.91	4.03	2.52		
NT2RM2002072	9.26	9.26	12.88	12.28	19.12	12.82		
NT2RM2002088	4.82	4.82	13.85	11.35	11.7	15.28		
NT2RM2002091	4.98	4.98	8.44	5.92	3.82	4.61		
NT2RM2002100	3.26	3.26	6.05	4.82	4.24	3.19		
NT2RM2002109	1.31	1.31	3.57	2.57	4.88	4.92		
NT2RM2002126	21.41	21.41	32.24	35.28	22.31	31.52		
NT2RM2002128	3.7	3.7	5.17	2.74	3.86	2.41		
NT2RM2002129	6.43	6.43	11.48	8.53	13.03	10.66		
NT2RM2002142	5.72	5.72	9.74	5.26	8.91	6.4		
NT2RM2002144	3.27	3.27	3.76	1.85	1.73	1.62	**	-
NT2RM2002145	2.63	2.63	8.69	6.1	5.18	5.98		
NT2RM2002153	2.61	2.61	6.37	6.31	7.62	5.75		
NT2RM2002163	0.97	0.97	3.41	1.87	3.4	0.64		
NT2RM2002170	3.28	3.28	7.03	6.62	7.5	7.65		
NT2RM2002178	3.99	3.99	3.67	3.5	5.48	2.9		
NT2RM2002179	7.82	7.82	8.69	6.17	8.15	6.02		
NT2RM2002270	4.51	4.51	4.56	2.28	1.76	1.67	**	-
NT2RM2002326	2.47	2.47	3.86	2.13	3.69	2.34		
NT2RM2002337	1.88	1.88	3.97	5.4	4.22	4.79	*	+
NT2RM2002339	2.83	2.83	6.29	5.26	5.22	3.85		
NT2RM2002345	5.16	5.16	6.03	4.04	4.2	4.21	*	-
NT2RM2002368	2.43	2.43	5.86	6.05	7.01	4.96		
NT2RM2002381	2.23	2.23	5.16	3.47	3.65	2.8		
NT2RM2002424	4.64	4.64	7.1	6.69	8.5	6.3		
NT2RM2002450	4.17	4.17	3.87	2.29	2.39	1.87	**	-
NT2RM2002482	3.93	3.93	4.65	2.66	3.2	3.79		
NT2RM2002492	9.39	9.39	24.31	29.13	24.65	29.29		
NT2RM2002575	3.26	3.26	5.23	5.99	6.03	5.07		
NT2RM2002580	4.23	4.23	4.68	4.82	7.79	7.42		
NT2RM2002592	7.7	7.7	12.59	13.07	15.28	14.69	*	+
NT2RM2002608	27.33	27.33	45.49	57.07	65.96	48.3	*	+
NT2RM2002615	6.01	6.01	9.38	13.15	20.32	14.42	*	+
NT2RM2002622	14.35	14.35	16.22	18.38	24.99	13.44		
NT2RM2002630	4.86	4.86	6.63	8.05	7.37	6.7		
NT2RM2002634	1.72	1.72	4.66	4.71	4.6	3.94		
NT2RM2002645	27.02	27.02	68.46	30.66	14.59	31.46		
NT2RM2002646	12.09	12.09	25.03	29.45	22.88	34.8		

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NT2RM2002647	7.68	7.68	17.56	19.5	17.74	23.44		
NT2RM2002652	5.11	5.11	4.71	4.3	6.43	3.73		
NT2RM2002692	4.59	4.59	4.48	2.5	2.86	2.02	**	-
NT2RM2002721	30.26	30.26	46.01	62.71	84.18	61.02	*	+
NT2RM2002748	18.37	18.37	43.62	87.35	119.27	102.35	**	+
NT2RM2002764	2.28	2.28	5.3	5.05	5.95	4.07		
NT2RM2002772	3.15	3.15	9.32	9.66	7.81	5.44		
NT2RM2002811	5.79	5.79	12.3	14.01	9.18	10.45		
NT2RM2002818	2.03	2.03	7.94	5.86	5.42	7.13		
NT2RM2002879	4.21	4.21	7.17	8.39	7.87	9.11	*	+
NT2RM2002979	11.79	11.79	19.66	24.49	23.23	21.79	*	+
NT2RM2002981	4.42	4.42	3.78	3.58	4.95	2.63		
NT2RM2002995	5.13	5.13	3.29	3.42	3.74	3.5		
NT2RM2003031	1.37	1.37	2.63	3	2.58	1.9		
NT2RM2003042	4.1	4.1	10.77	10.59	6.02	6.07		
NT2RM2003044	1.88	1.88	4.11	2.13	5.11	1.2		
NT2RM2003090	4.4	4.4	7.64	9.36	7.91	10.68	*	+
NT2RM2003095	11.98	11.98	25.25	15.63	16.43	19.04		
NT2RM2003116	11.16	11.16	16.09	17.96	21.43	22.08	*	+
NT2RM2003222	3.98	3.98	3.63	2.67	3.64	2.35		
NT2RM2003224	11.29	11.29	15.33	24.29	29.77	20.76	*	+
NT2RM2003250	14.18	14.18	86.06	85.79	96.6	94.15		
NT2RM2003258	4.59	4.59	6.32	6.54	5.11	5.69		
NT2RM2003262	5.07	5.07	7.33	5.06	7.76	5.72		
NT2RM4000023	2.15	2.15	7.02	3.57	4.91	4.29		
NT2RM4000024	2.28	2.28	6.78	3.17	4.98	4.33		
NT2RM4000027	4.74	4.74	7.77	4.85	6.94	11.32		
NT2RM4000030	2.95	2.95	5.73	3.16	4.9	2.64		
NT2RM4000033	2.51	2.51	4.77	2.36	3.89	4.61		
NT2RM4000034	1.93	1.93	5.35	3.74	4.84	6.09		
NT2RM4000046	1.37	1.37	3.79	1.57	3.5	2.32		
NT2RM4000052	1.82	1.82	3.55	1.72	2.96	1.98		
NT2RM4000054	10.43	10.43	13.85	12.07	12.83	24.7		
NT2RM4000061	1.65	1.65	4.17	1.66	4.54	0.83		
NT2RM4000074	15.83	15.83	43.57	27.9	34.24	30.79		
NT2RM4000085	5.35	5.35	10.1	8.41	10.19	10.17		
NT2RM4000086	3.06	3.06	4.5	3.84	5.25	3.71		
NT2RM4000100	6.62	6.62	15.05	12.74	15.6	14.84		
NT2RM4000101	3.77	3.77	9.11	7.17	7.71	8.78		

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NT2RM4000102	32.35	32.35	42.47	27.24	19.34	70.54		
NT2RM4000104	2.78	2.78	7.13	3.41	5.12	4.3		
NT2RM4000115	2.87	2.87	6.1	3.91	5.86	4.08		
NT2RM4000129	2.17	2.17	4.75	2.62	3.48	2.18		
NT2RM4000139	3.17	3.17	3.31	3.58	4.82	6.49		
NT2RM4000149	2.74	2.74	1.49	2.41	2.55	7.32		
NT2RM4000155	2.73	2.73	5.5	2.13	4.51	3.71		
NT2RM4000156	5.94	5.94	16.74	20.45	21	21.96	*	+
NT2RM4000167	1.36	1.36	2.58	2.61	4.34	1.75		
NT2RM4000169	9.95	9.95	36.53	29.12	24.89	23.57		
NT2RM4000191	4.29	4.29	7.56	5.49	5.57	5.66		
NT2RM4000197	2.73	2.73	4.78	1.83	3.86	2.2		
NT2RM4000198	3.38	3.38	7.42	5.26	5.45	4.21		
NT2RM4000199	2	2	3.51	2.8	4	3.76		
NT2RM4000200	0.67	0.67	3.19	2.25	1.84	1.2		
NT2RM4000202	1	1	3.24	2.11	2.42	1.84		
NT2RM4000210	1.46	1.46	3.72	2.41	3.08	2.21		
NT2RM4000215	2.54	2.54	5.43	3.3	4.09	3.06		
NT2RM4000220	6.42	6.42	10.52	8.68	11.08	15.14		
NT2RM4000229	3.26	3.26	6.62	1.46	2.34	1.76		
NT2RM4000231	6.37	6.37	7.06	6.13	7.85	6.24		
NT2RM4000233	4.83	4.83	17.3	11.9	14.34	13.4		
NT2RM4000244	2.35	2.35	5.22	3.86	4.14	5.17		
NT2RM4000251	3.85	3.85	10.97	4.82	6.52	4.59		
NT2RM4000255	2.28	2.28	4.7	3.79	4.89	1.42		
NT2RM4000265	2.23	2.23	5.69	4.29	8.21	1.99		
NT2RM4000283	18.14	18.14	26.21	37.17	39.88	44.79	**	+
NT2RM4000284	13.85	13.85	33.72	31.96	42.88	40.67		
NT2RM4000290	6.31	6.31	7.76	3.77	4.92	4	*	-
NT2RM4000295	2.36	2.36	2.16	2.32	2.13	0.88		
NT2RM4000306	3.79	3.79	7.76	7.1	6.14	5.02		
NT2RM4000307	5.04	5.04	9.13	9.95	9.99	11.72	*	+
NT2RM4000309	2.48	2.48	5.34	3.92	6.52	5.52		
NT2RM4000313	3.92	3.92	9.61	5.75	7.77	8.52		
NT2RM4000318	3.38	3.38	6.87	4.35	6.36	3.28		
NT2RM4000324	4.93	4.93	5.93	2.79	4.98	2.12		
NT2RM4000326	5.32	5.32	4.61	2.59	2.45	2.01	**	-
NT2RM4000327	4.97	4.97	10.95	7.94	10.32	7.71		
NT2RM4000344	5.46	5.46	16.67	11.16	10.17	19.18		

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NT2RM4000349	3.68	3.68	9.99	11.87	10.88	13.8	*	+
NT2RM4000354	1.65	1.65	3.13	4.2	4.31	3.1		
NT2RM4000356	1.5	1.5	3.11	2.5	4.07	1.64		
NT2RM4000366	15.75	15.75	44.48	38.81	44.07	58.06		
NT2RM4000368	3.04	3.04	5.9	4.36	5.48	3.48		
NT2RM4000373	6.49	6.49	12.29	12.72	15.96	16.47	*	+
NT2RM4000386	4.92	4.92	4.71	3.81	4.57	4.6		
NT2RM4000395	2.7	2.7	4.69	6.36	6.51	5.68	*	+
NT2RM4000414	1	1	2.76	2.38	2.9	2.19		
NT2RM4000417	1.66	1.66	2.83	3.9	3.95	3.25	*	+
NT2RM4000421	2.99	2.99	5.17	4.96	5.47	4.13		
NT2RM4000425	10.56	10.56	26.8	26.49	31.48	45.28		
NT2RM4000433	2.78	2.78	5.39	1.67	2.21	1.79		
NT2RM4000436	3.8	3.8	9.47	11.84	16.75	16.38	*	+
NT2RM4000444	4.51	4.51	12.97	7.29	8.54	7.38		
NT2RM4000457	3.35	3.35	8.69	13.35	12.38	13.25	*	+
NT2RM4000471	1.73	1.73	4.01	4.17	4.87	2.49		
NT2RM4000472	2.2	2.2	7.62	6.64	7.61	5.39		
NT2RM4000486	2.98	2.98	5.92	6.85	7.54	6		
NT2RM4000490	3.85	3.85	6.41	7.16	5.1	5.86		
NT2RM4000496	3.68	3.68	3.86	2.16	2.36	2.04	**	-
NT2RM4000505	26.85	26.85	60.33	68.9	80.59	70.67	*	+
NT2RM4000511	22.8	22.8	45.35	64.6	89.95	75.97	*	+
NT2RM4000514	2.61	2.61	6.75	10.47	7.53	9.25	*	+
NT2RM4000515	3.75	3.75	8.81	7.27	7.94	4.66		
NT2RM4000517	34.51	34.51	74.2	76.45	53.07	79.47		
NT2RM4000520	2.24	2.24	3.08	3.21	3.3	5.49		
NT2RM4000531	2.76	2.76	5.71	4.41	5.5	4.22		
NT2RM4000532	3.03	3.03	5.56	2.72	3.54	2.39		
NT2RM4000533	3.55	3.55	5.43	4.73	6.98	3.23		
NT2RM4000534	5.17	5.17	2.92	2.73	4.62	1.94		
NT2RM4000563	5.21	5.21	16.69	17.05	16.8	19.36		
NT2RM4000566	1.79	1.79	4.6	7.14	5.27	7.91	*	+
NT2RM4000568	10.48	10.48	19.4	28.18	22.91	33.06	*	+
NT2RM4000585	1.97	1.97	2.52	0.82	1.99	1.26		
NT2RM4000587	3.88	3.88	6.15	6.66	5.75	5.15		
NT2RM4000590	3.73	3.73	4.12	1.64	2.48	2.3	**	-
NT2RM4000593	4.46	4.46	7.83	10.21	12.36	7.45		
NT2RM4000595	3.94	3.94	3.91	2.27	4.36	2.45		

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NT2RM4000603	4.18	4.18	6.98	6.95	7.23	7.26		
NT2RM4000611	9.81	9.81	18.02	17.1	17.38	25.49		
NT2RM4000616	2.05	2.05	6.19	2.73	4.14	4.53		
NT2RM4000621	26.04	26.04	70.86	57.5	62.2	59.07		
NT2RM4000648	2.78	2.78	7.83	2.66	2.67	3.88		
NT2RM4000649	5.53	5.53	11.03	7.34	8.4	13.12		
NT2RM4000658	3.22	3.22	8.18	4.22	6.14	8.14		
NT2RM4000661	57.68	57.68	140.68	141.09	135.49	177.49		
NT2RM4000673	3.02	3.02	5.72	3.69	3.8	4.59		
NT2RM4000674	2.23	2.23	4.27	2.89	2.63	2.99		
NT2RM4000689	3.81	3.81	6.47	5.34	6.36	7.74		
NT2RM4000698	14.85	14.85	20.92	25.12	23.66	26.39	*	+
NT2RM4000700	2.39	2.39	5.53	2.41	6.95	5.61		
NT2RM4000701	10.07	10.07	54.36	61.81	67.75	63.17		
NT2RM4000712	3.5	3.5	7.9	5.97	8.03	9.55		
NT2RM4000717	2.14	2.14	6.66	3.67	2.94	4.3		
NT2RM4000733	4.37	4.37	7.8	4.16	6.93	11.03		
NT2RM4000734	2.17	2.17	5.92	2.35	5.23	4.7		
NT2RM4000741	2.14	2.14	6.11	3.59	4.75	4.66		
NT2RM4000744	1.76	1.76	7.05	2.76	4.4	10.18		
NT2RM4000749	15.53	15.53	23.13	26.26	27.8	34.67	*	+
NT2RM4000751	2.88	2.88	6.54	6.23	6.11	5.94		
NT2RM4000752	4.11	4.11	4.88	4.78	5.12	38.58		
NT2RM4000760	3.5	3.5	9.69	4.54	6.31	5.26		
NT2RM4000761	237.9	237.9	478.3	219.65	302.54	336.34		
NT2RM4000764	66.05	66.05	178	212.33	205.98	232.75	*	+
NT2RM4000768	6.11	6.11	11.21	15.56	10.14	21.17		
NT2RM4000778	1.6	1.6	4.7	4.27	5.18	6.18		
NT2RM4000779	4.52	4.52	8.28	6.87	7.19	7.33		
NT2RM4000787	2.55	2.55	7.49	3.64	4.9	4.53		
NT2RM4000790	2.99	2.99	5.03	5.47	5.82	12.06		
NT2RM4000795	1.99	1.99	3.67	2.36	1.2	2.51		
NT2RM4000796	3.26	3.26	5.86	4.29	3.48	4.28		
NT2RM4000798	1.77	1.77	5.53	3.72	3.08	3.47		
NT2RM4000800	4.15	4.15	8.16	8.7	9.44	9.06		
NT2RM4000813	3.31	3.31	8.79	7.14	7.95	10.09		
NT2RM4000820	4.89	4.89	9.14	5.39	6.27	5.44		
NT2RM4000827	7.1	7.1	18.55	16.3	15.8	17.88		
NT2RM4000830	3.27	3.27	7.35	5.28	7.8	8.38		

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NT2RM4000833	2.51	2.51	6.84	4.48	3.35	4.87		
NT2RM4000841	4	4	15	10.57	8.84	10.1		
NT2RM4000846	1.66	1.66	8.83	4.74	6.83	5.09		
NT2RM4000848	2.61	2.61	5.75	4.15	6.32	3.12		
NT2RM4000852	3.89	3.89	9.81	8.16	8.67	8.29		
NT2RM4000855	5.12	5.12	7.64	5.99	6.08	7.19		
NT2RM4000859	11.18	11.18	16.28	16.48	19.12	17.62		
NT2RM4000868	3.06	3.06	6.47	5.23	6.91	7.05		
NT2RM4000870	4	4	9.82	7.06	3.87	6.59		
NT2RM4000879	1.67	1.67	6	4.15	3.31	3.11		
NT2RM4000882	18.99	18.99	28.36	20.33	16.5	12.55		
NT2RM4000887	2.16	2.16	6.01	3.53	4.91	1.6		
NT2RM4000895	2.33	2.33	5.33	3.16	5.9	3.08		
NT2RM4000897	5.78	5.78	6.99	8.89	9.73	7.02		
NT2RM4000901	5.22	5.22	6.41	4.37	6.2	6.12		
NT2RM4000950	4.04	4.04	5.09	3.57	4.06	2.91		
NT2RM4000965	2.89	2.89	4.54	5.98	4.04	6.18		
NT2RM4000971	2.49	2.49	4.78	4.84	4.29	7.62		
NT2RM4000979	5.16	5.16	12.71	10.23	10.46	7.87		
NT2RM4000987	1.9	1.9	4.59	3.64	4.22	3.21		
NT2RM4000989	2.51	2.51	5.17	4.2	5.16	4.99		
NT2RM4000991	3.1	3.1	4.83	2.87	3.53	8.73		
NT2RM4000992	3.39	3.39	5.41	3.6	4.54	3.19		
NT2RM4000996	6.22	6.22	7.86	7.14	8	7.28		
NT2RM4000997	3.53	3.53	13.96	9.81	10.96	10.89		
NT2RM4001001	26.06	26.06	55.43	37.67	34.22	54.29		
NT2RM4001002	5.13	5.13	11.03	11.54	11.33	19.44		
NT2RM4001016	1.63	1.63	2.73	4.07	5.31	3.76	*	+
NT2RM4001025	65.77	65.77	133.97	148.39	181.87	171.5	*	+
NT2RM4001027	2.49	2.49	3.66	1.67	1.77	4.31		
NT2RM4001032	2.55	2.55	6.74	4.94	5.46	3.84		
NT2RM4001047	3.87	3.87	3.7	2.61	2.73	2.7	**	–
NT2RM4001049	3.97	3.97	10.12	18.29	20.63	26.25	**	+
NT2RM4001051	2.72	2.72	12.54	11.17	10.12	13.68		
NT2RM4001052	14.95	14.95	72.14	75.49	75.01	79.12		
NT2RM4001053	14.96	14.96	39.3	41.36	28.95	25.87		
NT2RM4001054	3.13	3.13	5.17	5.34	5.69	5.01		
NT2RM4001059	3.65	3.65	6.37	4.91	3.52	4.48		
NT2RM4001071	4.03	4.03	7.35	6.8	7.34	6.55		

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NT2RM4001084	8.04	8.04	6.52	9.49	10.53	9.53	*	+
NT2RM4001092	12.61	12.61	109.97	76.93	98.78	73.14		
NT2RM4001100	6.72	6.72	20.93	22.35	15.18	18.98		
NT2RM4001116	1.17	1.17	2.5	2.77	2.96	2.16		
NT2RM4001119	1.74	1.74	4.82	4.72	4.22	4.15		
NT2RM4001140	2.65	2.65	7.49	8.27	7.78	9.03		
NT2RM4001148	6.59	6.59	13.68	12.1	12.92	15.83		
NT2RM4001151	3.7	3.7	4.31	1.94	3.65	1.68		
NT2RM4001155	5.51	5.51	6.36	3.55	5.37	4.63		
NT2RM4001157	1.68	1.68	4.95	4.86	2.81	3.82		
NT2RM4001160	1.57	1.57	3.39	2.99	1.9	2.41		
NT2RM4001163	42.35	42.35	86.27	106.63	52.13	98.56		
NT2RM4001187	2.64	2.64	7.25	3.96	4.87	5.2		
NT2RM4001191	3.2	3.2	9.95	8.59	6.36	8.72		
NT2RM4001200	3.83	3.83	6.35	5.52	4.41	4.11		
NT2RM4001203	9.93	9.93	20.29	22.65	25.36	21.82		
NT2RM4001204	3.23	3.23	3.59	3.17	2.83	2.6		
NT2RM4001217	4.62	4.62	12.16	11.26	13.39	13.72		
NT2RM4001245	7.31	7.31	17.14	13.76	14.49	17.16		
NT2RM4001247	3.23	3.23	9.1	5.73	6.57	5.03		
NT2RM4001256	2.51	2.51	6.39	3.57	5.48	4.14		
NT2RM4001258	8.2	8.2	24.68	25.02	24.16	22.89		
NT2RM4001267	3.43	3.43	4.83	3.93	4.3	8.08		
NT2RM4001273	4.23	4.23	8.38	7.39	6.96	8.77		
NT2RM4001281	4	4	10.54	10.15	9.05	10		
NT2RM4001286	345.27	345.27	526.77	215.2	220.51	552.53		
NT2RM4001290	23.51	23.51	61.5	56.51	48.6	59.58		
NT2RM4001309	2.64	2.64	6.81	3.17	5.42	4.05		
NT2RM4001313	2.63	2.63	8.62	3.81	6.36	7.03		
NT2RM4001316	3.14	3.14	6.12	3.39	3.85	5.25		
NT2RM4001320	2.4	2.4	6.43	2.83	3.16	5.6		
NT2RM4001321	3.98	3.98	8.62	6.17	7.03	6.24		
NT2RM4001325	2.54	2.54	5.2	4.76	2.93	5.25		
NT2RM4001333	8.65	8.65	18.06	8.57	10.76	9.51		
NT2RM4001340	4.81	4.81	12.27	6.99	7.72	11.24		
NT2RM4001344	4.09	4.09	4.69	3.04	3.44	4.93		
NT2RM4001347	6.49	6.49	9.8	10.53	9.72	17.71		
NT2RM4001357	7.59	7.59	12.09	8.58	11.68	9.37		
NT2RM4001360	2.79	2.79	5.11	3.82	2.85	3.07		

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NT2RM4001371	4.71	4.71	8.57	6.58	13.16	12.93		
NT2RM4001377	8.01	8.01	13.74	8.66	9.23	10.58		
NT2RM4001382	17.31	17.31	56.74	35.57	28.32	38.22		
NT2RM4001384	2.17	2.17	4.11	2.35	3.34	3.75		
NT2RM4001400	3.78	3.78	5.76	4.87	4.66	5.07		
NT2RM4001409	2.55	2.55	6.82	4.82	4.63	5.27		
NT2RM4001410	5.48	5.48	21.69	17.34	21.09	18.91		
NT2RM4001411	2.66	2.66	6.5	5.86	6.64	6.77		
NT2RM4001412	1.75	1.75	3.33	2.39	2.52	2.79		
NT2RM4001414	2.18	2.18	4.83	2.45	2.4	3.77		
NT2RM4001436	8.35	8.35	16.65	10.45	10.13	15.55		
NT2RM4001437	2.77	2.77	8.85	8.31	11.26	7.67		
NT2RM4001444	11.57	11.57	25.93	21.1	18.36	18.42		
NT2RM4001454	3.62	3.62	7.89	6.16	5.03	4.79		
NT2RM4001455	5.85	5.85	22.19	18.03	25.08	26.16		
NT2RM4001483	4.37	4.37	8.77	4.97	5.43	6.46		
NT2RM4001489	3.12	3.12	7.04	3.64	4.19	5.46		
NT2RM4001495	1.35	1.35	5.13	2.85	3.29	3.37		
NT2RM4001499	1.74	1.74	4.98	3.65	2.77	3.3		
NT2RM4001515	0.95	0.95	3.38	2.65	5.38	3.41		
NT2RM4001519	1.86	1.86	4.6	2.24	4.38	2.85		
NT2RM4001522	3.8	3.8	7.66	5.36	7.42	9.13		
NT2RM4001523	5.46	5.46	9.11	4.82	7.58	5.79		
NT2RM4001550	11.9	11.9	17.38	16.49	16.76	15.01		
NT2RM4001553	7.88	7.88	13.4	23.26	23.53	23.87	**	+
NT2RM4001554	0.86	0.86	1.74	1.85	1.11	2.2		
NT2RM4001557	2.5	2.5	6.33	5.05	3.36	4.89		
NT2RM4001565	1.87	1.87	4.05	2.46	3.34	3.23		
NT2RM4001566	3.23	3.23	8.57	8.91	10.49	11.42		
NT2RM4001569	1.47	1.47	5.4	3.35	4.15	1.56		
NT2RM4001579	6.57	6.57	16.69	19.23	23.83	18.22		
NT2RM4001582	4.06	4.06	5.97	2.16	3.17	2.67	*	-
NT2RM4001589	21.51	21.51	37.16	42.45	55.76	47.57	*	+
NT2RM4001592	1.37	1.37	2.96	3.02	2.14	3.71		
NT2RM4001594	1.98	1.98	4.09	5.4	5.24	5.67	*	+
NT2RM4001597	2.65	2.65	5.64	5.17	4.97	4.33		
NT2RM4001605	2.7	2.7	6.18	5.71	5.92	5.93		
NT2RM4001609	23.65	23.65	45	61.08	78.89	77.31	*	+
NT2RM4001610	48.1	48.1	69.16	132.54	132.39	115.22	**	+

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NT2RM4001611	3.31	3.31	4.56	2.33	2.32	2.02	*	–
NT2RM4001618	7.05	7.05	7.95	6.68	8.98	12.95		
NT2RM4001622	13.53	13.53	19.88	14.67	24.67	28.46		
NT2RM4001624	1.6	1.6	3.02	3.92	2.66	4.43		
NT2RM4001625	4.89	4.89	39.6	41.63	47.1	46.46		
NT2RM4001629	3.82	3.82	8.82	12.09	12.08	13.38	*	+
NT2RM4001632	15.28	15.28	24.55	31.07	26.16	25.6		
NT2RM4001642	3.29	3.29	4.17	2.89	3.62	2.1		
NT2RM4001647	4.44	4.44	6.83	4.04	5.48	4.67		
NT2RM4001650	4.96	4.96	4.94	2.66	2.87	3.79	**	–
NT2RM4001662	2.18	2.18	5.47	8.31	6.54	9.39	*	+
NT2RM4001666	2.28	2.28	6.5	6.24	6.17	8.14		
NT2RM4001670	3.52	3.52	10.77	11.16	10.82	14.91		
NT2RM4001682	12.66	12.66	31.6	33.03	26.04	37.07		
NT2RM4001710	6.7	6.7	38.5	40.58	58.41	40.31		
NT2RM4001712	4.06	4.06	7.61	10.19	10.7	9.98	*	+
NT2RM4001714	10.88	10.88	19.37	18.67	19.3	17.65		
NT2RM4001715	10.77	10.77	11.6	13.55	16.86	12.99		
NT2RM4001727	3.41	3.41	5.92	4.83	5.89	7.6		
NT2RM4001731	2.6	2.6	10.72	13.46	11.23	11.73		
NT2RM4001735	12.84	12.84	21.53	22.01	20.88	34.93		
NT2RM4001739	2.46	2.46	7.3	8.13	5.17	7.14		
NT2RM4001741	14.41	14.41	29.88	26.98	27.21	32.35		
NT2RM4001746	3.65	3.65	6.76	6.89	6.5	5.33		
NT2RM4001754	3.16	3.16	4.17	3.39	3.62	3.84		
NT2RM4001757	5.02	5.02	5.78	4.7	6.31	7.97		
NT2RM4001758	1	1	0.76	1.98	0.65	1.46		
NT2RM4001768	4.83	4.83	10.19	8.48	6.91	7.83		
NT2RM4001775	3.23	3.23	2.76	1.9	1.85	1.71	**	–
NT2RM4001776	2.56	2.56	4.77	2.47	2.68	2.69		
NT2RM4001783	2.88	2.88	3.22	3.12	3.48	3.68		
NT2RM4001793	4.67	4.67	11.44	12.02	9.6	10.75		
NT2RM4001810	3.31	3.31	4.46	3.33	3.63	3.11		
NT2RM4001813	3.9	3.9	4.15	4.71	4.19	5.36		
NT2RM4001818	4.06	4.06	11.34	10.43	8.67	10.53		
NT2RM4001819	2.35	2.35	5.6	2.37	3.02	4.58		
NT2RM4001823	1.76	1.76	4.48	2.47	4.04	4.27		
NT2RM4001828	5.01	5.01	11.49	5.67	7.54	7.51		
NT2RM4001835	9.75	9.75	18.65	21.12	16.5	26.55		

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NT2RM4001836	3.27	3.27	8.32	3.65	3.54	5.58		
NT2RM4001841	7.94	7.94	15.82	20.15	20.96	23.33	*	+
NT2RM4001842	2.1	2.1	4.44	3.5	3.35	4.85		
NT2RM4001843	5.65	5.65	14.54	13.34	12.25	14.94		
NT2RM4001856	4.42	4.42	7.16	7.65	4.71	16.83		
NT2RM4001858	5.91	5.91	15.86	16.09	17.03	16.93		
NT2RM4001861	2.91	2.91	9.57	6.31	8.66	9.28		
NT2RM4001863	8.06	8.06	9.5	15.16	15.68	11.77	*	+
NT2RM4001865	5.04	5.04	11.25	7.44	10.24	9.03		
NT2RM4001869	5.1	5.1	5.96	5.22	8.45	21.88		
NT2RM4001873	9.62	9.62	18.43	13.33	15.49	19.21		
NT2RM4001876	2.24	2.24	6.94	3.65	4.39	7.25		
NT2RM4001880	3.6	3.6	8.57	5.13	5.41	7.67		
NT2RM4001885	5.71	5.71	11.11	7.11	6.56	11.98		
NT2RM4001889	10.25	10.25	18.24	16.31	15.85	21.33		
NT2RM4001894	2.61	2.61	6.07	3.58	3.65	3.49		
NT2RM4001897	7.87	7.87	20.24	18.41	20.4	23.46		
NT2RM4001899	3.36	3.36	7.43	4.92	8.19	8.54		
NT2RM4001905	3	3	4.84	3.3	4.53	7.1		
NT2RM4001922	2.55	2.55	6.05	3.97	4.84	5.11		
NT2RM4001930	2.64	2.64	8.9	2.88	6.53	6.38		
NT2RM4001938	2.65	2.65	4.91	5.09	5.65	6.43		
NT2RM4001940	2.73	2.73	6.17	5.91	4.46	5.48		
NT2RM4001942	37.36	37.36	32.02	53.86	59.28	82.77	*	+
NT2RM4001953	4.65	4.65	9.68	5.04	6.79	4.91		
NT2RM4001965	4.96	4.96	8.82	10.18	8.54	8.39		
NT2RM4001966	3	3	5.14	6.3	7.45	8.19	*	+
NT2RM4001969	2.22	2.22	7.29	5.01	2.95	4.5		
NT2RM4001974	1.19	1.19	4.61	1.89	2.96	4.83		
NT2RM4001979	2.09	2.09	6.37	3.39	4.65	7.36		
NT2RM4001980	4.3	4.3	7.59	7.58	8.02	9.33		
NT2RM4001984	2.31	2.31	5.36	2.68	3.49	4.57		
NT2RM4001987	3.36	3.36	9.66	2.92	4.6	5.01		
NT2RM4002013	6.62	6.62	15.13	13.47	17.16	19.8		
NT2RM4002018	2.31	2.31	5.15	4.09	5.53	7.1		
NT2RM4002033	3.19	3.19	8.16	4.91	3.27	5.93		
NT2RM4002034	1.89	1.89	6.19	4.82	4.38	4.03		
NT2RM4002044	7.71	7.71	17.9	18.75	12.3	18.5		
NT2RM4002047	3.88	3.88	5.19	2.68	5.38	9.2		

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NT2RM4002054	4.54	4.54	6.97	2.56	4.3	3.89		
NT2RM4002055	13.72	13.72	74.75	60.51	91.27	61.53		
NT2RM4002059	23.73	23.73	31.85	48.05	63.09	52.61	**	+
NT2RM4002061	3.72	3.72	5.32	3.59	3.69	4.81		
NT2RM4002062	1.9	1.9	5.41	3.66	2.84	4.26		
NT2RM4002063	2.21	2.21	8.1	7.64	7.35	3.79		
NT2RM4002066	2.07	2.07	5.29	4.42	6.32	4.07		
NT2RM4002067	2.51	2.51	4.27	3.07	5.19	4.41		
NT2RM4002073	3.73	3.73	7.24	5.51	7.69	5.16		
NT2RM4002074	5.19	5.19	7.35	5.67	7.47	4.49		
NT2RM4002075	5.13	5.13	5.9	3.16	3.18	2.91	**	-
NT2RM4002076	3.13	3.13	3.05	1.94	2.52	1.71	*	-
NT2RM4002078	10.3	10.3	28.06	23.95	20.81	26.64		
NT2RM4002081	10.47	10.47	30.87	19.18	17.8	18.22		
NT2RM4002082	1.25	1.25	3.02	3.85	2.58	1.23		
NT2RM4002093	2.82	2.82	3.9	4.79	4.66	4.79	*	+
NT2RM4002109	4.42	4.42	11.51	13.95	15.12	15.21	*	+
NT2RM4002115	2.86	2.86	4.51	4.81	4.8	2.52		
NT2RM4002118	4.48	4.48	6.14	4.3	4.86	4.27		
NT2RM4002128	3.78	3.78	4.57	2.84	3.31	3.13	*	-
NT2RM4002137	3.96	3.96	8.14	10.27	7.51	8.92		
NT2RM4002139	3.78	3.78	8.98	7.03	7.84	7.87		
NT2RM4002140	4.04	4.04	9.45	8.87	7.81	10.17		
NT2RM4002145	5.99	5.99	17.51	25.81	31.07	24.47	*	+
NT2RM4002146	4.51	4.51	8.23	8.56	9	8.92		
NT2RM4002161	2.33	2.33	4.97	1.38	3.15	5.3		
NT2RM4002174	4.86	4.86	8.02	3.12	4.53	6.15		
NT2RM4002178	7.3	7.3	24.43	28.61	33.13	29.27	*	+
NT2RM4002180	3.47	3.47	11.93	9.27	10.02	11.28		
NT2RM4002185	5.94	5.94	35.51	31.59	32.34	31.69		
NT2RM4002189	1.6	1.6	3.24	3.68	5.59	4.91	*	+
NT2RM4002194	9.3	9.3	25.94	37.2	29.64	38.23	*	+
NT2RM4002198	6.09	6.09	7.61	9.37	8.4	10.04	*	+
NT2RM4002205	4.01	4.01	9.05	6.76	7.86	8.76		
NT2RM4002213	5.36	5.36	8.79	8.05	11.99	14.41		
NT2RM4002216	7.35	7.35	12.58	16.58	23.93	18.16	*	+
NT2RM4002226	3.84	3.84	9.71	20.85	16.65	16.5	**	+
NT2RM4002237	4.19	4.19	10.13	10.37	7.64	13.22		
NT2RM4002240	1.96	1.96	3.64	3.73	3.71	7.59		

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NT2RM4002251	2.11	2.11	6.2	7.87	5.48	5.17		
NT2RM4002256	4.38	4.38	10.68	10.7	9.46	9.64		
NT2RM4002262	2.85	2.85	6.25	3.34	4.43	9.66		
NT2RM4002266	3.93	3.93	4.76	2.76	3.55	4.47		
NT2RM4002276	11.23	11.23	15.55	16.5	28.25	20.64		
NT2RM4002278	1.89	1.89	4.59	4.33	3.99	5.11		
NT2RM4002281	17.71	17.71	59.08	62.68	51.19	59.89		
NT2RM4002287	2.08	2.08	3.84	2.46	4.21	3.32		
NT2RM4002294	3.19	3.19	6.99	6.28	6.09	8.69		
NT2RM4002298	18.59	18.59	60.14	86.09	89.9	88.75	*	+
NT2RM4002301	3.2	3.2	6.85	4.63	5.94	4.02		
NT2RM4002306	4.71	4.71	8.24	4.99	5.31	4.2		
NT2RM4002323	3.9	3.9	4.06	4.11	4.39	3.11		
NT2RM4002334	11.54	11.54	20.76	17.92	20.72	16.95		
NT2RM4002339	1.78	1.78	3.52	1.33	1.3	1.38		
NT2RM4002344	2.36	2.36	5.74	2.87	3.57	7.92		
NT2RM4002345	3.56	3.56	10.59	5.06	4.63	7.5		
NT2RM4002352	2.04	2.04	7.67	3.99	5.14	3.74		
NT2RM4002362	20.38	20.38	24.92	11.23	14.32	15.17	*	-
NT2RM4002373	2.1	2.1	3.96	3.21	2.55	3.63		
NT2RM4002374	2.28	2.28	4.39	2.29	3.58	4.3		
NT2RM4002376	4.02	4.02	6.03	3.31	2.97	5.52		
NT2RM4002383	2.8	2.8	8.49	4.76	5.79	4.28		
NT2RM4002390	3.03	3.03	6.01	4.06	5.27	7.37		
NT2RM4002398	5.16	5.16	43.18	33.97	50.73	30.41		
NT2RM4002409	2.11	2.11	5.93	3.37	4.29	1.9		
NT2RM4002414	4.73	4.73	6.21	7.37	9.12	14.53		
NT2RM4002438	2.07	2.07	5.28	3.03	4.38	7.18		
NT2RM4002440	2.99	2.99	6.92	5.78	5.32	9.49		
NT2RM4002446	2.23	2.23	6.08	2.95	4.45	5.7		
NT2RM4002450	3.36	3.36	10.01	6.15	7.75	7.24		
NT2RM4002452	2.13	2.13	6.3	3.67	5.15	7.23		
NT2RM4002457	2.68	2.68	4.44	2.66	3.26	4.52		
NT2RM4002458	3.06	3.06	5.77	3.32	5.34	4.04		
NT2RM4002460	2.43	2.43	3.68	1.57	2.45	1.43		
NT2RM4002464	5.4	5.4	12.62	14.39	13.72	14.3		
NT2RM4002479	4.66	4.66	6.69	4.91	7.98	11.54		
NT2RM4002482	4.26	4.26	16.18	10.19	11.5	12.2		
NT2RM4002489	6.74	6.74	16.91	8.79	5.81	11.68		

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NT2RM4002493	1.35	1.35	3.22	1.96	3.51	2.73		
NT2RM4002499	34.96	34.96	72.9	59.42	52.07	54.3		
NT2RM4002504	5.15	5.15	10.68	10.57	13.51	9.8		
NT2RM4002506	4.77	4.77	9.4	4.93	7.59	8.53		
NT2RM4002510	2.03	2.03	3.27	1.66	2.97	2.48		
NT2RM4002527	1.57	1.57	3.14	1.83	2.31	4.47		
NT2RM4002532	2.45	2.45	7.75	5.88	3.37	5.19		
NT2RM4002534	1.79	1.79	4.8	2.1	3.45	2.94		
NT2RM4002535	2.5	2.5	6.51	5.89	8.1	6.37		
NT2RM4002554	3.29	3.29	5.31	3.31	5.47	3.12		
NT2RM4002558	6.91	6.91	32.57	32.58	41.54	25.61		
NT2RM4002565	5.38	5.38	13.6	8.22	9.85	10.53		
NT2RM4002567	3.34	3.34	5.43	4.21	4.49	7.22		
NT2RM4002571	4.48	4.48	15.61	11.95	16.47	15.24		
NT2RM4002572	5.57	5.57	17.2	13.7	9.59	13.48		
NT2RM4002577	7.76	7.76	15.25	6.59	5.87	5.65		
NT2RM4002583	1.08	1.08	3.58	2.28	4.83	2.44		
NT2RM4002584	1.64	1.64	5.67	3.24	5.74	5.56		
NT2RM4002593	3.29	3.29	5.17	2.75	3.91	4.61		
NT2RM4002594	11.26	11.26	46.5	38.21	55.32	43.58		
NT2RM4002604	4.83	4.83	4.64	1.77	2.03	2.89	**	−
NT2RM4002614	3.48	3.48	3.48	2.52	3.66	2.81		
NT2RM4002616	1.07	1.07	2.73	2.88	2.71	2.38		
NT2RM4002623	1.39	1.39	4.89	3.92	3.72	5.06		
NT2RM4002634	1.41	1.41	4.38	3.42	4.91	2.96		
NT2RM4002636	2.22	2.22	3.93	3.92	4.18	4.12		
NT2RP1000002	8.82	8.82	52.94	75.1	92.89	81.45	*	+
NT2RP1000006	4.68	4.68	6.28	4.25	4.48	2.56		
NT2RP1000015	4.86	4.86	5.27	2.74	1.99	2.28	**	−
NT2RP1000018	5.45	5.45	5	5.55	4.83	4.96		
NT2RP1000034	18.22	18.22	49.95	38.04	30.76	50.07		
NT2RP1000035	1.93	1.93	3.2	5.26	3.23	3.96		
NT2RP1000040	1.77	1.77	3.33	2.93	3.28	4.28		
NT2RP1000042	1.3	1.3	3.44	1.99	3.22	2.38		
NT2RP1000048	3.6	3.6	10.24	7.25	9.9	9		
NT2RP1000050	2.21	2.21	4.71	2.89	4	3.57		
NT2RP1000056	4.03	4.03	3.74	1.09	0.61	1.96	**	−
NT2RP1000058	3.49	3.49	2.03	1.84	2.07	2.48		
NT2RP1000063	1.77	1.77	3.65	4.09	4	3.83		

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NT2RP1000068	1.89	1.89	3.99	3.12	3.33	2.43		
NT2RP1000072	22.9	22.9	74.07	82.91	66.26	95.85		
NT2RP1000073	2.18	2.18	2.45	2.68	3.69	3.86	*	+
NT2RP1000078	2.72	2.72	3.17	2.93	2.3	3.13		
NT2RP1000079	4.13	4.13	5.32	3.6	4.48	2.5		
NT2RP1000080	4.99	4.99	8.13	9.46	12.46	9.46	*	+
NT2RP1000086	4.15	4.15	3.63	1.31	2.1	3.75		
NT2RP1000087	1.3	1.3	4.36	3.51	3.21	3.45		
NT2RP1000089	4.5	4.5	9.98	12.69	11.3	14.93	*	+
NT2RP1000090	45.76	45.76	96.6	94.37	53.44	93.42		
NT2RP1000100	2.17	2.17	4.05	5.23	4.13	3.66		
NT2RP1000101	3.44	3.44	5.22	4.41	2.88	4.81		
NT2RP1000111	3.24	3.24	5.56	4.51	3.9	3.69		
NT2RP1000112	3.29	3.29	4.08	1.85	3.33	3		
NT2RP1000124	5.57	5.57	4.96	3.11	5.73	5.5		
NT2RP1000125	7.28	7.28	19.39	13.69	10.68	16.86		
NT2RP1000129	1.81	1.81	4.35	5.14	3.91	4.27		
NT2RP1000130	2.31	2.31	4.11	5.31	5.62	16.86		
NT2RP1000154	7.5	7.5	15.63	17.16	12.72	16.37		
NT2RP1000163	2.42	2.42	3.51	2.72	2.99	3.59		
NT2RP1000170	3.42	3.42	4.2	4.96	5.17	5.85	*	+
NT2RP1000174	3.5	3.5	3.42	1.3	2.38	2.12	**	-
NT2RP1000181	6.14	6.14	7.22	10.97	14.98	9.38	*	+
NT2RP1000191	1.08	1.08	5.61	4.94	3.59	5.71		
NT2RP1000202	1.06	1.06	1.66	2.02	1.2	2.24		
NT2RP1000239	1.53	1.53	4.1	2.15	0.94	2.07		
NT2RP1000243	2.37	2.37	2.04	1.31	1.14	1.64	**	-
NT2RP1000255	1.94	1.94	3.02	2.11	2.26	1.78		
NT2RP1000259	5.27	5.27	9.55	5.53	6.33	4.29		
NT2RP1000261	2.76	2.76	4.4	2.07	1.64	2.64		
NT2RP1000269	5.16	5.16	5.01	7.7	10.51	7.39	*	+
NT2RP1000271	7.79	7.79	15.88	13.16	15.11	18.48		
NT2RP1000272	7.71	7.71	13.07	10.72	11.74	11.3		
NT2RP1000279	2.19	2.19	5.24	2.23	3.91	2.62		
NT2RP1000290	6.61	6.61	9.02	12.65	13.52	9.92	*	+
NT2RP1000293	6.86	6.86	10.91	9.75	8.45	10.92		
NT2RP1000300	12.42	12.42	11.93	9.96	11.37	10.2	*	-
NT2RP1000324	5.16	5.16	6	4.69	5.92	6.97		
NT2RP1000325	54.42	54.42	101.4	70.46	57.52	78.6		

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NT2RP1000326	4.01	4.01	7.67	3.82	4.56	7.85		
NT2RP1000331	12.16	12.16	24.08	12.19	10.5	20.1		
NT2RP1000333	4.18	4.18	7.52	6.66	6.53	6.98		
NT2RP1000336	1.45	1.45	4.45	1.35	3.76	1.78		
NT2RP1000347	3.05	3.05	8.75	7.26	8.31	6.38		
NT2RP1000348	2.11	2.11	4.14	2.76	3	2.75		
NT2RP1000349	2.12	2.12	3.92	3	4.39	4.11		
NT2RP1000353	40.87	40.87	83.5	51.49	47.8	66.02		
NT2RP1000356	39.53	39.53	93.37	50.3	56.48	74.42		
NT2RP1000357	3.89	3.89	9.63	8.43	8.7	8.72		
NT2RP1000358	2.85	2.85	6.11	4.23	3.04	5.09		
NT2RP1000360	11.04	11.04	19.39	12.08	18.42	19.44		
NT2RP1000363	13.09	13.09	15.39	13.13	13.38	10.01		
NT2RP1000376	1.81	1.81	3.8	2.09	1.9	2.24		
NT2RP1000386	118	118	191.31	146.98	187.97	155.47		
NT2RP1000407	0.72	0.72	3.16	0.58	0.89	1.2		
NT2RP1000409	2.05	2.05	5.39	2.84	6.59	3.83		
NT2RP1000413	4.78	4.78	8.03	5.86	8.89	10.19		
NT2RP1000416	1.5	1.5	2.01	0.93	3.17	0.7		
NT2RP1000418	2.27	2.27	6.69	5.08	6.67	4.85		
NT2RP1000420	1.77	1.77	5.19	7.32	7.64	3.7		
NT2RP1000434	1.48	1.48	4.39	1.27	3.12	1		
NT2RP1000439	5.02	5.02	9.31	20.62	28.73	24.75	**	+
NT2RP1000443	1.8	1.8	3.46	2.24	1.61	1.63		
NT2RP1000447	2.21	2.21	5.57	2.49	2.87	3.1		
NT2RP1000448	1.39	1.39	3.58	3.09	4.4	1.41		
NT2RP1000451	4.2	4.2	6.37	5.72	7.27	7.04		
NT2RP1000458	15.1	15.1	10.53	19.73	8.72	23.03		
NT2RP1000460	7.55	7.55	13.82	8.76	11.49	8.62		
NT2RP1000465	4.58	4.58	20.97	20.41	19.98	22.46		
NT2RP1000468	3.25	3.25	4.64	3.82	4.1	4.45		
NT2RP1000470	2.38	2.38	5.67	3.99	2.35	3.8		
NT2RP1000477	1.11	1.11	3.81	1.1	0.84	0.83		
NT2RP1000478	4.53	4.53	12.55	19.87	18.75	20.39	*	+
NT2RP1000481	1.23	1.23	3.89	2.48	4.09	1.2		
NT2RP1000493	2.44	2.44	3.8	1.74	3.83	0.87		
NT2RP1000513	13.07	13.07	16.37	17.06	17.57	18.97	*	+
NT2RP1000522	6.13	6.13	12.69	13.13	13.08	10.32		
NT2RP1000533	3.72	3.72	6.17	2.92	4.49	2.17		

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NT2RP1000544	1.53	1.53	2.45	1.38	1.24	1.44		
NT2RP1000547	0.88	0.88	2.45	2	1.63	1.23		
NT2RP1000551	1.7	1.7	2.62	2.13	3.2	1.1		
NT2RP1000567	1.66	1.66	4.29	2.54	4.29	1.77		
NT2RP1000574	1.99	1.99	4.28	1.5	3.43	1.38		
NT2RP1000577	3.14	3.14	6.01	3.16	5.31	2.05		
NT2RP1000579	4.64	4.64	6.24	3.27	3.97	2.04		
NT2RP1000581	5.22	5.22	3.58	2.07	1.61	0.93	**	-
NT2RP1000593	1.74	1.74	4.39	2.48	3.28	2.3		
NT2RP1000604	3.85	3.85	7.75	17.25	13.78	16.39	**	+
NT2RP1000609	1.15	1.15	2.21	2.84	2.61	1.55		
NT2RP1000613	1.12	1.12	2.56	1.82	4.29	0.82		
NT2RP1000622	5.94	5.94	15.9	14.91	19.42	15.46		
NT2RP1000627	9.18	9.18	18.96	23.88	21.9	14.86		
NT2RP1000629	4.18	4.18	5.9	5.92	5.32	3.17		
NT2RP1000630	6.54	6.54	7.84	7.21	7.67	7.92		
NT2RP1000639	0.64	0.64	0.31	1.53	2.04	0.28		
NT2RP1000640	130.14	130.14	307.77	227.5	176.05	232.29		
NT2RP1000646	4.14	4.14	9.59	10.19	11.87	12.15	*	+
NT2RP1000659	2.65	2.65	7	8.91	7.99	6.04		
NT2RP1000674	13.48	13.48	28.08	43.62	45.82	56.95	**	+
NT2RP1000677	3.9	3.9	10.76	11.84	10.19	9.87		
NT2RP1000679	2.38	2.38	3.76	2.3	2.35	1.05		
NT2RP1000688	4.72	4.72	3.34	2.76	2.73	1.83	*	-
NT2RP1000689	1.44	1.44	1.86	2.03	1.22	1.13		
NT2RP1000695	1.11	1.11	2.5	2.09	2.44	1.52		
NT2RP1000701	0.89	0.89	1.08	2.62	2.74	1.71	*	+
NT2RP1000702	1.12	1.12	2.28	3.74	4.07	3.15	*	+
NT2RP1000713	2.29	2.29	2.79	2.8	3.56	2.38		
NT2RP1000721	4.14	4.14	4.49	4.48	3.92	3.78		
NT2RP1000730	3.5	3.5	4.83	2.61	4.5	2.41		
NT2RP1000733	6.08	6.08	6.56	4.91	8.12	5.65		
NT2RP1000738	3.18	3.18	8.04	5.16	5.71	7.11		
NT2RP1000739	1.11	1.11	2.65	4.02	3.09	2.86		
NT2RP1000740	1.41	1.41	3.13	3.63	3.57	3.77	*	+
NT2RP1000746	1.15	1.15	3.58	2.28	3.74	1.37		
NT2RP1000750	4	4	8.31	10.25	10.72	9.39	*	+
NT2RP1000751	33.15	33.15	59.65	67.84	64.22	66.55		
NT2RP1000767	3.8	3.8	3.64	1.7	2.62	0.62	*	-

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NT2RP1000769	9.31	9.31	13.98	7.42	8.59	7.19		
NT2RP1000780	0.86	0.86	1.01	1.87	1.13	0.89		
NT2RP1000782	4.25	4.25	12.21	10.24	7.96	9.13		
NT2RP1000796	3.17	3.17	2.69	4.23	2.99	2.86		
NT2RP1000797	12.31	12.31	22.78	19.44	18.64	21.78		
NT2RP1000800	1.13	1.13	3.74	2.46	2.66	1.46		
NT2RP1000825	2.38	2.38	2.91	1.04	1.88	0.87	*	-
NT2RP1000833	2.5	2.5	2.85	0.92	2.39	1.26		
NT2RP1000834	35.44	35.44	66.57	73.98	90.28	71.45		
NT2RP1000836	1.83	1.83	3.43	1.01	2.39	1.04		
NT2RP1000837	3.36	3.36	6.66	3.22	4.71	3.67		
NT2RP1000846	1.29	1.29	5.48	1.67	2.84	1.4		
NT2RP1000847	1.99	1.99	5.49	2.15	5.12	1.64		
NT2RP1000851	4.67	4.67	9.32	6.18	7.94	6.72		
NT2RP1000856	14.31	14.31	17.46	20.38	23.22	19.37	*	+
NT2RP1000860	2.09	2.09	4.54	4.02	2.74	4.04		
NT2RP1000902	5.31	5.31	11.6	6.94	9.91	7.34		
NT2RP1000903	2.45	2.45	6.26	4.04	3.42	4.24		
NT2RP1000905	1.76	1.76	4.87	5.36	5.66	10		
NT2RP1000915	5.51	5.51	10.01	6.72	8.59	9.91		
NT2RP1000916	2.31	2.31	5.51	1.78	3.82	2.09		
NT2RP1000921	9.38	9.38	8.73	8.23	9.13	7.92		
NT2RP1000943	5.14	5.14	10.76	8.51	8.55	7.2		
NT2RP1000944	1.59	1.59	2.21	1.78	1.74	1.15		
NT2RP1000947	8.5	8.5	14.91	16.51	15.04	14.22		
NT2RP1000954	2.11	2.11	4.96	2.74	5.55	3.04		
NT2RP1000958	6.48	6.48	14.73	4.54	10.17	10.21		
NT2RP1000959	124.81	124.81	209.45	128.43	72.65	206.1		
NT2RP1000966	9.96	9.96	12.96	14.28	15.36	21.39		
NT2RP1000974	2.46	2.46	5.38	3.98	6.08	3.71		
NT2RP1000980	3.07	3.07	5.5	4.04	4.53	4.02		
NT2RP1000981	4.3	4.3	8.09	5.68	7.26	5.27		
NT2RP1000988	6.45	6.45	10.46	9.62	6.44	7.87		
NT2RP1001002	2.8	2.8	7.36	3.94	4.57	4.3		
NT2RP1001004	4.72	4.72	8.25	3.65	4.9	5.37		
NT2RP1001007	1.42	1.42	3.42	1.69	3.84	2.03		
NT2RP1001011	1.94	1.94	5.93	3.82	5.46	4.83		
NT2RP1001013	4.45	4.45	9.41	5.92	8.62	5.04		
NT2RP1001014	2.21	2.21	5.89	3.76	6.64	3.49		

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NT2RP1001020	1.87	1.87	4.11	2.08	3.75	2.36		
NT2RP1001023	62.79	62.79	145.09	101.48	105.86	143.96		
NT2RP1001027	18.11	18.11	82.66	51.63	59.05	68.9		
NT2RP1001031	1.83	1.83	3.31	2.05	3.53	2.25		
NT2RP1001033	2.43	2.43	6.09	5.68	5.98	4.27		
NT2RP1001042	2.94	2.94	6.47	2.99	3.85	2.04		
NT2RP1001045	15.95	15.95	23.24	40.66	47.04	44.53	**	+
NT2RP1001073	6.64	6.64	10.57	8.32	10.46	7.33		
NT2RP1001079	2.91	2.91	6.37	2.16	2.58	1.48		
NT2RP1001080	2.16	2.16	4.89	6.88	4.2	4.56		
NT2RP1001113	1.07	1.07	3.64	3.55	3.94	3.26		
NT2RP1001159	21.42	21.42	43.84	22.89	23.31	34.25		
NT2RP1001173	1.7	1.7	3.07	1.38	4.28	1.52		
NT2RP1001176	7.4	7.4	10.13	13	9.31	13.95		
NT2RP1001177	5.31	5.31	5.75	3.01	5.5	2.02		
NT2RP1001185	6.42	6.42	9.37	3.79	4.63	2.73	*	-
NT2RP1001199	3.9	3.9	7.67	6.93	5.22	3.28		
NT2RP1001205	7.78	7.78	19.46	16.66	12.64	23.28		
NT2RP1001215	1.82	1.82	5.02	3.79	4.12	3.15		
NT2RP1001225	4.54	4.54	7.96	7.56	8.77	6.31		
NT2RP1001245	7.27	7.27	10.86	19.68	21.03	22.13	**	+
NT2RP1001247	2.04	2.04	4.01	1.77	2.89	1.67		
NT2RP1001248	2.81	2.81	6.79	3.94	4.63	2.4		
NT2RP1001253	5.02	5.02	6.39	4.48	4.38	3.32		
NT2RP1001286	6.18	6.18	7.69	3.79	3.88	4.12	**	-
NT2RP1001294	2.4	2.4	4.47	3.6	2.73	4.18		
NT2RP1001302	2.46	2.46	4.51	4.89	2.9	5.39		
NT2RP1001310	15.54	15.54	34.01	21.13	20.75	27.15		
NT2RP1001311	1.9	1.9	3.22	2.66	3.16	2.38		
NT2RP1001313	2.6	2.6	7.72	5.45	7.85	5.78		
NT2RP1001324	2.47	2.47	5.3	3.34	4.17	2.35		
NT2RP1001349	3.3	3.3	6.29	3.63	3.92	2.14		
NT2RP1001361	19.41	19.41	18.28	23.28	28.33	24.16	*	+
NT2RP1001379	3.82	3.82	9.52	4.97	7.97	7.06		
NT2RP1001385	2.06	2.06	4.51	4.09	3.89	4.4		
NT2RP1001395	4.96	4.96	7.86	6.01	6.32	8.13		
NT2RP1001410	8.75	8.75	20.39	15.74	15.66	9.94		
NT2RP1001424	2.39	2.39	3.34	3	3	1.73		
NT2RP1001432	4.33	4.33	3.86	2.19	1.76	2.05	**	-

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NT2RP1001449	6.23	6.23	7.5	6.29	8.21	4.63		
NT2RP1001457	4.09	4.09	4.21	2.11	2.26	2.63	**	-
NT2RP1001459	21.54	21.54	132.97	90.96	107.97	81.08		
NT2RP1001466	5.73	5.73	14.97	11.31	9.39	10.99		
NT2RP1001475	2.45	2.45	6.31	5.98	6.67	3.9		
NT2RP1001482	3.93	3.93	9.18	15.88	13.03	8.2		
NT2RP1001494	1.61	1.61	4.6	4.34	4.18	2.25		
NT2RP1001500	3.39	3.39	8.13	8.09	8.65	7.42		
NT2RP1001517	5.11	5.11	7.37	4.41	5.38	2.36		
NT2RP1001540	4.74	4.74	5.03	4.6	4.86	3.11		
NT2RP1001543	1.02	1.02	1.83	1.49	1.12	0.98		
NT2RP1001546	22.51	22.51	51.51	34.99	22.76	33.42		
NT2RP1001550	9.33	9.33	21.4	14.35	12.21	13.42		
NT2RP1001553	2.07	2.07	6.07	5.69	6.04	4.45		
NT2RP1001555	36.28	36.28	58.55	41.1	53.63	54.35		
NT2RP1001563	2.28	2.28	3.44	2.07	2.24	1.31		
NT2RP1001569	9.43	9.43	16	17.31	18.21	13.04		
NT2RP1001584	15.6	15.6	19.66	28.1	32.53	25.83	**	+
NT2RP1001599	1.18	1.18	1.95	1.27	1.19	1.24		
NT2RP1001616	5	5	11.95	9.49	6.7	8.95		
NT2RP1001654	11.78	11.78	18.07	16.27	16.54	18.38		
NT2RP1001665	2.77	2.77	4.72	2.73	2.05	2.05		
NT2RP1001679	76.31	76.31	195.7	199.2	240.87	222.46		
NT2RP1001681	10.11	10.11	15.1	20.39	21.03	23.99	**	+
NT2RP1001694	3.58	3.58	3.82	2.45	2.38	1.97	**	-
NT2RP2000001	5.23	5.23	5.53	4.17	4.54	3.74	**	-
NT2RP2000006	3.49	3.49	7.32	4.12	3.88	3.4		
NT2RP2000007	3.18	3.18	6.56	4.68	5.66	4.92		
NT2RP2000008	2.77	2.77	6.72	3.66	5.3	4.9		
NT2RP2000010	2.89	2.89	5.59	2.99	5.06	2.5		
NT2RP2000011	7.08	7.08	17.96	14.55	14.74	15.15		
NT2RP2000027	2.28	2.28	7.42	4.52	4.89	3.61		
NT2RP2000028	22.93	22.93	62.54	46.48	51.47	53.47		
NT2RP2000032	2.5	2.5	5.85	3.11	3.71	6.42		
NT2RP2000040	11.57	11.57	23.92	14.38	14.5	23.1		
NT2RP2000042	5.28	5.28	10.32	6.89	7.21	12.64		
NT2RP2000045	5.7	5.7	9.42	5.27	6.45	6.3		
NT2RP2000051	3.16	3.16	6.29	9.23	9.96	9.53	**	+
NT2RP2000054	2.55	2.55	6.42	3.81	5.42	2.53		

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NT2RP2000056	3.68	3.68	6.23	5.67	6.89	5.8		
NT2RP2000057	60.79	60.79	174.83	212.63	239.81	221.98	*	+
NT2RP2000067	3.1	3.1	3.86	2.98	4.36	5.72		
NT2RP2000070	2.91	2.91	6.27	5.7	5.95	8.21		
NT2RP2000076	1.66	1.66	4.45	2.98	3.58	3.23		
NT2RP2000077	1.67	1.67	4.73	2.43	4.94	3.14		
NT2RP2000079	3.76	3.76	9.24	5.15	4.81	5.47		
NT2RP2000088	2.9	2.9	5.22	2.18	3.07	2.21		
NT2RP2000091	5.84	5.84	6.54	6.62	8.28	6.72		
NT2RP2000092	4.37	4.37	6.7	6.06	7.67	5.65		
NT2RP2000097	2.74	2.74	3.39	3.4	4.13	4.13	*	+
NT2RP2000098	3.44	3.44	6.83	6.69	9.01	6.27		
NT2RP2000108	1.93	1.93	7.24	4.8	6.31	6.68		
NT2RP2000114	1.95	1.95	3.65	2.58	4.41	2.9		
NT2RP2000116	3.17	3.17	7.36	5.35	3.85	9.42		
NT2RP2000119	3.14	3.14	7.16	4.58	7.96	5.6		
NT2RP2000120	3.91	3.91	7.62	5.57	8.5	5.8		
NT2RP2000126	2.86	2.86	4.86	3.88	5.1	3.44		
NT2RP2000133	1.83	1.83	3.66	3.13	4.05	2.01		
NT2RP2000147	6.28	6.28	12.88	11.64	6.51	8.58		
NT2RP2000153	4.61	4.61	9.55	10.57	6.49	12.05		
NT2RP2000156	3.27	3.27	8.24	5.59	6.55	4.07		
NT2RP2000157	3.7	3.7	6.33	6.57	5.02	4.15		
NT2RP2000161	4.45	4.45	8.82	7.52	7.5	6.02		
NT2RP2000168	4.22	4.22	12.63	3.94	6.03	3.88		
NT2RP2000173	12.56	12.56	81.37	72.12	92.12	78.68		
NT2RP2000175	1.9	1.9	3.78	2.03	3.33	4.43		
NT2RP2000178	2.06	2.06	6.06	3.23	3.01	3.81		
NT2RP2000183	1.64	1.64	7.82	5.82	6.21	6.03		
NT2RP2000195	3.1	3.1	6.65	6	6.71	3.22		
NT2RP2000204	73.6	73.6	93.43	102.95	40.16	62.34		
NT2RP2000205	4	4	6.56	3.91	5.74	4.5		
NT2RP2000208	3.06	3.06	9.42	4.23	6.77	3.36		
NT2RP2000224	13.3	13.3	31.75	18.34	21.15	20.93		
NT2RP2000230	9.96	9.96	18.99	12.16	16.4	11.95		
NT2RP2000231	4.3	4.3	7.41	4.24	3.43	4.54		
NT2RP2000232	1.08	1.08	2.75	1.53	2.45	0.74		
NT2RP2000233	8.04	8.04	60.44	47.2	64.72	52.31		
NT2RP2000239	3	3	4.7	8.93	8.93	7.01	**	+

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NT2RP2000240	2.01	2.01	5.25	2.49	3.41	1.45		
NT2RP2000248	4.29	4.29	6.09	2.82	2.39	0.96	*	-
NT2RP2000256	5.7	5.7	8.25	5.62	6.22	5.44		
NT2RP2000257	3.47	3.47	6.92	4.86	6.52	4.34		
NT2RP2000258	1.53	1.53	3.83	3.88	2.93	3.02		
NT2RP2000261	2.95	2.95	3.94	4.47	3.59	2.91		
NT2RP2000270	3.12	3.12	6.26	6.66	4.06	4.3		
NT2RP2000274	1.78	1.78	3.87	3.48	5.16	2.56		
NT2RP2000277	2.18	2.18	6.13	3.19	4.02	2.98		
NT2RP2000279	2.26	2.26	4.92	2.43	2.52	2.17		
NT2RP2000283	5.75	5.75	27.65	21.53	27.32	24.78		
NT2RP2000288	6.29	6.29	7.46	8.9	10.89	8.64	*	+
NT2RP2000289	1.12	1.12	2.79	3.09	2.77	1.93		
NT2RP2000297	2.57	2.57	5.7	4.8	4.53	6.09		
NT2RP2000298	3.61	3.61	9.64	8.51	7.66	8.24		
NT2RP2000310	1.43	1.43	2.3	2.46	3.41	1.7		
NT2RP2000327	2.12	2.12	3.96	3.13	3.49	1.57		
NT2RP2000328	6.95	6.95	11.56	13.43	16.7	14.68	*	+
NT2RP2000329	10.73	10.73	10.17	17.55	23.92	18.52	**	+
NT2RP2000333	6.35	6.35	6.4	6.83	7.17	4.64		
NT2RP2000337	2.05	2.05	5.16	4.43	5.32	5.31		
NT2RP2000346	2.55	2.55	5.18	7.2	5.63	4.95		
NT2RP2000357	1.57	1.57	6.87	5.48	5.14	5.35		
NT2RP2000358	2.09	2.09	4.52	5.03	4.9	4.01		
NT2RP2000366	3.23	3.23	4.08	4.16	4.25	2.32		
NT2RP2000369	7.22	7.22	9.94	44.13	45.2	44.34	**	+
NT2RP2000376	26.92	26.92	108.62	84.48	134.63	85.95		
NT2RP2000394	6.49	6.49	5.92	5.08	8.52	4.21		
NT2RP2000396	2.71	2.71	6.55	7.52	6.8	5.02		
NT2RP2000412	4.48	4.48	23.45	21.42	24.93	20.49		
NT2RP2000414	8.03	8.03	18.69	23.83	18.98	23.37		
NT2RP2000420	1.12	1.12	4.11	3.54	3.25	1.97		
NT2RP2000422	6.41	6.41	13.18	17.56	17.88	18.67	*	+
NT2RP2000426	21.59	21.59	80.94	87.94	110.97	74.98		
NT2RP2000428	24.92	24.92	43.91	34.21	35.59	30.95		
NT2RP2000438	5.06	5.06	5.17	5.62	6.94	5.11		
NT2RP2000447	4.14	4.14	9.68	7.3	7.08	7.16		
NT2RP2000448	3.03	3.03	4.63	4.57	3.57	3.17		
NT2RP2000459	2.47	2.47	4.93	2.82	3.15	2.09		

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NT2RP2000479	3.3	3.3	7.51	5.33	5.71	5.06		
NT2RP2000498	3.07	3.07	6.25	4.48	5.09	3.9		
NT2RP2000503	2.47	2.47	4.46	2.54	2.82	1.52		
NT2RP2000510	4.01	4.01	6.19	5.08	6.45	3.7		
NT2RP2000514	2.65	2.65	2.51	1.94	2.25	1.63	*	-
NT2RP2000516	4.72	4.72	9.77	4.92	5.29	5.18		
NT2RP2000523	2.21	2.21	3.17	1.92	2.44	2.63		
NT2RP2000533	17.82	17.82	29.05	22.57	27.56	30.78		
NT2RP2000540	1.98	1.98	4.66	3.01	5.41	5.18		
NT2RP2000547	3.1	3.1	5.26	4.38	5.27	3.71		
NT2RP2000557	4.26	4.26	6.96	4.34	6.5	3.32		
NT2RP2000558	3.43	3.43	7.17	6.43	7.11	8.26		
NT2RP2000564	3.04	3.04	7.2	3.49	8.03	4.77		
NT2RP2000565	4.54	4.54	11.07	7.64	9.24	9.98		
NT2RP2000583	14.8	14.8	44.9	49.6	34.93	49.08		
NT2RP2000591	0.81	0.81	3.81	1.53	2.61	1.21		
NT2RP2000599	1.85	1.85	4.1	1.97	3.43	2.36		
NT2RP2000601	1.78	1.78	4.67	1.28	2.48	1.3		
NT2RP2000603	2.58	2.58	4.44	2.54	2.84	2.98		
NT2RP2000610	3.77	3.77	7.23	6.32	7.62	5.53		
NT2RP2000614	75.85	75.85	129.42	130.63	184.38	188.58	*	+
NT2RP2000616	1.81	1.81	4.89	3.9	5.1	3.83		
NT2RP2000617	2.17	2.17	6.73	5.78	6.82	6.26		
NT2RP2000623	3.1	3.1	5.36	3.46	5.1	3.49		
NT2RP2000634	1.56	1.56	3.92	2.29	3.34	2.02		
NT2RP2000636	3.78	3.78	8.64	6.27	7.6	6.62		
NT2RP2000638	4.37	4.37	8.91	4.57	7.41	5.69		
NT2RP2000644	2.22	2.22	5.47	3.41	4.16	3.45		
NT2RP2000649	8.96	8.96	15.76	13.65	17.22	13.07		
NT2RP2000652	3.35	3.35	4.58	3.57	4.36	2.72		
NT2RP2000656	3.73	3.73	6.93	4.83	3.91	4.08		
NT2RP2000658	1.08	1.08	2.64	1.51	3.18	1.43		
NT2RP2000663	4.23	4.23	6.9	5.98	7.21	5.9		
NT2RP2000664	4.24	4.24	10.24	12.72	12.54	16.44	*	+
NT2RP2000668	7.49	7.49	26.84	16.92	20.41	17.17		
NT2RP2000678	1.77	1.77	3.19	1.77	2.09	1.13		
NT2RP2000694	4.89	4.89	8.39	11.06	13	13.36	**	+
NT2RP2000704	1.8	1.8	5.63	2.99	3.13	3.67		
NT2RP2000710	4.51	4.51	9.96	6.72	8.08	7.23		

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NT2RP2000712	1.43	1.43	5.35	3.39	3.57	2.95		
NT2RP2000715	3.42	3.42	7.43	6.04	7.56	4.49		
NT2RP2000720	4.92	4.92	11.76	7.24	8	7.11		
NT2RP2000731	3.92	3.92	9.15	3.7	4.5	2.61		
NT2RP2000739	3.23	3.23	5.67	2.62	3.32	5.65		
NT2RP2000748	1.59	1.59	4.2	1.42	1.81	1.62		
NT2RP2000749	11.84	11.84	21.88	14.4	8.47	13.91		
NT2RP2000758	1.6	1.6	3.17	2.65	6	1.17		
NT2RP2000764	1.51	1.51	5.74	2.95	5.22	1.95		
NT2RP2000766	9.08	9.08	52.24	46.37	59.37	52.89		
NT2RP2000777	12.28	12.28	18.43	26.91	28.56	24.47	**	+
NT2RP2000786	21.32	21.32	73.91	55.85	67.59	58.16		
NT2RP2000793	5.32	5.32	6.9	4.32	3.57	4.38	*	-
NT2RP2000796	5.32	5.32	7.41	7.38	9.17	6.66		
NT2RP2000809	3.25	3.25	8.3	6.46	4.69	5.45		
NT2RP2000812	6.65	6.65	17.51	16.43	14.35	16.89		
NT2RP2000814	4.16	4.16	4.97	3.75	4.6	3.29		
NT2RP2000816	1.84	1.84	5.64	4.64	5.19	3.58		
NT2RP2000818	3.28	3.28	5.19	3.18	3.66	1.95		
NT2RP2000819	2.76	2.76	5.79	3.03	3.05	1.94		
NT2RP2000841	4.35	4.35	4.51	2.17	2.48	1.65	**	-
NT2RP2000842	7.8	7.8	9.57	13.62	14.25	12.66	**	+
NT2RP2000845	2.52	2.52	8.31	7.51	6.76	6.93		
NT2RP2000863	2.45	2.45	3.48	3.82	3.37	2.47		
NT2RP2000880	5.96	5.96	11.61	9.5	11.13	10.25		
NT2RP2000892	4.3	4.3	6.43	6.54	6.97	5.01		
NT2RP2000894	5.59	5.59	11.88	5.41	5.59	2.16		
NT2RP2000903	5.71	5.71	9.12	10.73	11.92	7.44		
NT2RP2000906	4.56	4.56	5.39	2.63	3.78	2.19	*	-
NT2RP2000910	4.34	4.34	4.26	2.9	2.7	1.68	**	-
NT2RP2000931	10.97	10.97	18.36	20.51	19.28	24.6		
NT2RP2000932	2.86	2.86	5.43	4.8	4.72	4.21		
NT2RP2000938	18.41	18.41	42.99	35.71	30.01	43.52		
NT2RP2000943	7.02	7.02	14.98	18.7	14.88	14.48		
NT2RP2000957	3.19	3.19	4.11	4.26	3.66	2.71		
NT2RP2000958	7	7	6.84	10.43	12.36	7.8		
NT2RP2000959	9.88	9.88	14.99	13.92	17.38	10.69		
NT2RP2000965	5.05	5.05	7.82	15.73	18.97	16.02	**	+
NT2RP2000970	2.31	2.31	6.72	5.14	5	4.62		

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NT2RP2000973	0.9	0.9	1.47	2.56	2.64	1.57	*	+
NT2RP2000985	2.69	2.69	6	9.28	6.29	13.98		
NT2RP2000987	1.89	1.89	3.31	4.54	3.17	1.66		
NT2RP2000997	13.83	13.83	23.99	38.12	29.73	40.96	*	+
NT2RP2001024	2.86	2.86	5.34	3.61	3.12	2.36		
NT2RP2001028	4.66	4.66	4.2	2.65	4.09	0.99		
NT2RP2001036	5.14	5.14	8.86	6.16	6.44	4.91		
NT2RP2001039	1.08	1.08	3.18	3.47	1.14	2.24		
NT2RP2001044	1.13	1.13	2.5	2.53	1.89	2.8		
NT2RP2001056	4.97	4.97	28.32	20.16	26.9	18.16		
NT2RP2001065	2.38	2.38	6.24	7.45	7.4	5.69		
NT2RP2001067	2.98	2.98	5.38	4.12	5.29	2.41		
NT2RP2001070	3.3	3.3	7.63	4.72	6.17	3.58		
NT2RP2001081	2.91	2.91	8.19	4.8	6.68	3.9		
NT2RP2001087	3.93	3.93	2.36	2.06	2.92	1.61		
NT2RP2001094	0.69	0.69	1.37	1.25	1.15	1.04		
NT2RP2001119	2.02	2.02	6.11	5.86	4.44	4.35		
NT2RP2001127	1.53	1.53	4.04	2.69	1.85	2.1		
NT2RP2001133	2.45	2.45	4.73	4.06	3.61	3.6		
NT2RP2001137	2.68	2.68	4.07	2.3	2.82	2.9		
NT2RP2001142	3.88	3.88	7.47	3.37	2.83	2.42		
NT2RP2001149	2.7	2.7	2.98	2.11	3.39	1.32		
NT2RP2001168	6	6	7.81	6.8	7.01	5.75		
NT2RP2001173	4.15	4.15	7.88	3.98	3.09	5.44		
NT2RP2001174	9.23	9.23	14.98	14.12	15.45	18.01		
NT2RP2001184	2.78	2.78	5.46	4.21	7.18	4.64		
NT2RP2001196	1.62	1.62	5.93	3.14	3.28	2.94		
NT2RP2001200	3.85	3.85	9.36	5.02	4.25	7.88		
NT2RP2001218	2.29	2.29	5.69	2.55	3.89	3.6		
NT2RP2001223	2.65	2.65	5.03	1.95	3.69	3.31		
NT2RP2001226	4.34	4.34	10.19	6.95	5.72	7.35		
NT2RP2001227	4.45	4.45	6.12	3.2	3.62	6.01		
NT2RP2001232	6.44	6.44	13.95	7.13	9.79	13.66		
NT2RP2001233	4.02	4.02	10.57	7.04	7.77	8.01		
NT2RP2001245	4.21	4.21	8.03	9.47	11.82	11.16	*	+
NT2RP2001246	6.3	6.3	9.84	9	11.28	11.57		
NT2RP2001268	6.19	6.19	18.1	17.61	16.26	18.55		
NT2RP2001270	4.78	4.78	9.11	5.68	8.7	10.04		
NT2RP2001276	4.92	4.92	13.29	12.73	10.92	12.73		

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	NT2RP2001277	3.11	3.11	7.02	4.91	6.22	10.82	
	NT2RP2001290	2.71	2.71	6.46	4.42	5.61	6.01	
	NT2RP2001295	5.46	5.46	9.44	5.13	5.98	7.92	
	NT2RP2001297	118.17	118.17	120.73	139.11	97.16	145.76	
	NT2RP2001301	9.12	9.12	18.56	15.89	19.62	14.24	
	NT2RP2001312	2.7	2.7	5.68	5.6	4.59	6.04	
	NT2RP2001327	4.73	4.73	5.69	6.39	8.53	11.86	
	NT2RP2001328	8.44	8.44	20.87	16.32	23.25	23.16	
	NT2RP2001341	4.59	4.59	9.22	3.06	7.65	7.21	
	NT2RP2001347	3.09	3.09	8.54	5.54	9.55	6.9	
	NT2RP2001366	10.33	10.33	48.06	54.83	51.5	52.33	
	NT2RP2001378	2.33	2.33	3.77	3.74	4.64	5.02	
	NT2RP2001381	2.82	2.82	6.86	5.79	6.62	8.37	
	NT2RP2001388	3.25	3.25	6.71	4.54	5.11	5.2	
	NT2RP2001391	443.52	443.52	734.13	742.83	990.71	747.95	
	NT2RP2001392	2.98	2.98	6.43	4.58	3.16	4.18	
	NT2RP2001394	3.3	3.3	8.55	8.35	6.09	10.15	
	NT2RP2001397	5.04	5.04	6.79	7.33	5.68	12.2	
	NT2RP2001400	3.1	3.1	6.4	3.43	6.25	2.92	
	NT2RP2001408	3.31	3.31	6.13	4.02	5.97	5.62	
	NT2RP2001420	5.63	5.63	12.09	8.09	9.97	9.17	
	NT2RP2001423	4.71	4.71	9.71	6.21	8.29	7.19	
	NT2RP2001427	2.68	2.68	5.32	3.69	4.61	5.49	
	NT2RP2001428	2.71	2.71	7.13	5.49	3.78	3.03	
	NT2RP2001436	4.27	4.27	8.85	5.84	2.85	4.84	
	NT2RP2001440	2.89	2.89	7.34	10.24	10.15	11.98	* +
	NT2RP2001445	2.43	2.43	6.75	5.86	5.55	5.89	
	NT2RP2001449	4.37	4.37	6.41	5	4.74	5.02	
	NT2RP2001450	3.19	3.19	6.75	2.26	5.4	8.59	
	NT2RP2001467	4.53	4.53	10.28	5.32	4.72	6.5	
	NT2RP2001469	4.74	4.74	6.79	8.22	11.04	7.18	
	NT2RP2001480	6.54	6.54	26.68	14.98	12.63	15.42	
	NT2RP2001495	5.86	5.86	11.96	8.16	9.04	10.39	
	NT2RP2001499	8.25	8.25	16.78	10.05	14.46	9.66	
	NT2RP2001506	2.79	2.79	7.24	5.32	8.19	5.33	
	NT2RP2001508	10.59	10.59	13.66	18.74	20.49	21.92	** +
	NT2RP2001511	6.41	6.41	9.74	6.08	8.63	6.53	
	NT2RP2001514	7.04	7.04	7.02	7.24	6.44	6.38	
	NT2RP2001520	2.93	2.93	4.84	2.6	3.19	2.87	

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NT2RP2001526	3.88	3.88	8.49	7.01	5.27	3.83		
NT2RP2001529	9.87	9.87	53.78	44.74	55.72	60.88		
NT2RP2001536	1.63	1.63	4.17	3.81	4.52	4.71		
NT2RP2001538	83.44	83.44	178.68	132.75	146.73	155.87		
NT2RP2001547	4.96	4.96	14.87	16.77	19.21	17.77	*	+
NT2RP2001560	6.28	6.28	21.64	25.41	28.19	27.75	*	+
NT2RP2001562	5.56	5.56	5.57	5.94	6.75	4.64		
NT2RP2001566	7.96	7.96	9.24	8.22	7.91	8.56		
NT2RP2001569	4.26	4.26	8.71	6.09	5.65	8.28		
NT2RP2001576	3.95	3.95	11.58	13.42	9	12.82		
NT2RP2001581	47.15	47.15	130.15	121.19	112.28	129.54		
NT2RP2001597	3.73	3.73	7.88	8.57	8.3	13.3		
NT2RP2001601	2.37	2.37	4.81	3.67	4.81	3.34		
NT2RP2001613	2.74	2.74	4.87	2.83	2.72	4.15		
NT2RP2001628	3.42	3.42	3.97	3.14	3.04	7.84		
NT2RP2001634	8.64	8.64	13.94	16.57	23.67	17.67	*	+
NT2RP2001635	2.51	2.51	5.92	5.63	5.53	4.72		
NT2RP2001660	4.27	4.27	16.91	5.9	5.54	10.06		
NT2RP2001662	1.49	1.49	4.07	4.5	4.44	3.47		
NT2RP2001663	2.82	2.82	5.09	10.37	8.21	9.74	**	+
NT2RP2001672	3.28	3.28	3.82	3.88	4.09	4	*	+
NT2RP2001675	4.1	4.1	5.01	5.23	4.73	5.06		
NT2RP2001677	9.58	9.58	18.2	20.9	26.67	19.74	*	+
NT2RP2001678	4.84	4.84	6.73	4.6	4.83	4.5		
NT2RP2001683	1.89	1.89	3.12	4.6	4.72	2.78		
NT2RP2001699	3.15	3.15	6.16	6.5	5.84	4.88		
NT2RP2001707	1.24	1.24	3.19	3.42	4.13	4.8	*	+
NT2RP2001720	1.47	1.47	3.6	3.91	3	2.72		
NT2RP2001721	2.26	2.26	4.57	5.53	3.96	3.66		
NT2RP2001740	12	12	60.21	52.38	79.71	54.73		
NT2RP2001748	6.43	6.43	10.8	8.75	10.25	8.55		
NT2RP2001755	5.51	5.51	4.96	3.71	4.62	2.69	*	-
NT2RP2001762	1.25	1.25	2.01	3.87	2.56	3.52	*	+
NT2RP2001768	1.91	1.91	4.7	6.7	5.55	4.55		
NT2RP2001769	3.06	3.06	5.86	10.42	5.06	11.86		
NT2RP2001784	3.62	3.62	6.23	7.06	6.02	6.91		
NT2RP2001805	2.33	2.33	5.61	6.02	4.93	6.6		
NT2RP2001813	2.75	2.75	3.73	1.84	1.98	1.94	*	-
NT2RP2001817	3.16	3.16	4.49	4.03	5.32	3.45		

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NT2RP2001818	2.72	2.72	2.45	2.35	3.62	2.66		
NT2RP2001837	5.13	5.13	13.43	10.29	10.16	12.33		
NT2RP2001839	17.02	17.02	83.84	60.14	71.06	82.26		
NT2RP2001861	2	2	6.37	3.16	3.52	3.87		
NT2RP2001869	2.64	2.64	6.54	4.35	5.77	8.84		
NT2RP2001876	12.15	12.15	27.71	24.54	24.93	23.67		
NT2RP2001878	2.32	2.32	3.96	2.95	3.32	4.95		
NT2RP2001881	3.72	3.72	5.4	9.67	12.64	12.16	**	+
NT2RP2001883	2.63	2.63	6.8	4.33	5.42	6.35		
NT2RP2001884	13.59	13.59	23.56	15.33	10.54	23.6		
NT2RP2001885	3.27	3.27	5.49	2.88	4.39	4.82		
NT2RP2001898	10.76	10.76	80.37	69.48	88.43	73.46		
NT2RP2001900	3.38	3.38	4.03	2.61	4.93	10.26		
NT2RP2001903	3.73	3.73	7.71	5.57	5.7	8.2		
NT2RP2001907	3.1	3.1	8.56	5.05	7.56	6.72		
NT2RP2001915	2.89	2.89	5.06	4.06	3.08	7.19		
NT2RP2001921	4.04	4.04	10.3	13.02	12.45	19.33	*	+
NT2RP2001926	2.75	2.75	8.25	3.55	5.3	5.64		
NT2RP2001933	5.65	5.65	52.55	43.62	43.55	48.58		
NT2RP2001936	1.54	1.54	5.03	2.8	2.96	3.8		
NT2RP2001943	25.33	25.33	49.4	47.71	40.48	51.65		
NT2RP2001946	3.05	3.05	4.3	3.41	4.51	6.1		
NT2RP2001947	3.18	3.18	3.44	3.93	3.21	6.88		
NT2RP2001948	3.59	3.59	10.79	5.71	7.29	19.72		
NT2RP2001956	5.24	5.24	12.73	11.54	9.42	9.89		
NT2RP2001969	4.05	4.05	7.82	3.24	5.7	6		
NT2RP2001976	2.9	2.9	6.39	5.68	6.95	6.41		
NT2RP2001978	3.26	3.26	6.08	4.18	4.83	6.03		
NT2RP2001985	2.14	2.14	3.8	2.56	4.63	2.51		
NT2RP2001991	3.34	3.34	5.7	1.53	4.62	5.19		
NT2RP2001997	3.16	3.16	8.43	5.31	7.47	6.98		
NT2RP2002015	136.21	136.21	265.98	266.8	340.89	272.43		
NT2RP2002017	3.24	3.24	6.06	2.06	3.3	2.57		
NT2RP2002025	6.08	6.08	51.73	31.83	26.94	37.84		
NT2RP2002030	6.06	6.06	11.95	9.77	8.07	8.76		
NT2RP2002032	2.31	2.31	4.95	2.39	3.81	2.55		
NT2RP2002033	3	3	6.71	3.53	7.57	8.05		
NT2RP2002041	3.5	3.5	6.37	2.76	3.15	9		
NT2RP2002046	3	3	6.88	2.99	7.4	6.01		

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NT2RP2002047	2.71	2.71	3.86	2.06	3.87	3.83		
NT2RP2002050	7.67	7.67	11.66	9.78	6.47	7.77		
NT2RP2002052	3.77	3.77	8.39	6.6	3.99	6.28		
NT2RP2002058	2.07	2.07	4.11	3.1	4.82	3.39		
NT2RP2002060	1.48	1.48	3.44	2.1	5.9	3.18		
NT2RP2002063	3.61	3.61	5.83	3.3	5.2	6.65		
NT2RP2002066	10.11	10.11	13.47	5.47	9.88	9.73		
NT2RP2002070	3.74	3.74	6.3	2.15	3.1	3.83		
NT2RP2002076	3.72	3.72	5.1	3.35	5.58	3.63		
NT2RP2002078	13.09	13.09	105.74	73.87	88.51	76.08		
NT2RP2002079	5.76	5.76	36.34	31.87	32.66	36.54		
NT2RP2002099	4.19	4.19	5.82	4.7	6.75	6.03		
NT2RP2002105	2.66	2.66	12.25	11.41	14.04	11.23		
NT2RP2002115	1.63	1.63	5.21	1.98	3.42	1.52		
NT2RP2002124	3.66	3.66	6	4.56	5.38	3.88		
NT2RP2002137	3.99	3.99	4.83	2.21	2.1	1.76	**	-
NT2RP2002139	24.08	24.08	45.74	51.88	77.99	62.3	*	+
NT2RP2002154	1.37	1.37	4.13	3.56	2.36	3.2		
NT2RP2002155	351.63	351.63	869.83	623.53	501.61	620.68		
NT2RP2002172	1.5	1.5	3.33	2.78	3.53	5.13		
NT2RP2002185	3.29	3.29	7.65	7.3	8.56	8.12		
NT2RP2002188	1.74	1.74	5.95	4.15	4.31	4.95		
NT2RP2002192	2.9	2.9	7.6	6.65	6.42	5.83		
NT2RP2002193	5.21	5.21	5.22	4.76	4.95	5.75		
NT2RP2002208	5.96	5.96	7.31	4.7	5.67	5.14		
NT2RP2002219	2.2	2.2	1.8	2.22	3.2	2.26		
NT2RP2002231	1.72	1.72	3.1	4.11	2.76	5.76		
NT2RP2002232	2.59	2.59	5.17	3.93	4.7	6.08		
NT2RP2002235	5.62	5.62	15.07	16.26	16.18	15.18		
NT2RP2002239	37.02	37.02	67.99	72.09	67.21	63.77		
NT2RP2002252	2.64	2.64	3.66	2.63	2.76	2.94		
NT2RP2002256	4.62	4.62	15.3	11.37	16.99	12.91		
NT2RP2002257	7.01	7.01	22.77	18.65	25.09	20.6		
NT2RP2002259	1.58	1.58	13.91	9.9	12.15	10.49		
NT2RP2002264	0.6	0.6	3.14	3.2	3.12	3.92		
NT2RP2002267	3.66	3.66	8.75	8.95	8.3	11.16		
NT2RP2002270	4.26	4.26	8.23	16.09	10.47	14.71	*	+
NT2RP2002281	2.85	2.85	5.66	8.18	6.48	6.54	*	+
NT2RP2002288	4.32	4.32	6.6	5.33	5.56	4.23		

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NT2RP2002292	5.42	5.42	8.4	6.64	8.08	6.95		
NT2RP2002299	9.6	9.6	9.22	11.75	19.42	15.97	*	+
NT2RP2002304	1.37	1.37	4.78	6.99	5.08	5.52		
NT2RP2002312	1.21	1.21	2.33	3.78	5.3	3.28	*	+
NT2RP2002316	3.28	3.28	5.43	7.57	7.21	8.2	**	+
NT2RP2002325	1.95	1.95	3.46	2.79	2.22	4.95		
NT2RP2002333	2.13	2.13	3.03	3.53	4.86	5.69	*	+
NT2RP2002371	5.43	5.43	9.14	9.72	12.07	11.65	*	+
NT2RP2002373	10.65	10.65	40.1	36.72	58.84	33.58		
NT2RP2002381	4.68	4.68	2.35	2.66	3.19	3.71		
NT2RP2002385	5.71	5.71	11.84	9.95	11.34	9.47		
NT2RP2002394	0.94	0.94	1.52	1.24	0.96	1.26		
NT2RP2002408	2.7	2.7	5.08	3.89	3.12	4.29		
NT2RP2002409	3.73	3.73	10.81	10.78	7.95	8.35		
NT2RP2002424	2.98	2.98	4.22	5.84	6.22	7.85	*	+
NT2RP2002426	6.44	6.44	11.38	7.59	8.46	8.93		
NT2RP2002429	17.2	17.2	24.73	27.87	33.96	20.83		
NT2RP2002437	4.61	4.61	5.98	4.83	6.47	4.79		
NT2RP2002439	3.83	3.83	6.69	2.68	3.22	4		
NT2RP2002442	13.63	13.63	71.65	57.78	63.05	78.84		
NT2RP2002457	3.27	3.27	5.31	4.35	4.87	5.82		
NT2RP2002464	2.17	2.17	5.34	3.29	4.59	4.24		
NT2RP2002475	3.11	3.11	7.88	5.3	2.83	5.43		
NT2RP2002479	3.09	3.09	4.25	1.95	2.99	1.93		
NT2RP2002487	1.73	1.73	5.15	1.98	2.1	3.04		
NT2RP2002498	1.52	1.52	2.2	2.62	2.82	4.47		
NT2RP2002503	7.63	7.63	31.85	29.32	32.02	31.84		
NT2RP2002504	3.81	3.81	5.73	6	7.23	11.28		
NT2RP2002510	2.65	2.65	8.92	4.68	6.59	6.85		
NT2RP2002520	3.57	3.57	7.17	6.26	8.86	6.61		
NT2RP2002527	5.18	5.18	6.02	9	12.37	11.22	**	+
NT2RP2002533	3.34	3.34	6.27	4.83	6.94	5.88		
NT2RP2002537	3.22	3.22	4.02	4.09	5.91	10.08		
NT2RP2002542	4.81	4.81	4.64	5.99	5.93	9.73		
NT2RP2002546	4.31	4.31	5.85	6.5	4.91	5.24		
NT2RP2002549	4.06	4.06	9.33	7.68	10.49	11.65		
NT2RP2002564	4.11	4.11	11.18	10.67	9.21	9.29		
NT2RP2002591	2.45	2.45	7.03	3.31	4.79	5.79		
NT2RP2002595	9.67	9.67	12.41	12.06	13.39	14.79		

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NT2RP2002602	4.19	4.19	7.53	5.68	8.96	10.42		
NT2RP2002606	1.27	1.27	2.93	2.26	2.97	3.95		
NT2RP2002609	6.12	6.12	9.95	4.79	5.48	7.74		
NT2RP2002618	2.74	2.74	6.83	4.2	6.34	5.44		
NT2RP2002621	4.24	4.24	10.22	6.58	7.52	9.79		
NT2RP2002643	1.79	1.79	4.84	3.11	5.98	3.94		
NT2RP2002672	4.48	4.48	9.23	8.03	9.37	9.87		
NT2RP2002673	4.13	4.13	5.01	8	12.88	17.73	*	+
NT2RP2002674	2.4	2.4	4.06	2.78	2.37	1.84		
NT2RP2002686	2.73	2.73	4.61	3.17	5.19	6.49		
NT2RP2002688	10.73	10.73	28.07	22.34	33.34	28.71		
NT2RP2002695	2.62	2.62	7.03	5.26	4.34	5.52		
NT2RP2002701	7.29	7.29	13.37	11.85	5.18	10.04		
NT2RP2002706	3.02	3.02	5.58	6.47	8.14	6.19	*	+
NT2RP2002710	11.2	11.2	36.97	39.43	33.9	42.75		
NT2RP2002721	5.53	5.53	9.42	7.33	7.34	8.45		
NT2RP2002727	3.56	3.56	6.87	2.17	3.96	3.52		
NT2RP2002734	3.59	3.59	6.65	5.71	7.65	7.54		
NT2RP2002736	5.25	5.25	13.13	13.17	13.59	17.58		
NT2RP2002740	2	2	5.11	3.18	2.81	3.13		
NT2RP2002741	2.12	2.12	4.8	4.68	5.39	5.78		
NT2RP2002750	2.5	2.5	9.22	7.73	9.57	8.18		
NT2RP2002752	4.59	4.59	10.39	7.93	7.66	8.03		
NT2RP2002753	4.49	4.49	9.91	8.66	9.04	14.67		
NT2RP2002760	4.79	4.79	10.31	3.56	4.5	4.13		
NT2RP2002769	4.42	4.42	6.06	3.89	5.67	6.43		
NT2RP2002778	4.13	4.13	10.59	6.8	8.2	9.12		
NT2RP2002791	8.89	8.89	54.27	48.75	53.08	50.19		
NT2RP2002800	1.66	1.66	4.52	4	5.19	5.38		
NT2RP2002805	3.38	3.38	5.46	4.75	6.44	3.81		
NT2RP2002811	3.27	3.27	8.23	5.87	8.13	10.61		
NT2RP2002824	18.29	18.29	25.05	29.95	34.29	25.05		
NT2RP2002839	13.26	13.26	31.21	16.09	23.42	16.27		
NT2RP2002845	5.87	5.87	7.93	4.61	6.12	5.5		
NT2RP2002857	2.95	2.95	3.6	2.35	4.23	2.99		
NT2RP2002862	4.56	4.56	12.49	12.55	9.84	11.34		
NT2RP2002880	5.27	5.27	13.89	13.5	11.56	11.1		
NT2RP2002885	8.6	8.6	17.12	7.56	10.07	10.02		
NT2RP2002891	1.9	1.9	7.78	4.65	6.63	7.56		

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NT2RP2002907	2.95	2.95	6.91	5.95	5.5	4.9		
NT2RP2002925	5.67	5.67	6.73	10.04	11.6	8.45	*	+
NT2RP2002927	10.08	10.08	10.63	19.05	21.85	15.48	**	+
NT2RP2002928	4.32	4.32	4.56	2.65	2.34	2.51	**	-
NT2RP2002929	3.96	3.96	9.74	8.09	7.86	9.87		
NT2RP2002934	1.5	1.5	1.4	2.81	3.01	2.49	**	+
NT2RP2002939	2.96	2.96	5.09	5.15	6.71	4.91		
NT2RP2002942	2.4	2.4	5.06	4.35	5.07	10.81		
NT2RP2002954	5.41	5.41	11.46	7.21	9.1	8.65		
NT2RP2002959	8.15	8.15	12.55	13.81	16.28	16.69	*	+
NT2RP2002974	5.03	5.03	6.53	4.7	3.45	4.54		
NT2RP2002976	6.92	6.92	17.08	11.84	14.66	12.42		
NT2RP2002979	4.41	4.41	8.12	7.03	8.66	7.6		
NT2RP2002980	6.44	6.44	15.09	15.56	11	17.45		
NT2RP2002986	3.87	3.87	7.6	6.68	7.4	7.39		
NT2RP2002987	3.52	3.52	8.23	11.1	9.18	9.4	*	+
NT2RP2002988	14.96	14.96	22.92	30.07	31.87	31.36	**	+
NT2RP2002993	2.97	2.97	4.18	3.8	3.84	2.84		
NT2RP2003000	4.88	4.88	8.34	6.97	9.62	9.97		
NT2RP2003008	4.85	4.85	5.06	3.34	4.76	4.78		
NT2RP2003020	4.45	4.45	44.26	28.35	46.52	34.33		
NT2RP2003032	1.91	1.91	4.02	5.82	6.48	6.59	**	+
NT2RP2003034	4.21	4.21	13.47	13.16	11.15	16.31		
NT2RP2003042	2.15	2.15	3.81	4.57	3.65	4.92		
NT2RP2003050	2.32	2.32	3.56	2.55	2.17	1.83		
NT2RP2003060	7.27	7.27	15.51	21.53	18.91	17.46	*	+
NT2RP2003073	5.61	5.61	8.73	7.06	10.51	8.17		
NT2RP2003099	5.05	5.05	3.67	3.21	3.73	2.84		
NT2RP2003108	3.6	3.6	4.23	5.29	3.91	6.62		
NT2RP2003115	1.68	1.68	5	7.75	4.69	4.84		
NT2RP2003117	2.71	2.71	5.69	3.6	4.66	4.13		
NT2RP2003121	1.83	1.83	3.47	4.03	2.69	3.33		
NT2RP2003125	4.13	4.13	11.44	15.42	12.55	13.66	*	+
NT2RP2003127	2.36	2.36	3.94	1.53	1.66	1.75		
NT2RP2003129	3.43	3.43	7.09	6.08	6.05	5.42		
NT2RP2003137	4.49	4.49	6.14	7.58	8.4	6.46	*	+
NT2RP2003138	4.66	4.66	20.24	16.55	17.45	16.92		
NT2RP2003146	6.2	6.2	24.78	18.5	23.25	25.96		
NT2RP2003148	3.09	3.09	6.73	3.06	4.6	4.04		

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NT2RP2003150	1.45	1.45	5.71	3.98	5.2	4.3		
NT2RP2003157	6.93	6.93	34.27	34.29	31.85	32.84		
NT2RP2003158	6.3	6.3	25.32	26.87	28.69	59.31		
NT2RP2003161	2.73	2.73	3.36	2.51	2.82	6.12		
NT2RP2003164	1.96	1.96	2.1	1.28	1.87	2.46		
NT2RP2003165	2.18	2.18	5.94	3.1	3.69	4.84		
NT2RP2003177	1.63	1.63	4.37	2.79	3.03	4.42		
NT2RP2003179	1.23	1.23	4.98	4.08	3.63	7.96		
NT2RP2003194	4.04	4.04	7.2	5.73	6.29	14.77		
NT2RP2003206	1.59	1.59	4.47	1.64	3.52	1.44		
NT2RP2003210	5.06	5.06	15.15	16.14	12.93	15.9		
NT2RP2003227	1.62	1.62	3.97	2.04	3.66	6.28		
NT2RP2003228	6.57	6.57	29.53	29.56	43.94	44.24		
NT2RP2003230	3.51	3.51	7.91	4.49	8.04	8.46		
NT2RP2003231	2.22	2.22	5.59	2.46	3.23	3.83		
NT2RP2003237	2.52	2.52	4.59	4.59	6.4	6.46	*	+
NT2RP2003239	2.3	2.3	4.46	2.97	4.46	4.05		
NT2RP2003243	2.16	2.16	4.13	2.38	3.28	3.98		
NT2RP2003265	3.93	3.93	5.33	4.22	4.88	4.92		
NT2RP2003267	2.73	2.73	3.15	3.24	4.17	7.42		
NT2RP2003272	6.03	6.03	14.8	16.93	23.85	32.58	*	+
NT2RP2003277	3.85	3.85	11.29	5.53	8.39	6.39		
NT2RP2003280	3.47	3.47	9.38	7.67	7.25	6.09		
NT2RP2003286	2.18	2.18	4.23	4.13	5	9.61		
NT2RP2003293	2.98	2.98	6.9	5.66	7.05	7.94		
NT2RP2003295	4.67	4.67	8.45	8.73	12.39	6.35		
NT2RP2003297	3.43	3.43	7.57	4.32	6.89	5.28		
NT2RP2003300	20.38	20.38	32.04	45.7	53.51	48.07	**	+
NT2RP2003302	2.88	2.88	4.52	3.46	3.81	7.26		
NT2RP2003307	0.57	0.57	2.62	1.43	1.49	1.38		
NT2RP2003308	1.44	1.44	4.5	2.77	4.44	5.44		
NT2RP2003311	4.18	4.18	5.83	7.35	4.25	8.2		
NT2RP2003329	2.99	2.99	4.41	2.63	3.89	4.44		
NT2RP2003339	3.06	3.06	7.01	3.76	4.92	3.64		
NT2RP2003345	4.15	4.15	8.38	2.77	3.97	6.33		
NT2RP2003347	2.55	2.55	4.23	2.08	1.98	3.46		
NT2RP2003367	2.15	2.15	4.65	2.7	1.98	1.44		
NT2RP2003369	1.34	1.34	4.71	2.16	2.36	0.89		
NT2RP2003383	4.05	4.05	6.75	7.66	7.17	6.99		

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NT2RP2003390	9.1	9.1	17.93	16.66	14.27	12.94		
NT2RP2003391	9.39	9.39	12.9	11.96	9.91	12.84		
NT2RP2003393	4.23	4.23	6.99	6.14	5.03	9.44		
NT2RP2003394	8.67	8.67	16.21	17.56	21.75	17.23		
NT2RP2003401	4.39	4.39	5.97	3.52	3.72	2.9		
NT2RP2003403	3.42	3.42	7.64	6.62	8.55	7.79		
NT2RP2003433	3.02	3.02	15.54	13.62	13.5	13.08		
NT2RP2003445	3.2	3.2	4.74	4.08	3.5	3.93		
NT2RP2003446	2.67	2.67	6.23	5.06	6.05	4.47		
NT2RP2003456	2.04	2.04	6.57	4.26	5.89	3.81		
NT2RP2003466	3.56	3.56	20.09	17.34	25.96	23.53		
NT2RP2003469	6.2	6.2	5.65	6.19	7.53	6.33		
NT2RP2003470	5.64	5.64	6.47	5.06	6.11	6.44		
NT2RP2003471	2.72	2.72	3.88	3.22	2.78	3.38		
NT2RP2003480	7.15	7.15	20.74	19.77	19.89	21.14		
NT2RP2003495	3.99	3.99	6.03	8.07	7.24	10.72	*	+
NT2RP2003499	1.52	1.52	4.58	3.67	4.05	2.75		
NT2RP2003505	0.98	0.98	3.21	2.62	3.88	1.4		
NT2RP2003506	2.54	2.54	6.53	5.65	5.36	4.78		
NT2RP2003511	3.67	3.67	5.57	4.22	3.1	2.96		
NT2RP2003513	3.79	3.79	6.01	5.49	5.57	5.71		
NT2RP2003517	2.9	2.9	2.52	1.32	1.11	0.85	**	-
NT2RP2003522	11.08	11.08	19.77	10.55	11.42	16.52		
NT2RP2003525	5.12	5.12	14.93	12.19	10.72	11.79		
NT2RP2003533	3.36	3.36	10.44	12.12	10.72	12.94		
NT2RP2003541	6.72	6.72	11.29	12.02	13.42	11.7		
NT2RP2003543	2.48	2.48	5.96	4.17	3.55	6.54		
NT2RP2003545	2.59	2.59	4.85	2.22	3.6	1.85		
NT2RP2003559	4.92	4.92	4.81	3.97	3.84	3.37	**	-
NT2RP2003564	4.46	4.46	3.93	2.53	1.97	2.42	**	-
NT2RP2003565	4.94	4.94	50.48	41.12	48.32	37.82		
NT2RP2003567	3.51	3.51	16.65	16.25	19.43	16.05		
NT2RP2003575	4.44	4.44	18.78	19.56	22.63	20.7		
NT2RP2003576	102.12	102.12	203.44	206.62	128.42	171.89		
NT2RP2003579	11.45	11.45	26.58	38.62	39.51	39.88	*	+
NT2RP2003581	3.85	3.85	6.1	4.33	4.38	3.96		
NT2RP2003587	8.37	8.37	11.47	13.35	14.11	12.14	*	+
NT2RP2003590	7.15	7.15	9.08	11.06	13.15	14.91	*	+
NT2RP2003593	1.58	1.58	4.57	7.84	4.43	8.59		

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NT2RP2003596	4.86	4.86	10.86	14.43	13.12	17.96	*	+
NT2RP2003599	6.49	6.49	12.46	14.29	10.17	11.98		
NT2RP2003600	1.88	1.88	2.95	3.02	3.64	6.36		
NT2RP2003604	7.09	7.09	8.97	16.39	13.03	16.68	**	+
NT2RP2003629	3.72	3.72	5.25	3.11	4.56	2.38		
NT2RP2003630	4.09	4.09	6.66	4.79	6.78	3.84		
NT2RP2003643	5.49	5.49	4.88	7.15	9.8	8.51	*	+
NT2RP2003655	4.27	4.27	11.12	7.52	6.38	7.59		
NT2RP2003664	12.29	12.29	24.31	17.9	18.07	17.11		
NT2RP2003668	2.52	2.52	5.01	3.3	3.18	3.62		
NT2RP2003687	1.61	1.61	2.77	1.63	2.42	1.71		
NT2RP2003691	3.03	3.03	5.07	3.7	4.21	4.57		
NT2RP2003702	3.99	3.99	6.14	2.89	3.02	2.89		
NT2RP2003704	3.31	3.31	4.12	2.65	3.84	1.99		
NT2RP2003706	2.44	2.44	1.24	1.72	1.42	1.6		
NT2RP2003713	4.11	4.11	5.49	4.16	3.89	3.87		
NT2RP2003714	3.39	3.39	7.8	5.19	5.31	5.32		
NT2RP2003727	3.96	3.96	11.63	4.81	6.08	10.46		
NT2RP2003737	2.52	2.52	8.58	4.88	6.47	4.6		
NT2RP2003751	1.66	1.66	4.84	1.24	1.67	1.37		
NT2RP2003760	2.52	2.52	5.47	3.87	4.19	5.45		
NT2RP2003764	2.1	2.1	2.81	1.44	1.87	4.62		
NT2RP2003769	5.52	5.52	11.45	7.41	8.17	10.64		
NT2RP2003770	7.43	7.43	12.42	7.17	5.67	12.82		
NT2RP2003777	3.44	3.44	6.78	5.01	5.6	9.57		
NT2RP2003781	4.93	4.93	15.85	13.04	11.91	13.48		
NT2RP2003785	9.69	9.69	13.44	11.1	10.68	8.99		
NT2RP2003793	9.32	9.32	9.5	8.29	13.22	10.51		
NT2RP2003806	5.6	5.6	12.03	8.54	8.75	12.97		
NT2RP2003825	10.73	10.73	62.01	57.88	71.84	82.78		
NT2RP2003840	3.19	3.19	6.07	3.86	4.44	4.71		
NT2RP2003857	4.02	4.02	4.94	3.15	4.61	6.12		
NT2RP2003859	1.82	1.82	6	3.35	4.16	4.21		
NT2RP2003871	5.22	5.22	9.43	5.1	4.59	7.79		
NT2RP2003876	3.82	3.82	8.8	5.92	5.87	7.92		
NT2RP2003878	3.38	3.38	6.49	3.8	4.9	4.11		
NT2RP2003885	2.46	2.46	3.09	1.66	3.29	2.37		
NT2RP2003898	5.39	5.39	8.91	12.3	12.73	18.25	*	+
NT2RP2003902	5.09	5.09	10.78	8.24	8.23	10.42		

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NT2RP2003912	3.83	3.83	14.48	5.91	7.43	6.74		
NT2RP2003931	1.81	1.81	6.03	3.95	6.86	4.42		
NT2RP2003940	2.31	2.31	9.51	7.1	6.2	7.3		
NT2RP2003950	2.81	2.81	5.48	3.84	5.57	2.98		
NT2RP2003952	1.86	1.86	5.63	2.58	4.23	2.98		
NT2RP2003968	4.82	4.82	7.38	9.86	11.76	13.51	*	+
NT2RP2003976	5.35	5.35	9.56	12.56	12.6	13.2	*	+
NT2RP2003981	3.27	3.27	7.41	4.62	2.03	4.07		
NT2RP2003984	5.57	5.57	15.87	10.21	4.25	10.34		
NT2RP2003986	2.79	2.79	6.22	6.29	6.32	5.17		
NT2RP2003988	2.36	2.36	6.84	4.51	7.42	5		
NT2RP2004013	8.46	8.46	13.75	14.68	13.19	17		
NT2RP2004014	4.24	4.24	10.07	4.06	5.12	4.08		
NT2RP2004036	6.88	6.88	14.85	14.08	19.02	16.03		
NT2RP2004041	2.77	2.77	5.02	3.96	4.43	5.19		
NT2RP2004042	1.99	1.99	4.6	4.41	2.02	4.09		
NT2RP2004049	4.68	4.68	19.13	14.24	15.5	16.3		
NT2RP2004060	5.7	5.7	10.41	7.09	8.67	10.84		
NT2RP2004066	2.17	2.17	4.31	3.05	4.83	3.65		
NT2RP2004069	3.99	3.99	7.24	3.54	6	4.26		
NT2RP2004076	3.73	3.73	5.82	1.92	4.2	3.61		
NT2RP2004080	4.21	4.21	9.26	4.45	6.47	6.15		
NT2RP2004081	3.27	3.27	5.39	3.51	3.71	4.5		
NT2RP2004098	2.32	2.32	6.48	5.4	3.1	5.75		
NT2RP2004108	3.82	3.82	9.56	7.18	5.89	7.56		
NT2RP2004124	3.13	3.13	5.9	3.68	5.82	3.92		
NT2RP2004130	3.67	3.67	9.32	5.51	9.12	8.4		
NT2RP2004133	2.05	2.05	6.41	3.69	6.54	6.25		
NT2RP2004141	5.72	5.72	7.15	5.14	7.05	7.05		
NT2RP2004142	5.33	5.33	8.1	4.18	5.45	3.93		
NT2RP2004152	3.34	3.34	4.78	5.7	7.49	4.39		
NT2RP2004165	3.71	3.71	8.3	5.87	5.92	6.54		
NT2RP2004170	1.86	1.86	5.97	5.37	4.17	4.94		
NT2RP2004172	2.93	2.93	5.24	4.69	5.58	4.26		
NT2RP2004176	3.45	3.45	8.4	7.77	10.21	8.98		
NT2RP2004179	4.01	4.01	9.17	3.94	5.07	4.15		
NT2RP2004187	3.16	3.16	6.36	3.87	3.88	4.59		
NT2RP2004190	5.1	5.1	5.46	5.49	7.33	9.98		
NT2RP2004194	7.54	7.54	14.57	18.5	23.44	19.83	*	+

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NT2RP2004196	4.28	4.28	13.77	10.02	7.87	14.61		
NT2RP2004205	2.67	2.67	8.14	8.64	6.62	7.81		
NT2RP2004207	2.57	2.57	4.38	4.15	4.97	3.59		
NT2RP2004226	2.09	2.09	4.95	4.11	6.15	5.33		
NT2RP2004232	2.79	2.79	6.52	6	6.59	5.33		
NT2RP2004239	3.57	3.57	4.49	2.71	3.97	5.6		
NT2RP2004240	7.07	7.07	12.57	13	15.8	8.95		
NT2RP2004242	3.87	3.87	6.52	5.77	6.94	7.27		
NT2RP2004245	1.74	1.74	3.47	2.42	3.29	3.15		
NT2RP2004270	9.77	9.77	33.78	28.39	27.43	29.48		
NT2RP2004300	2	2	5.22	4.34	4.52	3.26		
NT2RP2004304	6.46	6.46	15.37	17.41	12.33	13.9		
NT2RP2004313	3.17	3.17	3.78	5.51	4.18	4.63	*	+
NT2RP2004316	3.46	3.46	5.84	4.9	4.96	4.04		
NT2RP2004321	4.71	4.71	6.06	6.79	7.43	6.29	*	+
NT2RP2004336	4.19	4.19	4.97	2.73	4.28	4.53		
NT2RP2004339	5.3	5.3	20.89	17.11	18.07	15.39		
NT2RP2004347	1.39	1.39	3.99	4.78	5	4.19		
NT2RP2004364	2.26	2.26	6.52	5.08	6.72	4.76		
NT2RP2004365	3.18	3.18	6.58	6.68	6.34	7.7		
NT2RP2004366	2.49	2.49	6.06	4.49	4.71	3.08		
NT2RP2004373	8.17	8.17	14.38	7.1	7.22	5.91		
NT2RP2004375	9.27	9.27	13.98	20.89	26.85	20.68	**	+
NT2RP2004389	5.25	5.25	5.62	5.01	6.26	5.61		
NT2RP2004392	8.88	8.88	23.7	13.04	19.48	20.89		
NT2RP2004396	1.98	1.98	6.27	6.65	4.98	6.17		
NT2RP2004399	5.24	5.24	8.12	12.56	7.74	9.52		
NT2RP2004400	2.07	2.07	3.55	2.36	3.47	2		
NT2RP2004404	15.79	15.79	46	45.56	40.89	41.74		
NT2RP2004410	16.64	16.64	24.04	27.99	33.46	32.69	*	+
NT2RP2004412	5.84	5.84	6.74	7.37	9.71	7.37		
NT2RP2004414	4.27	4.27	5.09	3.81	4.89	3.8		
NT2RP2004425	3.71	3.71	6.53	3.73	3.18	4.04		
NT2RP2004447	1.93	1.93	5.68	2.75	5.22	3.56		
NT2RP2004463	13.57	13.57	16.23	16.84	16.25	20.26		
NT2RP2004476	9.11	9.11	12.69	11.89	12.66	15.87		
NT2RP2004488	3.82	3.82	8.52	4.59	6.02	5.37		
NT2RP2004490	2.88	2.88	3.86	2.31	2.96	4.1		
NT2RP2004495	35.59	35.59	88.76	96.31	109.31	123.5	*	+

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	NT2RP2004512	4.25	4.25	7.62	5.84	6.41	7.12	
	NT2RP2004523	5.18	5.18	11.04	8.44	7.56	10.21	
	NT2RP2004524	2.19	2.19	6.33	4.97	5.32	5.56	
	NT2RP2004536	8.99	8.99	16.96	14.1	14.51	17.51	
	NT2RP2004538	8.03	8.03	24.44	20.15	25.59	22.24	
	NT2RP2004548	4.45	4.45	9.92	7.39	9.1	10.51	
	NT2RP2004551	4.95	4.95	5.62	7.17	9.98	6.21	
	NT2RP2004556	83.73	83.73	210.17	226.48	298.92	241.84	
	NT2RP2004568	5.19	5.19	11.18	6.52	9.16	9.99	
	NT2RP2004580	3.98	3.98	7.71	5.71	7.88	7.04	
	NT2RP2004585	11.28	11.28	49.82	36.69	46.91	64.56	
	NT2RP2004587	1.85	1.85	4.16	2.07	2.89	3	
	NT2RP2004594	4.56	4.56	9.24	11.47	12.21	28.18	
	NT2RP2004600	3.49	3.49	5.76	2.22	3.22	3.09	
	NT2RP2004602	4.62	4.62	6.32	6	8.49	6.26	
	NT2RP2004606	392.21	392.21	581.19	612.4	897.5	764.63	* +
	NT2RP2004614	2.92	2.92	4.73	2.69	3.63	3.81	
	NT2RP2004648	2.52	2.52	4.96	3.24	5.01	4.12	
	NT2RP2004655	5.69	5.69	10.1	8.37	6.76	9.46	
	NT2RP2004664	3.64	3.64	5.35	3.59	4.62	5.97	
	NT2RP2004670	1.98	1.98	3.81	1.98	3.71	4.27	
	NT2RP2004675	3.37	3.37	9.29	4.08	5.87	5.33	
	NT2RP2004681	3.46	3.46	7.56	5.72	8.92	7.55	
	NT2RP2004689	2.63	2.63	5.75	5.75	4.73	7.87	
	NT2RP2004709	3.93	3.93	7.79	4.46	2.89	5.25	
	NT2RP2004710	3.15	3.15	8.37	5.63	4.61	6.88	
	NT2RP2004721	1.79	1.79	5.99	3.39	4.41	2.78	
	NT2RP2004736	3.26	3.26	5.81	6.11	4.79	4.63	
	NT2RP2004743	4.94	4.94	7.96	5.94	6.67	7.36	
	NT2RP2004750	6.21	6.21	17.46	11.9	15.49	11.01	
	NT2RP2004755	11.65	11.65	19.9	14.84	22.87	19.91	
	NT2RP2004767	3.54	3.54	9	4.05	5.8	4.81	
	NT2RP2004768	3.48	3.48	29.51	18.48	18.73	19.6	
	NT2RP2004775	4.68	4.68	5.68	7.71	5.62	8.26	
	NT2RP2004791	7.23	7.23	16.58	9.33	10.24	11.68	
	NT2RP2004794	14.01	14.01	25.74	23.04	16.86	22.78	
	NT2RP2004795	5.15	5.15	7.97	6.96	5.67	11.2	
	NT2RP2004799	6.74	6.74	10.99	5.35	8.58	6.3	
	NT2RP2004802	6.35	6.35	11.79	6.1	7.62	6.24	

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NT2RP2004810	3.44	3.44	8.83	7.37	7.84	6.03		
NT2RP2004816	5.58	5.58	12.1	11.22	8.76	11.15		
NT2RP2004837	4.13	4.13	9.89	10.43	7.23	12.98		
NT2RP2004841	0.91	0.91	2.86	3.69	4.03	8.87		
NT2RP2004847	3.25	3.25	13.75	13.82	13.87	17.16		
NT2RP2004861	2.3	2.3	5.23	2.33	4.23	2.46		
NT2RP2004897	3.35	3.35	6.43	4.26	3.27	3.35		
NT2RP2004932	6.64	6.64	10.16	7.96	8.53	6.91		
NT2RP2004933	4.63	4.63	3.41	2.98	2.93	3.2	*	-
NT2RP2004936	3.69	3.69	6.41	4.56	4.42	7.53		
NT2RP2004951	2.98	2.98	10.48	5.09	5.22	19.28		
NT2RP2004959	3.13	3.13	6.61	6.43	6.26	6.5		
NT2RP2004961	2.1	2.1	4.79	4.89	6.49	5.44		
NT2RP2004962	2.27	2.27	7.28	4.5	5.57	4.47		
NT2RP2004966	2.26	2.26	6.07	4.1	4.1	2.97		
NT2RP2004967	3.87	3.87	6.16	4.07	4.82	3.26		
NT2RP2004974	5.27	5.27	5.43	3.59	3.47	3.89	**	-
NT2RP2004978	2.68	2.68	5.26	4.17	6.39	5.09		
NT2RP2004982	0.57	0.57	1.82	2.2	1.94	1.72		
NT2RP2004985	16.03	16.03	45.34	44.65	46.12	54.4		
NT2RP2004999	2.21	2.21	5.64	4.27	8.86	10.34		
NT2RP2005000	3.62	3.62	5.76	4.33	4.76	4.65		
NT2RP2005001	5.41	5.41	7.91	8.26	9.15	8.32		
NT2RP2005003	3.8	3.8	7.2	6.11	7.91	6.2		
NT2RP2005012	6.61	6.61	20.14	18.41	20.96	17.87		
NT2RP2005018	1.9	1.9	4.24	3.29	2.24	2.91		
NT2RP2005020	6.12	6.12	23.58	19.97	19.94	22.96		
NT2RP2005022	1.65	1.65	5.01	5.09	7.24	4.77		
NT2RP2005027	5.96	5.96	38.61	42.51	40.08	33.77		
NT2RP2005031	1.54	1.54	4.99	3.94	4.53	3.92		
NT2RP2005035	44.19	44.19	94.82	116.52	107.36	106.69	*	+
NT2RP2005037	4.28	4.28	5.87	7.91	10.26	7.09	*	+
NT2RP2005038	4.86	4.86	4.84	1.85	2.29	3.1	**	-
NT2RP2005048	9.92	9.92	30.91	30.14	33.38	32.48		
NT2RP2005069	16.01	16.01	34.88	21.99	20.63	27.64		
NT2RP2005073	7.36	7.36	30.35	29.36	28.24	30.33		
NT2RP2005097	2.39	2.39	5.6	5.27	5.2	4.6		
NT2RP2005108	1.76	1.76	3.95	2.84	4.21	7.12		
NT2RP2005116	3.53	3.53	5.96	6.27	5.42	5.89		

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NT2RP2005126	5.88	5.88	8.31	8.9	14.96	8.51		
NT2RP2005135	5.08	5.08	5.22	4.65	6.59	5.47		
NT2RP2005139	1.94	1.94	2.77	1.87	1.81	2.45		
NT2RP2005140	3.82	3.82	4.86	12.39	6.72	8.55	*	+
NT2RP2005144	4.04	4.04	6.31	6.69	5.97	9.7		
NT2RP2005147	2.23	2.23	5.49	5.61	6.15	6.25		
NT2RP2005148	2.86	2.86	5.63	3.83	6.65	4.83		
NT2RP2005159	3.92	3.92	5.6	4.94	6.38	7.41		
NT2RP2005162	3.23	3.23	5.56	4.57	5.4	4.21		
NT2RP2005163	9.15	9.15	20.61	24.53	28.92	23.77	*	+
NT2RP2005168	2.87	2.87	6.14	5.24	4.79	4.88		
NT2RP2005181	2.64	2.64	5.42	3.4	2.11	1.98		
NT2RP2005204	5.4	5.4	7.81	9.08	11.94	11.81	*	+
NT2RP2005219	4.61	4.61	9.64	7.09	10.28	8.7		
NT2RP2005227	3.59	3.59	10.43	7.55	5.36	9.97		
NT2RP2005237	26.49	26.49	94.81	86.96	105.8	93.92		
NT2RP2005239	2.24	2.24	6.07	2.62	4.27	4.34		
NT2RP2005247	10.63	10.63	37.59	35.58	46.1	46.95		
NT2RP2005254	4.35	4.35	9.14	5.7	6.44	6.93		
NT2RP2005270	9.06	9.06	17.44	10.82	9.28	17.11		
NT2RP2005276	7.19	7.19	11.53	10.88	11.68	15.71		
NT2RP2005287	7.98	7.98	11.97	8.37	7.7	13.36		
NT2RP2005288	2.51	2.51	5.14	2.89	5.59	5.22		
NT2RP2005289	4.26	4.26	8.48	6.68	9.08	7.49		
NT2RP2005293	5	5	6.93	13.68	14.37	15.66	**	+
NT2RP2005315	5.79	5.79	10.64	8.04	12.95	16.68		
NT2RP2005322	5.05	5.05	15.42	18.91	11.33	22.43		
NT2RP2005325	8.45	8.45	18.4	15.57	13.63	20.01		
NT2RP2005336	1.71	1.71	6.68	4.18	5.74	5.3		
NT2RP2005343	2.44	2.44	7.48	3.91	4.11	5.89		
NT2RP2005344	3.39	3.39	4.83	2.37	2.67	3.32		
NT2RP2005347	3.14	3.14	3.61	3.34	2.96	3.53		
NT2RP2005354	6.49	6.49	11.79	10.37	13	11.38		
NT2RP2005358	35.87	35.87	109.04	101.37	134.72	117.96		
NT2RP2005360	2.93	2.93	5	3.59	4.97	3.84		
NT2RP2005378	5.27	5.27	13.12	7.54	8.7	13.93		
NT2RP2005391	3.06	3.06	5.41	4.21	6.76	7.72		
NT2RP2005393	1.61	1.61	6.34	4.86	6.16	4.07		
NT2RP2005407	2.59	2.59	5.71	4.28	5.65	4.64		

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NT2RP2005419	2.65	2.65	9.05	6.37	8.5	6.77		
NT2RP2005425	5.63	5.63	18.38	15.27	18.89	15.46		
NT2RP2005429	3.23	3.23	5.85	5.41	6.65	5.64		
NT2RP2005436	4.65	4.65	10.5	7.02	4.28	4.97		
NT2RP2005441	2.28	2.28	5.62	3.36	3.77	5.79		
NT2RP2005442	24.92	24.92	40.66	34.62	25.56	41.66		
NT2RP2005444	10.72	10.72	19.24	21.92	21.07	25.56	*	+
NT2RP2005453	2.79	2.79	7.44	2.63	4.09	3.15		
NT2RP2005457	15.12	15.12	23.21	28.69	37.38	31.61	*	+
NT2RP2005458	2.47	2.47	5.27	3.55	4.16	4.95		
NT2RP2005463	7.73	7.73	15.23	15.65	22.11	25.05	*	+
NT2RP2005464	5.96	5.96	11.91	9.22	4.67	10.35		
NT2RP2005465	1.81	1.81	6.69	3.86	3.75	3.74		
NT2RP2005472	10.98	10.98	32.59	28.21	27.9	25.85		
NT2RP2005476	5.01	5.01	8.99	7.01	6.98	6.08		
NT2RP2005490	7.51	7.51	21.09	18.18	25.55	23.45		
NT2RP2005491	4.99	4.99	12.47	8.63	10.12	8.78		
NT2RP2005495	3.56	3.56	5.77	3.38	4.55	4.3		
NT2RP2005496	4.84	4.84	18.25	11.3	13.16	11.28		
NT2RP2005498	2.92	2.92	7.45	5.18	5.03	4.98		
NT2RP2005501	2.04	2.04	5.54	3.12	4.34	2.46		
NT2RP2005506	124.3	124.3	217.82	139.27	121.83	104.81		
NT2RP2005509	6.97	6.97	10.45	11.4	9.61	15.73		
NT2RP2005514	3.93	3.93	6	4.06	7.05	4.39		
NT2RP2005520	14.95	14.95	32.39	27.11	39.97	33.03		
NT2RP2005525	6.19	6.19	7.01	7.81	7.68	4.79		
NT2RP2005531	2.18	2.18	3.33	1.67	2.12	1.9		
NT2RP2005535	4.66	4.66	9.09	9.34	7.79	8.91		
NT2RP2005539	3.39	3.39	6.22	6.43	5.84	7.45		
NT2RP2005540	3.2	3.2	7.15	4.79	5.58	6.59		
NT2RP2005541	21.25	21.25	39.57	25.85	38.31	39.61		
NT2RP2005549	2.69	2.69	7.66	6.72	4.85	7.11		
NT2RP2005555	7.97	7.97	10.1	14.96	16.19	15.37	**	+
NT2RP2005557	4.89	4.89	8.47	4.03	6.52	6.26		
NT2RP2005581	3.93	3.93	9.61	6.32	7.95	6.89		
NT2RP2005586	1.56	1.56	3.18	3.21	2.92	4.74		
NT2RP2005597	2.77	2.77	2.93	2.98	4.1	3.84		
NT2RP2005600	1.81	1.81	3.71	4.03	4.29	4.44	*	+
NT2RP2005605	4.93	4.93	14.29	13.17	15.14	15.75		

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NT2RP2005614	3.06	3.06	5.62	3.68	4.11	2.45		
NT2RP2005620	3.47	3.47	6.26	3.6	3.92	3.11		
NT2RP2005622	6.14	6.14	5.07	6.21	7.43	4.61		
NT2RP2005632	5.72	5.72	10.95	11.57	10.42	14.89		
NT2RP2005635	2.22	2.22	19.06	18.14	23.77	18.14		
NT2RP2005637	1.53	1.53	8	3.73	3.71	4.14		
NT2RP2005640	1.72	1.72	7.22	7.49	8.73	6.06		
NT2RP2005645	4.68	4.68	11.8	10.61	11.47	9.67		
NT2RP2005651	3.45	3.45	7.88	7.64	6.78	10.15		
NT2RP2005654	4.08	4.08	4.14	3.02	2.52	3.8		
NT2RP2005666	4.91	4.91	5.27	4.34	7.7	4.74		
NT2RP2005669	7.15	7.15	7.95	7.05	11.14	8.21		
NT2RP2005670	2.35	2.35	6.91	7.77	5.04	5.2		
NT2RP2005671	3.12	3.12	7.83	10.77	8.9	9.78	*	+
NT2RP2005675	7.32	7.32	37.84	34.46	40.94	40.02		
NT2RP2005683	2.56	2.56	7.01	7.16	5.19	7.16		
NT2RP2005690	2.84	2.84	4.48	2.82	3.74	3.4		
NT2RP2005694	4.07	4.07	5.49	3.77	6.26	3.54		
NT2RP2005701	5.97	5.97	8.82	10.39	10.35	9.52	*	+
NT2RP2005712	5.67	5.67	5.28	4.83	7.94	6.33		
NT2RP2005719	1.86	1.86	3.26	4.42	3.8	3.76	*	+
NT2RP2005722	4.16	4.16	11.13	13.39	15.7	15.94	*	+
NT2RP2005723	2.71	2.71	4.2	3.65	4.58	3.67		
NT2RP2005726	2.55	2.55	4.13	2.86	4.01	3.22		
NT2RP2005729	4.64	4.64	9.94	10.21	10.7	10.62		
NT2RP2005731	3.05	3.05	3.39	2.51	2.16	1.27	*	-
NT2RP2005732	9.41	9.41	57.73	48.37	75.21	41.64		
NT2RP2005737	10.75	10.75	22.28	27.16	25.02	17.59		
NT2RP2005741	3.03	3.03	5.35	3.68	3.31	3.37		
NT2RP2005748	1.86	1.86	5.94	3.8	3.72	2.95		
NT2RP2005752	2.46	2.46	5.55	3.27	4.37	3.8		
NT2RP2005753	8.45	8.45	14.76	11.12	11.69	14.45		
NT2RP2005763	3	3	8.03	4.22	4.77	5		
NT2RP2005767	3.72	3.72	7.79	5.55	6.75	6.29		
NT2RP2005773	8.11	8.11	10.02	10.6	11.59	13.37	*	+
NT2RP2005774	4.25	4.25	12.72	6.86	12.24	14.61		
NT2RP2005775	3.75	3.75	7.2	3.35	4.83	5.63		
NT2RP2005781	5.11	5.11	9.88	9.82	7.19	12.94		
NT2RP2005784	5.41	5.41	11.51	7.68	12.12	14.06		

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NT2RP2005789	3.98	3.98	11.24	7.89	9.52	8.86		
NT2RP2005799	2.45	2.45	6.35	2.64	4.67	3.7		
NT2RP2005804	9.01	9.01	25	27.85	27.32	30.57		
NT2RP2005812	2.63	2.63	4.83	2.9	3.89	5.21		
NT2RP2005815	2.48	2.48	3.15	2.38	3.21	5.2		
NT2RP2005835	5.99	5.99	11.26	7.13	13.74	11.69		
NT2RP2005841	2.32	2.32	10.04	4.89	7.43	11.23		
NT2RP2005853	1.29	1.29	4.44	2.71	4.6	4.96		
NT2RP2005857	7.37	7.37	9.87	13.46	7.93	20.27		
NT2RP2005859	2.76	2.76	5	2.91	6.14	4.78		
NT2RP2005860	1.41	1.41	3.54	1.45	1.89	2.22		
NT2RP2005863	3.03	3.03	6.55	10.76	18.29	15.94	*	+
NT2RP2005868	3.86	3.86	5.85	5.1	6.3	7.77		
NT2RP2005876	5.7	5.7	12.31	7.84	8.29	8.2		
NT2RP2005878	2.26	2.26	8.44	5.25	4.95	6.32		
NT2RP2005883	13.54	13.54	21.06	23.75	9.57	28.09		
NT2RP2005886	7.18	7.18	50.05	51.13	62.09	50.14		
NT2RP2005887	3.76	3.76	6.51	4.74	8.05	4.81		
NT2RP2005890	4.17	4.17	9.77	11.87	17.13	12.15	*	+
NT2RP2005901	3.19	3.19	5.69	3.91	6.18	5.14		
NT2RP2005902	3.17	3.17	4.33	4.78	4.77	6.25		
NT2RP2005908	3.09	3.09	7.86	4.89	3.7	6.34		
NT2RP2005927	1.77	1.77	2.66	2.25	4.36	3.07		
NT2RP2005933	2.5	2.5	5.59	6.4	4.77	6.42		
NT2RP2005941	2.09	2.09	5.2	3.31	4.41	3.9		
NT2RP2005942	4	4	6.86	3.08	4.59	4.64		
NT2RP2005946	4.63	4.63	9.49	5.33	7.06	6.24		
NT2RP2005970	5.44	5.44	14	16.16	22.05	18.9	*	+
NT2RP2005980	3.71	3.71	5.25	2.69	3.46	2.37		
NT2RP2005994	2.99	2.99	6.76	4.28	3.28	5.14		
NT2RP2006004	1.31	1.31	2.89	2.07	6.09	2.58		
NT2RP2006013	1.38	1.38	4.91	3.1	5.07	4.92		
NT2RP2006023	8.37	8.37	17.77	20	21.43	21.14	*	+
NT2RP2006028	5.03	5.03	10.23	7.47	9.89	9.71		
NT2RP2006038	4.67	4.67	5.86	2.79	5.4	1.09		
NT2RP2006042	8.3	8.3	7.22	6.63	5.89	6.3	*	-
NT2RP2006043	5.65	5.65	7.59	7.6	10.99	8.29		
NT2RP2006052	1.48	1.48	4.48	4.13	3.12	4.54		
NT2RP2006057	3.73	3.73	6.23	5.69	3.83	4.95		

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NT2RP2006064	4.16	4.16	7.73	5.86	6.81	9.08		
NT2RP2006068	2.76	2.76	6.75	6.8	7.81	5.81		
NT2RP2006069	1.46	1.46	4.94	3.56	3.95	3.3		
NT2RP2006071	8.37	8.37	7.8	9.28	10.48	9.11	*	+
NT2RP2006090	6.62	6.62	5.78	3.27	3.55	3.64	**	−
NT2RP2006092	3.78	3.78	8.3	6.18	8.04	7.07		
NT2RP2006097	14.05	14.05	40.38	31.2	25.81	40.02		
NT2RP2006098	1.94	1.94	4.27	4.52	4.61	7.65		
NT2RP2006099	3.84	3.84	11.02	10.65	10.99	13.34		
NT2RP2006100	2.87	2.87	5.78	3.63	7.31	5.19		
NT2RP2006103	2.39	2.39	5.54	2.6	3.93	1.71		
NT2RP2006106	6.48	6.48	21.51	18.05	24.81	22.3		
NT2RP2006127	3.17	3.17	4.92	1.62	1.26	1.21	*	−
NT2RP2006134	4.25	4.25	4.41	6.08	6.7	5.47	**	+
NT2RP2006141	3.91	3.91	7.94	7.45	6.04	9.08		
NT2RP2006166	3.1	3.1	10.65	9.01	8.94	7.85		
NT2RP2006176	2.15	2.15	4.26	3.95	5.73	4.69		
NT2RP2006181	1.68	1.68	2.84	3.21	3.14	2.45		
NT2RP2006184	8.85	8.85	17.16	20.8	19.95	17.1		
NT2RP2006186	3.01	3.01	4.57	2.77	2.29	4.33		
NT2RP2006196	5.24	5.24	7.21	5.25	5.23	4.16		
NT2RP2006199	5.06	5.06	4.38	3.81	3.65	3.64	**	−
NT2RP2006200	0.87	0.87	3.43	4.37	4.52	2.17		
NT2RP2006210	20.08	20.08	59.85	75.37	70.55	96.59	*	+
NT2RP2006219	2.88	2.88	6.26	5.97	5.11	7.36		
NT2RP2006224	3.7	3.7	7.55	9	7.7	8.93		
NT2RP2006237	1.97	1.97	4.79	3.45	2.74	4.14		
NT2RP2006238	3.9	3.9	6.33	4.2	4.69	3.93		
NT2RP2006258	4.5	4.5	6.73	3.07	4.27	4.39		
NT2RP2006261	7.32	7.32	3.98	2.04	3.19	7.69		
NT2RP2006269	4.11	4.11	7.96	9.52	5.46	9.06		
NT2RP2006275	3.67	3.67	30.36	23.46	35.36	25.14		
NT2RP2006282	3.16	3.16	8.89	8.85	8.4	7.05		
NT2RP2006302	5.69	5.69	12.68	13.12	12.4	11.87		
NT2RP2006312	4.88	4.88	8.22	8.47	9.13	9.8		
NT2RP2006320	4.27	4.27	9.87	6.42	9.32	9.69		
NT2RP2006321	3.27	3.27	4.23	2.79	4.99	4.13		
NT2RP2006323	4.1	4.1	2.59	2.39	3.6	1.83		
NT2RP2006333	0.67	0.67	1.82	1.7	1.04	1.17		

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NT2RP2006334	2.24	2.24	4.02	4.57	2.72	3.54	
NT2RP2006338	2.4	2.4	5.26	4.73	5.11	4.04	
NT2RP2006339	2.24	2.24	2.94	2.47	1.93	2.06	
NT2RP2006355	3.61	3.61	4.59	3.14	3.39	2.22	
NT2RP2006365	3.3	3.3	4.44	2.42	2.6	1.3	*
NT2RP2006374	16.34	16.34	111.62	108.73	174.7	73.65	
NT2RP2006393	4.93	4.93	7.68	7.38	8	6.95	
NT2RP2006394	8.59	8.59	17.91	11.3	11.18	15.38	
NT2RP2006400	2.25	2.25	4.51	2.08	3.58	1.95	
NT2RP2006411	27.71	27.71	42.11	23.61	17.25	37.31	
NT2RP2006429	2.22	2.22	7.3	2.82	5.3	2.21	
NT2RP2006435	1.46	1.46	5.29	1.76	2.65	1.98	
NT2RP2006436	2.33	2.33	6.43	4.33	5.28	3.75	
NT2RP2006441	4.69	4.69	8.19	7.76	8.89	8.37	
NT2RP2006447	2.41	2.41	4.78	3.18	2.63	3.87	
NT2RP2006454	2.58	2.58	5.38	4.39	3.37	4.03	
NT2RP2006455	3.79	3.79	7.14	2.91	4.62	9.23	
NT2RP2006456	1.96	1.96	5.99	2.51	4.49	3.17	
NT2RP2006464	5.44	5.44	8.28	4.47	8.85	7.9	
NT2RP2006467	4.17	4.17	10	8.56	12.47	12.58	
NT2RP2006472	5.05	5.05	6.84	7.24	6.92	7.37	
NT2RP2006474	4.69	4.69	16.3	18.19	32.31	21.3	
NT2RP2006475	2.5	2.5	9.54	6.14	6.86	7.66	
NT2RP2006476	5.34	5.34	14.94	7.62	13.82	17.24	
NT2RP2006501	2.44	2.44	7.28	4.6	7.45	7.74	
NT2RP2006512	10.25	10.25	19.79	16.72	7.89	29.01	
NT2RP2006526	2.09	2.09	5.19	2.24	2.78	2.31	
NT2RP2006527	3.61	3.61	7.05	4.56	6.14	6.46	
NT2RP2006534	2.24	2.24	4.49	2.08	2.95	2.73	
NT2RP2006537	6.08	6.08	15.7	11.72	17.73	12.82	
NT2RP2006543	7.83	7.83	14.8	6.52	5.4	6.88	
NT2RP2006554	1.33	1.33	3.71	1.79	3.76	2.2	
NT2RP2006565	3.78	3.78	8.91	5.79	8.42	7.55	
NT2RP2006571	1.38	1.38	3.88	2.77	4.01	2.29	
NT2RP2006573	2.1	2.1	4.02	3.05	3.6	2.41	
NT2RP2006598	2.25	2.25	7.04	4.34	6.56	4.78	
NT2RP2006601	24.92	24.92	35.13	38.45	45.47	31.69	
NT2RP3000002	5.04	5.04	6.09	4.7	5.04	8.18	
NT2RP3000011	1.82	1.82	5.9	2.59	1.85	2.22	

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NT2RP3000014	3.29	3.29	7.66	4.22	3.06	4.95		
NT2RP3000016	3.42	3.42	7	5.29	6.56	6.11		
NT2RP3000022	1.71	1.71	3.93	1.72	4.68	0.59		
NT2RP3000024	3.74	3.74	7.03	4.31	4.92	4.06		
NT2RP3000031	4.66	4.66	8.66	4	6.75	4.86		
NT2RP3000034	3.76	3.76	6.24	4.44	7.13	3.23		
NT2RP3000037	2.76	2.76	6.5	9.41	13.44	11.06	*	+
NT2RP3000040	2.04	2.04	5.96	3.21	3.46	3.56		
NT2RP3000041	2.15	2.15	7.35	3.71	3.01	3.16		
NT2RP3000046	1.95	1.95	4.42	3.67	7.11	3.84		
NT2RP3000047	3.25	3.25	5.55	5.85	6.2	5.94		
NT2RP3000049	2.54	2.54	6.94	5.26	7.78	3.58		
NT2RP3000050	4.99	4.99	9.03	3.76	8.5	6.22		
NT2RP3000051	5.99	5.99	10.69	8.51	11.19	9.72		
NT2RP3000054	4.31	4.31	6.5	4.38	5.35	3.22		
NT2RP3000055	1.98	1.98	4.76	3.81	2.67	3.96		
NT2RP3000056	2.87	2.87	7.09	5.59	3.32	3.91		
NT2RP3000059	2.54	2.54	5.1	1.89	4.07	1.6		
NT2RP3000063	2.18	2.18	5.51	3.34	5.19	2.27		
NT2RP3000068	3.76	3.76	24.22	25.83	37.88	23.13		
NT2RP3000069	17.44	17.44	20.58	22	28.87	18.2		
NT2RP3000072	5.9	5.9	6.18	4.96	5.39	4.19	*	-
NT2RP3000080	4.38	4.38	6.72	3.78	5.28	3.93		
NT2RP3000085	1.9	1.9	4.84	5.13	4.66	5.5		
NT2RP3000087	3.77	3.77	9.1	6.22	5.61	6		
NT2RP3000092	1.92	1.92	3.6	2.72	3.2	2.52		
NT2RP3000109	1.74	1.74	5.05	5.63	7.94	4.24		
NT2RP3000119	4.66	4.66	14.27	11.29	13.7	14.28		
NT2RP3000125	3.02	3.02	5.56	3.42	4.53	2		
NT2RP3000131	7.84	7.84	14.37	16.23	19.96	12.93		
NT2RP3000134	5.96	5.96	9.01	6.61	7.25	6.46		
NT2RP3000137	3.88	3.88	6.48	5.58	6.3	6.11		
NT2RP3000142	2.87	2.87	7.77	7.28	5.03	5.31		
NT2RP3000148	1.84	1.84	6.28	4.9	5.04	5.34		
NT2RP3000149	2.51	2.51	6.97	6.14	7.77	8.24		
NT2RP3000163	2.16	2.16	6.17	3.27	3.9	2.5		
NT2RP3000168	5.53	5.53	14.55	12.8	11.65	11.73		
NT2RP3000169	3.74	3.74	6.01	6.03	8.47	5.72		
NT2RP3000171	10.86	10.86	16.71	28.33	38.98	25.93	*	+

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NT2RP3000172	0.86	0.86	1.53	1.66	1.2	1.46		
NT2RP3000186	4.32	4.32	10.6	19.18	15.43	15.82	*	+
NT2RP3000197	1.22	1.22	3.66	4.03	4.29	3.39		
NT2RP3000201	2.4	2.4	7.2	10.49	8.4	7.88		
NT2RP3000204	2.16	2.16	4.44	3.88	4.1	4.25		
NT2RP3000207	2.87	2.87	4.71	3	2.6	2.45		
NT2RP3000216	5.38	5.38	10.1	5.87	9.5	5.73		
NT2RP3000220	5.14	5.14	5.66	3.68	5.69	2.92		
NT2RP3000221	2.18	2.18	5.45	6.26	6.63	5.93		
NT2RP3000232	2.7	2.7	8.01	7.1	5.52	5.92		
NT2RP3000233	1.55	1.55	6.01	6.9	5.91	4.06		
NT2RP3000234	3.23	3.23	9.09	12.89	10.4	11.41	*	+
NT2RP3000235	1.57	1.57	3.3	2.35	2.92	1.38		
NT2RP3000239	4.61	4.61	11.11	9.51	9.71	14.92		
NT2RP3000247	3.25	3.25	5.82	2.92	4.04	1.96		
NT2RP3000251	6.11	6.11	6.52	5.22	5.82	3.25		
NT2RP3000252	3.73	3.73	7.99	7.61	8.53	8.4		
NT2RP3000255	2.18	2.18	2.96	3.26	3.13	1.97		
NT2RP3000262	6.72	6.72	9.43	11.67	7.95	9.13		
NT2RP3000266	6.47	6.47	15.5	13.38	10.83	12.64		
NT2RP3000267	2.71	2.71	4.04	2.9	2.64	3.03		
NT2RP3000271	4.38	4.38	5.57	5.11	4.84	3.72		
NT2RP3000278	7.84	7.84	56.85	48.55	82.07	42.57		
NT2RP3000281	4.94	4.94	10.72	8.19	8.22	7.27		
NT2RP3000292	5.63	5.63	14.1	9.17	6.77	6.93		
NT2RP3000299	2.31	2.31	4.92	3.73	4.89	4.98		
NT2RP3000304	2.15	2.15	3.48	2.85	3.36	1.64		
NT2RP3000310	7.24	7.24	24.22	18.94	23.07	19.88		
NT2RP3000312	2.99	2.99	8.16	3.31	5.25	3.87		
NT2RP3000320	7.06	7.06	6.17	5.25	4.74	4.74	**	-
NT2RP3000322	11.05	11.05	18.76	32.59	45.13	46.95	**	+
NT2RP3000324	6.91	6.91	46.42	36.64	43.53	39.68		
NT2RP3000326	1.95	1.95	6.17	4.02	5.75	3.53		
NT2RP3000329	2.5	2.5	5.96	4.97	8.84	5.9		
NT2RP3000330	4.1	4.1	6.18	4.62	5.53	6.12		
NT2RP3000333	3.23	3.23	7.45	4.36	5.28	4.52		
NT2RP3000341	8.8	8.8	12.85	14.81	18.59	14.41	*	+
NT2RP3000344	2.73	2.73	3.75	2.69	3.54	2.29		
NT2RP3000345	3.09	3.09	3.57	1.65	1.97	2.66	*	-

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NT2RP3000348	444.59	444.59	802.63	824.621016.01		909.68		
NT2RP3000350	4.25	4.25	10.34	4.57	9.28	6.4		
NT2RP3000359	9.53	9.53	24.44	8.54	11.36	16.62		
NT2RP3000361	7.5	7.5	11.12	7.89	7.81	8.95		
NT2RP3000366	7.38	7.38	14.27	9.52	11.84	16.13		
NT2RP3000378	2.67	2.67	5.75	3.92	4.78	2.47		
NT2RP3000384	5.42	5.42	10.88	9.52	13.1	9.28		
NT2RP3000389	12.54	12.54	21.49	23.95	35.02	27.32	*	+
NT2RP3000393	3.74	3.74	6.16	5.03	4.53	4.77		
NT2RP3000395	110.27	110.27	212	108.33	38.18	148.45		
NT2RP3000397	2.83	2.83	5.28	2.51	5.26	3.31		
NT2RP3000398	3.39	3.39	10.12	11.46	11.18	12.26		
NT2RP3000403	3.22	3.22	9.39	10.1	8.2	8.44		
NT2RP3000418	3.4	3.4	10.22	7.12	11.08	13.42		
NT2RP3000424	2.86	2.86	9.43	6.25	9.52	6.86		
NT2RP3000427	4.65	4.65	9.05	11.55	13.43	12.35	*	+
NT2RP3000431	2.05	2.05	4.93	3.43	3.26	3.93		
NT2RP3000433	2.63	2.63	8.65	5.65	7.09	6.65		
NT2RP3000436	11.39	11.39	20.93	18.76	9.35	18.86		
NT2RP3000439	1.4	1.4	3.61	2.54	3.56	2		
NT2RP3000441	3.88	3.88	7.4	7.56	7.92	6.39		
NT2RP3000444	3.31	3.31	7.29	2.36	3.25	2.2		
NT2RP3000448	4.45	4.45	10.15	4.05	6.54	3.93		
NT2RP3000449	2.84	2.84	4.59	3.1	3.94	2.93		
NT2RP3000451	1.76	1.76	5.12	3.7	5	2.96		
NT2RP3000456	1.69	1.69	5.48	4.23	6.67	4.21		
NT2RP3000460	18.87	18.87	36.67	24.52	25.24	26.25		
NT2RP3000471	3.14	3.14	6.49	2.74	4.98	5.84		
NT2RP3000477	19.96	19.96	23.67	28.98	17.78	32.78		
NT2RP3000478	5.86	5.86	8.95	5.21	8.98	2.6		
NT2RP3000481	5.48	5.48	5.76	2.76	3.61	1.52	**	-
NT2RP3000484	3.51	3.51	4.26	2.32	2.55	1.76	*	-
NT2RP3000487	1.77	1.77	7.4	5.07	4.03	4.97		
NT2RP3000512	3.29	3.29	17.7	15.17	15.9	14.52		
NT2RP3000523	13.05	13.05	30.74	31.75	27.83	34.4		
NT2RP3000526	3.07	3.07	7.38	5.18	6.31	4.64		
NT2RP3000527	2.83	2.83	6.5	3.76	7.25	5.03		
NT2RP3000531	2.9	2.9	7.71	5.11	5.51	4.69		
NT2RP3000532	5.74	5.74	5.6	5.75	8.39	4.26		

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NT2RP3000542	6.23	6.23	8.1	7.21	7.3	6.39		
NT2RP3000554	8.81	8.81	15.22	13.78	10.56	14.95		
NT2RP3000561	1.21	1.21	3.51	3.11	2.76	2.25		
NT2RP3000562	1.84	1.84	3.5	3.7	3.87	3.23		
NT2RP3000578	1.56	1.56	2.54	2.54	3.37	2.36		
NT2RP3000582	1.26	1.26	4.66	2.24	2.52	0.41		
NT2RP3000584	2.82	2.82	6.52	3.2	2.5	2.02		
NT2RP3000586	4.08	4.08	4.59	3.28	3.9	2.87		
NT2RP3000590	5.69	5.69	4.61	3.78	4.35	2.57		
NT2RP3000592	1.8	1.8	2.99	2.97	2.75	3.15		
NT2RP3000596	2.27	2.27	4.89	4.5	3.33	3.03		
NT2RP3000599	1.67	1.67	3.07	3.88	4.98	3.82	*	+
NT2RP3000603	6.09	6.09	39.25	40.43	44.88	35.89		
NT2RP3000605	2.84	2.84	6.66	4.56	4.23	2.56		
NT2RP3000607	5.35	5.35	7.59	5.74	8.46	7.55		
NT2RP3000616	3.26	3.26	5.45	2.56	2.38	1.21		
NT2RP3000621	5.18	5.18	8.48	10.28	10.29	6.01		
NT2RP3000622	2.36	2.36	8.76	5.85	6.21	4.72		
NT2RP3000624	1.53	1.53	3.19	3.97	3.06	2.78		
NT2RP3000628	2.44	2.44	8.04	10.27	7.85	5.58		
NT2RP3000631	4.71	4.71	14.95	22.82	16.45	14.2		
NT2RP3000632	2.35	2.35	5.5	7.78	8.91	5.91	*	+
NT2RP3000638	6.95	6.95	17.93	11.8	11.6	9.97		
NT2RP3000644	25.72	25.72	48.41	57.98	72.01	52.49	*	+
NT2RP3000645	5.85	5.85	10.48	9.84	12.55	8.43		
NT2RP3000652	3.39	3.39	5.34	6.22	5.9	7.74	*	+
NT2RP3000658	2.26	2.26	5.01	6.16	4.24	4.86		
NT2RP3000660	2.34	2.34	6.25	6.98	6.91	5.14		
NT2RP3000661	1.98	1.98	4.49	4.06	3.87	3.1		
NT2RP3000665	4.79	4.79	12.26	11.83	11.92	7		
NT2RP3000676	4.46	4.46	7.55	6.65	7.81	5.42		
NT2RP3000677	2.87	2.87	4.13	2.44	3.07	1.54		
NT2RP3000681	19.85	19.85	30.12	32.94	41.51	34.34	*	+
NT2RP3000683	2.68	2.68	9.67	6.69	7.09	6.69		
NT2RP3000685	1.7	1.7	2.5	3.63	2.36	3.44		
NT2RP3000690	2.77	2.77	3.29	3.82	3.75	2.72		
NT2RP3000698	10	10	22.49	25.66	17.08	27.43		
NT2RP3000708	3.45	3.45	5.5	8.17	9.22	8.56	**	+
NT2RP3000719	2.83	2.83	2.83	1.16	1.7	1.91	**	-

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NT2RP3000721	5.63	5.63	24.61	23.43	39.76	21.55		
NT2RP3000728	3.33	3.33	2.57	1.4	1.64	1.05	**	-
NT2RP3000730	2.06	2.06	5.04	2.76	4.23	1.86		
NT2RP3000733	2.87	2.87	6.32	3.48	4.47	4.25		
NT2RP3000735	1.74	1.74	4.22	1.81	2.22	1.26		
NT2RP3000736	2.71	2.71	6.35	3.29	5.05	3.65		
NT2RP3000739	13.76	13.76	12.16	18.05	9.37	20.19		
NT2RP3000742	3.89	3.89	10.06	4.54	4.97	4.43		
NT2RP3000753	2.29	2.29	3.9	2.17	2.65	6.3		
NT2RP3000759	9.07	9.07	15.99	11.11	17.14	23.05		
NT2RP3000789	1.58	1.58	5.76	4.89	4.23	3.69		
NT2RP3000815	1.91	1.91	5.92	4.49	5.57	3.08		
NT2RP3000818	4.35	4.35	11.29	6.64	10.49	8.27		
NT2RP3000820	9.01	9.01	18.49	18.58	20.1	16.9		
NT2RP3000821	2.13	2.13	4.83	3.28	5.19	2.02		
NT2RP3000825	1.87	1.87	4.94	1.92	1.47	2.27		
NT2RP3000826	4.04	4.04	13.59	10.86	13.8	12.94		
NT2RP3000836	5.33	5.33	11.61	11.55	14.11	13.3		
NT2RP3000838	319.2	319.2	741.74	710.2	743.55	1049.86		
NT2RP3000839	2.35	2.35	6.67	4.53	6.38	4.36		
NT2RP3000841	2.17	2.17	4.32	3.79	5.55	4.72		
NT2RP3000845	3.96	3.96	8.89	5.76	6.71	7.85		
NT2RP3000847	3.7	3.7	7.94	4.48	5.94	5.28		
NT2RP3000848	2.84	2.84	8.34	5.36	6.81	6.3		
NT2RP3000850	5.67	5.67	7.04	6.58	11.29	7.47		
NT2RP3000852	3.27	3.27	3.17	4.02	5.23	5.8	*	+
NT2RP3000859	2.76	2.76	7.12	4.46	7.11	8.43		
NT2RP3000861	2.58	2.58	10.51	6.13	10.36	6.43		
NT2RP3000862	15.29	15.29	24.16	16.36	9.81	23.13		
NT2RP3000865	1.58	1.58	4.26	2.54	4.21	1.83		
NT2RP3000866	2.08	2.08	5.03	2.37	3.59	5.22		
NT2RP3000868	2.2	2.2	7.09	3.04	3.84	2.28		
NT2RP3000869	3.54	3.54	11.36	9.61	15.76	7.9		
NT2RP3000871	1.75	1.75	3.79	1.81	3.24	1.94		
NT2RP3000875	0.99	0.99	4.25	2.57	2.71	3.64		
NT2RP3000895	2.54	2.54	5.56	2.84	3.55	4.93		
NT2RP3000900	6.01	6.01	11.86	11.3	7.7	14.58		
NT2RP3000901	3.67	3.67	7.03	4.11	6.39	5.3		
NT2RP3000903	3.76	3.76	7.87	3.12	5.92	3.93		

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NT2RP3000904	3.83	3.83	8.67	3.05	4.87	3.16		
NT2RP3000907	5.66	5.66	10.03	8.94	10.67	10.14		
NT2RP3000913	6.04	6.04	15.01	17.87	25.57	17.37	*	+
NT2RP3000917	7.64	7.64	16.58	7.66	6.56	13.51		
NT2RP3000919	1.99	1.99	5.15	3.5	4.3	2.68		
NT2RP3000921	2.26	2.26	7.67	4.88	4.07	6.51		
NT2RP3000942	2.66	2.66	3.89	2.68	4.12	2.63		
NT2RP3000968	70.24	70.24	87.55	105.89	110.05	115.38	**	+
NT2RP3000974	5.36	5.36	9.06	3.21	4.48	2.64		
NT2RP3000980	5.77	5.77	5.77	2.09	4.14	2.26	*	-
NT2RP3000984	3.17	3.17	7.65	6.33	6.68	4.58		
NT2RP3000994	2.09	2.09	4.88	2.4	3.14	3.37		
NT2RP3001001	1.46	1.46	3.45	3.75	4.14	1.31		
NT2RP3001004	3.37	3.37	6.52	3.51	5.63	5.01		
NT2RP3001007	4.46	4.46	9.87	10.02	10.62	6.81		
NT2RP3001012	2.78	2.78	5.4	4.99	6.83	3.65		
NT2RP3001042	4.74	4.74	5.52	2.99	5.18	1.38		
NT2RP3001044	6.26	6.26	7.12	7.16	6.76	4.92		
NT2RP3001048	2.52	2.52	3.01	3.5	3.93	2.42		
NT2RP3001050	1.79	1.79	4.99	4.68	5.94	4.7		
NT2RP3001055	6.55	6.55	15.6	16.48	12.44	20.49		
NT2RP3001057	2.79	2.79	10.84	5.57	6.05	5.67		
NT2RP3001061	3.18	3.18	6.57	5.03	7.85	5.42		
NT2RP3001069	6.03	6.03	14.95	18.49	17.53	15.08		
NT2RP3001074	4.2	4.2	7.22	8.72	10	6.64		
NT2RP3001078	5.11	5.11	7.29	7.51	8.72	5.18		
NT2RP3001081	4	4	5.72	4.65	5.19	3.52		
NT2RP3001084	2.7	2.7	7.92	6.85	6.71	6.23		
NT2RP3001095	1.57	1.57	3.88	3.69	3.68	3.42		
NT2RP3001096	2.52	2.52	7.33	16.78	8.08	18.7	*	+
NT2RP3001097	3.65	3.65	4.28	6.42	8.11	8.5	**	+
NT2RP3001107	3.69	3.69	4.79	3.77	4.03	2.37		
NT2RP3001109	3.2	3.2	5.5	6.01	9.56	7.26	*	+
NT2RP3001111	4.58	4.58	4.19	3.41	3.51	2.29	*	-
NT2RP3001112	12.61	12.61	18.48	25.73	29.85	24.61	**	+
NT2RP3001113	1.21	1.21	2.59	2.47	3.24	2.19		
NT2RP3001115	1.51	1.51	3.32	2.57	3.77	2.19		
NT2RP3001116	1.01	1.01	2.66	2.55	4.4	2.91		
NT2RP3001119	3.69	3.69	6.75	9.07	6.67	5.44		

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NT2RP3001120	5.02	5.02	8.24	8.85	7.87	6.71		
NT2RP3001126	6.16	6.16	12.34	17.84	19.66	17.49	**	+
NT2RP3001127	6.93	6.93	6.76	4.79	7.63	6.36		
NT2RP3001133	3.95	3.95	4.95	3.95	4.16	3.62		
NT2RP3001140	1.46	1.46	2.43	3.21	2.38	6.71		
NT2RP3001147	3.16	3.16	6.96	16.08	14.49	13.84	**	+
NT2RP3001150	1.99	1.99	4.32	4.06	5.68	3.76		
NT2RP3001152	1.7	1.7	3.29	3.15	3.62	2.51		
NT2RP3001155	2.95	2.95	4.35	3.68	4.35	3.58		
NT2RP3001156	4.38	4.38	6.57	2.91	5.72	5.67		
NT2RP3001159	5.38	5.38	10.5	7.87	10.86	7.25		
NT2RP3001170	7.38	7.38	5.96	6.12	8.01	4.56		
NT2RP3001176	3.49	3.49	10.75	6.27	8.23	9.49		
NT2RP3001195	2.35	2.35	4.81	6.79	5.79	6.22	*	+
NT2RP3001209	3.47	3.47	5.98	5.96	4.64	5.22		
NT2RP3001214	1.63	1.63	4.91	3.44	3.87	3.81		
NT2RP3001216	3.58	3.58	6.38	6.25	4.33	3.6		
NT2RP3001221	3.33	3.33	4.27	3.07	3.06	1.79		
NT2RP3001226	5.96	5.96	29.04	21.93	31.45	17.76		
NT2RP3001230	3.17	3.17	2.41	3.09	3.14	1.56		
NT2RP3001232	1.8	1.8	4.72	2.36	3.7	2.85		
NT2RP3001236	1.68	1.68	4.3	1.7	3.26	1.47		
NT2RP3001239	1.58	1.58	5.21	2.81	4.31	2.01		
NT2RP3001240	12.83	12.83	22.18	23.01	24.3	14.46		
NT2RP3001245	3.53	3.53	9.88	4.08	6.36	3.39		
NT2RP3001253	2.79	2.79	4.87	3.34	4.53	5.21		
NT2RP3001259	6.62	6.62	11.97	12.33	15.62	11.83		
NT2RP3001260	3.74	3.74	5.15	3.45	5.44	3.97		
NT2RP3001264	2.2	2.2	10.29	5.99	6.92	6.38		
NT2RP3001268	2.25	2.25	7.18	4.93	4.72	4.35		
NT2RP3001271	7.06	7.06	16.29	13.07	12.27	14.24		
NT2RP3001272	3.73	3.73	12.45	9.43	11.09	10.15		
NT2RP3001274	6.08	6.08	8.09	6.72	6.35	5.11		
NT2RP3001275	9.78	9.78	11.58	21.56	26.84	22.59	**	+
NT2RP3001280	3.39	3.39	5.5	3.58	5.24	4.18		
NT2RP3001281	3.15	3.15	3.89	3.08	4.48	5.14		
NT2RP3001288	49.31	49.31	103.24	124.07	142.92	164.41	*	+
NT2RP3001297	6.39	6.39	42.01	37.04	42.75	41.14		
NT2RP3001300	5.23	5.23	15.92	16.78	17.41	17.76		

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NT2RP3001301	2.91	2.91	6.59	3.96	4.58	3.9		
NT2RP3001307	1.76	1.76	7.67	2.07	2.81	2.06		
NT2RP3001310	11.55	11.55	17.04	25.54	26.07	28.13	**	+
NT2RP3001318	2.11	2.11	3.4	2.49	3.37	2.37		
NT2RP3001322	3.58	3.58	5.23	2.62	3.84	5.48		
NT2RP3001325	2.7	2.7	8.39	5.82	6.82	5.58		
NT2RP3001338	2.67	2.67	6.19	4.1	4.21	3.5		
NT2RP3001339	2.53	2.53	5.64	3.08	4.89	2.91		
NT2RP3001340	2.9	2.9	8.42	6.36	7.07	5.79		
NT2RP3001341	2.26	2.26	6.97	5.1	5.62	4.73		
NT2RP3001354	3.22	3.22	9.77	4.28	6.93	9.35		
NT2RP3001355	1.9	1.9	5.41	2.65	3.82	2.74		
NT2RP3001356	2	2	5.34	2.59	3.2	3.55		
NT2RP3001359	1.09	1.09	4.05	1.63	2.5	1.75		
NT2RP3001364	2.34	2.34	5.31	3.26	6.67	2.67		
NT2RP3001373	1.12	1.12	3.22	2.1	3.74	1.71		
NT2RP3001374	1.9	1.9	4.17	3.18	3.92	3.1		
NT2RP3001383	3.84	3.84	8.96	3.92	6.65	3.85		
NT2RP3001384	4.11	4.11	9.47	3.54	4.46	2.41		
NT2RP3001388	3.98	3.98	8.79	9.48	10.99	9.4		
NT2RP3001392	4.61	4.61	6.19	3.91	6.14	3.23		
NT2RP3001396	1.7	1.7	6.39	4.04	4.66	4.53		
NT2RP3001398	2.51	2.51	6.55	3.85	7.05	2.94		
NT2RP3001399	4.91	4.91	20.67	15.86	16.12	12.44		
NT2RP3001402	6.46	6.46	36.36	33.37	41.61	39.66		
NT2RP3001407	6.96	6.96	19.16	13.69	17.65	12.35		
NT2RP3001416	7.92	7.92	15.88	13.02	18.3	14.72		
NT2RP3001420	5.33	5.33	6.4	3.27	3.64	1.8	*	-
NT2RP3001425	3.73	3.73	4.92	4.74	5.67	3.15		
NT2RP3001426	2.39	2.39	6.08	5.45	4.45	5.11		
NT2RP3001427	1.82	1.82	5.61	3.46	2.89	3.59		
NT2RP3001428	2.42	2.42	6.29	5.69	4.81	3.77		
NT2RP3001429	3.08	3.08	5.91	4.15	7.37	4.73		
NT2RP3001432	2.14	2.14	6.61	3.72	4.44	3.58		
NT2RP3001439	4.14	4.14	6.39	5.87	7.27	4.41		
NT2RP3001441	6.45	6.45	12.63	11.13	14.61	11.2		
NT2RP3001446	4.99	4.99	4.99	4.64	5.22	4.39		
NT2RP3001447	2.72	2.72	5.21	6.64	5.14	6.33		
NT2RP3001449	3.95	3.95	11.85	16.9	14.57	13.16	*	+

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NT2RP3001453	1.84	1.84	3.66	3.5	4.4	2.81		
NT2RP3001457	3.86	3.86	7.71	6.06	6.93	5.5		
NT2RP3001459	2.39	2.39	6.03	2.64	2.78	1.17		
NT2RP3001463	2.77	2.77	6.74	5.93	5.94	3.98		
NT2RP3001466	2.87	2.87	3.56	1.19	1.43	0.78	**	-
NT2RP3001472	5.74	5.74	4.02	3.7	4.85	4.32		
NT2RP3001475	3.54	3.54	7.61	6.91	6.65	7.39		
NT2RP3001479	2.54	2.54	6.66	4.37	5.69	5.16		
NT2RP3001490	3.18	3.18	9.26	4.4	6.02	5.21		
NT2RP3001492	4.36	4.36	7.84	7.59	7.08	5.72		
NT2RP3001495	4.14	4.14	3.85	2.75	2.92	1.76	*	-
NT2RP3001497	5.8	5.8	6.32	7.47	9.96	6.8		
NT2RP3001501	5.36	5.36	5.52	3.12	4.49	3.43	*	-
NT2RP3001527	4.89	4.89	6.71	4.9	5.14	3.52		
NT2RP3001529	1.51	1.51	3.5	4.12	3.95	4.18	*	+
NT2RP3001538	1.78	1.78	6.2	6.93	7.81	6.23		
NT2RP3001539	5.81	5.81	14.5	15.19	14.15	16.47		
NT2RP3001542	1.52	1.52	5.26	4.23	4.38	2.13		
NT2RP3001549	4.75	4.75	11.12	14.57	11.37	13.44		
NT2RP3001554	3.06	3.06	6.16	6.37	7.5	5.05		
NT2RP3001560	4.96	4.96	5.73	4.67	6.35	2.36		
NT2RP3001561	8.85	8.85	20.77	20.38	27.2	17.15		
NT2RP3001564	1.54	1.54	8.24	6.43	4.53	5.96		
NT2RP3001568	2.1	2.1	7.68	11.84	10.29	8.49	*	+
NT2RP3001575	3.94	3.94	7.24	6.39	6.97	6.16		
NT2RP3001580	1.78	1.78	4.49	4.35	3.8	3.11		
NT2RP3001587	4.38	4.38	8.74	10.75	10.04	7.77		
NT2RP3001589	3.17	3.17	8.21	5.6	7.79	4.36		
NT2RP3001592	4.52	4.52	21.6	19	32.62	14.54		
NT2RP3001607	3.42	3.42	1.86	1.59	2.8	1		
NT2RP3001608	1.05	1.05	3.59	2.41	1.73	2.31		
NT2RP3001613	3.08	3.08	2.77	3.89	2.91	3.99		
NT2RP3001619	4.31	4.31	8.15	7.69	6.45	7.62		
NT2RP3001621	1.18	1.18	2.69	2.39	2.28	2.02		
NT2RP3001629	2.58	2.58	3.28	2.68	2.41	1.7		
NT2RP3001630	3.39	3.39	4.56	1.67	2.02	1.17	**	-
NT2RP3001631	9.01	9.01	14.34	18.65	21.16	15.24	*	+
NT2RP3001634	4	4	5.29	4.51	6.89	5.11		
NT2RP3001642	3.71	3.71	7.45	5.77	4.41	5.09		

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NT2RP3001646	1.56	1.56	3.7	0.89	2.79	0.95		
NT2RP3001650	2.06	2.06	5.81	4.86	7.03	2.08		
NT2RP3001667	4.66	4.66	11.91	6.93	9.95	5.13		
NT2RP3001671	2.28	2.28	7.98	7.7	4.69	5.99		
NT2RP3001672	1.33	1.33	4.55	1.66	1.47	1.72		
NT2RP3001676	2.18	2.18	5.02	2.35	3.14	2.24		
NT2RP3001678	2.86	2.86	9.24	5.12	5.14	6.03		
NT2RP3001679	6.12	6.12	9.19	6.74	4.73	6.91		
NT2RP3001682	1.82	1.82	5.09	4.45	6.18	3.35		
NT2RP3001685	3.02	3.02	6.74	3.52	6.53	3.01		
NT2RP3001688	3.01	3.01	9.42	5.46	8.21	6.43		
NT2RP3001690	3.21	3.21	4.87	2.91	3.54	2.99		
NT2RP3001693	5.69	5.69	10.93	16.59	18.34	16.12	**	+
NT2RP3001696	2.28	2.28	3.63	1.77	3.68	3.39		
NT2RP3001698	35.35	35.35	79.65	85.09	91.88	105.32		
NT2RP3001708	4.82	4.82	8.78	6.34	6.95	9.01		
NT2RP3001712	8.69	8.69	16.06	10.22	14.19	13		
NT2RP3001716	1.44	1.44	5.45	2.14	3.42	2.31		
NT2RP3001724	2.75	2.75	6	4.08	4.54	2.63		
NT2RP3001727	11.73	11.73	38.73	39.17	49.36	31.26		
NT2RP3001729	3.36	3.36	4.7	5.69	6.55	3.06		
NT2RP3001730	12.54	12.54	26.52	12.53	19.94	16.4		
NT2RP3001733	1.46	1.46	3.04	2.09	3.7	1.62		
NT2RP3001737	3.02	3.02	7.12	4.62	5.49	2.78		
NT2RP3001738	1.59	1.59	8.22	3.38	6.01	3.03		
NT2RP3001739	3.26	3.26	5.25	5.63	6.1	2.51		
NT2RP3001742	2.54	2.54	5.36	3.86	4.55	4.03		
NT2RP3001751	3.61	3.61	11.54	9.94	12.82	8.76		
NT2RP3001752	2.58	2.58	7.01	2.1	3.59	2.76		
NT2RP3001753	5.73	5.73	9.48	10.83	15.3	13.69	*	+
NT2RP3001754	4.63	4.63	9.08	5.86	3.73	5.33		
NT2RP3001756	4.66	4.66	7.36	9.37	5.75	8.03		
NT2RP3001764	2.1	2.1	3.76	2.54	4.25	2.49		
NT2RP3001771	2.63	2.63	3.2	1.52	4.14	1.22		
NT2RP3001777	2.59	2.59	5.99	3.25	5.19	3.26		
NT2RP3001782	3.52	3.52	14.68	6.47	6.63	6.47		
NT2RP3001792	2.27	2.27	4.35	2.91	4.09	1.35		
NT2RP3001799	1.76	1.76	5.18	5.71	6.36	5.68		
NT2RP3001819	1.36	1.36	4.54	1.7	1.52	2.06		

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NT2RP3001829	21.63	21.63	43.14	35.64	17.14	24.87		
NT2RP3001836	7.31	7.31	10.67	15.24	7.26	11.37		
NT2RP3001839	18.86	18.86	31.77	31.97	19.23	17.53		
NT2RP3001844	4.15	4.15	11.37	8.33	9.59	8.54		
NT2RP3001848	9.61	9.61	52.04	44.52	74.75	43.87		
NT2RP3001854	6.41	6.41	11.29	12.86	16.75	13.26	*	+
NT2RP3001855	2.27	2.27	3.94	1.87	1	1.74		
NT2RP3001857	3.1	3.1	5.22	5.13	5.6	3.33		
NT2RP3001858	1.53	1.53	4.45	4.41	6.04	2.97		
NT2RP3001861	7.35	7.35	16.34	11.85	14.46	10.42		
NT2RP3001866	4.35	4.35	9.63	5.52	10.42	7.93		
NT2RP3001871	4.82	4.82	6.34	5.55	6.38	4.55		
NT2RP3001874	6.8	6.8	9.73	7.72	11.19	6.14		
NT2RP3001878	5.98	5.98	6.35	4.59	6.89	5.02		
NT2RP3001885	3.21	3.21	5.3	5.65	5.25	4.42		
NT2RP3001896	1.64	1.64	3.49	3.37	2.13	2.02		
NT2RP3001898	9.03	9.03	17.69	14.71	8.69	11.94		
NT2RP3001899	3.21	3.21	7.33	4.52	6.9	5.81		
NT2RP3001901	4.58	4.58	9.18	8.19	9.44	9.21		
NT2RP3001915	4.84	4.84	11.12	14.09	15.67	14.04	*	+
NT2RP3001926	2.8	2.8	4.88	2.47	2.45	1.65		
NT2RP3001929	3.74	3.74	4.06	2.56	3.38	0.86		
NT2RP3001931	4.63	4.63	5.26	3.9	5.62	2.98		
NT2RP3001938	2.27	2.27	5.53	4.93	3.93	4.75		
NT2RP3001943	3.27	3.27	5.36	5.77	6.5	5.56		
NT2RP3001944	1.77	1.77	3.72	4.08	5.91	4.34		
NT2RP3001945	4.25	4.25	12.2	11.86	11.78	6.11		
NT2RP3001947	2.94	2.94	5.89	4.06	5.41	3.4		
NT2RP3001949	4.21	4.21	8.9	10.49	11.08	8.08		
NT2RP3001952	23.54	23.54	43.64	48.59	88.56	41.86		
NT2RP3001954	5.06	5.06	3.68	4.34	4.79	1.85		
NT2RP3001956	4.97	4.97	9.44	7.76	8.22	6.29		
NT2RP3001967	3.78	3.78	7.74	6.7	5.37	5.66		
NT2RP3001969	1.71	1.71	2.91	4.05	4.39	3.62	*	+
NT2RP3001976	2.25	2.25	4.67	6.22	6.25	4.84	*	+
NT2RP3001986	3.55	3.55	3.88	3.43	2.82	2.19		
NT2RP3001989	3.76	3.76	5.23	2.86	3.58	2.54		
NT2RP3002002	6.68	6.68	9.47	6.25	8.85	3.86		
NT2RP3002004	5.02	5.02	6.23	3.79	5.74	3.55		

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NT2RP3002007	1.29	1.29	2.3	3.46	4.05	1.69		
NT2RP3002014	1.38	1.38	6.23	6.04	6.24	4.21		
NT2RP3002015	3.61	3.61	10.33	14.17	9.94	8.85		
NT2RP3002033	1.54	1.54	5.03	7.29	5.03	3.65		
NT2RP3002045	1.89	1.89	5.29	4.67	4.36	2.5		
NT2RP3002054	5.26	5.26	8.12	6.27	9.17	5.42		
NT2RP3002056	5.67	5.67	5.52	4.24	4.24	2.7	*	−
NT2RP3002057	4.35	4.35	3.5	2.87	2.41	0.81	*	−
NT2RP3002061	4.71	4.71	13.94	8.64	8.9	10.74		
NT2RP3002062	0.8	0.8	2.42	3.58	3.26	1.11		
NT2RP3002063	5.61	5.61	10.31	9.29	9.3	7.31		
NT2RP3002064	2.6	2.6	3.37	2.72	3.74	2.52		
NT2RP3002071	1.6	1.6	3.91	1.99	3.29	1.45		
NT2RP3002073	6.47	6.47	9.55	10.45	11.13	8.64		
NT2RP3002074	4.2	4.2	7.25	6.33	7.82	4.24		
NT2RP3002075	7.58	7.58	11.93	21.64	30.17	18.15	*	+
NT2RP3002077	3.81	3.81	5.95	2.48	3.05	2.78		
NT2RP3002081	4.25	4.25	7.55	13.22	12.62	11.13	**	+
NT2RP3002086	3.86	3.86	9.77	5.59	8.66	6.95		
NT2RP3002094	7.34	7.34	10.28	13.84	14.79	11.67	*	+
NT2RP3002096	1.98	1.98	4.53	1.28	3.12	1.73		
NT2RP3002097	3.77	3.77	6.16	6.1	8.34	6.88		
NT2RP3002098	1.61	1.61	4.3	1.04	1.8	1.46		
NT2RP3002102	2	2	4.86	3.11	3.4	3.16		
NT2RP3002106	2.74	2.74	4.98	2.83	4.9	2.51		
NT2RP3002108	3.69	3.69	7.8	3.11	3.39	3.15		
NT2RP3002109	12.49	12.49	32.04	31.61	27.15	25.12		
NT2RP3002110	36.38	36.38	54.93	55.24	58.94	46.55		
NT2RP3002113	11.15	11.15	13.99	10.66	15.22	11.44		
NT2RP3002120	2.22	2.22	4.42	2.31	4.13	2.7		
NT2RP3002121	5.93	5.93	14.39	13.38	14.39	15.06		
NT2RP3002126	34.03	34.03	108.96	121.18	130.55	142.49	*	+
NT2RP3002128	4.06	4.06	8.23	3.36	6.87	3.92		
NT2RP3002130	8.29	8.29	18.59	11.69	10.7	14.03		
NT2RP3002133	14.24	14.24	18.31	10.06	8.3	19.51		
NT2RP3002136	10.32	10.32	15.42	12.49	17.64	17.49		
NT2RP3002140	3.13	3.13	6.35	6.15	3.9	4.16		
NT2RP3002142	16.86	16.86	50.85	56.54	81.25	62.65	*	+
NT2RP3002146	4	4	7.22	5.14	9.31	6.56		

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NT2RP3002147	3.8	3.8	10.45	6.06	7.4	6.2	
NT2RP3002151	5.62	5.62	10.64	6.27	4.43	7.33	
NT2RP3002155	1.62	1.62	3.27	2.01	4.98	0.8	
NT2RP3002156	3.15	3.15	4.82	2.55	4.08	2.42	
NT2RP3002160	1.57	1.57	3.43	1.36	3.43	1.56	
NT2RP3002163	20.86	20.86	55.1	35.13	44.03	32.6	
NT2RP3002165	4.17	4.17	3.67	6.21	8.31	4.86	
NT2RP3002166	4.04	4.04	10.53	7.76	8.79	5.58	
NT2RP3002173	2.24	2.24	5.75	2.95	3.34	3.53	
NT2RP3002174	8.41	8.41	15.8	13.21	7.82	14.77	
NT2RP3002181	1.1	1.1	3.46	1.87	3.51	1.61	
NT2RP3002185	2.69	2.69	4.51	2.94	4.35	2.61	
NT2RP3002193	5.51	5.51	13.38	16.39	15.35	11.36	
NT2RP3002204	5.66	5.66	12.49	17.04	24.14	18.95	* - +
NT2RP3002244	4.03	4.03	8.29	5.28	6.11	4.8	
NT2RP3002248	5.42	5.42	11.1	8.19	11.78	6.52	
NT2RP3002253	2.61	2.61	9.3	9.66	11.26	6.18	
NT2RP3002255	11.07	11.07	26.56	22.78	11.53	20.93	
NT2RP3002264	3.06	3.06	5.54	5.88	7.37	4.07	
NT2RP3002267	1.26	1.26	4.33	3.1	4.65	1.82	
NT2RP3002273	7.51	7.51	12.98	10.15	13.8	12.11	
NT2RP3002276	5.22	5.22	7.89	3.08	7.68	3.48	
NT2RP3002281	6.37	6.37	6.83	7.45	8.46	3.44	
NT2RP3002286	3	3	4.79	3.54	4.34	3.88	
NT2RP3002297	10.62	10.62	29.36	22.26	20.57	23.93	
NT2RP3002301	5.73	5.73	13.24	9.47	7.55	6.21	
NT2RP3002303	3.01	3.01	6.39	5.29	6.65	4.58	
NT2RP3002304	2.66	2.66	7.17	6.3	7.3	4.91	
NT2RP3002309	2.3	2.3	7.18	9.26	13	4.39	
NT2RP3002311	4.54	4.54	6.67	3.17	4.02	1.83	
NT2RP3002315	15.27	15.27	20.91	25.82	33.13	21.82	
NT2RP3002319	2.37	2.37	5.06	3.07	3.51	2.38	
NT2RP3002324	8.97	8.97	61.42	49.85	51.23	55.4	
NT2RP3002330	4.74	4.74	8.33	10.31	8.24	8.15	
NT2RP3002333	5.13	5.13	14.32	13.14	13.65	8.12	
NT2RP3002337	2.61	2.61	5.14	4.8	5.57	4.87	
NT2RP3002342	5.16	5.16	11.56	5.52	7.51	6.43	
NT2RP3002343	3.38	3.38	7.29	5.8	7.03	4.13	
NT2RP3002351	4.32	4.32	4.55	4.38	3.9	2.55	

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NT2RP3002352	6.3	6.3	8.01	4.4	6.76	4.31		
NT2RP3002353	3	3	4.85	4.87	6.18	5.9		
NT2RP3002362	5	5	11.74	15.86	11.03	10.49		
NT2RP3002363	2.41	2.41	3.67	5.53	6.17	2.32		
NT2RP3002377	2.61	2.61	5.47	6.8	7.31	4.73		
NT2RP3002377	4.47	4.47	7.73	11.4	5.31	7.09		
NT2RP3002394	5.58	5.58	7.35	7.82	10.17	4.46		
NT2RP3002397	3.77	3.77	4.81	2.7	3.12	1.68	*	-
NT2RP3002399	4.61	4.61	7.69	14.65	13.02	16.16	**	+
NT2RP3002402	2.84	2.84	6.99	8.94	8.7	6.99		
NT2RP3002404	2.88	2.88	5.6	3.12	3.73	1.83		
NT2RP3002410	4.85	4.85	15.65	17.05	14.13	10.65		
NT2RP3002411	2.98	2.98	5.68	3.7	5.29	2.85		
NT2RP3002414	5.62	5.62	9.35	10.28	6.81	7.92		
NT2RP3002430	5.11	5.11	14.63	18.24	19.29	14.51		
NT2RP3002448	5.4	5.4	4.6	4.35	5.25	3.62		
NT2RP3002454	7.3	7.3	15.31	12.9	12.71	9.32		
NT2RP3002455	4.62	4.62	12.11	14.31	9.11	13.25		
NT2RP3002456	3.21	3.21	7.75	7.09	6.57	5.9		
NT2RP3002462	2.79	2.79	4.16	4.94	6.17	4.79	*	+
NT2RP3002469	3.84	3.84	6.38	9.24	6.78	8.07	*	+
NT2RP3002470	6.7	6.7	14.71	17.86	16.99	13.48		
NT2RP3002484	4.01	4.01	6.86	6.81	8.01	4.59		
NT2RP3002491	3.62	3.62	4.1	2.05	2.51	1.46	**	-
NT2RP3002494	79.24	79.24	131.02	118.47	163.2	105.2		
NT2RP3002497	1.07	1.07	1.57	2.37	1.39	1.37		
NT2RP3002500	1.23	1.23	1.13	2.72	2.02	2.07	**	+
NT2RP3002501	5.25	5.25	8.49	8.45	8.11	9.69		
NT2RP3002512	2.85	2.85	3.97	3.3	2.74	3.57		
NT2RP3002529	3.94	3.94	7.5	6.59	5.14	5.85		
NT2RP3002533	7.95	7.95	10.26	9.79	10.51	8.18		
NT2RP3002539	4.39	4.39	4.32	5.66	6.61	2.85		
NT2RP3002540	5.24	5.24	5.5	3.48	4.76	3.65	*	-
NT2RP3002543	3.44	3.44	7.17	4.93	6.21	5.31		
NT2RP3002545	7.34	7.34	7.46	5.17	5.52	6.8	*	-
NT2RP3002549	3.27	3.27	7.8	4.98	6.11	4.54		
NT2RP3002552	3.05	3.05	6.04	4.17	5.81	4.06		
NT2RP3002558	9.54	9.54	9.39	9.93	4.26	11.27		
NT2RP3002565	1.94	1.94	4.83	1.73	2.48	1.52		

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NT2RP3002566	3.62	3.62	7.02	4.03	8.51	3.65		
NT2RP3002571	2.53	2.53	4.85	3.77	5.41	3.74		
NT2RP3002572	2.98	2.98	5.28	4.75	4.74	5.21		
NT2RP3002573	4.31	4.31	11.38	7.06	9.48	7.06		
NT2RP3002577	1.57	1.57	4.61	2.71	2.32	1.9		
NT2RP3002579	3.92	3.92	6.41	4.03	7.75	11.16		
NT2RP3002582	5.02	5.02	7.17	11.51	14.07	8.45	*	+
NT2RP3002587	1.9	1.9	3.13	2.68	3.04	1.97		
NT2RP3002590	3.16	3.16	5.65	9.06	10.39	8.06	**	+
NT2RP3002602	3.02	3.02	4.24	3.95	5.85	3.77		
NT2RP3002603	71.53	71.53	214.41	268.41	257.84	298.26	*	+
NT2RP3002621	1.95	1.95	3.42	2.13	5.13	1.85		
NT2RP3002622	2.63	2.63	7.38	3.7	7.36	4.67		
NT2RP3002624	2.29	2.29	7.4	4.04	4.9	3.64		
NT2RP3002628	6.36	6.36	16.17	19.57	22.15	16.21		
NT2RP3002629	8.96	8.96	13.58	15.4	18.26	15.57	*	+
NT2RP3002631	1.95	1.95	1.67	0.91	1.65	1.69		
NT2RP3002647	4.04	4.04	4.01	5.44	7.16	4.6		
NT2RP3002649	2.99	2.99	5.99	2.15	5.84	3.23		
NT2RP3002650	3.32	3.32	11.62	4.98	8.53	6.88		
NT2RP3002652	2.27	2.27	6.59	4.91	6.83	4.25		
NT2RP3002654	3.05	3.05	7.5	5.58	5.4	4.2		
NT2RP3002657	14.14	14.14	13.87	17.27	26.08	18.87		
NT2RP3002659	1.92	1.92	6.01	3.91	5.78	3.47		
NT2RP3002660	3.09	3.09	4.84	3.77	7.72	3.52		
NT2RP3002663	2.39	2.39	3.33	2.54	3.13	2.84		
NT2RP3002664	2.74	2.74	7.28	3.65	2.56	2.13		
NT2RP3002667	2.92	2.92	6.59	6.63	5.46	5.35		
NT2RP3002671	2.37	2.37	5.02	3.91	5.52	4.11		
NT2RP3002682	6.34	6.34	20.62	14.37	17.64	21.7		
NT2RP3002684	4	4	6.34	3.32	6.16	3.18		
NT2RP3002687	3.25	3.25	6.22	2.7	3.87	6.41		
NT2RP3002688	3.22	3.22	4.98	2.63	3.91	2.61		
NT2RP3002698	2.2	2.2	3.99	3.07	4.28	2.38		
NT2RP3002701	2.93	2.93	6.73	3.45	3.07	3.6		
NT2RP3002705	2.17	2.17	8.01	4.36	8.76	4.72		
NT2RP3002708	3.69	3.69	9.88	5.64	7.34	4.9		
NT2RP3002711	6.67	6.67	7.85	7.77	7.56	6.69		
NT2RP3002712	55.99	55.99	75.28	146.74	168.42	130.64	**	+

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NT2RP3002713	4.31	4.31	7.06	2.66	2.19	1.87	*	-
NT2RP3002721	5.77	5.77	10.06	11.06	16.94	8.96		
NT2RP3002722	7.11	7.11	10.08	7.8	6.45	6.62		
NT2RP3002723	42.31	42.31	75.85	60.39	46.74	58.76		
NT2RP3002737	8.35	8.35	18.1	10.97	11.6	9.37		
NT2RP3002738	1.9	1.9	6.13	3.09	5.23	3.54		
NT2RP3002742	14.11	14.11	23.22	30.39	28.27	27.66	*	+
NT2RP3002744	4.09	4.09	5.24	3.92	4.92	1.71		
NT2RP3002756	5.8	5.8	5.8	3.19	2.68	1.55	**	-
NT2RP3002757	12	12	17.79	19.76	24.24	19.75	*	+
NT2RP3002758	21.11	21.11	42.35	44.47	63.91	36.38		
NT2RP3002762	5.07	5.07	8.82	7.21	7.43	7.76		
NT2RP3002763	1.62	1.62	4.86	3.76	4.99	2.18		
NT2RP3002770	1.78	1.78	5.14	3.46	3.7	2.93		
NT2RP3002771	17.04	17.04	39.53	24.93	40.21	34.4		
NT2RP3002785	2.42	2.42	5.45	3.36	4.09	2.66		
NT2RP3002790	4.65	4.65	4.22	3.16	3.57	2.33	*	-
NT2RP3002799	4.73	4.73	6.33	3.42	2.7	1.43	*	-
NT2RP3002801	4.14	4.14	3.59	3.6	3.22	2.49		
NT2RP3002802	2.31	2.31	6.3	6.78	5.43	4.4		
NT2RP3002810	2.98	2.98	5.41	7.44	12.32	13.27	*	+
NT2RP3002818	1.5	1.5	2.44	2.18	4.16	2.47		
NT2RP3002821	12.8	12.8	33.14	26.1	35.81	23.02		
NT2RP3002823	3.85	3.85	8.98	4.65	5.92	3.87		
NT2RP3002825	5.47	5.47	13.04	13.47	19.19	7.12		
NT2RP3002829	5.37	5.37	6.25	4.75	4.89	3.8		
NT2RP3002831	4.01	4.01	6.13	9.07	8.77	5.19		
NT2RP3002836	7.33	7.33	19.42	11.56	16.91	20.66		
NT2RP3002845	4.17	4.17	6.63	7.87	8.6	8.45	*	+
NT2RP3002852	3.37	3.37	7.57	7.8	8.72	8.21		
NT2RP3002861	3.82	3.82	6.4	7.34	7.35	4.63		
NT2RP3002869	3.66	3.66	3.26	2.49	1.86	0.49	*	-
NT2RP3002874	11.25	11.25	21.44	25.33	31.95	25.54	*	+
NT2RP3002876	6.98	6.98	11.06	12.8	14.93	14.39	*	+
NT2RP3002877	4.7	4.7	5.96	3.3	5.24	2.53		
NT2RP3002887	0.47	0.47	3.42	2.81	3.53	3.91		
NT2RP3002900	6.46	6.46	19.64	21.86	21.54	22.3		
NT2RP3002902	4.01	4.01	10.25	11.72	8.52	8.06		
NT2RP3002909	2.61	2.61	6.19	6.67	5.38	3.93		

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NT2RP3002911	3.05	3.05	3.68	3.09	3.73	2.24		
NT2RP3002948	4.09	4.09	4.81	2.73	4.44	2.07		
NT2RP3002953	3.85	3.85	3.6	2.27	2.52	0.84	*	-
NT2RP3002955	6.55	6.55	3.78	1.93	2.47	0.86	*	-
NT2RP3002958	5.85	5.85	11.4	16.5	10.57	16.64		
NT2RP3002969	4.28	4.28	8.27	12.91	7.49	7.33		
NT2RP3002972	3.55	3.55	4.82	4.41	6.18	2.29		
NT2RP3002978	1.48	1.48	2.99	2.61	3.7	1.49		
NT2RP3002983	2.89	2.89	4.69	4.46	6.12	4.37		
NT2RP3002985	4.23	4.23	17.87	13.64	20.26	11.12		
NT2RP3002988	3.97	3.97	4.6	4.12	5.64	4.13		
NT2RP3003000	3.11	3.11	3.46	2.46	3.2	1.51		
NT2RP3003008	3.26	3.26	5.87	3.95	4.55	2.96		
NT2RP3003012	3.43	3.43	6.06	3.9	4.96	2.79		
NT2RP3003015	1.35	1.35	4.9	1.5	2.5	0.54		
NT2RP3003018	2.15	2.15	6.09	3.45	7.24	2.59		
NT2RP3003028	3.53	3.53	7.23	3.5	5.05	4.01		
NT2RP3003029	111.75	111.75	149.73	175.13	159.77	181.4	*	+
NT2RP3003032	7.06	7.06	9.05	11.87	18.84	9.94		
NT2RP3003041	2.07	2.07	1.88	1.61	1.41	0.69		
NT2RP3003044	3.06	3.06	7.45	5.72	6.11	7.57		
NT2RP3003047	3.09	3.09	5.16	2.4	4.67	2.06		
NT2RP3003050	5.96	5.96	12.03	6.74	10.3	8.42		
NT2RP3003053	7.46	7.46	18	14.42	17.14	13.72		
NT2RP3003059	1.93	1.93	4.76	2.88	4.41	3.06		
NT2RP3003061	2.8	2.8	8.59	5.49	5.68	5.16		
NT2RP3003068	5.99	5.99	11.77	9.41	8.75	10.04		
NT2RP3003071	7.22	7.22	10.77	10.39	14.52	10.39		
NT2RP3003076	2.67	2.67	9.49	6.57	6.57	4.01		
NT2RP3003078	1.5	1.5	4.12	2.09	4.52	2.43		
NT2RP3003081	6.21	6.21	10.54	9.94	9.6	9.97		
NT2RP3003090	1.49	1.49	5.95	3.28	3.57	3.25		
NT2RP3003097	2.42	2.42	7.15	2.71	3.72	2.93		
NT2RP3003098	2.75	2.75	4.22	2.73	3.43	1.73		
NT2RP3003101	5.56	5.56	7.24	7.73	10.35	7.18		
NT2RP3003109	16.11	16.11	27.38	27.36	41.03	21.91		
NT2RP3003121	3.39	3.39	11.03	4.61	8	2.44		
NT2RP3003133	2.09	2.09	5.78	4.93	8.58	3.96		
NT2RP3003137	3.42	3.42	5.74	6.32	7.59	5.29		

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NT2RP3003138	2.36	2.36	5.27	5.26	5.7	3.74		
NT2RP3003139	2.53	2.53	7.8	3.15	5.74	2.7		
NT2RP3003145	5.08	5.08	32.56	25.8	29.74	19.72		
NT2RP3003150	2.03	2.03	5.17	3.56	3.76	1.97		
NT2RP3003157	2.52	2.52	8.34	6.4	10.1	4.94		
NT2RP3003185	1.77	1.77	3.88	1.91	3.34	2.62		
NT2RP3003193	2.62	2.62	5.75	6.03	4.59	2.65		
NT2RP3003197	2.38	2.38	3.8	3.11	4.02	2.2		
NT2RP3003203	11.82	11.82	14.35	16.85	10.17	15.27		
NT2RP3003204	3.76	3.76	7.93	4.04	6.17	3.79		
NT2RP3003210	14.48	14.48	75.3	58.97	84.6	68.66		
NT2RP3003212	5.15	5.15	9.44	9.21	10.67	7.36		
NT2RP3003213	4.16	4.16	5.68	5.15	7.02	5.44		
NT2RP3003224	1.7	1.7	4.75	2.43	2.11	2.64		
NT2RP3003226	3.25	3.25	5.68	6.57	5.94	3.63		
NT2RP3003230	7.79	7.79	11.47	12.39	8.89	6.72		
NT2RP3003235	7.61	7.61	10.79	7.77	7.73	6.89		
NT2RP3003242	12.17	12.17	23.49	26.68	32.03	19.25		
NT2RP3003251	5.61	5.61	9.47	3.73	4.95	4.08		
NT2RP3003252	3.95	3.95	5.95	2.19	3.7	2.42		
NT2RP3003258	4.92	4.92	7.89	19.94	24.95	15.47	**	+
NT2RP3003260	4.54	4.54	12.34	13.46	11.52	12.68		
NT2RP3003264	1.64	1.64	5.99	3.18	4.32	1.86		
NT2RP3003273	2.18	2.18	4.93	4.57	3.58	1.72		
NT2RP3003278	1.33	1.33	4	1.31	5.12	0.63		
NT2RP3003280	9.85	9.85	23.11	18.18	19.52	18.19		
NT2RP3003282	5.29	5.29	6.25	3.62	3.97	3.48	**	-
NT2RP3003290	6.64	6.64	9.09	4.8	5.38	3.78	*	-
NT2RP3003301	4.01	4.01	5.73	4.31	4.59	3.23		
NT2RP3003302	1.45	1.45	2.31	2.91	2.64	1.91		
NT2RP3003311	2.45	2.45	6.76	15.72	13.09	11.55	**	+
NT2RP3003312	1.81	1.81	3.35	3.73	3.87	2.41		
NT2RP3003313	1.61	1.61	4.2	2.91	5.4	2.87		
NT2RP3003327	1.62	1.62	6.24	4.81	4.95	3.34		
NT2RP3003330	5.13	5.13	8.01	15.68	16.13	12.78	**	+
NT2RP3003344	3.36	3.36	4.14	2.92	3.74	2.6		
NT2RP3003346	3.81	3.81	4.83	4.38	4.05	1.24		
NT2RP3003349	4.04	4.04	6.93	9.96	9.41	9.65	**	+
NT2RP3003353	1.95	1.95	3.24	4.06	5.37	2.45		

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NT2RP3003354	5.09	5.09	13.72	16.29	12.02	13.5		
NT2RP3003368	3.03	3.03	4.73	4.04	4.08	2.63		
NT2RP3003375	4.1	4.1	7.4	7.41	9.67	6.62		
NT2RP3003377	4.16	4.16	3.98	2.57	3.58	1.65		
NT2RP3003384	5.77	5.77	4.55	2.83	3.43	2.56	**	-
NT2RP3003385	4.55	4.55	3.12	1.9	2.36	1.47	*	-
NT2RP3003396	3.93	3.93	13.63	16.4	8.38	12.32		
NT2RP3003403	1.62	1.62	2.54	3.24	4.73	1.92		
NT2RP3003409	1.18	1.18	2.97	3.3	4.48	3.03		
NT2RP3003411	4.59	4.59	15.42	14.11	15.42	10.96		
NT2RP3003420	3.79	3.79	4.36	3.68	2.13	1.85		
NT2RP3003425	3.25	3.25	6.71	5.85	7.25	5.49		
NT2RP3003426	9.11	9.11	16.3	10.88	11.12	17.45		
NT2RP3003427	5.95	5.95	10.09	9.15	13.58	8.03		
NT2RP3003433	2.55	2.55	6.26	8.42	9.57	4.87		
NT2RP3003437	22.12	22.12	49.85	51.81	44	38.77		
NT2RP3003448	1.88	1.88	4.24	3.5	3.83	2.63		
NT2RP3003455	5.23	5.23	12.16	11.8	9.96	8.44		
NT2RP3003462	4.96	4.96	10.07	10.76	8.25	7.08		
NT2RP3003464	3.79	3.79	5.03	3.01	4.76	1.2		
NT2RP3003469	4.1	4.1	7.77	6.62	7.56	5.07		
NT2RP3003473	22.06	22.06	36.6	54.82	69.25	56.46	**	+
NT2RP3003474	8.26	8.26	23.04	13.23	12.04	13.52		
NT2RP3003475	2.84	2.84	4.04	4.55	4.45	3.28		
NT2RP3003490	2.7	2.7	5.81	4.21	4.43	3.12		
NT2RP3003491	2.26	2.26	3	2.14	2.75	1.26		
NT2RP3003493	11.75	11.75	30.77	34.59	28.9	34.45		
NT2RP3003500	4.93	4.93	5.26	4.99	7.46	3.65		
NT2RP3003527	2.73	2.73	3.09	2.42	2.92	1.72		
NT2RP3003532	2.7	2.7	1.81	2.14	3.33	2.13		
NT2RP3003535	3.14	3.14	4.37	1.92	3.4	2.19		
NT2RP3003536	3.04	3.04	5.95	3.45	5.2	4.97		
NT2RP3003543	2.61	2.61	6.24	3.21	4.81	3.83		
NT2RP3003549	1.43	1.43	6.66	2.18	4.07	1.55		
NT2RP3003552	1.8	1.8	5.76	0.64	0.84	1.58		
NT2RP3003555	4.4	4.4	14.14	12.16	17.43	16.23		
NT2RP3003559	2.81	2.81	6.7	3.88	5.11	5.49		
NT2RP3003564	3.11	3.11	5.9	2.24	4.6	5.25		
NT2RP3003572	2.1	2.1	4.21	1.88	3.02	2.32		

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NT2RP3003576	5.88	5.88	10.15	11.32	8.98	9.22	
NT2RP3003587	7.39	7.39	12.41	10.01	12.71	12.75	
NT2RP3003589	15.33	15.33	22.45	23.89	23.75	26.58	
NT2RP3003592	7.77	7.77	10.4	8.42	14.48	9.74	
NT2RP3003593	8.16	8.16	13.62	13.47	13.84	110.49	
NT2RP3003614	2.66	2.66	8.18	3.11	4.48	7.09	
NT2RP3003621	1.64	1.64	3.91	2.1	3.68	2.96	
NT2RP3003625	1.54	1.54	6.94	3.79	5.09	4.96	
NT2RP3003627	6.73	6.73	20.05	16.23	13.97	25.71	
NT2RP3003636	3.3	3.3	7.74	5.99	3.79	10.4	
NT2RP3003642	7.12	7.12	12.2	12.85	13.15	15.83	
NT2RP3003645	2.91	2.91	6.07	2.23	2.42	3.53	
NT2RP3003648	2.88	2.88	3.71	2.17	2.44	3.13	
NT2RP3003649	2.7	2.7	9.28	6.36	5.11	12.04	
NT2RP3003650	2.65	2.65	4.25	4.38	3.16	4.09	
NT2RP3003656	1.69	1.69	3.23	1.94	4.12	3	
NT2RP3003659	2.76	2.76	4.56	2.14	4.8	4.88	
NT2RP3003662	31.39	31.39	53.28	34.35	14.68	34.64	
NT2RP3003664	3.56	3.56	6.5	6.18	5.45	6.55	
NT2RP3003665	1.89	1.89	4.83	2.07	2.8	4.96	
NT2RP3003671	2.88	2.88	4.33	3.03	2.6	4.29	
NT2RP3003672	4.78	4.78	9.8	10.69	14.73	16.35	* +
NT2RP3003673	4.98	4.98	9.42	5.35	3.05	4.12	
NT2RP3003679	40.1	40.1	95.75	69.92	23.86	83.88	
NT2RP3003680	3.13	3.13	5.38	3.96	4.58	5.88	
NT2RP3003686	2.22	2.22	4.43	2.84	4.85	2.25	
NT2RP3003689	4.05	4.05	9.69	5.94	5.63	8.27	
NT2RP3003697	13.79	13.79	120.74	108.93	77.49	68.74	
NT2RP3003701	2.7	2.7	5.17	2.58	3.05	2.57	
NT2RP3003704	2.99	2.99	6.96	7.09	7.61	6.96	
NT2RP3003714	1.39	1.39	4.25	1.68	0.89	1.14	
NT2RP3003716	2.05	2.05	4.23	3	2.29	2.24	
NT2RP3003721	1.83	1.83	3.27	1.85	3.45	2.18	
NT2RP3003722	3.45	3.45	8.18	8.08	7.79	5.45	
NT2RP3003726	3.5	3.5	4.9	2.77	4.51	2.32	
NT2RP3003729	4.1	4.1	8.53	4.22	5.44	4.6	
NT2RP3003731	5.06	5.06	6.98	4.19	3.54	7.45	
NT2RP3003740	2.58	2.58	5.08	2.42	2.48	2.94	
NT2RP3003746	3.63	3.63	8.14	6.7	5.94	6.59	

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NT2RP3003749	0.67	0.67	2.58	1.55	2.08	1.73		
NT2RP3003754	3.32	3.32	7.31	4.66	5.87	5.81		
NT2RP3003759	1.16	1.16	4.44	2.49	4.41	1.43		
NT2RP3003764	3.97	3.97	7.08	6.85	7.41	5.06		
NT2RP3003766	6.93	6.93	7.84	3.3	5.87	3.79	*	-
NT2RP3003767	11.19	11.19	16.8	14.83	21.08	16.97		
NT2RP3003778	3.36	3.36	4.89	4.46	5.55	4.27		
NT2RP3003779	4.05	4.05	15.26	13.02	8.74	10.52		
NT2RP3003783	9.25	9.25	21.72	22.42	13.65	18.76		
NT2RP3003787	2.15	2.15	4.65	4.41	4.74	6.37		
NT2RP3003789	5.12	5.12	10.16	11.63	12.19	14.96	*	+
NT2RP3003795	1.48	1.48	6.48	4.09	2.82	2.24		
NT2RP3003799	2.67	2.67	5.5	3.08	2.38	1.75		
NT2RP3003800	4.36	4.36	5.92	4.14	4.57	6.91		
NT2RP3003805	8.15	8.15	6.78	8.4	5.48	5.89		
NT2RP3003809	1.94	1.94	7.2	5.83	5.4	4.82		
NT2RP3003819	3.39	3.39	6.07	7.3	5.97	6.35		
NT2RP3003824	5.69	5.69	10.69	14.08	14.85	13.32	*	+
NT2RP3003825	9.06	9.06	16.31	12.87	16.88	16.75		
NT2RP3003828	4.7	4.7	14.38	13.36	15.69	14.55		
NT2RP3003831	4.01	4.01	6.38	5.77	6.54	7.23		
NT2RP3003833	5.12	5.12	7.5	6.44	8.88	6.96		
NT2RP3003836	6.37	6.37	5.05	5.74	6.47	4.31		
NT2RP3003842	2.7	2.7	9.08	6.84	6.51	7.09		
NT2RP3003843	9.26	9.26	26.77	16.67	12.71	16.2		
NT2RP3003844	20.38	20.38	46.56	42.84	27.94	44.32		
NT2RP3003846	4.04	4.04	8.45	8.94	7.18	8.05		
NT2RP3003849	2.27	2.27	2.68	2.67	2.73	1.68		
NT2RP3003862	28.91	28.91	45.63	32	37.58	44.88		
NT2RP3003870	4.76	4.76	4.81	2.54	2.93	2.05	**	-
NT2RP3003874	21.46	21.46	20.88	33.11	47.25	36.44	*	+
NT2RP3003876	1.62	1.62	8.08	5.45	7.49	6.81		
NT2RP3003880	1.74	1.74	4.63	5.31	4.66	4.73		
NT2RP3003889	1.69	1.69	3.04	3.41	3.53	9.53		
NT2RP3003891	1.88	1.88	2.98	2.56	3.19	1.37		
NT2RP3003914	3.1	3.1	7.35	6.88	5.15	7.39		
NT2RP3003915	5.03	5.03	8.44	9.52	11.35	8.6		
NT2RP3003918	6.79	6.79	10.39	10.04	13.71	12.42		
NT2RP3003920	6.9	6.9	9.13	8.31	10.22	8.96		

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NT2RP3003924	2.25	2.25	9.57	6.49	5.34	6.91		
NT2RP3003932	1.41	1.41	3.85	5.17	5.26	3.85		
NT2RP3003939	3.48	3.48	11.88	9.86	14.05	11.09		
NT2RP3003940	11.34	11.34	27.33	23.54	20.59	23.06		
NT2RP3003943	2.6	2.6	2.83	2.85	2.78	3.88		
NT2RP3003959	3.52	3.52	6.96	6.54	5.93	5.49		
NT2RP3003963	4.83	4.83	7.59	4.01	4.61	2.52		
NT2RP3003965	11.14	11.14	13.85	18.75	20.67	17.22	**	+
NT2RP3003972	26.1	26.1	40.32	22.13	17.98	38.48		
NT2RP3003973	2.85	2.85	4.33	1.96	3.6	3.96		
NT2RP3003979	5.89	5.89	12.53	6.92	8.49	8.84		
NT2RP3003980	3.52	3.52	9.41	9.34	8.89	7.92		
NT2RP3003982	4.2	4.2	4.63	2.44	1.6	4.61		
NT2RP3003989	6.24	6.24	4.69	9.61	5.62	16.05		
NT2RP3003992	2.13	2.13	4.89	2.47	5.12	4.8		
NT2RP3004000	2.81	2.81	6	1.72	3.22	2.62		
NT2RP3004001	11.38	11.38	19.94	11.62	11.37	21.11		
NT2RP3004005	2.89	2.89	7.79	4.7	4.48	6.84		
NT2RP3004013	2.23	2.23	7.2	2.66	4.87	3.57		
NT2RP3004016	1.5	1.5	7.1	2.22	3.14	2.88		
NT2RP3004025	4.02	4.02	7.69	7.48	12.19	9.01		
NT2RP3004030	7.05	7.05	12.64	13.97	15.8	17.66	*	+
NT2RP3004041	5.65	5.65	11.38	10.48	9.57	19.81		
NT2RP3004042	15.22	15.22	102.33	97.27	103.6	99.67		
NT2RP3004044	2.13	2.13	6.51	5.14	7.21	4.22		
NT2RP3004051	2.6	2.6	5.79	2.23	5.51	4.69		
NT2RP3004052	7.1	7.1	11.22	5.63	4.98	9.78		
NT2RP3004053	15.87	15.87	35.04	23.12	40.67	40.17		
NT2RP3004055	2.38	2.38	5.33	2.98	3.3	4.47		
NT2RP3004059	4.05	4.05	8.8	8.15	7.03	11		
NT2RP3004063	5.13	5.13	11.23	8.78	11.27	12.33		
NT2RP3004067	4.24	4.24	8.4	6.62	6.42	4.47		
NT2RP3004070	3.58	3.58	9.92	6.26	4.4	5.47		
NT2RP3004075	4.16	4.16	11.23	12.62	11.88	13.3		
NT2RP3004078	2.6	2.6	5.25	4.94	4.19	2.79		
NT2RP3004083	2.93	2.93	6.23	4.57	6.8	11.37		
NT2RP3004084	4.65	4.65	20.29	6.18	8.56	5.32		
NT2RP3004087	4.2	4.2	7.86	7.14	10.81	9.03		
NT2RP3004090	4.11	4.11	6.42	9	8.19	8.61	**	+

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NT2RP3004093	2.38	2.38	7.49	4.07	3.51	4.47		
NT2RP3004095	5.02	5.02	13.11	11.57	10.17	18.55		
NT2RP3004102	3.32	3.32	5.59	5.25	4.27	3.21		
NT2RP3004110	12.74	12.74	18.66	22.12	14.31	19.97		
NT2RP3004119	3.3	3.3	7.71	3.91	4.08	3.73		
NT2RP3004125	5.55	5.55	12.05	8.13	10.88	8.38		
NT2RP3004129	4.62	4.62	7.38	3.36	2.95	6.08		
NT2RP3004130	11.81	11.81	28.12	21.92	31.13	21.05		
NT2RP3004133	4.51	4.51	12.95	14.62	8.94	16.81		
NT2RP3004145	1.43	1.43	4.17	2.62	4.87	3.59		
NT2RP3004148	2.67	2.67	7.07	5.26	6.24	4.5		
NT2RP3004155	2.37	2.37	4.82	4.7	4.57	6.59		
NT2RP3004165	17.94	17.94	29.96	29.58	31.82	39.18		
NT2RP3004179	7.34	7.34	6.72	2.71	5.41	3.3	*	-
NT2RP3004185	5.2	5.2	5.53	2.76	2.76	1.95	**	-
NT2RP3004188	4.77	4.77	10.82	7.74	11.35	7		
NT2RP3004189	4.23	4.23	5.91	4.97	4.82	6.28		
NT2RP3004190	2.6	2.6	5.57	5.84	4.36	5.26		
NT2RP3004191	14.09	14.09	23.4	31.41	29.45	30.09	*	+
NT2RP3004202	2.04	2.04	4.56	4.16	4.42	2.3		
NT2RP3004205	8.75	8.75	21.54	21.27	25.35	20.28		
NT2RP3004206	4.5	4.5	9.74	5.14	6.37	9		
NT2RP3004207	5.19	5.19	4.99	3.09	3.25	1.77	**	-
NT2RP3004209	4.74	4.74	7.74	8.2	11.23	9.08	*	+
NT2RP3004215	1.86	1.86	6.7	3.96	2.41	4.55		
NT2RP3004219	5.15	5.15	11.25	10.04	8.81	13.65		
NT2RP3004242	4.65	4.65	10.36	9.8	10.19	14.56		
NT2RP3004246	4.5	4.5	9.39	9.18	10.95	3.8		
NT2RP3004253	1.89	1.89	4.85	3.64	4.99	2.8		
NT2RP3004258	5.45	5.45	10.89	12.77	11.07	11.39		
NT2RP3004262	4.26	4.26	5.71	2.63	2.99	2.01	*	-
NT2RP3004275	5.59	5.59	3.43	1.4	2.97	2.34	*	-
NT2RP3004282	5.45	5.45	68.08	51.29	52.72	53.57		
NT2RP3004289	1.79	1.79	2.95	1.9	2.18	3.99		
NT2RP3004294	2.74	2.74	6.02	6.95	6.93	7.24	*	+
NT2RP3004298	8.76	8.76	48.63	46.33	60.89	50.83		
NT2RP3004309	3.3	3.3	6.46	5.2	5.22	5.31		
NT2RP3004321	3.71	3.71	6.11	3.29	3.74	3.34		
NT2RP3004322	5.61	5.61	6.86	6.06	6.43	6.56		

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NT2RP3004332	11.69	11.69	100.11	78.54	102.41	76.72		
NT2RP3004334	1.49	1.49	6.97	8.56	6.06	9.06		
NT2RP3004336	2.11	2.11	6.24	6.02	4.44	5.63		
NT2RP3004338	3.09	3.09	8.41	10.22	9.52	16.47		
NT2RP3004341	1.81	1.81	4.56	6.13	5.17	9.13		
NT2RP3004345	4.1	4.1	8.68	9.3	9.63	8.48		
NT2RP3004348	5.06	5.06	11.25	13.04	10.79	12.54		
NT2RP3004349	5	5	7.5	4.89	7.75	5.76		
NT2RP3004355	5.57	5.57	7.09	7.55	7.07	7.18		
NT2RP3004356	5.76	5.76	21.51	11.29	15.14	15.56		
NT2RP3004360	3.4	3.4	5.26	6.01	5.32	7.85		
NT2RP3004361	2.6	2.6	6.26	7.67	7.3	8.87	*	+
NT2RP3004374	3.06	3.06	10.09	8.8	6.6	5.75		
NT2RP3004378	10.48	10.48	18.57	28.26	24.09	34.81	*	+
NT2RP3004399	3.88	3.88	5.77	3.53	3.17	9.06		
NT2RP3004405	4.07	4.07	6.77	3.03	5.52	3.93		
NT2RP3004406	5.36	5.36	6.23	5.19	6.03	6.12		
NT2RP3004411	5.93	5.93	13.28	8.08	6.39	9.51		
NT2RP3004424	1.53	1.53	2.43	3.27	1.81	2.83		
NT2RP3004428	3.03	3.03	5.36	5.07	3.82	4.09		
NT2RP3004432	3.3	3.3	3.52	3.61	3.11	4.38		
NT2RP3004434	3.42	3.42	8.41	7.28	9.09	7.99		
NT2RP3004446	3.29	3.29	4.6	3.29	4.1	2.63		
NT2RP3004451	3.2	3.2	6.01	3.89	3.38	2.48		
NT2RP3004454	2.96	2.96	4.16	2.69	3.5	2.5		
NT2RP3004466	3.5	3.5	7.89	5.25	3.85	5.61		
NT2RP3004470	7.42	7.42	24.53	18.4	16.35	24.72		
NT2RP3004472	2.49	2.49	4.4	3.97	3.84	3.88		
NT2RP3004475	1.71	1.71	5.52	2.72	5.93	3.9		
NT2RP3004480	14.12	14.12	17.04	18.94	10.5	18.82		
NT2RP3004481	5.42	5.42	11.37	5.04	7.37	12.39		
NT2RP3004490	2.66	2.66	8.45	3.92	7.03	8.25		
NT2RP3004496	4.8	4.8	14.38	7.22	9.3	11.08		
NT2RP3004498	6.39	6.39	21.39	16.86	15.11	18.92		
NT2RP3004503	2.78	2.78	9.34	4.85	6.23	5.88		
NT2RP3004504	3.91	3.91	11.09	6.05	10.67	11.52		
NT2RP3004505	17.38	17.38	28.56	37.35	26.72	37.82		
NT2RP3004507	1.57	1.57	6.6	2.52	5.52	1.68		
NT2RP3004519	4.9	4.9	7.73	4.93	8.36	8.75		

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NT2RP3004524	10.04	10.04	29.21	26.88	26.43	29.62		
NT2RP3004527	3.03	3.03	3.22	1.29	2.23	2.08	*	-
NT2RP3004534	3.08	3.08	10.44	5.58	12	7.38		
NT2RP3004539	4.45	4.45	12.17	9.8	8.97	12		
NT2RP3004541	2.65	2.65	11.06	5.48	9.44	8.25		
NT2RP3004544	3.54	3.54	8.89	6.62	5.24	9.48		
NT2RP3004551	3.46	3.46	6.75	6.6	6.6	6.98		
NT2RP3004552	2.76	2.76	4.33	2.84	3.22	4.98		
NT2RP3004557	5.68	5.68	8.73	9.74	15.44	13.16	*	+
NT2RP3004561	1.96	1.96	3.77	2.55	4.46	4.1		
NT2RP3004566	3.09	3.09	11.55	7.2	10.05	8.79		
NT2RP3004569	2.21	2.21	7.09	4.63	5.36	6.91		
NT2RP3004572	4.37	4.37	6.83	7.08	5.55	7.07		
NT2RP3004578	2.35	2.35	5.38	4.15	4.27	3.24		
NT2RP3004584	4.76	4.76	28.36	34.99	37.13	30.29		
NT2RP3004588	2.38	2.38	4.89	1.6	3.7	3.28		
NT2RP3004594	2.25	2.25	5.9	5.67	6.49	8.94		
NT2RP3004603	34.16	34.16	99.64	80.2	102.6	97.27		
NT2RP3004612	4.71	4.71	12.17	5.3	3.36	5.34		
NT2RP3004617	1.09	1.09	2.32	2.49	3.3	2.39		
NT2RP3004618	4.61	4.61	5.9	2.49	5.21	5.9		
NT2RP3004625	3.97	3.97	8.17	4.55	6.92	7.1		
NT2RP3004635	4.76	4.76	7.83	1.52	2.86	3.47		
NT2RP3004640	10.61	10.61	62.15	59.33	67.97	48.32		
NT2RP3004642	8.04	8.04	29.31	22.82	26.12	25.12		
NT2RP3004647	3.5	3.5	5.65	5.89	7.35	6.88	*	+
NT2RP3004652	1.76	1.76	10.37	4.2	3.71	4.34		
NT2RP3004669	2.01	2.01	5.36	4.01	5.33	3.46		
NT2RP3004670	5.04	5.04	10.58	12.4	9.19	14.23		
NT2RP4000008	45.17	45.17	71.24	49.77	32.43	48.77		
NT2RP4000018	11.64	11.64	14.61	11.69	14.8	14.87		
NT2RP4000023	6.96	6.96	8.91	4.86	7.38	5.98		
NT2RP4000025	16.2	16.2	22.16	26.22	29.89	24.7	*	+
NT2RP4000035	6.3	6.3	12.01	11.28	15.33	11.01		
NT2RP4000041	14.46	14.46	34.8	22.01	17.41	23.68		
NT2RP4000049	2.64	2.64	6.34	6.59	6.88	5.3		
NT2RP4000050	2.24	2.24	6.87	3.54	4.48	4.05		
NT2RP4000051	4.66	4.66	10.5	10.58	10.02	8.96		
NT2RP4000063	20.51	20.51	33.5	26.77	31	18.33		

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NT2RP4000065	7.54	7.54	9.24	11.85	15.01	11.47	*	+
NT2RP4000070	6.63	6.63	5.29	3.79	4.54	3.84	*	-
NT2RP4000074	6.55	6.55	13.63	10.29	15.39	9.52		
NT2RP4000078	3.41	3.41	9.55	12.2	11.66	12.56	*	+
NT2RP4000080	3.52	3.52	7.01	5.06	6.84	6.81		
NT2RP4000099	128.86	128.86	236.22	149.44	161.1	211.56		
NT2RP4000102	3.55	3.55	6.48	5.27	4.97	5.54		
NT2RP4000103	2	2	5.47	2.57	2.85	3.96		
NT2RP4000108	4.66	4.66	7.91	9.33	10.73	10.61	*	+
NT2RP4000109	18.89	18.89	22.84	19.87	24.15	16.14		
NT2RP4000111	4.56	4.56	6.38	4.87	5.27	4.85		
NT2RP4000112	5.62	5.62	10.14	12.45	8.7	11.81		
NT2RP4000115	2.94	2.94	3.62	4.95	7.82	10.93		
NT2RP4000129	2.18	2.18	4.58	3.02	5.04	5.03		
NT2RP4000137	3.36	3.36	10.05	5.34	8.72	11.4		
NT2RP4000138	7.21	7.21	10.91	17.75	20.19	19.17	**	+
NT2RP4000141	3.25	3.25	6.1	5.22	4.9	3.57		
NT2RP4000147	6.21	6.21	4.49	4.27	5.2	3.47		
NT2RP4000150	5.96	5.96	6.93	7.33	10.41	7.06		
NT2RP4000151	2.82	2.82	7.82	5.69	6.24	5.05		
NT2RP4000157	73.27	73.27	222.87	169.53	97.5	173.8		
NT2RP4000159	2.02	2.02	5.03	3.38	5.03	2.92		
NT2RP4000163	5.21	5.21	8.74	10.89	9.18	6.63		
NT2RP4000167	3.26	3.26	4.35	4.32	3.22	3.69		
NT2RP4000171	5.72	5.72	7	5.72	7.45	5.03		
NT2RP4000175	62.48	62.48	94.56	144.06	214.73	147.88	*	+
NT2RP4000180	17.17	17.17	106.15	88.61	123.6	81.8		
NT2RP4000185	7.64	7.64	31.76	31.82	23.23	34.01		
NT2RP4000192	1.04	1.04	4.78	4.19	3.6	3.05		
NT2RP4000194	3.13	3.13	7.53	7.58	4.98	6.36		
NT2RP4000196	6.81	6.81	43.94	35.57	46.56	41.91		
NT2RP4000210	5.63	5.63	9.71	9.96	8.35	9.27		
NT2RP4000212	5.59	5.59	8.88	8.57	8.41	9.08		
NT2RP4000214	5.53	5.53	10.21	5.72	6.68	11.29		
NT2RP4000216	8.89	8.89	7.36	7	12.63	10.08		
NT2RP4000218	3.45	3.45	9.78	7.25	6.07	5.77		
NT2RP4000223	21.18	21.18	177.28	121.8	125.75	125.3		
NT2RP4000243	16.52	16.52	54.51	42.94	41.61	51.74		
NT2RP4000246	17.75	17.75	37.97	26.43	11.42	27.5		

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NT2RP4000250	16.86	16.86	31.23	24.92	23.85	26.39	
NT2RP4000256	4.38	4.38	8.45	4.99	6.44	4.67	
NT2RP4000257	32.45	32.45	44.22	48.67	57.52	39.19	
NT2RP4000259	7.07	7.07	6.96	8.48	13.07	9.08	
NT2RP4000261	4.18	4.18	8.13	4.07	4.55	6.48	
NT2RP4000262	8.36	8.36	11.02	7.11	10.05	7.64	
NT2RP4000263	2.6	2.6	5.14	3.47	3.67	3.78	
NT2RP4000280	5.84	5.84	11.62	9.05	11.58	14.23	
NT2RP4000286	4.73	4.73	10.16	4.38	6.77	11.94	
NT2RP4000290	5.77	5.77	5.42	3.18	3.19	5.5	
NT2RP4000291	42.53	42.53	73.59	62.12	70.23	70.61	
NT2RP4000301	3.31	3.31	20.59	22.93	34.62	26.63	* +
NT2RP4000312	7.76	7.76	45.27	39.01	43.59	45.92	
NT2RP4000321	3.73	3.73	8.16	7.88	7.14	9.75	
NT2RP4000323	1.44	1.44	4.26	2.27	2.55	2.12	
NT2RP4000324	7.77	7.77	16.76	8.33	10.2	11.08	
NT2RP4000334	20.97	20.97	77.78	63.81	71.76	68.24	
NT2RP4000343	2.48	2.48	5.54	1.57	3.16	2.38	
NT2RP4000348	3.4	3.4	10.81	8.38	6.75	13.2	
NT2RP4000349	1.78	1.78	0.83	0.37	0.72	2.48	
NT2RP4000355	3.98	3.98	14.84	7.18	9.13	9.04	
NT2RP4000356	8.3	8.3	22.64	9.22	11.44	21.13	
NT2RP4000360	3.04	3.04	6.98	5.06	5.43	4.73	
NT2RP4000367	2.18	2.18	3.72	2.04	2.58	2.83	
NT2RP4000370	4.21	4.21	7.51	3.62	7.12	5.99	
NT2RP4000373	3.33	3.33	5.18	3.19	5.23	2.95	
NT2RP4000376	4.2	4.2	5.5	4.85	5.53	6.5	
NT2RP4000381	1.97	1.97	6.46	4.31	7.01	5.59	
NT2RP4000388	85.82	85.82	204.63	128.93	93.38	116.03	
NT2RP4000390	12.16	12.16	94.1	78.97	76.6	82.02	
NT2RP4000393	8.66	8.66	9.77	9.09	5.99	10.79	
NT2RP4000398	5.51	5.51	26.52	22.08	28.3	26.61	
NT2RP4000406	6.68	6.68	15.61	12.95	15.02	10.08	
NT2RP4000407	6.17	6.17	11.52	9.41	14.74	9.13	
NT2RP4000413	1.79	1.79	3.63	1.15	2.35	2.12	
NT2RP4000415	7.59	7.59	26.11	18.6	21.68	21.68	
NT2RP4000417	7.76	7.76	26.64	14.47	12.79	19.19	
NT2RP4000423	3.52	3.52	7.56	7	6.98	6.46	
NT2RP4000424	2.51	2.51	7.2	3.07	5.03	3.27	

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NT2RP4000447	10.3	10.3	64.21	64.91	71.82	68.48		
NT2RP4000448	5.59	5.59	6.67	4.32	3.56	6.27		
NT2RP4000449	5.67	5.67	20.48	14.2	19.45	14.67		
NT2RP4000453	3.53	3.53	6.32	9.02	10.32	10.12	**	+
NT2RP4000455	2.64	2.64	3.98	1.81	1.75	2.4		
NT2RP4000456	12.57	12.57	21.7	14.7	9.86	13.58		
NT2RP4000457	1.54	1.54	7.12	3.9	7.55	2.98		
NT2RP4000461	5.7	5.7	9.84	7.65	6.41	4.6		
NT2RP4000462	11.76	11.76	15.32	11.86	11.53	17.37		
NT2RP4000463	10.2	10.2	52.59	50.66	69.3	48.36		
NT2RP4000471	6.36	6.36	10.74	5.74	6.23	4.98		
NT2RP4000472	3.97	3.97	4.41	1.27	1.27	1.66	**	-
NT2RP4000476	27.14	27.14	52.56	74.95	94.93	65.35	*	+
NT2RP4000480	11.56	11.56	29.27	19.08	9.95	26.66		
NT2RP4000481	2.29	2.29	4.76	3.73	4.16	4.33		
NT2RP4000483	1.38	1.38	7.59	7.58	7.85	6.26		
NT2RP4000487	1.54	1.54	4.9	2.26	3.17	0.91		
NT2RP4000496	2.16	2.16	4.98	2.95	4.07	3.65		
NT2RP4000497	17.15	17.15	22.33	34.9	44.46	29.9	*	+
NT2RP4000498	10.46	10.46	21.39	20.15	30.33	24.49		
NT2RP4000500	2.43	2.43	3.21	2.03	1.49	1.39	*	-
NT2RP4000507	5.63	5.63	9.02	12.49	10.62	17.51	*	+
NT2RP4000515	12.85	12.85	88.89	90.3	101.29	96.12		
NT2RP4000516	8.77	8.77	26.09	19.63	21.76	21.82		
NT2RP4000517	3.22	3.22	5.73	4.69	5.89	4.79		
NT2RP4000518	3.42	3.42	7.4	4.47	6.05	3.82		
NT2RP4000519	2.9	2.9	5.76	2.18	2.22	1.77		
NT2RP4000524	4.2	4.2	3.44	2.05	1.72	1.3	**	-
NT2RP4000528	3.67	3.67	3.06	3.01	3.27	8.01		
NT2RP4000537	35.4	35.4	62.6	36.23	30.93	44.52		
NT2RP4000541	2.04	2.04	2.45	3.34	4.33	3.09	*	+
NT2RP4000543	2.93	2.93	8.94	7.96	9.72	8.75		
NT2RP4000545	4.03	4.03	6.38	4.99	6.43	4.78		
NT2RP4000546	3.34	3.34	5.93	5.53	4.9	6.03		
NT2RP4000549	23.81	23.81	56.48	41.6	51.57	38.82		
NT2RP4000556	7.36	7.36	13.04	14.69	15.54	12.07		
NT2RP4000557	6.1	6.1	4.53	1.82	3.97	6.27		
NT2RP4000558	30.12	30.12	94.28	68.16	57.01	73.2		
NT2RP4000560	14.8	14.8	52.31	49.75	58.69	56.12		

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NT2RP4000568	1.72	1.72	3.83	5.6	6.08	4.46	*	+
NT2RP4000583	11.61	11.61	20.2	23.65	14.97	20.56		
NT2RP4000585	3.04	3.04	4.14	3.12	2.55	3.24		
NT2RP4000588	8.65	8.65	12.77	14.58	16.96	13.55	*	+
NT2RP4000590	24.89	24.89	41.97	41.86	50.81	32.65		
NT2RP4000599	4.29	4.29	3.24	2.44	2.23	3.59		
NT2RP4000603	14.08	14.08	33.32	31.06	21.01	29.12		
NT2RP4000607	2.41	2.41	10.04	4.45	7.87	15.35		
NT2RP4000614	6.14	6.14	15.21	15.57	12.53	15.19		
NT2RP4000634	6.61	6.61	11	7.78	9.84	10.31		
NT2RP4000638	3.59	3.59	7.77	8.45	5.8	4.73		
NT2RP4000648	3.13	3.13	4.26	2.54	2.69	2.19		
NT2RP4000657	9.94	9.94	15.38	15.95	18.93	14.49		
NT2RP4000691	5.76	5.76	5.82	4.92	7.47	7.73		
NT2RP4000697	3.74	3.74	8.5	5.55	6.56	6.12		
NT2RP4000704	8.91	8.91	47.2	44.17	54.81	38.14		
NT2RP4000710	40.22	40.22	98.85	90.4	59.28	83.71		
NT2RP4000713	4.35	4.35	19.92	16.67	20.85	15.52		
NT2RP4000724	6.29	6.29	12.5	8.19	9.81	7.83		
NT2RP4000725	3.61	3.61	4	1.88	1.74	2.33	**	-
NT2RP4000728	10.13	10.13	41.12	43.53	66.46	39.83		
NT2RP4000737	4.07	4.07	2.15	3.63	3.09	3.28		
NT2RP4000739	5.07	5.07	7.71	4.61	3.63	5.84		
NT2RP4000749	2.4	2.4	5.29	2.59	3.97	1.68		
NT2RP4000769	4.93	4.93	10.12	4.67	6.27	6.2		
NT2RP4000774	3.34	3.34	8.87	5.12	6.63	4.27		
NT2RP4000781	2.15	2.15	5.12	2.06	2.26	1.55		
NT2RP4000783	6.81	6.81	15.16	13.48	15.44	12.67		
NT2RP4000787	1.45	1.45	2.27	0.31	0.51	0.54	*	-
NT2RP4000788	3.58	3.58	23.26	16	18.3	18.73		
NT2RP4000792	3.68	3.68	5.64	5.5	5.8	9.45		
NT2RP4000809	43.7	43.7	56.09	46.75	50.47	81.62		
NT2RP4000817	3.65	3.65	7.83	7.92	7.25	5.82		
NT2RP4000821	31.34	31.34	38.66	28.32	33.11	25.22		
NT2RP4000822	2.46	2.46	5.91	4.29	6.19	2.6		
NT2RP4000823	697.74	697.74	127.48	923.16	1026.8	947.85		
NT2RP4000831	9.98	9.98	61.97	44.37	68.47	50.69		
NT2RP4000833	3.19	3.19	11.26	6.73	7.19	11.91		
NT2RP4000837	1.41	1.41	4.03	1.56	3.65	2.29		

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NT2RP4000839	12.23	12.23	97.13	79.71	85.74	86.06		
NT2RP4000846	3.8	3.8	10.13	4.65	3.46	6.65		
NT2RP4000848	4.63	4.63	10.74	8.65	8.58	6.07		
NT2RP4000855	2.91	2.91	4.7	4	3.85	3.43		
NT2RP4000863	3.08	3.08	4.33	3.11	5.3	3.78		
NT2RP4000865	6.43	6.43	25.36	20.09	39.64	21.24		
NT2RP4000873	9.64	9.64	88.25	63.22	69.65	71.33		
NT2RP4000874	1.76	1.76	3.98	2.37	3.67	2.03		
NT2RP4000875	3.31	3.31	9.24	6.88	6.52	7.19		
NT2RP4000878	24.17	24.17	42.53	28.01	16.35	29.04		
NT2RP4000879	2.56	2.56	5.1	2.95	5.29	2.62		
NT2RP4000880	5.17	5.17	21.59	20.97	27.22	16.8		
NT2RP4000891	81.07	81.07	192.57	252.29	351.53	221.08	*	+
NT2RP4000894	5.16	5.16	9.81	8.53	4.8	6.97		
NT2RP4000898	0.86	0.86	2.74	1.88	2.14	1.64		
NT2RP4000899	9.63	9.63	29.48	24.01	20.85	23.95		
NT2RP4000907	2.14	2.14	3.58	1.74	4.04	0.81		
NT2RP4000908	4.62	4.62	9.67	7.51	5.9	5.87		
NT2RP4000910	14.4	14.4	104.68	124.04	197.74	160.9	*	+
NT2RP4000918	2.85	2.85	4.76	4.73	4.26	5.35		
NT2RP4000925	3.9	3.9	5.53	2.81	3.15	1.86		
NT2RP4000927	1.99	1.99	2.5	0.46	1.08	0.6	**	-
NT2RP4000928	3.11	3.11	6.8	4.48	4.22	5.18		
NT2RP4000929	1.44	1.44	3.68	1.94	2.86	0.84		
NT2RP4000946	0.92	0.92	3.41	1.78	3.22	1.47		
NT2RP4000947	1.71	1.71	3.51	1.94	3.31	1.79		
NT2RP4000949	4.94	4.94	7.84	3.88	5.48	2.38		
NT2RP4000955	4.17	4.17	6.34	2.07	2.86	0.54	*	-
NT2RP4000959	20.55	20.55	28.14	36.21	42.82	36.14	*	+
NT2RP4000962	3.4	3.4	4.24	8.33	10.09	4.53		
NT2RP4000973	8.6	8.6	16.04	10.31	8.92	9.03		
NT2RP4000975	2.18	2.18	5.84	3.29	3.05	2.62		
NT2RP4000979	3.83	3.83	8.67	5.55	8.13	7.1		
NT2RP4000984	1.61	1.61	4.31	3.15	3.93	1.85		
NT2RP4000986	7.32	7.32	13.27	12.66	12.35	2.52		
NT2RP4000988	5.74	5.74	8.37	4	5.2	2.63		
NT2RP4000989	6.24	6.24	6.55	4.05	3.48	2.89	**	-
NT2RP4000990	3.16	3.16	4	1.92	1.69	2.16	**	-
NT2RP4000994	4.04	4.04	7.67	16.48	10.13	15.95	*	+

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NT2RP4000996	3.54	3.54	7.49	6.77	6.52	7.38		
NT2RP4000997	21.59	21.59	36.81	28.52	15.18	34.38		
NT2RP4001001	5.53	5.53	9.17	16.66	18.38	15.09	**	+
NT2RP4001004	1.71	1.71	4.88	2.84	3.09	1.37		
NT2RP4001006	3.46	3.46	8.12	6.85	6.52	6.13		
NT2RP4001009	9.3	9.3	10.45	15.44	20.46	8.25		
NT2RP4001010	7.33	7.33	9.13	7.38	9.75	6.68		
NT2RP4001013	23.29	23.29	50.16	30.87	28.1	30.91		
NT2RP4001029	2.49	2.49	5.95	4.05	2.84	3.63		
NT2RP4001036	7.55	7.55	13.55	9.11	11.51	13.16		
NT2RP4001041	6.57	6.57	14.4	9.89	12.3	6.35		
NT2RP4001042	4.34	4.34	8.11	9.44	12.5	8.79		
NT2RP4001046	6.98	6.98	9.95	13.24	16.28	15.36	**	+
NT2RP4001050	5.28	5.28	4.81	3.79	4.64	3.35	*	-
NT2RP4001051	6.48	6.48	8.44	5.43	6.82	5.26		
NT2RP4001057	0.76	0.76	2.19	2.34	2.43	1.87		
NT2RP4001063	1.48	1.48	4.39	3.34	3.53	1.8		
NT2RP4001064	3.51	3.51	9.18	12.02	9.13	11.57		
NT2RP4001067	4.42	4.42	9.77	10.96	9.63	6.6		
NT2RP4001078	2.12	2.12	3.43	2.67	2.53	1.82		
NT2RP4001079	5.3	5.3	9.35	8.51	8.02	8.98		
NT2RP4001080	4.1	4.1	5.27	3.52	4.52	2.3		
NT2RP4001086	5.08	5.08	4.19	3.93	6.64	2.85		
NT2RP4001095	2.49	2.49	7.25	7.96	6.49	6.85		
NT2RP4001098	0.92	0.92	3.38	3.87	2.95	3.41		
NT2RP4001100	6.47	6.47	24.34	20.89	20.64	16.99		
NT2RP4001105	3.13	3.13	7.23	6.51	5.58	4.61		
NT2RP4001110	1.75	1.75	3.5	7.07	8.35	5.29	*	+
NT2RP4001115	9.95	9.95	17.68	20.6	18.48	15.31		
NT2RP4001117	19.81	19.81	30.49	35.35	42.53	27.5		
NT2RP4001122	6.06	6.06	6.09	5.17	6.25	3.27		
NT2RP4001123	3.62	3.62	7.76	7.95	5.96	6.27		
NT2RP4001126	4.36	4.36	11.28	10.87	9.09	8.04		
NT2RP4001127	3.25	3.25	4.59	3.39	3.08	2.17		
NT2RP4001138	2.46	2.46	5.8	3.41	2.56	1.62		
NT2RP4001143	2.73	2.73	5.98	6.44	6.54	5.66		
NT2RP4001148	3.72	3.72	6.76	3.77	3.03	2.05		
NT2RP4001149	5.07	5.07	7.28	6.76	9.03	6.37		
NT2RP4001150	3.8	3.8	3.17	3.15	3.7	2.88		

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NT2RP4001159	7.08	7.08	11.61	7.69	5.58	10.46		
NT2RP4001162	3.77	3.77	6.14	4.07	6.06	3.41		
NT2RP4001170	1.15	1.15	4.53	1.28	3.2	2.15		
NT2RP4001174	4.16	4.16	12.27	7.91	11.95	5.02		
NT2RP4001175	9.65	9.65	19.14	15.72	21.29	13.28		
NT2RP4001176	99.19	99.19	161.51	174.03	241.92	194	*	+
NT2RP4001184	4.83	4.83	27.1	25.76	32.51	22.85		
NT2RP4001198	21.66	21.66	48.22	29.54	29.17	38.54		
NT2RP4001199	2.52	2.52	6.45	2.59	4.74	3.71		
NT2RP4001206	8.25	8.25	33.2	25.92	32.07	25.48		
NT2RP4001207	2.38	2.38	5.15	2.21	3.11	4.01		
NT2RP4001210	2.73	2.73	5.2	3.62	4.26	2.64		
NT2RP4001213	3.42	3.42	5.11	3.99	4.23	3.63		
NT2RP4001214	3.34	3.34	4.3	3.51	3.76	2.16		
NT2RP4001219	7.4	7.4	12.05	14.35	19.28	13.39	*	+
NT2RP4001228	5.26	5.26	9.63	12.15	15.74	20.07	*	+
NT2RP4001235	2.42	2.42	7.45	3.46	6.02	4.48		
NT2RP4001256	2.11	2.11	4.24	1.66	3.41	2.66		
NT2RP4001257	2.48	2.48	7.27	4.05	4.35	4.05		
NT2RP4001260	3.16	3.16	5.79	2.52	3.86	2.92		
NT2RP4001261	3.84	3.84	6.63	8.42	6.47	5		
NT2RP4001274	22.92	22.92	38.08	25.02	31.56	21.25		
NT2RP4001276	5.24	5.24	10.03	11.38	15.97	11.63	*	+
NT2RP4001283	20.72	20.72	122.55	87.44	93.43	86.47		
NT2RP4001299	9.62	9.62	15.14	14.95	10.52	15.18		
NT2RP4001313	1.45	1.45	3.26	1.72	2.96	0.97		
NT2RP4001315	6.06	6.06	11.14	7.45	9.92	7.74		
NT2RP4001320	14.6	14.6	42.74	32.02	38.13	29.24		
NT2RP4001325	32.53	32.53	146.14	142.88	178.36	128.89		
NT2RP4001336	6.69	6.69	40.75	38.55	46.66	32.11		
NT2RP4001339	4.12	4.12	5.6	3.35	5.56	2.76		
NT2RP4001343	10.46	10.46	83.37	54.71	61.01	60.06		
NT2RP4001344	6.7	6.7	60.08	49.79	55.21	42.62		
NT2RP4001345	1.65	1.65	6.68	5.64	5.7	3.87		
NT2RP4001351	4.1	4.1	15.97	10.01	20.05	11.42		
NT2RP4001353	2.8	2.8	5.91	1.63	2.94	1.86		
NT2RP4001355	2.57	2.57	8.67	1.83	3.12	2.08		
NT2RP4001367	10.64	10.64	17.66	11.92	17.06	13.16		
NT2RP4001372	2.26	2.26	3.82	2.1	2.06	2.07		

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NT2RP4001373	8.86	8.86	16.4	10.99	8.59	11.48		
NT2RP4001375	2.71	2.71	6.06	4.91	7.42	2.94		
NT2RP4001379	1.74	1.74	3.52	2.34	4.67	1.38		
NT2RP4001381	5.6	5.6	12.51	12.8	12.66	8.27		
NT2RP4001386	6.39	6.39	14.52	14.77	20.11	12.32		
NT2RP4001389	7.28	7.28	8.66	5.43	9.25	4.09		
NT2RP4001396	5.76	5.76	6.42	2.83	4.61	2.12	*	-
NT2RP4001407	2.92	2.92	2.98	3.07	2.04	1.76		
NT2RP4001409	13.6	13.6	28.28	8.87	5.85	8.84		
NT2RP4001410	33.56	33.56	61.26	40.57	18.92	37.8		
NT2RP4001414	16.59	16.59	37.89	14.29	21.3	16.8		
NT2RP4001424	3.55	3.55	8.85	7.99	10.45	7.41		
NT2RP4001433	3.85	3.85	6	8.39	9.79	3.38		
NT2RP4001438	9.95	9.95	27.94	46.22	53.63	30.76	*	+
NT2RP4001442	4.33	4.33	4.97	3.3	3.41	2.64	*	-
NT2RP4001447	4.42	4.42	4.69	5.08	5.51	3.41		
NT2RP4001466	3.74	3.74	5.45	7.38	3.23	5.57		
NT2RP4001467	21.67	21.67	58.89	54.18	44.07	55.8		
NT2RP4001472	8.05	8.05	12.19	11.7	11.76	11.97		
NT2RP4001474	2.83	2.83	4.81	3.2	5.73	1.98		
NT2RP4001483	1.48	1.48	4.33	2.61	3.7	1.19		
NT2RP4001488	21.03	21.03	32.41	39.07	46.9	33.42		
NT2RP4001492	4.18	4.18	6.73	3.21	3.81	1.91		
NT2RP4001498	4.3	4.3	2.43	2.95	3.52	2.13		
NT2RP4001502	28.2	28.2	57.38	27.65	34.81	41.83		
NT2RP4001503	3.83	3.83	6.74	5.51	4.1	3.37		
NT2RP4001507	2.39	2.39	3.69	5.03	5.95	5.18	**	+
NT2RP4001510	1.74	1.74	4.63	5.64	5.05	3.02		
NT2RP4001516	3.54	3.54	4.16	2.52	1.9	1.27	*	-
NT2RP4001520	25.33	25.33	70.64	73.93	107.21	85.05		
NT2RP4001523	5.57	5.57	9.99	8.4	7.79	6.19		
NT2RP4001524	6.1	6.1	10.17	8.92	11.45	5.98		
NT2RP4001529	29.8	29.8	74.89	59.39	60.69	55.29		
NT2RP4001531	2.88	2.88	10.96	8.63	11.05	7.81		
NT2RP4001546	143.48	143.48	388.31	316.63	215.6	309.45		
NT2RP4001547	9.05	9.05	26.31	28.76	23.06	18.81		
NT2RP4001551	2.27	2.27	3.93	3.87	4.08	2.02		
NT2RP4001555	2.95	2.95	5.8	4.14	3.58	1.74		
NT2RP4001567	6.54	6.54	6.88	5.82	7.12	5.68		

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NT2RP4001568	7.58	7.58	11.65	10.02	19.33	12.97		
NT2RP4001569	15.49	15.49	41.42	32.56	40.11	27.18		
NT2RP4001571	5.75	5.75	13.28	9.06	7.43	8.13		
NT2RP4001574	8.5	8.5	19.03	15.54	17.52	15.29		
NT2RP4001575	2.46	2.46	5.86	5.71	5.53	4.24		
NT2RP4001578	17.21	17.21	45.64	52.76	53.63	40.92		
NT2RP4001592	9.76	9.76	13.68	14.13	19.64	11.68		
NT2RP4001593	9.4	9.4	18.11	22.12	27.3	18.04		
NT2RP4001605	5.97	5.97	4.78	4.1	7.77	4.66		
NT2RP4001606	2.9	2.9	8.34	6.01	3.51	6.75		
NT2RP4001607	2.04	2.04	5.24	4.57	3.26	3.78		
NT2RP4001610	1.74	1.74	2.42	2.6	2.48	1.7		
NT2RP4001614	2.17	2.17	7.19	5.38	4.34	6.86		
NT2RP4001623	2.38	2.38	5.26	2.43	2.65	2.02		
NT2RP4001626	9.48	9.48	11.67	18.67	23.9	19.44	**	+
NT2RP4001634	2.74	2.74	4.93	3.67	5.24	4.26		
NT2RP4001638	3.41	3.41	3.03	2.36	2.11	1.87	**	-
NT2RP4001644	7.86	7.86	33.73	24.36	26.04	24.99		
NT2RP4001646	11.61	11.61	15.02	7.42	10.74	11.21		
NT2RP4001656	3.75	3.75	5.23	2.89	4.51	2.07		
NT2RP4001666	1.99	1.99	4.68	3.26	6.25	2.02		
NT2RP4001670	11.74	11.74	15.51	12.45	7.09	8.31		
NT2RP4001677	28.27	28.27	42.75	42.01	45.48	47.53		
NT2RP4001679	8.82	8.82	33.83	33.23	51.5	29.78		
NT2RP4001695	7.71	7.71	12.76	15.66	20.35	12.87		
NT2RP4001696	2.64	2.64	5.45	3.13	3.92	3.72		
NT2RP4001699	3.58	3.58	8.03	3.18	4.12	4.42		
NT2RP4001717	2.79	2.79	7.03	3.29	5.84	4.15		
NT2RP4001719	3.59	3.59	9.11	7.6	9.27	6.28		
NT2RP4001725	2.27	2.27	4.79	2.28	5.07	1.43		
NT2RP4001726	7.07	7.07	11.18	5.85	6.91	4.98		
NT2RP4001730	3.11	3.11	12.82	11.96	19.81	16.3		
NT2RP4001739	2.83	2.83	5.83	5.79	6.55	4.98		
NT2RP4001741	7.25	7.25	15.93	9.28	12.42	10.97		
NT2RP4001753	3.04	3.04	8.4	4.39	4.64	6.64		
NT2RP4001760	4.32	4.32	6.6	7.79	7.73	12.96		
NT2RP4001787	67.61	67.61	173.05	169.17	187.1	193.22		
NT2RP4001790	2	2	5.29	3.42	2.97	2.58		
NT2RP4001795	9.31	9.31	12.31	14.38	19.76	12.34		

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NT2RP4001803	3.35	3.35	3.6	3.94	4.78	3.67		
NT2RP4001805	2.64	2.64	3.57	3.64	2.47	2.95		
NT2RP4001809	4.84	4.84	26.35	18.18	23.17	11.33		
NT2RP4001817	11.55	11.55	19.09	9.5	10.78	12.71		
NT2RP4001822	2.09	2.09	5.36	3.73	5.11	3.33		
NT2RP4001823	1.91	1.91	3.95	1.14	3.34	1.24		
NT2RP4001827	14.88	14.88	25.96	35.78	40.37	29.5	*	+
NT2RP4001828	9.76	9.76	34.37	27.78	34.21	26.3		
NT2RP4001836	7.74	7.74	33.26	27.19	39.14	26.78		
NT2RP4001838	1.59	1.59	7.49	2.09	4.5	2.71		
NT2RP4001841	8.75	8.75	80.37	61.67	50.27	56.46		
NT2RP4001849	1.9	1.9	4.55	2.51	5.08	1.58		
NT2RP4001861	7.27	7.27	34.6	36.09	41.9	34.39		
NT2RP4001877	6.59	6.59	8.44	12.87	9.04	14.1	*	+
NT2RP4001879	9.64	9.64	15.47	11.58	14.24	10.73		
NT2RP4001889	5.09	5.09	10.66	6.68	11.25	8.91		
NT2RP4001893	3.97	3.97	7.34	3.19	6.11	2.72		
NT2RP4001896	3.18	3.18	6.86	5.38	7.87	4.92		
NT2RP4001898	7.83	7.83	26.41	22.98	20.13	20.15		
NT2RP4001901	1.73	1.73	4.69	4.08	5.87	2.69		
NT2RP4001910	39.51	39.51	58.21	53.45	33.59	45.93		
NT2RP4001925	4.1	4.1	10.21	6.69	6.32	6.12		
NT2RP4001926	6.41	6.41	7.22	7.1	9.54	5.52		
NT2RP4001927	6.26	6.26	9.97	5.83	8.13	2.82		
NT2RP4001931	8.64	8.64	14.16	15.49	17.54	11.89		
NT2RP4001933	38.49	38.49	87.13	96.81	133.51	91.22		
NT2RP4001938	2.93	2.93	4.53	4.27	3.31	3.55		
NT2RP4001942	13.44	13.44	27.12	31.34	24.8	18.71		
NT2RP4001945	1.41	1.41	4	1.55	3.67	1.77		
NT2RP4001946	1.97	1.97	5.67	3.04	3.96	1.66		
NT2RP4001947	4.42	4.42	8.93	5.92	9.81	5.16		
NT2RP4001950	4.13	4.13	5	2.25	2.84	1.34	*	-
NT2RP4001953	10.44	10.44	14.15	13.81	19.4	14.36		
NT2RP4001966	2.44	2.44	2.41	2.51	4.26	1.52		
NT2RP4001970	2.26	2.26	5.32	3.91	3.4	2.88		
NT2RP4001975	8.56	8.56	20.03	18.32	13.05	12.02		
NT2RP4001988	6.72	6.72	18.78	22.92	24.78	29.44	*	+
NT2RP4001996	5.27	5.27	12.83	10.65	16.35	12.42		
NT2RP4002014	3.4	3.4	8.14	43.19	37.87	33.17	**	+

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NT2RP4002018	6.19	6.19	13.71	10.47	11.39	10.36		
NT2RP4002035	5.35	5.35	5.95	5.4	4.17	2.54		
NT2RP4002043	7.1	7.1	10.8	9.64	12.2	6.5		
NT2RP4002046	9.74	9.74	20.08	21.94	15.28	17.11		
NT2RP4002047	8.37	8.37	19.18	22.28	24.07	28.83	*	+
NT2RP4002052	5.78	5.78	10.36	9.02	9.36	9.37		
NT2RP4002056	32.58	32.58	71.49	58.09	76.58	49.75		
NT2RP4002057	6.37	6.37	11.06	12.13	13.58	7.41		
NT2RP4002058	3.85	3.85	6.6	4.1	4.2	3.22		
NT2RP4002064	5.93	5.93	4.39	2.6	4.16	2.07	*	-
NT2RP4002071	6.67	6.67	7.07	6.95	10.06	6.27		
NT2RP4002075	1.16	1.16	2.11	2.27	2.35	1.27		
NT2RP4002078	2.25	2.25	8.63	6.86	8.24	4.97		
NT2RP4002081	8.11	8.11	26.15	18.73	18.78	19.42		
NT2RP4002083	1.39	1.39	5.25	3.36	3.16	1.88		
NT2RP4002099	3.26	3.26	4.73	2.84	3.56	2.51		
NT2RP4002106	10.35	10.35	20.34	22.36	25.93	20.55		
NT2RP4002111	11.7	11.7	12.37	19.77	30.44	17.72		
NT2RP4002112	6.15	6.15	10.97	8.9	8.34	3.22		
NT2RP4002116	12.6	12.6	47.19	37.43	41.25	28.65		
NT2RP4002122	5.34	5.34	9.29	14.84	14.86	12.67	**	+
NT2RP4002126	6.42	6.42	14.44	16.82	14.35	10.42		
NT2RP4002133	7.56	7.56	20.82	29.17	26.14	21		
NT2RP4002136	3.63	3.63	5.74	4.89	5.38	2.69		
NT2RP4002139	26.89	26.89	31.12	60.65	61.92	32.88		
NT2RP4002174	139.27	139.27	232.64	240.71	275.01	193.19		
NT2RP4002185	7.77	7.77	13.2	12.36	19.06	11.58		
NT2RP4002186	4.5	4.5	9.83	7.82	4.72	6.78		
NT2RP4002187	15.42	15.42	32.13	26.94	19.84	21.17		
NT2RP4002188	3.01	3.01	8.34	8.3	7.75	6.41		
NT2RP4002199	1.85	1.85	3.73	2.6	2.91	3.78		
NT2RP4002206	2.08	2.08	3.39	2.48	2.34	1.29		
NT2RP4002210	3.13	3.13	4.75	2.02	2.86	0.98		
NT2RP4002222	4.2	4.2	6.63	5.56	6.28	4.16		
NT2RP4002241	7.97	7.97	8.24	10.82	11.75	7.19		
NT2RP4002248	5.08	5.08	16.69	10.74	8.9	8.13		
NT2RP4002250	1.54	1.54	3.22	0.73	1.69	0.56		
NT2RP4002259	4.86	4.86	9.82	3.21	4.85	1.75		
NT2RP4002268	16.62	16.62	29.54	28.9	28.18	25.68		

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NT2RP4002288	6.42	6.42	12.57	13.29	14.36	11.97
NT2RP4002290	7.55	7.55	7.61	7.96	7.67	5.87
NT2RP4002298	3.92	3.92	4.18	5.54	5.03	4.18
NT2RP4002306	2.38	2.38	5.79	2.97	5.77	2.64
NT2RP4002308	2.04	2.04	6.03	5.31	5.23	4.1
NT2RP4002336	2.71	2.71	6.33	3.71	4.19	4.63
NT2RP4002340	1.09	1.09	3.96	1.28	2.75	0.49
NT2RP4002361	2.77	2.77	5.78	3.73	4.03	2.48
NT2RP4002367	2.27	2.27	5.84	3.23	2.48	2.77
NT2RP4002368	9.87	9.87	17.2	18.26	19.27	16
NT2RP4002377	3.3	3.3	23.8	25.46	30.75	23.93
NT2RP4002408	2.22	2.22	3.87	3.75	6.37	4.11
NT2RP4002425	2.84	2.84	5.81	8.24	7.98	5.23
NT2RP4002432	12.33	12.33	85.4	61.06	72.53	67.82
NT2RP4002447	2.97	2.97	7.68	3.96	5.4	4.59
NT2RP4002451	5.48	5.48	6.2	5.84	5.85	6.83
NT2RP4002461	9.8	9.8	32.09	32.76	38.91	29.04
NT2RP4002486	3.5	3.5	6.71	2.47	4.15	2.87
NT2RP4002517	3.65	3.65	9.11	7.02	8.53	7.18
NT2RP4002556	4.29	4.29	3.91	5.68	10.03	6.41
NT2RP4002569	3.36	3.36	7.36	4.93	5.29	3.42
NT2RP4002587	2.26	2.26	4.19	2.8	3.4	2.02
NT2RP4002591	2.21	2.21	4.89	2.89	4.5	3.08
NT2RP4002607	1.43	1.43	3.34	2.87	4.63	1.58
NT2RP4002627	17.83	17.83	61.9	55.9	76.17	65.3
NT2RP4002628	7.28	7.28	15.48	14.53	23.95	12.54
NT2RP4002630	4.19	4.19	5.25	6.72	9.4	7.16
NT2RP4002639	9.43	9.43	70.25	52.38	77.24	57.28
NT2RP4002641	1.58	1.58	9.03	3.94	4.07	4.1
NT2RP4002658	114.62	114.62	166.93	76.49	34.96	109.83
NT2RP4002669	3.5	3.5	5.67	5.4	5.33	4.68
NT2RP4002677	6.24	6.24	9.41	10.14	7.99	13.62
NT2RP4002715	8.42	8.42	34.92	40.1	48.46	32.3
NT2RP4002750	2.6	2.6	8.29	1.68	2.04	1.33
NT2RP4002784	3.71	3.71	9.51	9.44	11.22	7.06
NT2RP4002791	4.91	4.91	9.44	4.88	9.76	5.33
NT2RP4002811	1.63	1.63	6.38	3.17	2.95	3.43
NT2RP4002830	4.26	4.26	7.45	3.9	5.9	5.46
NT2RP4002832	2.12	2.12	3.13	2.38	5.59	2.54

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NT2RP4002850	5.07	5.07	12.04	14.36	12.63	8.06		
NT2RP4002874	5.17	5.17	6.67	3.41	5.14	1.96		
NT2RP4002884	28.81	28.81	49.75	43.57	74.75	52.87		
NT2RP4002888	5.55	5.55	4.83	3.67	4.32	3.08	*	-
NT2RP4002891	5.48	5.48	15.79	13.16	19.42	11.91		
NT2RP4002894	12.04	12.04	24.47	18.44	12.76	16.4		
NT2RP4002896	5.54	5.54	12.2	8.96	6.18	7.78		
NT2RP4002905	1.71	1.71	4.27	2.32	3.58	1.28		
NT2RP4002907	5.11	5.11	7.62	6.94	10.72	1.41		
NT2RP5003459	68.11	68.11	133.25	154.61	146.15	164.37	*	+
NT2RP5003461	7.34	7.34	10.14	10.85	14.36	8		
NT2RP5003471	106.6	106.6	168.71	124.4	148.85	112.14		
NT2RP5003477	2.71	2.71	2.62	2.59	2.33	1.9		
NT2RP5003487	157.44	157.44	424.89	292.71	256.56	354.93		
NT2RP5003492	3.1	3.1	4.91	5.25	6.17	5.91	*	+
NT2RP5003500	1.5	1.5	3.28	2.38	2.54	2.59		
NT2RP5003506	4.96	4.96	9.3	7.83	10.37	9.04		
NT2RP5003512	2.21	2.21	4.35	2.63	3.46	2.15		
NT2RP5003522	4.1	4.1	5.97	4.62	4.19	2.34		
NT2RP5003524	4.38	4.38	3.86	1.61	1.54	0.84	**	-
NT2RP5003527	24.72	24.72	71.27	76.81	87.24	60.59		
NT2RP5003531	7.16	7.16	17.2	15.58	14.06	14.11		
NT2RP5003534	2.68	2.68	5.49	5.54	6.82	4.55		
NT2RP6000020	8.69	8.69	19.96	14.65	15.13	16.29		
NT2RP6000022	3.19	3.19	4.05	4.06	3.96	2.44		
NT2RP6000050	3.95	3.95	3.99	4.98	5.82	2.88		
NT2RP6000063	3.91	3.91	6.04	3.61	2.52	2.56		
NT2RP6000074	5.38	5.38	4.88	3.41	3.27	2.17	**	-
NT2RP6000083	7.76	7.76	11.18	11.49	16	9.91		
NT2RP6000100	2.49	2.49	4.58	4.04	4.71	3.3		
NT2RP6000123	1.94	1.94	3.29	5.1	4.26	4.22	*	+
NT2RP6000129	1.9	1.9	4.47	4.06	4.27	2.74		
NT2RP6000147	3.75	3.75	11.74	10.8	11.03	7.48		
NT2RP6000163	2.62	2.62	4.23	2.28	1.95	1.71		
NT2RP6000181	8.03	8.03	12.4	9.44	13.25	9.01		
NT2RP6000182	5.44	5.44	6.42	4.82	5.56	3.88		
OVARC1000001	4.97	4.97	5.24	6.04	7.48	2.35		
OVARC1000003	3.21	3.21	8.31	8.51	7.66	7.05		
OVARC1000004	9.87	9.87	116.19	88.04	109.99	85.44		

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OVARC1000006	3.57	3.57	6.58	9.04	7.88	4.73		
OVARC1000013	6.51	6.51	9.19	7.32	8.36	8.33		
OVARC1000014	3.39	3.39	5.02	4.23	5.02	4.17		
OVARC1000017	3.11	3.11	6.81	4.2	4.45	2.72		
OVARC1000026	24.79	24.79	32.1	56.82	69.34	44.53	*	+
OVARC1000035	11.11	11.11	20.26	20.41	23.65	15.36		
OVARC1000037	8.73	8.73	19.12	15.64	9.13	15.9		
OVARC1000058	6.06	6.06	11.69	13.84	7.56	10.6		
OVARC1000060	1.89	1.89	6.28	5.98	5.24	5.13		
OVARC1000068	2.38	2.38	5.33	5.31	3.56	2.42		
OVARC1000069	74.66	74.66	101.53	75.95	84.36	86.42		
OVARC1000071	4.4	4.4	4.77	6.47	5.35	4.04		
OVARC1000075	55.43	55.43	125.63	120.89	150.97	117.03		
OVARC1000083	9.58	9.58	9.24	13.12	12.7	10.64	*	+
OVARC1000085	106.6	90.9	156.14	214.2	177.05	273.14	*	+
OVARC1000086	3.98	6.82	9.23	11.98	11.3	14.09	*	+
OVARC1000087	1.51	2.83	1.79	4.03	3.57	3.35	*	+
OVARC1000090	1.48	4.1	6.14	10.88	9.58	8.79	*	+
OVARC1000091	4.88	8.33	8.01	7.99	7.76	6.82		
OVARC1000092	2.83	6.81	4.18	4.68	6.25	4.85		
OVARC1000105	9.73	14.86	17.21	26.29	25.62	22.88	*	+
OVARC1000106	26.02	23.03	46.38	66.36	50.1	53.01	*	+
OVARC1000109	9.12	13.08	18.04	16.72	12.91	17.46		
OVARC1000113	4.12	6.25	6.53	6.83	8.19	7.65		
OVARC1000114	2.14	3.44	5.77	5.94	5.86	4.98		
OVARC1000133	2.53	4.96	6.36	4.05	4.97	2.95		
OVARC1000137	6.14	10.05	13.51	13.3	18.59	14.39		
OVARC1000139	14.75	20.77	83.44	71.14	98.1	69.29		
OVARC1000145	0.72	6.64	2.89	1.78	2.42	2		
OVARC1000148	5.09	4.98	7.88	4.91	5.32	7.91		
OVARC1000151	1.41	2.11	2.4	3.58	4.08	3.58	**	+
OVARC1000157	10.99	14.16	17.51	21.21	25.06	22.76	*	+
OVARC1000162	1.22	4.4	2.5	2.93	2.49	2.59		
OVARC1000168	1.98	8.46	6.2	8.01	9.61	9.96		
OVARC1000169	32.03	45.07	49.48	70.63	69.6	89.08	*	+
OVARC1000178	0.84	5.08	2.53	3.37	3.18	2.78		
OVARC1000182	0.8	3.3	1.42	2.02	1.95	1.78		
OVARC1000186	2.51	3.72	3.23	5.95	3.27	4.77		
OVARC1000188	1.04	2.67	2.33	2.48	2.87	1.9		

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OVARC1000191	1.01	3.8	2.63	3.12	2.85	2.54		
OVARC1000198	2.09	3.59	4.32	5.62	5.12	5.06	*	+
OVARC1000208	6.49	10.37	22.5	17.79	24.54	22.02		
OVARC1000209	7.99	13.69	22.82	23.42	27.81	29.16		
OVARC1000212	2.47	5.63	3.59	4.76	5.03	4.88		
OVARC1000216	1.72	4.96	4.36	15.43	11.3	12.54	**	+
OVARC1000240	2.98	3.53	8.13	5.39	5.46	4.87		
OVARC1000241	1.29	2.47	3.18	2.65	3.17	1.4		
OVARC1000249	4.14	5.43	8.17	5.46	5	6.13		
OVARC1000254	33.15	39.39	100.99	100.41	131.42	100.89		
OVARC1000255	0.85	4.83	2.51	2.98	2.45	1.95		
OVARC1000267	2.37	6.41	6.71	6.66	7.16	7.31		
OVARC1000275	79.02	93.7	161.08	199.43	240.76	175.96	*	+
OVARC1000287	226.67	224.66	236.08	433.91	512.76	470.31	**	+
OVARC1000288	3.2	4.25	7.38	6.23	5.32	4.47		
OVARC1000298	8.96	10.09	19.62	13.37	7.19	9.6		
OVARC1000302	1.12	2.14	2.13	2.47	1.85	2		
OVARC1000304	1.09	2.68	3.23	5.02	3.41	6		
OVARC1000307	2.95	6.19	4.74	7.59	4.7	6.29		
OVARC1000309	1.18	7.16	3.22	3.24	2.85	2.4		
OVARC1000312	2.83	11.64	6.03	4.17	5.4	2.46		
OVARC1000313	10.48	19.25	14.81	9.39	17.54	22.17		
OVARC1000321	31.6	24.05	47.79	30.5	31.37	15.43		
OVARC1000326	1.52	2.3	3.9	3.84	3.17	2.79		
OVARC1000327	1.52	3.28	4.24	3.13	1.49	2.46		
OVARC1000331	2.22	4.72	2.41	4.33	4.45	4.58		
OVARC1000335	2.3	5.84	4.02	2.72	5.16	4.75		
OVARC1000347	1.83	8.18	6.24	7.35	9.24	8.44		
OVARC1000348	1.61	10.62	3.73	2.84	4.59	3.05		
OVARC1000363	3.7	9.61	6.51	7.31	11.52	6.83		
OVARC1000377	1.07	2.09	2.43	2.28	2.51	2.45		
OVARC1000382	3.34	3.39	4.33	5.07	2.52	1.03		
OVARC1000384	4.2	5.42	8.35	5.32	4.4	6.04		
OVARC1000401	0.62	3.63	2.09	3.35	4.08	3.64		
OVARC1000406	18.98	23.3	49.12	57.09	74.48	54.63	*	+
OVARC1000407	1.99	6.28	3.99	4.11	6.42	3.16		
OVARC1000408	27.5	38.45	70.39	74.84	111.17	71.25		
OVARC1000410	6.83	12.72	10.41	4.78	6.65	5.01		
OVARC1000411	0.91	1.5	2.6	3.49	3	2.22		

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OVARC1000414	1.31	2.22	3.7	4.5	3.78	3.71		
OVARC1000420	1.44	2.76	3.29	3.3	2.59	2.1		
OVARC1000421	1.42	2.65	3.33	3.96	4.21	4.99	*	+
OVARC1000427	25.78	27.02	130.06	156.9	215.67	142.19		
OVARC1000431	10.51	17.6	19.12	33.66	31.78	25.78	*	+
OVARC1000437	3.14	6.37	7.31	5.97	7.63	6.36		
OVARC1000439	5.81	10.95	13.82	21.81	23.01	21.52	**	+
OVARC1000440	2.56	3.74	5.01	7.47	9.31	7.08	*	+
OVARC1000442	2.34	2.38	6.81	6.66	9.5	8.12		
OVARC1000443	2.09	2.2	2.88	3.29	3.41	2.62		
OVARC1000461	1.11	2.84	2.2	2.55	1.12	2.14		
OVARC1000465	3.27	5.01	3.51	3.94	4.62	3.95		
OVARC1000466	1.94	5.47	5.9	6.54	10.13	6.76		
OVARC1000467	1.01	5.08	2.41	3.65	2.98	3.78		
OVARC1000470	1.13	5.81	3.03	3.18	4.02	3.78		
OVARC1000473	1.81	1.95	2.65	2.44	4.16	1.39		
OVARC1000479	5.67	5.88	9.88	10.35	14.26	6.88		
OVARC1000484	3.99	5.74	6.54	8.66	9.93	6.87		
OVARC1000486	3.17	4.71	4.49	5.74	4.93	4.28		
OVARC1000496	0.93	3.55	0.66	0.31	1.07	0.62		
OVARC1000520	0.84	5.89	1.18	1.32	2.27	2		
OVARC1000522	4.1	7.19	12	13.85	14.03	10.34		
OVARC1000526	1.96	7.04	3.75	5.93	5.48	4.69		
OVARC1000529	2.38	2.57	4.44	3.66	4.16	3.08		
OVARC1000533	3.3	4.66	7.95	8.89	12.29	7.83		
OVARC1000543	0.84	2.44	2.06	2.57	3.08	2.72		
OVARC1000550	0.75	3.68	2.32	2.82	4.04	2.34		
OVARC1000553	2.1	5.63	7.02	7.72	7.69	6.95		
OVARC1000556	5.77	15.21	11.77	8.95	13.91	8.96		
OVARC1000557	0.83	5.12	1.4	1.61	2.29	1.88		
OVARC1000561	3.48	7.38	9.26	13	17.66	15.09	*	+
OVARC1000564	8.89	9.02	10.44	17.84	11.31	16.69	*	+
OVARC1000573	1.87	3.68	4.86	5.75	5.32	3.83		
OVARC1000576	24.12	29.23	124.94	83.09	93.83	98.58		
OVARC1000578	2.43	4.6	5.53	8.64	4.46	3.93		
OVARC1000581	0.34	3.28	1.15	1.75	1.27	1.23		
OVARC1000586	22.54	28.9	41.17	34.58	43.39	40.93		
OVARC1000588	0.74	5.23	2.03	2.75	3.72	2.05		
OVARC1000605	1.98	2.62	2.88	4.47	4.23	3.87	**	+

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OVARC1000622	3.86	4.59	11.57	12.7	11.13	11.6		
OVARC1000636	1.64	3.79	4.58	4.19	4.03	5.09		
OVARC1000640	1.97	4.72	3.93	4.21	3.67	3.09		
OVARC1000649	9.69	14.8	53.54	53.32	64.51	52.67		
OVARC1000661	1.14	9.33	2.99	5.34	5.24	5.24		
OVARC1000677	8.53	10.16	14.87	11.77	10.98	15.47		
OVARC1000678	1.21	4.49	2.71	3.28	4.17	3.26		
OVARC1000679	2.86	3.25	4.09	5.29	5.16	6.25	*	+
OVARC1000681	1.47	1.55	3.2	2.41	2.22	1.71		
OVARC1000682	10.09	11.33	50.91	33.79	47.49	44.31		
OVARC1000689	3.81	7.1	19.94	20.18	22.12	21.83		
OVARC1000700	1.8	10.37	3.18	4.98	4.37	5.14		
OVARC1000703	1.74	7.18	5.35	6.4	6.64	7.77		
OVARC1000722	10.59	11.92	47.93	43.41	60.06	39.34		
OVARC1000726	1.44	3.48	4.62	4.88	5.89	3.58		
OVARC1000727	1.93	2.09	4.13	3.78	3.79	3.89		
OVARC1000730	5.95	5.86	9.01	4.07	4.16	5.62		
OVARC1000741	4.85	6.13	8.74	15.19	10.58	13.71	*	+
OVARC1000746	0.89	3.61	2.43	2.06	2.9	2.84		
OVARC1000764	1.76	4.93	4.77	5.35	7.01	5.44		
OVARC1000769	1.13	4.3	3.6	3.76	4.42	5.2		
OVARC1000771	2.42	6.28	2.3	4.02	4.81	3.71		
OVARC1000773	19.09	24.7	31.93	44.69	56.24	46.24	*	+
OVARC1000775	11.67	8.94	16.44	12.16	8.7	4.26		
OVARC1000778	2.37	3.89	5.69	4.59	6.23	4.92		
OVARC1000779	0.8	2.02	1.85	2.23	2.45	1.46		
OVARC1000781	1.67	5.05	4.16	6.37	3.45	5.07		
OVARC1000787	1.64	4.79	4.22	2.97	5.44	3.25		
OVARC1000789	7.62	14.23	16.39	24.95	29.69	25.94	**	+
OVARC1000800	2.91	10.72	5.72	6.41	10.65	6.2		
OVARC1000802	1.55	8.77	2.97	2.99	5.34	2.76		
OVARC1000810	3.37	3.54	8.29	6.66	7.99	7.21		
OVARC1000811	2.41	2.73	7.5	4.88	3.67	4.95		
OVARC1000814	3.44	4.55	9.03	7.92	11.3	9.05		
OVARC1000816	7.64	10.41	12.41	10.99	10.58	14.11		
OVARC1000817	1.18	3.38	1.27	1.71	2.14	1.55		
OVARC1000834	2.46	8.3	3.39	4.84	5.81	4.01		
OVARC1000846	2.23	10.02	5.35	7.38	9.66	7.72		
OVARC1000850	1.74	8.37	3.38	3.39	2.51	3.1		

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OVARC1000853	23.21	24.23	43.4	30.67	37.81	18.39		
OVARC1000862	2.28	2.66	4.91	3.05	1.61	1.49		
OVARC1000873	2.56	2.98	4.14	4.4	3.79	3.85		
OVARC1000875	1.47	3.07	1.79	2.35	3.09	1.87		
OVARC1000876	3.71	5.67	4.46	5.11	6.06	5.45		
OVARC1000883	6.06	9.53	9.18	12.43	15.42	13.05	*	+
OVARC1000885	2.84	9.95	3.38	3.74	5.66	4.11		
OVARC1000886	4.31	8.19	4.29	3.74	5.15	4.39		
OVARC1000890	17.47	18.3	91.22	70.97	78.71	51.68		
OVARC1000891	1.28	1.44	3.03	2.85	2.19	3.22		
OVARC1000897	0.48	1.74	1.29	1.21	1.33	0.5		
OVARC1000912	2.06	3.22	4.33	5.21	6.1	5.86	*	+
OVARC1000914	1.48	6.18	1.61	3.68	3.02	2.18		
OVARC1000915	1.71	6.64	4.14	4.87	3.54	4.76		
OVARC1000916	1.91	5.19	2.56	4.05	4.32	3.88		
OVARC1000924	1.45	5.5	3.09	3.28	3.85	3.48		
OVARC1000928	6.05	5.46	8.78	4.22	5.83	5.35		
OVARC1000936	1.37	1.39	2.17	2.04	3.25	2.49		
OVARC1000937	1.69	3.01	1.94	4.17	3.26	3.24		
OVARC1000945	1.55	3.67	3.62	3.83	3.22	2.28		
OVARC1000948	1.57	3.85	2.66	3.15	3.68	1.99		
OVARC1000956	1.41	5.08	4.36	7.56	7.26	5.51		
OVARC1000959	1.8	4.87	3.39	4.88	3.02	3.9		
OVARC1000960	2.64	7.53	9.55	11.64	13.89	12.86	*	+
OVARC1000964	19.89	17.19	103.98	118.41	165.46	96.14		
OVARC1000971	0.42	1.58	1.4	2.53	2.27	2.28	*	+
OVARC1000975	5.93	8.3	36.1	31.27	51.54	30.22		
OVARC1000976	0.65	2.12	1.27	2.17	1.46	1.5		
OVARC1000981	4.06	7.18	4.94	7.97	12.1	8.53		
OVARC1000982	2.83	5.41	2.23	3.13	3.02	3.54		
OVARC1000984	1.78	5.43	3.32	3.01	3.08	2.16		
OVARC1000995	2.94	6.59	4.5	5.98	6.19	6.72		
OVARC1000996	1.68	1.87	4.29	3.58	4.15	4.56		
OVARC1000999	6.02	5.65	15.29	15.61	13.18	13.29		
OVARC1001000	1.96	4.5	6.2	6.26	7.09	6.86		
OVARC1001004	0.51	3.4	1.45	2.05	3.3	1.47		
OVARC1001010	1.35	3.99	1.66	3.04	1.4	1.54		
OVARC1001011	1.46	5.57	1.13	2.39	3.27	2.45		
OVARC1001030	96.19	101.41	143.98	119.24	154.26	133		

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OVARC1001032	1.42	5.34	1.89	1.83	2.82	1.92		
OVARC1001034	4.44	5.58	6.51	3.29	5.21	3.77		
OVARC1001038	3.62	5.03	7.4	10.3	10.88	8.61	*	+
OVARC1001040	2.63	3.77	6.93	5.25	6.51	4.25		
OVARC1001041	4.54	8.03	12.87	8.57	12.25	9.4		
OVARC1001044	1.05	2.92	1.83	1.96	2.43	1.84		
OVARC1001049	3.78	8.78	10.67	10.65	11.87	10.26		
OVARC1001051	40.95	55.97	80.66	66.89	109.71	87.49		
OVARC1001054	1.22	4.06	3.22	2.86	4.19	1.93		
OVARC1001055	2.13	3.38	3.82	4.32	5.61	5.22	*	+
OVARC1001062	5.8	6.15	12.54	8.04	9.94	9.57		
OVARC1001065	8.85	13.63	51.33	51.41	60.3	56.97		
OVARC1001068	2.82	5.62	4.76	4.72	4.02	5.52		
OVARC1001072	0.73	4.18	4.41	3.2	3.71	3.07		
OVARC1001073	0.92	5.7	2.65	2.91	2.54	1.79		
OVARC1001074	0.81	4.66	3.31	1.87	2.95	2.04		
OVARC1001078	2	5.12	2.79	3.57	3.08	2.83		
OVARC1001085	2.41	2.83	3.66	5.54	5.02	6.36	**	+
OVARC1001086	1.97	3.17	2.85	3.98	2.83	4.13		
OVARC1001091	16.24	19.32	92.73	76.48	96.74	77.99		
OVARC1001092	4.62	5.35	7.22	9.69	7.84	6.05		
OVARC1001104	1.05	4.37	2.66	3.16	2.58	2.03		
OVARC1001107	11.59	15.6	40.28	31.21	49.49	42.22		
OVARC1001113	1.04	5.81	1.59	2.46	3.05	2.39		
OVARC1001117	2.71	6.63	4.31	4.67	5.74	2.67		
OVARC1001118	2.38	3.69	7.08	7.36	6.91	8.28		
OVARC1001125	2.02	2.9	3	5.92	4.97	5.9	**	+
OVARC1001129	2.61	4.58	3.19	8.46	9.43	11	**	+
OVARC1001132	1.7	6.48	2.66	3.69	4.26	4.66		
OVARC1001138	9.52	15.82	23.8	48.95	45.16	44.97	**	+
OVARC1001141	1.68	4.97	3.48	3.77	3.68	3.84		
OVARC1001154	18.31	29.49	68.39	60.43	83.49	65.64		
OVARC1001161	2.49	5.55	6.15	7.03	6.69	5.89		
OVARC1001162	2.2	3.13	5.34	5.09	4.86	5.26		
OVARC1001163	0.69	3.59	2.77	2.2	3.98	2.54		
OVARC1001167	3.03	4.57	7.69	10.19	12.95	9.3	*	+
OVARC1001169	0.74	4.87	2.68	2.47	1.91	2.06		
OVARC1001170	7.81	15.04	17.59	14.61	19.45	14.99		
OVARC1001171	15.57	17.71	24.31	16.12	23.34	22.51		

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OVARC1001173	2.09	5.08	5.1	4.32	6.75	5.49		
OVARC1001176	22.57	21.48	89.96	76.74	102.3	70.7		
OVARC1001180	3.01	4.58	12.7	11.81	10.77	9.56		
OVARC1001188	2.66	3.7	3.95	3.62	3.44	4.16		
OVARC1001200	1.52	4.56	3.62	3.47	2.9	2.96		
OVARC1001202	3.75	6.65	6.53	9.26	7.79	10.23	*	+
OVARC1001206	1.52	5.52	1.15	1.59	1.13	1.9		
OVARC1001209	4.89	8.92	27.46	24.69	30.38	24.27		
OVARC1001219	1.81	6.36	4.71	5.33	3.95	3.62		
OVARC1001222	2.5	8.36	5.01	3.2	4.34	5.63		
OVARC1001232	2.91	4.18	7.74	6.75	6.02	5.65		
OVARC1001240	2.05	3.27	6.84	5.55	5.06	5.4		
OVARC1001243	0.94	2.59	1.76	3.64	2.64	1.86		
OVARC1001244	9.07	12.05	18	21.61	18.57	26.62		
OVARC1001246	30.48	50.95	48.51	80.54	100.83	101.88	**	+
OVARC1001247	3.64	9.86	7.7	6.57	7.02	4.49		
OVARC1001260	1.05	9.07	1.85	2.62	2.65	1.85		
OVARC1001261	4.23	10.5	6.99	3.46	2.08	2.94		
OVARC1001268	24.4	19.69	52.37	32.58	35.32	14.16		
OVARC1001270	14.46	15.1	20.83	9.69	9.8	8.65	*	−
OVARC1001271	2.62	3.62	3.88	3.95	7.02	4.26		
OVARC1001282	0.88	3.02	3.09	1.37	1.59	2		
OVARC1001296	3.02	8.06	2.3	3.04	4.11	5.41		
OVARC1001306	1.48	8.27	2.4	2.04	2.29	3.82		
OVARC1001314	0.49	8.47	1.57	1.06	1.79	1.32		
OVARC1001316	2.77	7.17	4.81	5.48	8.11	5.36		
OVARC1001329	6.12	6.18	21.11	17.09	19.29	16.22		
OVARC1001330	0.2	1.89	1.38	1.22	1.35	1.42		
OVARC1001336	1.92	3.7	3.59	5.67	4.09	4.02		
OVARC1001338	0.26	2.87	0.86	2.49	1.71	1.07		
OVARC1001339	12.07	18.29	22.73	33.65	32.72	37.29	**	+
OVARC1001340	0.72	4.83	1.23	1.33	2.44	1.3		
OVARC1001341	4.35	9.25	6.77	7.94	11.38	9.69		
OVARC1001342	90.37	98.53	136.12	129.68	163.22	127.78		
OVARC1001344	2.1	2.51	6.27	6.52	6.89	6.2		
OVARC1001357	5.61	8.93	16.02	15.52	11.34	11.69		
OVARC1001359	8.96	12.4	16.15	21.66	13.84	10.6		
OVARC1001360	0.44	2.52	0.99	1.97	2.6	1.62		
OVARC1001369	1.56	5.66	1.89	3.41	1.88	3.1		

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OVARC1001372	0.96	4.23	3.33	1.52	2.77	1.95		
OVARC1001376	1.82	5.1	3.62	5.79	5.79	4.18		
OVARC1001381	4.51	6.44	9.94	10.95	12.91	11.21		
OVARC1001391	0.5	1.62	1.44	1.88	1.27	1.26		
OVARC1001392	2.12	4.69	6.14	11.96	12.7	7.79	*	+
OVARC1001399	0.98	3.59	2.16	1.77	2.54	1.1		
OVARC1001417	1.01	3.07	1.76	2.39	3.61	2.81		
OVARC1001419	2.47	5.4	3.06	4.39	4.03	3.16		
OVARC1001425	2.29	5.58	5.15	8.76	8.5	8.07	*	+
OVARC1001436	1.37	5.85	2.54	2.9	3.57	3.18		
OVARC1001442	0.64	4.84	1.39	2.27	1.52	0.69		
OVARC1001451	3.09	2	3.89	5.18	5.98	4.75	*	+
OVARC1001452	1.35	2.41	2.87	2.96	4.69	3.13		
OVARC1001453	1.21	2.84	1.88	2.3	1.82	1.57		
OVARC1001476	10.67	14.38	16.52	17.22	12.9	13.09		
OVARC1001480	0.93	4.73	1.5	3.1	2.98	2.21		
OVARC1001489	0.97	6.89	2.51	3.01	2.83	2.09		
OVARC1001493	2.09	6.59	3.75	7.38	8.78	10.48	*	+
OVARC1001496	4.65	9.58	8.63	10.74	7.37	11.03		
OVARC1001499	1.24	1.18	2.6	3.47	2.68	2.84		
OVARC1001506	2.9	2.7	5.31	5.33	6.73	5.48		
OVARC1001509	1.73	3.89	3.69	4.07	4.59	3.07		
OVARC1001510	0.16	3.69	1.42	1.94	1.73	0.86		
OVARC1001516	2.57	5.78	3.85	6.04	4.97	4.39		
OVARC1001525	0.53	4.76	2.12	1.94	2.01	1.81		
OVARC1001542	8.8	12.86	13.01	15.91	13.63	17.23		
OVARC1001544	2.14	6.6	6.72	7.54	8.33	6.22		
OVARC1001546	4.08	4.32	4.6	6.12	5.31	7.23	*	+
OVARC1001547	1.29	2.53	1.68	2.44	1.85	2.22		
OVARC1001555	10.39	16.51	68.77	48.66	65.39	56.39		
OVARC1001560	3.35	4.91	5.52	5.36	4.93	5.34		
OVARC1001569	1.63	4.75	4.79	5.92	5.19	5.1		
OVARC1001570	3.96	7.9	6.93	7.72	10.7	8.55		
OVARC1001577	1.68	5.89	5.41	8.61	6.9	10.2		
OVARC1001578	0.25	3.47	-0.19	-0.47	0.24	0.15		
OVARC1001596	12.13	11.65	14.23	13.51	14.82	27.15		
OVARC1001600	1.13	2.9	1.48	2.81	2.67	3.67		
OVARC1001607	6.22	7.72	10.91	13.42	14.01	13.45	*	+
OVARC1001610	1.81	5.25	2.84	4.25	2.66	2.7		

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OVARC1001611	0.13	5.11	1.24	1.48	2.89	1.79		
OVARC1001615	0.58	5.42	1.93	1.54	2.56	1.74		
OVARC1001636	1.09	3.75	1.05	2.39	2.05	2.15		
OVARC1001668	3.77	6.75	10.04	10.5	11.4	10.48		
OVARC1001702	1.18	2.21	2.42	3.86	2.07	2.25		
OVARC1001703	2.82	3.18	2.97	2.64	4.71	4.65		
OVARC1001710	3.58	7.03	8.67	8.01	6.28	9.55		
OVARC1001711	1.96	7.3	3.36	5.01	4.15	5.4		
OVARC1001713	9.17	11.54	44.65	36.47	51.48	43.79		
OVARC1001725	1.01	5.45	6.11	2.56	3.77	4.01		
OVARC1001726	1.64	4.48	3.23	4.97	5.6	5.18		
OVARC1001727	1.4	2.41	1.52	1.43	2.35	1.14		
OVARC1001731	120.62	110.86	255.43	140.73	139.03	74.2		
OVARC1001735	1.29	3.44	3.54	3.75	3.25	2.89		
OVARC1001741	3.3	4.73	15.28	13.09	12.93	13.17		
OVARC1001745	2.72	5.39	6.83	9.17	10.23	8.89	*	+
OVARC1001759	3.31	9.01	6.31	7.61	7.61	11.95		
OVARC1001762	3.96	7.78	6.38	10.3	11.01	13.4	*	+
OVARC1001766	5.33	7.8	11.99	15.56	16.86	15.33	*	+
OVARC1001767	0.94	3.76	1.18	1.97	1.96	2.41		
OVARC1001768	3.31	3.86	3.76	5.35	4.59	3.54		
OVARC1001770	3.04	6.58	9.98	11.46	9.08	9.46		
OVARC1001776	2.11	4.7	3.5	4.72	3.64	2.92		
OVARC1001791	1.13	4.77	3.54	3.07	3.12	3.42		
OVARC1001795	0.89	6.19	1.24	2.31	2.87	2.11		
OVARC1001798	2.81	12.11	7.57	9.72	11.93	9.04		
OVARC1001802	1.73	11.64	4.9	5.6	5.93	4.01		
OVARC1001805	1.92	6.96	2.58	3.62	4.59	3.51		
OVARC1001807	1.9	2.53	4.18	3.06	3.12	2.46		
OVARC1001809	12.38	14.06	76.32	55.87	81.41	52.83		
OVARC1001812	1.44	3.39	3.15	3.23	4.63	3.71		
OVARC1001813	1.61	4.29	2.33	2.93	3.98	2.51		
OVARC1001820	1.67	7.15	3.21	3.47	3.76	3.22		
OVARC1001828	0.78	6.85	2.36	1.91	3.23	2.2		
OVARC1001833	1.07	8.12	2.02	2.4	2.1	1.92		
OVARC1001839	1.56	8.43	2.98	2.91	3.59	1.15		
OVARC1001846	1.91	1.38	2.9	2.15	2.11	1.8		
OVARC1001849	1.21	2.52	2.42	5.79	3.69	4.03	*	+
OVARC1001861	1.46	3.56	2.73	2.78	2.5	2.09		

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OVARC1001873	3.09	3.78	4.68	5.47	4.42	4.73		
OVARC1001879	1.44	6.08	3.48	2.35	2.93	2.22		
OVARC1001880	0.91	7.84	2.94	3.63	5.78	3.8		
OVARC1001883	0.99	7.61	3.12	2.61	3.42	2.52		
OVARC1001900	1.11	7.07	4.03	2.57	3.61	2.89		
OVARC1001901	0.54	1.84	1.21	2.42	1.37	2.43		
OVARC1001911	0.59	1.57	1.66	1.51	1.39	1.55		
OVARC1001916	1.86	3.13	3.35	4.16	4.61	3.51		
OVARC1001928	1.45	3.53	1.55	1.58	1.62	1.72		
OVARC1001937	5.12	11.69	8.13	17.41	11.63	15.16		
OVARC1001940	1.1	4.51	3.13	3.72	3.14	2.78		
OVARC1001942	3.85	7.4	8.03	11.47	13.91	12.77	*	+
OVARC1001943	7.16	10.07	11.08	9.62	13.85	11.87		
OVARC1001949	1.69	3.34	4.15	5.35	4.01	5.55		
OVARC1001950	1.53	2.41	3.79	6.3	4.35	3.98		
OVARC1001952	11.3	11.38	53.57	52.33	78.84	38.05		
OVARC1001954	1.12	2.99	2.2	3.09	2.67	2.05		
OVARC1001963	1	4.91	2.89	4.5	3.39	3.21		
OVARC1001983	3.62	14.16	14.25	20.96	19.21	21.67		
OVARC1001987	3.12	6.54	5.94	6.08	8.39	8.02		
OVARC1001989	1.41	5.2	4.96	4.54	5.59	5.26		
OVARC1001991	1.74	3.27	4.08	4.57	3.86	3.27		
OVARC1002005	4.14	3.55	7.66	10.01	9.06	8.2	*	+
OVARC1002044	3.73	3.94	6.17	6.57	8.32	6.99	*	+
OVARC1002046	10.28	16.21	20.07	29.4	37.78	37.02	**	+
OVARC1002050	1.7	5.6	2.43	3.96	3.82	2.53		
OVARC1002058	4.23	6.11	4.02	4.69	5.55	5.43		
OVARC1002066	11.47	13.5	25.49	26.02	28.69	22.63		
OVARC1002082	3.6	8.55	8.81	9.6	8.89	6.49		
OVARC1002091	3.17	5.67	8.37	9.49	5.49	7.64		
OVARC1002092	1.38	2.72	2.2	4	3.97	1.88		
OVARC1002093	1.79	3.1	4.51	5.01	4.44	3.88		
OVARC1002094	1.55	6.24	4.17	36.42	27.25	28.35	**	+
OVARC1002107	1.42	4.63	2.69	4.86	5.48	3.6		
OVARC1002112	6.17	11.59	8.5	13.47	17.48	11.92		
OVARC1002126	2.66	6.35	6.68	7.95	6.44	8.79		
OVARC1002127	0.73	5.04	1.86	1.92	2.61	1.52		
OVARC1002138	1.4	1.79	1.86	3.16	4.82	2.75	*	+
OVARC1002143	0.73	1.51	1.55	1.29	3.03	2.09		

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OVARC1002156	2.42	3.87	4.19	4.43	3.9	3.65		
OVARC1002158	0.88	2.63	1.6	2.36	1.57	1.51		
OVARC1002165	4.85	6.3	9.83	10.73	14.03	10.87		
OVARC1002176	0.86	5.08	3.59	2.01	3.46	2.64		
OVARC1002178	0.83	5.35	3.12	3.8	5.02	4.25		
OVARC1002182	1.29	2.89	3.77	2.45	4.64	3.12		
OVARC1002185	11.45	13.19	62.79	43.91	53.43	55.56		
PLACE1000004	1.42	3.23	2.35	3.87	4.25	4.05	*	+
PLACE1000005	1.18	3.06	3.3	5.27	5.31	4.83	*	+
PLACE1000006	2.01	8.33	3.23	4.2	5.44	4.67		
PLACE1000007	0.97	5.13	2.89	3.03	2.47	2.56		
PLACE1000014	2.9	8.06	6.26	6.67	8.18	6.55		
PLACE1000031	0.88	4.81	0.45	2.61	2.71	2.79		
PLACE1000033	1.23	2.15	2.75	2.42	3.17	2.56		
PLACE1000040	3.08	4.43	6.18	7.11	5.54	7.37		
PLACE1000048	1.83	3.24	2.14	3.32	3.96	3.74		
PLACE1000050	2.12	5.36	9.1	9	6.55	8.25		
PLACE1000061	138.29	147.36	249.77	165.55	233.98	230.37		
PLACE1000066	14.23	15	19.46	15.86	15.62	18.52		
PLACE1000075	3.03	6.24	9.08	4.98	6.93	7.11		
PLACE1000078	2.1	5.75	5	6.07	6.93	5.19		
PLACE1000081	1.08	1.88	1.52	1.13	1.89	1.27		
PLACE1000086	4.97	6.55	11.25	8.1	9.16	7.75		
PLACE1000094	0.7	4.18	1.72	1	3.44	2.96		
PLACE1000101	4.67	8.44	7.7	11.69	10.38	13.65	*	+
PLACE1000121	0.87	6.29	2.02	1.95	2.85	2.39		
PLACE1000133	6.65	11.93	17.66	15.19	17.59	21.71		
PLACE1000142	1.79	6.03	5.66	2.64	4.77	4.24		
PLACE1000146	1.95	4.51	2.89	3.71	5.02	2.82		
PLACE1000163	4.52	5.99	10.71	16.27	10.95	13.78		
PLACE1000172	1.12	2.63	1.48	1.81	3.21	2.29		
PLACE1000181	1.06	3	2.98	2.63	3.75	2.86		
PLACE1000184	1.17	3.08	1.48	1.87	3.28	2.27		
PLACE1000185	2.99	6.52	8.47	9.53	9.99	12.03		
PLACE1000198	0.78	4.09	2.49	2.19	2.17	1.93		
PLACE1000213	3.3	5.87	7.36	4.35	5.38	8.09		
PLACE1000214	1.37	4.29	4.54	5.22	6.72	4.22		
PLACE1000220	9.61	7.84	16.78	7.48	5.77	4.1		
PLACE1000231	2.48	4.1	4.92	4.57	4.65	3.91		

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PLACE1000236	0.66	3.33	2.43	2.8	3.63	2.37		
PLACE1000245	2.92	5.88	6.34	9.34	11.24	10.55	*	+
PLACE1000246	5.15	8.27	9.95	3.29	2.55	2.86	*	-
PLACE1000258	5.4	12.61	13.52	14.88	16.7	14.95		
PLACE1000288	1.68	7.22	2.96	2.83	4.02	2.48		
PLACE1000292	3.72	9.02	8.85	10.23	20.58	9.21		
PLACE1000302	0.56	1.01	1.39	1.07	0.92	0.62		
PLACE1000304	1.13	3.26	3.17	3.75	2.32	3.05		
PLACE1000308	2.54	4.35	4.17	4.42	3.87	1.34		
PLACE1000309	2.29	4.02	4	6.72	5.23	7.88	*	+
PLACE1000312	1.33	3.44	2.48	2.74	3.99	2.5		
PLACE1000330	0.46	5.76	3.02	1.32	1.93	1.35		
PLACE1000332	1.02	8.82	2.01	3.01	3.78	1.68		
PLACE1000347	2.3	9.48	3.89	2.59	5.81	3.22		
PLACE1000351	1.2	1.5	2.87	2.2	2.4	2		
PLACE1000374	2.01	3.03	7.02	8.89	6.55	6.85		
PLACE1000380	2.39	4.27	3.95	4.9	2.12	2.38		
PLACE1000383	1.03	2.62	1.9	2.53	3.64	2.4		
PLACE1000397	0.63	4.06	1.89	2.82	3.34	3.47		
PLACE1000401	1.22	6.39	2.24	2.23	3.05	2.36		
PLACE1000406	1.08	8.76	3.4	3.72	4.08	3.64		
PLACE1000412	1.61	6.38	1.56	1.62	3.45	1.46		
PLACE1000420	2.59	3.51	4.6	8.95	7.28	5.6	*	+
PLACE1000421	0.99	1.3	2.32	2.97	2	1.7		
PLACE1000423	16.6	23.29	32.85	10.67	8.02	8.09	*	-
PLACE1000424	1.36	3.09	2.12	3.35	2.65	1.97		
PLACE1000430	0.77	4.36	1.95	3.51	2.94	3.77		
PLACE1000433	1.06	5.9	1.65	1.89	2.6	1.8		
PLACE1000435	1.39	7.21	4.77	6.22	6.29	4.22		
PLACE1000437	6.06	10.65	10.14	17.29	20.07	18.79	**	+
PLACE1000442	3.75	3.85	6.27	7.81	5.7	6.7		
PLACE1000444	2.14	3.94	8.96	11.14	11.55	9.8		
PLACE1000453	5.57	11.03	14.16	10.42	7.4	2.99		
PLACE1000456	1.25	2.21	1.97	1.33	2.18	1.07		
PLACE1000465	2.09	5.63	6.62	12.97	11.8	10.69	**	+
PLACE1000481	2.32	8.1	3.73	6.89	6.64	6.45		
PLACE1000492	1.15	4.45	2.95	3.27	3.06	2.81		
PLACE1000508	1.36	4.64	4	3.91	4.24	3.71		
PLACE1000512	4.91	4.29	6.39	8.12	7.8	4.6		

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PLACE1000540	5.18	3.93	7.84	5.44	6.9	5.57		
PLACE1000541	13.59	15.07	48.84	60.62	81.24	41.96		
PLACE1000546	0.86	3.61	2.82	4.72	4.63	2.5		
PLACE1000547	2.16	4.61	3.83	6.31	5.64	5.92	*	+
PLACE1000560	2.08	5.97	2.1	1.62	2.8	1.72		
PLACE1000562	2.8	6.23	6.04	8.86	11.26	8.61	*	+
PLACE1000564	1.54	6.4	3.07	3.16	4.41	3.43		
PLACE1000583	3.75	3.28	6.32	6.78	11.53	6.8		
PLACE1000587	8.52	9.32	12.99	13.64	14.69	9.43		
PLACE1000588	1.92	4.36	3.99	8.79	8.15	4.48		
PLACE1000596	1.99	5.34	4.39	7.8	6.74	4.51		
PLACE1000599	2.39	5.51	7.05	7.92	7.79	6.46		
PLACE1000605	5.12	11.43	7.06	14.2	15.1	12.67	*	+
PLACE1000610	2.01	6.08	3.54	5.26	4.48	2.94		
PLACE1000611	13.18	19.13	24.68	16.45	20.37	22.79		
PLACE1000626	3.19	4.04	8.04	5.71	9.93	8.12		
PLACE1000633	1.32	2.12	3.95	4.8	6.06	3.59		
PLACE1000636	1.15	2.54	1.43	2.72	4.25	2.94		
PLACE1000653	5.07	8.56	9.29	11.07	11.87	14.08	*	+
PLACE1000656	4.2	12.9	25.22	16.66	16.71	12.92		
PLACE1000663	2	6.43	3.59	2.39	6.61	4.03		
PLACE1000706	2	6.3	5.04	5.37	7.27	6.26		
PLACE1000712	3.9	9.52	10.82	10.49	10.07	9.11		
PLACE1000716	0.98	2.75	3.44	2.44	3.2	2.82		
PLACE1000740	2.74	5.28	6.24	8.83	8.13	9.69	*	+
PLACE1000748	3.35	3.51	6.81	3.12	5.02	4.23		
PLACE1000749	3.49	6.35	5.94	4.61	4.65	6.02		
PLACE1000751	2.71	5.34	4.07	7.81	8.32	8.36	**	+
PLACE1000755	1.39	6.14	1.93	2.55	5.1	2.96		
PLACE1000769	2.29	6.8	3.45	3.33	4.58	2.6		
PLACE1000778	0.87	1.48	1.99	2.05	2.94	2.38		
PLACE1000785	9.56	12.21	27.18	28	24.34	29.54		
PLACE1000786	2.68	4.22	3.63	3.09	3.77	3.7		
PLACE1000793	4.05	7.21	6.7	6.06	7.6	9.1		
PLACE1000795	2.15	5.5	3.99	4.44	5.29	4.31		
PLACE1000798	0.88	8.44	3.24	3.13	3.8	3.72		
PLACE1000812	2.13	5.08	4.46	5.06	5.16	6.03		
PLACE1000823	1.71	5.2	4.89	5.67	7.28	4.84		
PLACE1000825	1.6	2.86	2.02	3.77	3.96	3.76	*	+

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PLACE1000838	16	15.77	23.73	13.88	15.6	15.65		
PLACE1000841	1.22	3.78	3.31	3.97	10.65	3.77		
PLACE1000843	2.14	6.2	5.68	5.79	7.7	5.38		
PLACE1000849	2.79	8.82	6.72	7.24	6.78	10.02		
PLACE1000856	2.01	5.3	3.59	3.42	4.79	4.19		
PLACE1000863	5.2	7.58	9.56	8.97	12.34	11.53		
PLACE1000876	3.65	7.6	6.02	6.7	9.95	9.06		
PLACE1000899	1.36	2.24	3.12	4.12	5.14	4.22	*	+
PLACE1000907	4.82	5.53	9.59	6.77	8.44	5.83		
PLACE1000909	1.18	3.31	2.45	3.65	3.88	3.44		
PLACE1000912	0.42	4.55	1.77	1.76	2.72	1.46		
PLACE1000914	1.05	4.41	3.5	3	6.09	4.22		
PLACE1000918	0.54	4.49	1.61	1.82	3.13	1.98		
PLACE1000927	10.48	12.41	16.9	20.91	23.21	25.47	*	+
PLACE1000931	0.69	3.44	2.12	2.44	3.94	3.3		
PLACE1000944	2.55	2.24	4.78	3.84	3.32	2.09		
PLACE1000948	0.52	2.31	2.96	2.21	2.72	1.72		
PLACE1000958	0.12	2.2	1.73	1.11	1.77	2.27		
PLACE1000972	1.01	3.43	2.89	4.49	5.33	3.75		
PLACE1000977	2.33	5.67	4.42	2.71	5.33	5.25		
PLACE1000979	1.63	8.01	3.93	4.24	5.92	4.57		
PLACE1000986	3.37	16.51	6.63	6.97	8.75	7.69		
PLACE1000987	1.76	10.13	4.79	4.17	4.74	5.11		
PLACE1001000	4.85	4.62	7.76	6.02	4.25	3.02		
PLACE1001007	7	6.94	14.66	5.39	3.76	3.47		
PLACE1001010	0.61	2.04	2.45	2.56	2.73	2.84		
PLACE1001015	0.88	2.55	1.84	2.36	1.72	2.42		
PLACE1001016	1.79	4.54	4.29	6.37	9	6.57	*	+
PLACE1001022	0.68	6.5	2.45	1.9	2.39	1.29		
PLACE1001024	1.05	8.89	1.83	1.34	2.49	2.35		
PLACE1001036	2.63	10.55	5.42	3.62	5.49	5.43		
PLACE1001038	50.16	49.81	118.83	82.67	64.83	52.8		
PLACE1001048	1.07	1.82	0.92	2.39	2.09	1.21		
PLACE1001054	9.95	10.74	63.88	62.96	79.44	66.71		
PLACE1001062	1.45	4.19	3.71	3.12	4.17	3.05		
PLACE1001063	1.35	3.74	2.2	4.06	3.65	2.74		
PLACE1001076	0.46	6.48	1	1.86	2.18	1.62		
PLACE1001081	1.53	7.95	3.33	3.65	5.24	4.8		
PLACE1001088	1.32	5.24	1.22	1.42	2.81	1.37		

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PLACE1001092	2.31	2.47	4.68	5.8	4.18	3.9		
PLACE1001098	0.93	2.62	4.53	5.49	4.05	3.17		
PLACE1001100	1.31	2.58	2.48	4.27	4.17	3.37	*	+
PLACE1001104	1.95	4.09	4.54	3.39	3.42	4.47		
PLACE1001114	1.56	6.54	4.33	5.17	3.78	3.27		
PLACE1001118	2.52	5.77	6.12	6.21	6.14	5.1		
PLACE1001123	2.86	5.3	7.53	7.08	8.51	7.63		
PLACE1001136	1.58	4.39	5.13	5.29	5.95	5.85		
PLACE1001144	6.27	5.67	13.43	10.34	11	10.08		
PLACE1001147	2.11	2.98	6.03	6.13	5.15	4.83		
PLACE1001148	1.72	1.31	1.89	1.76	2.39	2.31		
PLACE1001159	0.86	2.37	2.05	2.27	3.73	1.43		
PLACE1001168	8.87	14.52	15.09	25.46	23.18	30.79	*	+
PLACE1001171	0.69	3.89	1.23	2.53	1.42	1.53		
PLACE1001183	0.24	3.61	1.81	1.57	2.78	1.38		
PLACE1001185	3.13	7.43	3.76	5	6.4	5.64		
PLACE1001201	1.77	2.8	3.29	6.32	6.94	6.32	**	+
PLACE1001229	7.51	8.56	12.64	15.24	11.45	10.42		
PLACE1001231	1.83	2.73	3.07	4.09	5.1	2.3		
PLACE1001238	1.52	4.35	3.74	3.65	4.52	4.57		
PLACE1001241	1.63	5.58	2.92	5.73	8.13	7.04		
PLACE1001242	22.28	29.54	30.28	46.43	48.89	62.65	*	+
PLACE1001247	2.43	7.02	4.07	5.03	5.91	4.52		
PLACE1001250	1.01	5.36	3.61	4.68	4.39	4.81		
PLACE1001257	2.99	3.06	7.06	7.89	9.21	7.69		
PLACE1001272	3.19	4.27	5.68	7.13	6.43	5.14		
PLACE1001279	0.96	3.12	2.74	3.08	3.81	3.29		
PLACE1001280	1.08	4.75	2.68	4.98	4.45	2.86		
PLACE1001294	1.91	7.23	6.91	4.88	5.57	6.18		
PLACE1001295	4.16	9.94	7.53	8.55	11.85	8.43		
PLACE1001300	2.46	7.9	4.31	4.65	14.73	4.95		
PLACE1001304	3	8.27	10.47	8.57	10.81	10.64		
PLACE1001311	3.95	3.34	5.67	6.85	9.14	7.6	*	+
PLACE1001323	2.17	2.95	5.12	5.66	8.43	5.5		
PLACE1001325	0.88	1.95	3.71	2.84	3.56	3.27		
PLACE1001340	5.18	6.99	9.8	8.69	12.02	10.48		
PLACE1001344	1.52	3.49	1.77	2.34	2.06	1.75		
PLACE1001351	3.23	6.39	8.39	6.4	8.62	6.1		
PLACE1001366	1	4.49	4.02	4.19	4.6	3.72		

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PLACE1001377	3.02	4.97	5.1	7.91	7.28	5.83	*	+
PLACE1001383	2.31	4.13	3.53	2.62	5.5	5.72		
PLACE1001384	1.81	3.23	2.89	2.05	3.43	3.15		
PLACE1001387	1.65	3.64	3.7	3.03	4.83	3		
PLACE1001395	3.72	6.64	6.54	7.01	7.61	7.73		
PLACE1001399	3.71	6.58	9.31	7.37	8.61	9.22		
PLACE1001401	0.83	5.25	2.33	1.55	1.76	0.87		
PLACE1001407	11.65	21.8	24.47	22.63	18.09	26.24		
PLACE1001412	1.6	4.98	4.53	4.08	4.42	3.83		
PLACE1001414	2.3	3.02	5.86	7.57	5.13	6.83		
PLACE1001416	2.99	4.71	3.29	5.62	4.04	7.08		
PLACE1001433	33.62	33.05	51.64	49.1	58.33	55.88		
PLACE1001440	1.95	3.99	3.96	3.6	3.53	2.1		
PLACE1001456	1.64	5.5	4.26	4.15	4.87	4.49		
PLACE1001464	32.76	28.05	47.41	53.22	68.42	61.32	*	+
PLACE1001468	0.85	5.04	1.17	1.56	2.55	2.27		
PLACE1001484	1.31	4.85	2.96	4.25	5.8	3.04		
PLACE1001500	0.92	2.22	2.14	2.72	3.34	3.26	*	+
PLACE1001502	1.36	3.6	3.9	3.54	5.9	4.54		
PLACE1001503	1.7	4.58	6.72	7.47	8.2	8.05		
PLACE1001505	6.34	14.13	16.16	39.97	27.14	46.65	*	+
PLACE1001513	4.09	10.82	8.17	5.87	8.53	14.61		
PLACE1001516	0.61	4.33	1.33	1.71	3.49	1.99		
PLACE1001517	5.56	8.58	14.77	14.14	14.96	14.28		
PLACE1001523	12.83	14.09	20.42	22.79	19.74	32.9		
PLACE1001526	5.12	4.89	8.42	9.51	9.11	6.89		
PLACE1001534	2.12	5.12	3.58	3.62	5.55	3.99		
PLACE1001536	0.61	2.5	1.52	2.11	3.2	1.9		
PLACE1001545	17.97	23.9	38.46	33.78	45.13	66.08		
PLACE1001551	2.55	6.26	6.15	4.72	6.59	6.71		
PLACE1001564	1.37	4.87	2.88	4.01	3.57	3.7		
PLACE1001570	2.62	5.95	4.18	2.19	3.82	4.32		
PLACE1001571	2.04	4.51	6.07	5.69	6.27	5.81		
PLACE1001595	4.73	4.64	10.04	11.6	8.27	5.28		
PLACE1001602	7.23	8.39	18.65	20.38	18.68	19.71		
PLACE1001603	2.01	3.83	5.37	6.86	5.86	4.56		
PLACE1001608	3.44	7.22	5.9	5.82	7.73	8.7		
PLACE1001610	3.77	8.4	8.22	9.26	9.49	9.85		
PLACE1001611	1.94	7.34	3.65	2.28	3.85	1.88		

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	PLACE1001629	0.78	6.77	2.24	3.62	3.36	3.52	
	PLACE1001632	1.66	8.26	4.04	4.3	4.14	4.37	
	PLACE1001634	7.4	9.92	39.12	23.85	32.41	18.38	
	PLACE1001637	0.84	2.16	1.25	1.41	2.4	1.1	
	PLACE1001640	1.33	3.27	4.66	2.68	4.85	4.49	
	PLACE1001655	0.83	2.93	2.06	2.82	2.14	2.02	
	PLACE1001672	1.84	7.04	4.01	3.3	4.41	4.09	
	PLACE1001676	1.38	8.49	3.54	4.63	4.77	3.85	
	PLACE1001683	12.79	23.62	24.61	25.33	30.22	27.13	
	PLACE1001691	3.41	12.29	6.72	9.03	8.96	9.83	
	PLACE1001692	1.47	2.96	5.25	5.87	5.6	5.13	
	PLACE1001705	3.02	3.75	9.88	10.06	9.21	8.32	
	PLACE1001716	1.68	3	2.61	2.24	3.79	3.58	
	PLACE1001720	1.49	2.62	2.21	1.56	2.45	1.71	
	PLACE1001728	1.43	6.19	4.24	1.96	2.04	2.51	
	PLACE1001729	2.12	8.13	4.44	3.8	4.52	4.36	
	PLACE1001739	2.61	9.55	4.04	4.95	7.24	6.16	
	PLACE1001740	0.92	5.36	2.09	1.92	2.1	1.69	
	PLACE1001745	1.15	0.98	3.22	1.87	2.48	2.31	
	PLACE1001746	1.04	2.25	2.55	4.64	3.4	2.82	
	PLACE1001748	4.74	7.01	8.18	8.19	6.58	5.96	
	PLACE1001753	2.06	3.54	3.29	7.44	5.57	5.82	* +
	PLACE1001756	5.6	11.31	38.07	31.78	44.99	35.99	
	PLACE1001760	6.54	12.23	12.85	16.36	16.96	16.66	* +
	PLACE1001767	11.26	14.98	59.72	45.37	61.46	45.39	
	PLACE1001771	1.96	6.64	4.03	4.32	5.22	4.54	
	PLACE1001775	2.23	2.81	6.72	5.1	3.11	4.79	
	PLACE1001777	83.34	145.9	190.82	142.92	71.27	59.69	
	PLACE1001781	1.9	3.86	4.91	8.72	3.39	2.3	
	PLACE1001783	0.76	3.21	2.06	4.84	2.09	1.54	
	PLACE1001786	1.77	6.61	2.72	3.7	3.32	2.6	
	PLACE1001788	5.16	9.07	7.14	10.52	8.74	9.32	
	PLACE1001795	1.92	4.4	4.82	5.42	4.61	5.42	
	PLACE1001799	0.69	3.62	2.11	1.86	2.83	1.97	
	PLACE1001810	0.89	1.52	1.76	2.73	3.91	1.73	
	PLACE1001817	5.53	6.12	10.88	10.56	9.4	6.38	
	PLACE1001821	4.68	6.07	7.11	8.37	9.92	4.99	
	PLACE1001836	0.91	3.12	2.38	2.69	4.12	2.63	
	PLACE1001844	1.55	5.1	3.48	4.42	4.36	4.09	

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PLACE1001845	3.62	8.38	7.39	7.88	7.55	9.93		
PLACE1001858	2.56	6.58	3.52	5.26	7.48	6.05		
PLACE1001869	3.13	7.15	4.85	6.09	6.46	5.66		
PLACE1001890	11.74	11.92	21.45	173.44	255.31	125.13	*	+
PLACE1001897	9.19	13.85	16.44	22.22	23.13	12.95		
PLACE1001902	10.13	12.6	21.53	22.74	27.67	12.77		
PLACE1001904	1.38	3.72	1.51	2.45	2.53	2.35		
PLACE1001907	3.36	6.76	5.71	7.67	5.67	5.59		
PLACE1001910	83.6	82.16	135.34	301.29	325.42	244.59	**	+
PLACE1001912	1.53	6.6	3.36	5.54	5.48	4.85		
PLACE1001918	17.31	22.95	30.16	31.14	40.44	40.02	*	+
PLACE1001920	2.07	3.51	5.43	11.97	13.8	11.4	**	+
PLACE1001928	3.06	2.96	4.67	5.29	9.7	5.31		
PLACE1001930	1.17	3.92	2.2	2.9	4.73	3.22		
PLACE1001949	1.16	3.67	1.78	3.84	4.24	3.18		
PLACE1001959	1.36	4.7	3.16	2.63	3.17	2.26		
PLACE1001969	2.09	7.83	7.21	6.56	10.73	6.57		
PLACE1001974	7.39	11.98	11.87	11.43	16.09	16.06		
PLACE1001981	0.77	4.38	3.22	1.77	3.88	2.36		
PLACE1001983	3.81	4.12	5.32	5.92	6.16	5.72	*	+
PLACE1001989	2.34	4.15	5.02	4.37	5.91	3.72		
PLACE1002004	3.07	4.06	8.05	9.22	9.69	7.18		
PLACE1002008	8.4	11.76	17	23.36	22.19	22.42	*	+
PLACE1002015	26.96	30.92	67.62	105.75	88.42	94.15	*	+
PLACE1002044	3.79	8.07	5.86	4.64	6.39	6.4		
PLACE1002046	1.78	5.68	1.9	4.3	5.79	4.97		
PLACE1002052	1.09	4.98	2.26	1.38	2.41	2.32		
PLACE1002066	4.79	6.3	8.29	10.24	10.77	9.93	*	+
PLACE1002072	2.55	3.91	4.86	6	5.48	6	*	+
PLACE1002073	0.51	2.83	2.29	2.35	4.06	2.91		
PLACE1002080	1.81	6.49	6.13	4.76	6.82	5.72		
PLACE1002081	1.66	6.13	4.06	3.74	4.86	4.3		
PLACE1002090	7.74	16.55	13.87	12.53	14.4	19.41		
PLACE1002095	2.97	6.22	8.45	10.01	10.18	11.32	*	+
PLACE1002102	4.26	8.56	8.81	9.47	9.56	10.67		
PLACE1002109	2.57	5.08	3.81	4.66	6.17	6.32		
PLACE1002115	1.75	3.57	2.48	2.78	4.26	2.59		
PLACE1002119	15.65	15.3	35.78	37.28	32.59	38.23		
PLACE1002140	5.25	8.45	14.05	19.93	17.14	17.19	*	+

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PLACE1002150	1.54	8.26	4.25	3.23	5.36	4.12		
PLACE1002153	1.6	5.75	2.58	3.47	5.76	4.48		
PLACE1002157	0.87	2.96	1.72	1.76	3.28	3.73		
PLACE1002163	2.13	4.67	4.55	6.21	8.81	6.03		
PLACE1002168	2.39	4.04	4.42	4.68	6.28	3.22		
PLACE1002170	2.73	3.53	7.35	4.89	5.33	3.74		
PLACE1002171	3.09	6.11	10.02	18.44	14.63	13.93	*	+
PLACE1002180	3.16	6.23	6.77	4.63	8.54	8.39		
PLACE1002184	9.2	15.58	18.42	124.63	250.27	333.14	*	+
PLACE1002200	1.35	5.67	2.38	2.97	2.89	2.26		
PLACE1002205	3.3	6.47	18.07	17.08	18.38	14.61		
PLACE1002213	2.2	4.16	4.93	5.52	8.03	6.03		
PLACE1002219	1.05	1.91	2.23	3.33	3.53	1.96		
PLACE1002227	0.68	2.65	1.7	1.5	3.03	1.67		
PLACE1002253	0.32	2.67	1.28	1.47	0.76	0.43		
PLACE1002256	1.16	4.78	3.31	3.54	3.01	4.79		
PLACE1002259	1.46	5.69	4.48	3.22	2.98	2.31		
PLACE1002285	1.16	10.74	2.29	1.55	2.38	1.24		
PLACE1002301	9.42	17.5	14.68	12.7	10.48	11.7		
PLACE1002310	4.28	10.16	9.86	8.82	7.87	9.94		
PLACE1002311	1.84	2.94	3.87	2.96	2.87	2.03		
PLACE1002319	2.31	2.64	2.94	3.21	3.23	3.92	*	+
PLACE1002329	0.56	2.54	2.5	4.07	3.58	3.07		
PLACE1002333	1.34	3.1	1.96	1.22	2.44	2		
PLACE1002342	4.19	9.04	9.44	5.06	8.52	8.17		
PLACE1002343	0.49	6.98	2.94	2.08	1.9	2.52		
PLACE1002355	1.31	9.39	2.36	3.33	4.35	2.63		
PLACE1002358	1.15	7.94	3.3	2.6	2.65	2.13		
PLACE1002359	1.91	2.17	3.47	4.7	3.91	3.42		
PLACE1002374	29.69	28.18	54.19	53.9	34.73	36.14		
PLACE1002376	3.58	5.91	7.86	6.23	6.82	6.56		
PLACE1002379	6.24	7.66	6.63	10.13	9.68	10.9	**	+
PLACE1002386	0.86	5.32	1.35	1.87	2.05	1.51		
PLACE1002395	3.69	9.97	17.13	16.43	20.62	16.16		
PLACE1002399	2.38	11.09	3.42	5.31	10.38	7.39		
PLACE1002407	1.09	5.22	2.31	2.3	4.01	3.66		
PLACE1002433	1.63	2.17	2.97	2.96	4.35	3.66		
PLACE1002437	0.79	1.4	1.47	1.41	3.28	1.35		
PLACE1002438	0.74	2.38	1.96	1.8	2.43	3.38		

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PLACE1002446	4.64	8.42	5.95	10.27	8.88	11.99	*	+
PLACE1002447	1.26	6.06	2.05	3.92	3.14	4.32		
PLACE1002450	1.19	5.92	3.24	4.32	4.21	5.05		
PLACE1002462	0.81	4.02	2.94	3.51	2.99	3.13		
PLACE1002465	0.96	4.69	2.2	2.69	4.31	2.24		
PLACE1002474	1.61	2.26	3.23	3.85	4.41	3.6	*	+
PLACE1002477	11.11	14.51	32.39	44.06	41.42	26.68		
PLACE1002493	3.39	4.1	10.1	14.39	16.66	9.49		
PLACE1002497	0.68	2.81	0.67	1.45	0.93	0.99		
PLACE1002499	2.12	4.73	3	5.98	6.44	5.28	*	+
PLACE1002500	2.61	6.52	7.36	7.58	10.45	7.25		
PLACE1002514	0.3	4.49	1.84	1.74	2.47	1.75		
PLACE1002518	2.86	7.65	6.9	5.62	7.55	4.67		
PLACE1002529	1.14	1.56	2.21	3.19	3.4	1.44		
PLACE1002532	1.31	1.82	3.18	5.75	4.94	5.59	**	+
PLACE1002536	3.59	3.75	3.44	5.84	6.07	3.85		
PLACE1002537	1.63	4.06	2.7	2.69	4.07	3.08		
PLACE1002539	1.86	5.68	2.75	4.53	5.29	4.78		
PLACE1002547	6.09	8.06	7.3	12.32	11.02	11.26	**	+
PLACE1002571	2.84	6.85	5.19	6.84	8.65	6.23		
PLACE1002578	3.57	8.34	8.35	11.11	12.19	8.11		
PLACE1002583	1.33	1.61	2.32	3.18	4.02	2.46		
PLACE1002591	0.82	1.62	2.34	3.25	4.43	1.92		
PLACE1002598	6.56	10.95	12.39	11.93	9.04	7.74		
PLACE1002604	1.73	3.57	2.69	3.75	5.38	3.51		
PLACE1002612	2.89	8.47	5.95	11.25	10.88	8.06		
PLACE1002625	1.25	4.79	3.18	2.7	3.25	1.82		
PLACE1002638	2.94	8.01	6.66	7.78	6.81	7.29		
PLACE1002655	1.39	6.51	5.57	7.19	7.62	6.46		
PLACE1002665	4.57	3.88	5.4	7.47	12.16	10.75	*	+
PLACE1002685	0.58	1.12	1.3	0.67	2.43	0.98		
PLACE1002692	7.42	8.56	16.7	19.27	22.67	16.29		
PLACE1002714	1.8	3	2.11	2.43	3.14	2.24		
PLACE1002721	2.94	4.37	3.88	5.88	7.1	4.28		
PLACE1002722	0.92	5.42	1.97	1.37	3.28	1.85		
PLACE1002726	1.6	6.24	3.66	4.6	5.7	5.26		
PLACE1002756	1.57	4.5	7.04	5.92	9.63	7.78		
PLACE1002768	1.05	3.72	2.16	2.1	2.34	1.71		
PLACE1002772	0.54	2.15	1.32	2.49	2.86	2.3		

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PLACE1002775	4.33	4.71	9.15	7.05	7.08	8.67		
PLACE1002780	185.63	218.72	325.36	272.21	244.38	305.38		
PLACE1002782	0.4	3.76	1.1	1.62	1.69	1.14		
PLACE1002794	1.5	6.71	3.27	2.26	4.59	4.36		
PLACE1002795	1.92	6.45	0.81	2.37	3.63	2.77		
PLACE1002811	0.6	1.57	1.34	1.9	1.46	1.16		
PLACE1002815	6.39	7	10.49	7.24	3.16	9.21		
PLACE1002816	8.5	9.72	9.05	7.22	8.2	7.97	*	-
PLACE1002822	0.58	2.51	2.06	2.2	2.87	1.94		
PLACE1002833	9.98	15.11	16.78	15.42	15.99	16.56		
PLACE1002834	3.2	8.08	6.57	6.23	6.79	8.41		
PLACE1002835	0.62	4.14	1.72	0.85	1.83	1.79		
PLACE1002839	1.13	5.75	2.72	2.89	4.72	2.81		
PLACE1002851	1.52	1.87	1.41	1.98	2.15	2.7		
PLACE1002853	4.18	6.23	9.15	6.26	5.6	7		
PLACE1002881	3.42	5.2	11.04	8.35	11.57	10.26		
PLACE1002901	9.66	12.66	20.09	24.14	25.51	30.67	*	+
PLACE1002904	0.89	7.35	1.41	1.98	1.95	3.09		
PLACE1002905	1.36	5.46	3.26	4.04	4.46	3.4		
PLACE1002908	1.6	5.19	3.18	3.84	5.27	3.81		
PLACE1002911	3.91	6.96	6.9	4.66	7.89	6.75		
PLACE1002941	1.57	2.2	2.48	3.94	2.02	2.31		
PLACE1002950	9.59	9.15	14.74	5.31	8.02	14.51		
PLACE1002955	47.83	40.69	72.7	82.17	62.5	84.64		
PLACE1002958	19.36	26.92	35.27	35.6	35.35	59.02		
PLACE1002962	1.03	4.03	2.2	1.41	2.63	1.67		
PLACE1002967	1.34	4.83	3.19	4.37	3.62	2.81		
PLACE1002968	1.2	5.14	2.7	2.55	3.05	1.81		
PLACE1002976	8.94	12.08	24.23	24.5	36.89	30.05		
PLACE1002991	2.68	3.05	6.66	3.49	4.56	3.6		
PLACE1002993	2.72	3.86	5.52	8.21	6.92	5.56		
PLACE1002996	2.02	3.03	3.43	5.54	3.52	3.01		
PLACE1003010	1.91	3.69	4.27	4.31	3.86	3.32		
PLACE1003025	2.85	7.01	6.1	8.57	11.37	10.11	*	+
PLACE1003027	5.02	13.08	9.31	8.55	12.45	12.76		
PLACE1003044	1.95	8.24	2.61	3.64	4.16	2.74		
PLACE1003045	1.41	7.75	1.77	1.88	2.64	1.01		
PLACE1003052	2.19	3.16	5.74	4.44	3.6	1.99		
PLACE1003083	1.59	3.04	3.23	3.06	1.61	2.25		

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PLACE1003085	3.91	6.19	5.6	9.46	5.89	3.33		
PLACE1003092	3.94	4.87	6.25	7	5.6	6.17		
PLACE1003097	0.37	3.06	1.44	2.12	1.88	1.63		
PLACE1003100	1.65	7.1	4.2	3.88	4.74	4.29		
PLACE1003108	1.26	10.37	2.91	3.32	4.44	2.39		
PLACE1003115	11.39	18.3	58.59	73.64	99.24	69.1	*	+
PLACE1003120	3.1	3.08	9.71	11.34	8.32	10.19		
PLACE1003135	0.72	2.04	1.09	1.56	2.89	1.08		
PLACE1003136	3.95	5.82	6.05	9.03	6.55	7.34		
PLACE1003141	2.04	2.97	2.1	1.97	2.49	1.8		
PLACE1003145	1.21	4.17	2.52	6.24	6.88	7.67	*	+
PLACE1003147	2.87	7.85	5.71	5.02	5.25	6.28		
PLACE1003153	0.54	7.63	2.14	1.66	3.2	1.82		
PLACE1003163	6.09	13.55	8.19	8.39	14.09	12.26		
PLACE1003172	23.21	21.74	44.19	47.78	43.17	39.52		
PLACE1003174	2.31	2.49	3.75	4.3	3.55	1.68		
PLACE1003176	0.47	2	1.89	2.88	1.27	1.46		
PLACE1003181	1.72	4.19	2.72	2.5	2.76	2.36		
PLACE1003184	0.76	3.92	1.53	1.91	1.49	2.06		
PLACE1003190	2.39	9.81	8.67	10.73	7.98	10.34		
PLACE1003200	0.29	4.48	1.84	0.72	1.92	1.16		
PLACE1003205	3.94	7.07	9.68	6.82	10.38	7.2		
PLACE1003209	1.43	2.18	2.62	2.28	1.82	2.89		
PLACE1003214	0.83	1.3	2	2.15	2.44	1.81		
PLACE1003229	2.08	2.78	2.9	2.78	3.35	3.48		
PLACE1003238	0.46	2.34	1.24	1.35	2	0.75		
PLACE1003249	1.87	5.04	4.7	7.33	7.56	5.89		
PLACE1003256	3.47	7.69	7.94	8.82	7.68	6.08		
PLACE1003258	1.03	3.81	3.48	2.42	2.19	0.87		
PLACE1003279	3.09	7.19	9.02	11.15	13.56	11.58	*	+
PLACE1003294	0.95	1.54	1.59	1.57	1.25	2.64		
PLACE1003296	1.49	2.6	2.45	2.59	3.11	2.4		
PLACE1003297	7.52	10.15	31.88	23.01	23.49	19.3		
PLACE1003302	3.92	5.16	6.99	5.8	4.72	5.47		
PLACE1003334	1.51	4.41	1.91	2.4	3.59	3.09		
PLACE1003337	13.69	16.3	29.83	28.53	34.27	25.76		
PLACE1003342	1.05	4.07	1.89	2.15	2.35	1.97		
PLACE1003343	1.07	4.98	1.61	2.02	2.75	2.12		
PLACE1003344	6.25	5.33	12.83	11.18	11.35	11.98		

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PLACE1003353	19.67	16.04	40.09	37.78	42.55	40.26	
PLACE1003361	1.82	3.64	3.72	5.85	5.31	4.6	* +
PLACE1003366	1.45	4.35	3.63	3.22	3.33	2.97	
PLACE1003369	2.75	4.51	3.49	3.29	3.25	4.62	
PLACE1003372	2.08	5.73	2.68	5.45	4.72	3.39	
PLACE1003373	2.85	7.37	6.62	8.8	11.81	9.89	
PLACE1003375	1.42	4.91	1.92	2.59	2.95	3.21	
PLACE1003378	0.94	0.94	0.98	0.7	1.66	1.08	
PLACE1003383	0.87	1.55	2.33	1.59	3.15	1.57	
PLACE1003394	10.55	12.49	24.08	11.75	22.99	17.27	
PLACE1003401	0.79	3.91	1.34	1.03	2.13	1.04	
PLACE1003405	1.5	3.97	2.22	2.54	2.46	2.04	
PLACE1003407	2.39	6.06	5.16	3.96	6.3	4.02	
PLACE1003420	3.26	7.69	6.19	6.8	10.92	8.7	
PLACE1003428	0.63	3.3	2.62	2.07	2.94	1.96	
PLACE1003432	6.14	5.81	8.2	6.64	7.05	5.42	
PLACE1003438	0.45	2.66	0.93	2.41	2.34	1.99	
PLACE1003452	1.87	5.02	5.08	4.53	3.43	3.84	
PLACE1003454	2.49	5.59	7.34	7.31	6.95	5.61	
PLACE1003455	2.58	4.26	2.35	2.97	3.01	3.17	
PLACE1003456	3.22	7.74	8.62	6.9	7.2	7.79	
PLACE1003460	6.39	13.35	14.87	13.02	16.76	12.86	
PLACE1003478	1.15	1.71	0.86	2.33	2.07	1.24	
PLACE1003484	12.06	12.21	45.33	28.12	31.5	34.2	
PLACE1003493	1.61	4.72	4.9	3.84	5.96	5.08	
PLACE1003503	85.45	87.35	107.79	115.17	111.85	172.81	
PLACE1003505	1.99	6.77	4.78	7.44	6.63	8.87	
PLACE1003516	0.86	6.78	2.7	2.8	3.95	2.39	
PLACE1003519	17.58	26.29	50.41	45.77	36.97	58.75	
PLACE1003520	14.18	25.48	35.96	25.73	31.4	32.19	
PLACE1003521	2.71	3.64	4.93	5.97	4.71	7.4	
PLACE1003525	8.45	11.81	45.05	33.94	43.71	36.88	
PLACE1003528	39.18	44.68	136.4	106.04	122.76	127.22	
PLACE1003529	1.46	4.26	3.29	2.4	3.94	3.83	
PLACE1003537	4.41	9.05	11.05	11.36	13.77	13.3	
PLACE1003549	1.1	5.02	4.59	5.61	6.01	5.93	
PLACE1003553	1.6	5.89	3.88	4.02	4.17	4.23	
PLACE1003566	5.93	9.8	17.51	13.03	19.09	14.58	
PLACE1003568	3.01	2.71	5.76	5.69	4.43	4.04	

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PLACE1003573	0.98	2.43	1.19	2.16	1.87	1.48		
PLACE1003575	2.16	3.09	3.44	3.34	3.5	4.15		
PLACE1003583	0.97	3.45	3.34	2.29	4.16	2.23		
PLACE1003584	1.23	4.46	4.01	3.56	3.8	2.65		
PLACE1003592	4.4	8.48	9.48	7.11	10.48	9.53		
PLACE1003593	0.84	5.55	2.4	2.23	3.02	1.55		
PLACE1003594	4.24	6.76	6.01	5.78	6.68	7.36		
PLACE1003596	13.77	11.31	22.53	15.68	17.69	8.25		
PLACE1003598	2.83	3.63	5.02	4.89	3.7	2.95		
PLACE1003602	1.8	4.24	6.36	4.37	3.54	2.68		
PLACE1003605	17.43	21.72	45.86	94.65	95.6	91.55	**	+
PLACE1003611	2.34	5.18	6.07	5.65	7.14	6		
PLACE1003618	0.67	7.39	2.09	1.58	2.4	1.32		
PLACE1003625	1.78	10.41	2.75	3.33	5.48	2.8		
PLACE1003626	8.77	15.99	17.14	10.87	14.46	13.19		
PLACE1003630	1.8	2.57	5.8	7.05	4.67	5.86		
PLACE1003635	2.15	1.83	3.19	2.96	2.82	2.44		
PLACE1003638	1.3	2.58	3	5.21	4.19	3.13		
PLACE1003644	4.01	5.7	7.25	7.81	9.13	8.76	*	+
PLACE1003654	2.56	6.14	4.04	3.54	6.96	6.4		
PLACE1003656	2.69	7.79	6.12	6.54	5.63	4.77		
PLACE1003660	0.26	9.54	3.5	3.08	4.92	4.11		
PLACE1003669	2.43	9.05	3.67	2.59	4.26	3.08		
PLACE1003670	5.37	5.7	9.44	11.01	8.26	8.76		
PLACE1003671	1.66	1.22	3.57	3.11	2.57	1.57		
PLACE1003697	7.27	7.99	9.8	8.23	6.06	6.42		
PLACE1003704	3.12	3.97	5.17	5.96	7.25	5.97	*	+
PLACE1003709	0.89	2.63	0.8	1.19	1.24	2.44		
PLACE1003711	0.74	5.48	1.35	1.87	1.8	1.39		
PLACE1003723	1.07	6.99	4.7	4.2	5.31	4.16		
PLACE1003724	3.31	10.74	9.1	9.11	11.79	10.49		
PLACE1003737	2.14	2.21	4.72	3.35	3.1	3.29		
PLACE1003738	1.06	1.94	3.13	3.96	3.92	3.41		
PLACE1003742	2.25	3.58	5.71	6.81	6.18	2.85		
PLACE1003744	6.13	8.86	14.6	16.21	17.96	19.13	*	+
PLACE1003758	0.85	4.55	0.96	2	1.46	1.16		
PLACE1003760	13.44	18.68	27.23	31.82	20.52	22.79		
PLACE1003762	1.45	4.97	3.7	3.77	3.78	3.49		
PLACE1003765	1.18	5.23	3.45	2.01	3.1	2.11		

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PLACE1003768	0.36	1.14	1.36	1.45	2.75	1.07		
PLACE1003771	1.28	1.94	2.07	1.84	3.13	1.43		
PLACE1003772	34.15	38.19	97.86	62.42	64.06	52.43		
PLACE1003783	1.48	3.02	2.22	18.65	19.53	16.61	**	+
PLACE1003784	0.69	3.92	0.87	2.09	2.19	2.68		
PLACE1003788	0.4	4.92	1.06	1.85	1.71	0.32		
PLACE1003795	1.01	4.1	3.57	4.73	4.38	3.54		
PLACE1003827	13.83	20.46	20.72	22.48	30.84	25.92		
PLACE1003833	0.98	1.49	3.9	3.65	4.33	3.31		
PLACE1003839	22.55	19.18	52.95	50.39	56.11	43.86		
PLACE1003845	6.09	6.88	11.72	24.98	19.99	10.6		
PLACE1003850	3.16	4.84	7.19	5.45	5.95	6.39		
PLACE1003852	0.25	3.36	1.09	0.99	1.58	1.05		
PLACE1003858	1.34	4.42	1.99	2.04	1.85	2.92		
PLACE1003861	0.95	4.51	1.63	2.98	2.78	1.73		
PLACE1003864	0.94	5.5	2.74	2.88	3.86	2.69		
PLACE1003870	3.84	3.4	13.2	10.71	16.12	12.03		
PLACE1003885	1.33	1.42	1.59	3.07	3.76	2.38	*	+
PLACE1003886	4.56	6.01	5.75	9.27	6.87	4.3		
PLACE1003888	0.75	3.79	1.96	2.87	3.42	2.68		
PLACE1003892	4.93	6.91	20.79	17.21	22.33	14.87		
PLACE1003900	2.27	5.92	7.17	6.34	9.75	6.6		
PLACE1003902	1.91	7.39	5.25	5.43	8.07	6.29		
PLACE1003903	0.42	5.07	2.94	2.55	3.5	2.59		
PLACE1003915	8.15	7.04	10.78	8.31	9.79	9.84		
PLACE1003918	1.88	2.45	4.75	3.47	6.26	3.75		
PLACE1003923	2.06	3.73	5.63	2.7	5.54	3.32		
PLACE1003932	3.99	5.16	5.47	4.06	7.58	5.09		
PLACE1003936	1.02	3.82	2.81	3.63	2.42	2.78		
PLACE1003966	3.11	7.43	7.76	4.89	7.32	4.21		
PLACE1003968	1.68	5.68	5.94	3.33	4.26	4.57		
PLACE1004018	25.49	33.73	48.16	32.56	40.53	28.62		
PLACE1004020	8.91	10.18	13.26	11.42	18.03	24.15		
PLACE1004028	0.41	2.55	1.3	1.38	1.23	1.91		
PLACE1004034	3.56	4.53	5.22	8.42	9.03	13.04	*	+
PLACE1004042	17.25	20.19	68.35	79.51	93.32	79.44	*	+
PLACE1004078	1.14	4.1	3.3	4.95	6.51	4.45		
PLACE1004103	5.54	10.93	13.98	13.77	15.09	14.14		
PLACE1004104	5.94	12.29	27.78	24.18	34.98	29.71		

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PLACE1004113	1.37	3.7	3.28	2.75	3.27	1.29		
PLACE1004114	1.12	2.55	2.23	2.84	2.49	2.93		
PLACE1004118	1.58	3.52	2.09	2.74	3.64	2.5		
PLACE1004128	4.4	6.84	5.66	6.61	8.13	9.01		
PLACE1004130	2.25	4.83	8.35	6.86	9.26	6.73		
PLACE1004149	3.59	7.3	9.86	10.23	13.29	10.12		
PLACE1004156	3.61	7.91	10.12	11.66	17.62	13.31		
PLACE1004160	5.45	9.54	14.36	13.1	19.65	14.53		
PLACE1004161	2.2	4.86	3.54	4.85	5.73	7.48		
PLACE1004166	5.61	5.81	9.91	8.3	8.66	11.2		
PLACE1004168	3.35	4.97	3.73	4.73	6.65	6.79		
PLACE1004170	0.78	3.28	1.93	2.98	3.42	2.76		
PLACE1004178	0.83	5.23	2.37	2.4	2.59	2.36		
PLACE1004183	0.89	7.99	4.41	3.53	4.32	4.84		
PLACE1004197	0.64	5.14	1.55	1.73	3.54	1.65		
PLACE1004199	1.66	4.52	4.09	3.78	5.88	4.35		
PLACE1004203	1.8	3.57	4.17	2.43	3.62	2.83		
PLACE1004242	3.8	5.64	11.04	8.55	8.14	8.64		
PLACE1004249	31.4	56.31	117.88	127.93	152.54	151.22	*	+
PLACE1004255	0.79	2.65	1.26	2.59	2.15	1.93		
PLACE1004256	9.06	11.68	13.63	14.66	14.18	23.37		
PLACE1004257	2.63	7.95	6.48	7.89	8.8	8.64		
PLACE1004258	1.87	5.21	3.13	4.59	3.15	3.11		
PLACE1004270	0.72	3.8	2.5	2.7	4.01	1.65		
PLACE1004272	1.34	3.68	3.73	3.86	5.38	6.15		
PLACE1004273	92.91	89.59	212.62	212.05	129.56	99.82		
PLACE1004274	2.09	3.61	6.51	6.42	7.14	6.74		
PLACE1004277	2.3	4.4	5.76	6.45	7.7	6.04		
PLACE1004279	0.54	3.39	2.23	3.16	2.64	2.02		
PLACE1004282	2.43	8.25	6.62	4.22	5.56	4.49		
PLACE1004284	4.59	11.31	7.84	7.38	8.16	7.15		
PLACE1004289	1.28	7.85	2.46	3.06	3.63	2.1		
PLACE1004299	0.33	6.41	1.38	1.54	2.67	1.83		
PLACE1004302	1.01	2.98	3.27	2.41	2.45	1.12		
PLACE1004305	1.11	2.09	1.9	1.9	1.82	1.78		
PLACE1004316	2.3	4.48	5.4	6.06	3.85	4.52		
PLACE1004322	2.49	3.41	5.25	6.35	7.14	5.75	*	+
PLACE1004325	2.43	6.38	3.84	3.85	3.66	4		
PLACE1004332	1.21	7.18	2.8	3.72	3.46	3.01		

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PLACE1004336	2.87	9.6	5.36	6.88	9.21	6.71		
PLACE1004346	0.47	7.22	2.58	1.87	2.54	1.69		
PLACE1004358	1.3	2.41	2.41	2.46	2.09	2.03		
PLACE1004376	11.07	10.15	23.35	19.16	17.04	16.46		
PLACE1004384	0.65	3.46	1.46	1.92	2.48	2.1		
PLACE1004385	1.4	2.89	1.69	3.52	1.88	2.67		
PLACE1004388	1.79	5.73	4.27	3.44	4.87	3.04		
PLACE1004405	2.16	8.39	4.42	13.36	14.48	16.74	**	+
PLACE1004407	5.05	13.12	13.37	11.2	16.24	11.85		
PLACE1004424	0.37	5.78	0.85	1.7	1.81	1.58		
PLACE1004425	1.14	1.94	3.57	3.28	3.27	3.44		
PLACE1004427	1.96	3.31	4.56	4.67	4.22	3.24		
PLACE1004428	0.88	2.05	2.17	2.66	2.08	2.62		
PLACE1004433	5.7	8.3	10.82	12.94	15.67	12.05	*	+
PLACE1004435	0.72	4.17	1.43	1.95	1.9	2.15		
PLACE1004437	4.05	7.68	14.2	11.07	13.01	12.37		
PLACE1004441	7.82	11.68	34.06	30.75	43.19	26.41		
PLACE1004446	1.5	4.36	0.9	1.03	1.35	1.39		
PLACE1004450	0.33	1.46	1.34	2.57	1.71	0.7		
PLACE1004451	0.51	1.45	2.14	1.89	2.69	0.88		
PLACE1004456	8.22	9.7	10.97	16.68	10.4	4.18		
PLACE1004458	3.39	4.81	3.66	7.77	7.05	8.24	**	+
PLACE1004460	0.84	4.58	2.1	2.91	2.69	1.75		
PLACE1004467	5.31	6.81	10.65	7.67	10.14	10.48		
PLACE1004471	2.65	5.93	6.64	6.79	7.34	6.14		
PLACE1004473	1.16	4.66	3.5	3.18	3.23	3.21		
PLACE1004475	14.03	16.41	32.49	31.09	32.51	18.17		
PLACE1004482	8.37	6.7	10.79	10.04	9.76	9.15		
PLACE1004491	0.39	2.51	1.49	1.19	2.68	1.3		
PLACE1004492	61.52	74.8	127.94	129.92	127.64	123.82		
PLACE1004506	10.71	14.35	14.4	8.45	11.13	10.03		
PLACE1004507	2.9	7.37	5.09	7.15	6.87	6.18		
PLACE1004510	2.51	6.23	6.33	6.59	7.8	8.16		
PLACE1004516	0.98	7.36	2.12	2.79	3.78	2.22		
PLACE1004518	1.64	1.78	3.03	2.41	3.88	2.83		
PLACE1004519	0.17	0.82	0.62	1.43	2.79	1.51	*	+
PLACE1004520	6.08	8.09	10.06	7.44	9.11	2.52		
PLACE1004530	33.19	43.86	68.13	41.86	27.72	38.09		
PLACE1004545	1.13	3.83	2.12	3.03	3.31	3.65		

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PLACE1004547	5	7.61	7.82	8.66	11.2	10.28		
PLACE1004548	1.69	6.73	4.43	6.93	8.48	6.5		
PLACE1004550	2.27	6.24	6.67	5.92	6.78	6.15		
PLACE1004551	0.8	2.16	1.62	2.14	2.21	1.95		
PLACE1004559	2.9	2.89	5.11	4.45	6.75	4.82		
PLACE1004562	8.67	11.27	16.07	13.01	14.38	13.34		
PLACE1004564	1.84	5.19	4.36	4.64	5.98	4.49		
PLACE1004604	1.69	4.21	9.88	2.49	4.34	1.97		
PLACE1004611	2.73	5.87	4.89	3.86	4.17	3.99		
PLACE1004629	9.42	15.75	19.92	23.93	30.49	29.01	*	+
PLACE1004630	16.66	20.82	35.1	16.76	23.04	19.17		
PLACE1004637	5.03	8.82	10.34	6.61	9.17	8.29		
PLACE1004645	36.5	39.28	92.04	85.16	87.94	74.59		
PLACE1004646	1.07	2.91	2.87	3.68	2.19	2.28		
PLACE1004648	0.8	3.42	2.52	2.53	3.15	1.22		
PLACE1004655	45.95	58.09	130.94	112.14	126.25	99.01		
PLACE1004658	2.4	7.34	6.31	6.64	8.37	6		
PLACE1004664	1.26	4.83	1.3	3.02	2.65	1.89		
PLACE1004672	2.32	6.79	8.02	6.3	7.51	7.14		
PLACE1004674	9.4	11.97	14.7	8.3	9.75	15.25		
PLACE1004681	1.97	3.84	5.62	5.05	5.69	4.39		
PLACE1004686	2.74	4.33	7.46	9.22	10.77	8.59	*	+
PLACE1004690	10.64	13.43	19.62	21.75	19.21	31.72		
PLACE1004691	1.14	6.71	3.71	2.92	4.13	2.75		
PLACE1004693	1.34	7.54	4.89	3.91	4.59	5.97		
PLACE1004701	13.01	18.45	24.24	25.21	24.46	25.1		
PLACE1004705	1.29	3.33	2.27	1.8	1.96	1.47		
PLACE1004708	37.69	46.37	80.19	41.34	39.66	50.98		
PLACE1004716	6.37	8.81	11.08	4.22	12.55	14.26		
PLACE1004722	1.31	3.05	2.6	2.26	3.28	2.51		
PLACE1004736	5.25	7.71	7.6	9.16	8.89	11.63		
PLACE1004737	5.42	12.71	16.14	8.15	11.23	13.78		
PLACE1004740	4.88	9.06	8.22	7.37	7.93	8.2		
PLACE1004743	1.31	4.04	3.1	1.97	4	3.55		
PLACE1004751	0.98	2.89	2.88	2.75	3.74	3.06		
PLACE1004757	3.45	4.34	10.53	8.4	9.6	7.22		
PLACE1004761	6.41	7.32	12.59	9.99	10.44	9.72		
PLACE1004773	1.05	2.34	1.7	1.94	2.31	2.72		
PLACE1004775	0.35	3.26	1.37	1.29	2.14	1.07		

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PLACE1004777	2.1	7.57	2.97	3.68	4.25	4.4		
PLACE1004793	0.83	4.58	1.37	1.9	2.06	1.25		
PLACE1004796	6.65	8.7	13.08	7.79	8.57	7.88		
PLACE1004804	0.99	4.46	3.25	2.44	2.38	3.22		
PLACE1004813	4.55	7.11	9.84	6.45	5.19	5.45		
PLACE1004814	7.16	11.76	17.62	15.83	11.39	10.1		
PLACE1004815	0.7	2.81	2.43	3.12	2.61	3.44		
PLACE1004816	1.16	2.63	2.04	2.36	2.26	1.84		
PLACE1004824	3.25	7.37	5.27	8.1	9.13	8.85		
PLACE1004827	1.4	10.89	3.17	2.57	3.05	1.3		
PLACE1004836	1.72	12.95	4.26	6.25	7.99	4.49		
PLACE1004838	1.35	8.81	2.2	2.49	2.34	1.68		
PLACE1004840	1.59	2.06	2.21	1.85	2.08	1.37		
PLACE1004842	0.86	1.98	1.89	1.98	1.78	2.33		
PLACE1004850	0.81	2.35	1.63	1.83	2.76	2.36		
PLACE1004868	0.81	2.97	2.04	1.62	2.23	2		
PLACE1004885	1.5	7.09	3.51	3.4	6.03	4.77		
PLACE1004886	1.87	8.53	2.76	3.33	5.12	4.93		
PLACE1004887	18.14	34.01	58.51	36.9	38.66	30.33		
PLACE1004896	8.39	14.15	15.4	9.39	11.14	14.03		
PLACE1004900	1.75	2.7	6.69	5.66	5.74	4.44		
PLACE1004902	5.42	6.25	9.27	6.39	4.2	3.6		
PLACE1004904	1.7	4.66	2.52	6.49	4.78	3.03		
PLACE1004911	0.69	2.5	1.12	5.95	4.82	6.09	**	+
PLACE1004913	3.63	5.72	7.38	4.49	5.45	4.79		
PLACE1004918	1.3	6.69	2.05	2.39	3.24	2.64		
PLACE1004930	2.74	8.84	5.93	10.63	16.57	14.71	*	+
PLACE1004934	1.14	4.3	3.34	2.97	2.03	2.5		
PLACE1004937	2.1	4.03	4.91	2.74	3.59	2.36		
PLACE1004949	4.32	4.98	7.67	8.53	8.48	6.04		
PLACE1004969	0.74	1.74	1.99	1.39	2.34	1.4		
PLACE1004970	0.45	2.18	1.2	1.43	1.31	1.01		
PLACE1004972	1.63	6.56	2.69	5.66	3.17	4.76		
PLACE1004974	1.27	5.21	4.2	5.6	5.7	5.62		
PLACE1004975	0.59	2.84	1.11	1.94	1.98	1.24		
PLACE1004979	1.58	4.06	4.26	4.91	5.69	4.75		
PLACE1004982	5.66	6.45	9.74	10.03	10.67	5.65		
PLACE1004985	1.4	1.47	1.46	2.5	2.17	1.2		
PLACE1005003	2.85	4.22	6	6.05	6.37	5.78		

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PLACE1005004	0.47	3.36	0.92	1.5	0.73	0.85		
PLACE1005005	3.35	6.9	5.32	6.67	9.65	7.17		
PLACE1005011	6.03	11.12	35.8	37.66	56.97	36.62		
PLACE1005026	0.79	4.18	2.29	2.44	2.49	2.16		
PLACE1005027	2.46	6.72	6.69	5.36	6.92	5.68		
PLACE1005031	1.21	1.47	3.69	5.72	7.1	4.6	*	+
PLACE1005036	2.27	3.6	6.83	9.08	8.91	7.53	*	+
PLACE1005041	2.5	2.84	2.84	5.05	4.41	3.25	*	+
PLACE1005046	2.23	4.11	4.56	6.04	3.92	4.33		
PLACE1005047	0.23	3.19	2.6	1.43	1.23	2.1		
PLACE1005052	4.24	8.53	6.36	8.08	8.15	8.1		
PLACE1005055	2.54	7.45	4.66	7.2	6.45	5.62		
PLACE1005066	4.33	8.26	7.58	12.9	14.14	16.49	**	+
PLACE1005077	1.17	0.68	1.2	2.1	2.43	1.54	*	+
PLACE1005085	1.41	1.97	3.06	3.34	4.14	3.45		
PLACE1005086	1.93	3.77	5.17	5.62	7.78	4.79		
PLACE1005088	24.66	32.47	46.03	43.45	31.47	27.46		
PLACE1005089	1.57	4.78	3.15	2.52	3.67	3.14		
PLACE1005101	3.37	8.11	5.46	6.11	8.96	6.39		
PLACE1005102	2.56	7.14	5.01	4.11	5.51	3.8		
PLACE1005108	2	6.08	5.87	6.58	6.19	5.09		
PLACE1005110	1.34	1.89	3.08	1.75	2.75	2.15		
PLACE1005111	1.31	1.34	1.23	1.45	2.17	1.54		
PLACE1005123	26.23	26.21	47.58	34.26	49.34	34.98		
PLACE1005124	3.2	4.66	4.18	4.2	6.91	5.44		
PLACE1005128	9.54	8.89	18.22	16.37	16.36	16.13		
PLACE1005130	2.65	6.57	5.54	2.84	4.98	3.58		
PLACE1005141	6.3	9.92	11.25	16.15	20.75	18.95	**	+
PLACE1005146	1.3	2.71	3.03	2.17	2.53	2.29		
PLACE1005152	1.85	3.9	4.56	4.13	4.23	4.79		
PLACE1005157	2.66	5.19	5.3	4.38	4.09	7.01		
PLACE1005162	2.79	3.72	9.31	6.57	7.45	7.1		
PLACE1005170	17.34	18.92	29.76	21.38	18.18	23.73		
PLACE1005176	0.57	5.6	1.7	2.33	2.47	1.94		
PLACE1005181	0.53	5.14	0.96	0.89	1.36	0.37		
PLACE1005184	4.06	9.09	10.4	8.97	12.82	11.26		
PLACE1005186	3.5	3.41	8.56	8.05	5.79	5.73		
PLACE1005187	2.85	4	4.13	6.1	4.99	4.25		
PLACE1005189	6.12	7.71	5.34	10.84	10.65	12.22	**	+

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PLACE1005193	1.48	3.78	1.71	3.84	2.91	2.61		
PLACE1005200	1.35	4.68	2.61	2.47	3.75	3.1		
PLACE1005206	2.43	6.48	4.26	3.35	3.95	2.95		
PLACE1005216	1.53	5.46	4.44	5.6	6.51	4.12		
PLACE1005223	1.43	6.21	5	4.38	5.66	3.27		
PLACE1005225	1.36	3.01	3.49	3.33	3.32	4.65		
PLACE1005232	1.86	3.31	4.87	5.63	6.19	3.88		
PLACE1005239	1.06	4.3	2.32	2.84	2.86	2.41		
PLACE1005243	4.35	7.32	5.41	8.48	7.49	10.75		
PLACE1005250	4.24	10.31	7.98	4.38	5.9	8.88		
PLACE1005261	3.21	7.43	4.74	4.78	5.82	3.51		
PLACE1005266	1.05	4.47	2.82	2.28	4.43	2.76		
PLACE1005271	4.66	5.31	8.79	5.87	11.16	7.95		
PLACE1005277	2.06	3.48	2.35	2.62	1.98	2.64		
PLACE1005287	3.63	4.31	5.87	2.98	5.06	6.91		
PLACE1005299	24.16	22.75	48.29	35.17	24.24	41.06		
PLACE1005305	6.81	8.46	11.13	10.67	11.85	16.25		
PLACE1005307	1.59	5.44	4.14	3.15	5.42	4.84		
PLACE1005308	2.41	4.96	3.95	5.32	5.99	5.79		
PLACE1005313	1.08	3.83	1.6	1.8	2.05	1.8		
PLACE1005320	1.36	3.65	3.34	3.39	4.05	2.26		
PLACE1005327	10.78	8.74	16.8	10.36	7.95	4.43		
PLACE1005331	2.28	4.92	5.28	4.66	4.97	3.33		
PLACE1005335	1.53	3.8	2.24	2.03	3.22	2.42		
PLACE1005336	9.12	12.58	16.58	16.39	16.99	20.15		
PLACE1005351	2.62	8.18	10.17	9.28	8.66	9.52		
PLACE1005366	2.04	6.93	3	2.99	3.71	4.23		
PLACE1005373	1.77	6.34	4.44	3.91	5.36	3.37		
PLACE1005374	3.29	9.47	11.4	7.35	10.22	12.41		
PLACE1005383	8.16	7.54	12.81	7.21	5.93	4.03		
PLACE1005388	0.33	2.04	1.56	1.92	3.67	2.2		
PLACE1005409	2.97	5.02	4.99	3.9	4.23	2.97		
PLACE1005410	12.41	16.44	18.89	24.38	20.98	27.1	*	+
PLACE1005426	5.16	7.48	9.06	5.51	7.67	5.45		
PLACE1005431	12.6	15.65	22.53	19.64	26.25	23.75		
PLACE1005453	1.4	10.38	3.93	4.85	4.45	3.28		
PLACE1005467	3.09	11.87	7	5.57	11.63	7.28		
PLACE1005471	1.6	1.94	1.66	2.29	1.52	1.28		
PLACE1005476	0.42	1.73	1.24	1.6	1.57	1.46		

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PLACE1005477	1.58	2.26	2.51	3	2.93	2.74	
PLACE1005480	0.77	2.01	1.86	1.93	1.4	0.53	
PLACE1005481	0.44	4.81	2.3	2.77	3.62	2.44	
PLACE1005494	0.27	6.66	1.68	1.21	1.73	1.06	
PLACE1005495	3.86	12.83	8.31	6.85	9.25	7.62	
PLACE1005497	2.27	7.72	3.95	4.24	5.68	5.91	
PLACE1005499	5.71	5.86	11.07	10.82	7.9	6.49	
PLACE1005502	1.59	2.87	3.43	4.07	3.45	1.49	
PLACE1005513	1.77	4.14	3.35	1.86	2.85	1.98	
PLACE1005515	2.89	4.76	4.22	4.58	5.29	3.78	
PLACE1005519	1.04	4.53	3.29	2.85	2.85	2.83	
PLACE1005526	0.58	5.55	1.38	1.3	1.59	0.71	
PLACE1005528	2.08	7.71	5.57	5.94	7.12	5.33	
PLACE1005530	2.16	7.09	4.32	5.17	8.23	4.67	
PLACE1005536	1.74	1	2.74	3.12	2.43	2.88	
PLACE1005539	10.1	11.64	23.77	8.65	8.66	5.22	
PLACE1005543	1.7	3.57	5.62	3.54	4.32	2.57	
PLACE1005544	0.86	3.26	3.15	2.49	2.68	2.27	
PLACE1005550	4.32	7.61	7.85	10.16	7.25	6.86	
PLACE1005554	1.15	5.47	2.67	2.17	2.17	1.17	
PLACE1005557	1.76	7.21	4.95	8.22	7.64	7.7	
PLACE1005563	0.51	4	1.89	1.45	2.07	1.06	
PLACE1005569	0.6	0.5	1.56	1.59	1.81	1.09	
PLACE1005574	1.07	1.88	2.49	2.48	4.43	2.22	
PLACE1005584	1.3	2.68	3.91	3.91	5.58	3.03	
PLACE1005590	4.28	5.14	8.4	9.87	10.73	8.02	
PLACE1005595	3.08	4.03	2.89	3.65	3.81	3.89	
PLACE1005601	2	5.66	4.22	3.77	4	4.02	
PLACE1005603	1.08	4.9	1.04	2.49	0.95	1.94	
PLACE1005604	1.2	6.71	2.42	3.6	4.2	3.46	
PLACE1005611	2.22	2.3	3.98	5.15	5.65	2.89	
PLACE1005622	0.65	1.71	1.98	2.94	3.88	1.26	
PLACE1005623	1.42	3.08	3.27	3.71	3.65	1.61	
PLACE1005630	3.31	5.81	7.75	87.83	72.15	89.12	** +
PLACE1005639	0.75	4.36	1.28	1.66	2.02	1.18	
PLACE1005646	2.13	5.41	4.31	5.4	5.08	2.55	
PLACE1005647	2.77	9.69	6.72	7.34	9.11	6.25	
PLACE1005648	3	8.11	9.21	8.34	10.59	8.22	
PLACE1005653	1.99	1.43	2.74	2.74	2.13	2.67	

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PLACE1005656	0.92	2.48	2.24	1.68	2.78	1.58		
PLACE1005659	0.87	2.64	1.01	1.62	1.84	1.32		
PLACE1005660	3.91	8.03	5.77	8.87	8.88	8.34		
PLACE1005664	2.69	6.57	6.14	3.39	4.27	3.19		
PLACE1005666	0.89	5.91	3.55	4.63	4.93	3.97		
PLACE1005669	4.46	10.41	11.39	11.64	13.9	14.6		
PLACE1005682	1.94	5.27	4.49	6.2	5.2	5.47		
PLACE1005698	0.6	2.7	2.92	2.01	2.67	2.38		
PLACE1005708	25.32	34.08	53.46	53.89	59.98	53.76		
PLACE1005725	3.25	3.75	6.41	5.64	5.82	7.29		
PLACE1005727	2.97	4.54	4.15	3.9	3.49	4		
PLACE1005730	0.77	4.29	3.26	1.1	1.54	1.28		
PLACE1005736	5.37	7.55	5.73	9.25	12.55	10.19	*	+
PLACE1005739	0.81	4.96	1.38	2.46	3.17	1.74		
PLACE1005745	8.03	7.11	11.52	11.98	6.97	11.44		
PLACE1005752	1.31	3.15	2.96	2.55	2.24	1.25		
PLACE1005755	0.8	2.79	3.02	1.72	3.28	2.27		
PLACE1005756	10.79	12.06	17.2	18.22	19.3	21.47	*	+
PLACE1005760	10.22	15.24	68.06	49.69	68.81	53.09		
PLACE1005763	1.47	7.04	3.58	3.79	4.63	3.02		
PLACE1005768	1.25	5.63	3.69	4.58	5.13	4.19		
PLACE1005771	5.71	13.63	13.7	11.28	17.49	17.27		
PLACE1005783	1.82	2.44	3.64	3.05	3.71	3.47		
PLACE1005799	4.79	5.25	8.37	6.12	8.78	8.62		
PLACE1005802	1.07	3.78	3.64	2.7	3.64	1.96		
PLACE1005803	3.06	6.15	4.78	5.6	4.94	7.36		
PLACE1005804	0.92	8.41	1.33	2	1.91	2.44		
PLACE1005813	17.23	18.71	78.06	70.01	94.17	74.89		
PLACE1005815	1.43	5.6	4.38	3.8	5.01	4.1		
PLACE1005828	2.11	3.62	4.42	5.34	6.24	3.56		
PLACE1005833	119.17	92.82	182.22	122	114.37	107.96		
PLACE1005834	2.04	4.33	3.95	3.55	3.56	2.56		
PLACE1005835	22.7	19.1	51.52	72.32	60.34	68.56	*	+
PLACE1005836	2.39	4.21	4.97	2.61	3.83	2.55		
PLACE1005845	0.97	5.42	2.66	2.67	3.05	3.65		
PLACE1005850	1.82	3.91	3.04	2.84	2.85	2.15		
PLACE1005851	1.03	3.44	1.46	1.2	2.01	1.11		
PLACE1005856	0.92	4.01	2.42	2.24	3.37	3.37		
PLACE1005875	1.78	3.89	4.77	3.3	3.48	3.17		

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PLACE1005876	1.33	3.99	4.76	6.87	6.34	6.9	*	+
PLACE1005878	1.3	2.67	2.08	3.54	4.46	2.79		
PLACE1005880	2.36	4.09	4.31	4.16	3.07	3.45		
PLACE1005884	1.6	4.87	1.89	2.48	2.21	2.73		
PLACE1005890	1.9	9.57	3.7	2.26	3.09	1.88		
PLACE1005898	3.29	10.87	5.34	7.36	8.12	6.36		
PLACE1005913	1.46	9.31	8.05	4.99	6.47	4.33		
PLACE1005921	0.99	1.92	2.03	1.49	2.22	0.79		
PLACE1005923	0.74	1.61	1.17	1.47	2.42	1.43		
PLACE1005925	0.83	2.67	3.18	2.19	2.14	1.68		
PLACE1005927	1.26	2.49	1.93	1.95	2.56	2.3		
PLACE1005932	2.04	5.66	2.44	2.53	2.32	2.52		
PLACE1005934	0.88	7.91	3.16	3.9	5.61	4.19		
PLACE1005936	1.31	8.96	3.02	2.02	2.84	2.3		
PLACE1005939	54.61	68.58	111.22	157.61	194.58	212.18	**	+
PLACE1005951	2.36	3.39	4.98	5.56	4.48	2.35		
PLACE1005953	1.5	1.64	2.64	2.59	2.43	3.03		
PLACE1005955	1.64	2.01	3.8	4.07	3.43	2.55		
PLACE1005966	0.76	3.42	1.69	1.75	2	2.19		
PLACE1005968	1.52	4.96	3.2	4.71	5.15	6.12		
PLACE1005975	2.58	7.11	5.42	6.18	7.01	6.49		
PLACE1005990	0.7	7.7	1.54	2.1	1.87	0.88		
PLACE1005997	88.15	118.52	196.48	189.6	226.97	172.1		
PLACE1006002	3.38	3.97	8.87	8.4	7.71	9.18		
PLACE1006003	1.55	3.02	4.83	5.09	4.44	5.33		
PLACE1006011	1.85	3.63	3.46	4.48	2.68	1.91		
PLACE1006017	0.84	2.74	2.81	3.4	3.4	3.58		
PLACE1006037	2.99	7.05	2.48	6.14	3.64	4.29		
PLACE1006040	2.2	7.87	3.97	6.64	6.9	7.77		
PLACE1006063	0.94	4.64	2.59	2.11	3.15	2.25		
PLACE1006071	3.06	6.52	4.97	5.36	4.03	4.47		
PLACE1006073	2.74	3.53	6.43	7.19	6.81	6.93		
PLACE1006074	1.4	2.22	3.34	2.62	3.23	1.69		
PLACE1006076	1.36	2.51	2.98	3.15	2.47	2.75		
PLACE1006079	1.38	4.32	1.78	2.1	1.1	1.11		
PLACE1006093	0.49	3.76	1	3.56	3.85	1.83		
PLACE1006116	2.99	6.44	4.04	5.28	5.01	4.91		
PLACE1006119	3.15	6.81	7.07	9.22	10.4	8.03		
PLACE1006129	2.12	5.6	3.98	6.59	7.62	5.65		

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PLACE1006139	3.44	2.98	6.03	7.77	8.85	5.58		
PLACE1006143	0.5	1.48	1.87	3.18	4.13	3.17	*	+
PLACE1006157	1.55	2.54	4.82	2.96	3.9	2.44		
PLACE1006159	0.69	3.61	0.94	2.68	1.98	1.04		
PLACE1006164	0.35	3.18	1.37	1.73	1.85	1.21		
PLACE1006167	2.18	6.5	3.37	3.95	4.52	3.13		
PLACE1006170	2.79	6.09	6.09	4.34	5.31	3.68		
PLACE1006181	2.75	7.34	2.84	5.8	5.51	5.22		
PLACE1006187	0.76	1.3	2.15	2.01	2.41	1.48		
PLACE1006195	0.11	1.24	1.73	1.93	1.93	0.87		
PLACE1006196	1.8	4.01	4.15	4.32	5.77	2.19		
PLACE1006197	2.12	5.6	5.24	4	3.47	3.39		
PLACE1006198	0.27	3.68	1.21	0.84	1.63	0.5		
PLACE1006205	0.89	5.59	0.99	2.43	2.18	1.28		
PLACE1006208	7.28	13.32	13.46	14.09	14.99	12.5		
PLACE1006211	2.6	8.05	7.92	6.07	9.08	9.35		
PLACE1006219	6.77	5.77	8.94	14.88	22.25	15.35	*	+
PLACE1006223	1.55	1.46	3.19	1.39	3	1.64		
PLACE1006225	0.56	2.27	1.3	1.04	2.3	0.99		
PLACE1006236	1.53	3.2	2.92	3.06	5.01	2.29		
PLACE1006239	0.67	3.62	1.97	2.61	3.66	3.41		
PLACE1006245	3.86	7.13	5.45	4.43	7.44	3.28		
PLACE1006246	1.66	6.56	6.19	5.59	7.66	6.33		
PLACE1006248	1.58	4.47	5.6	2.77	3.1	2.82		
PLACE1006262	0.93	2.24	1.49	2.08	1.61	1.4		
PLACE1006269	2.28	4.71	3.42	2.06	2.47	2.33		
PLACE1006275	1.6	3.57	3.37	4.12	3.68	3.53		
PLACE1006277	1.01	2.42	1.4	1.79	3.01	0.88		
PLACE1006288	9.32	13.59	22.49	26.85	18.4	25.21		
PLACE1006290	1.79	6.81	5.99	8.87	7.56	9.13		
PLACE1006298	1.93	5.52	2.47	3.87	5.08	4.55		
PLACE1006311	0.65	3.38	1.75	225.97	161.43	251.12	**	+
PLACE1006318	3.52	4.03	4.17	4.04	3.17	4.01		
PLACE1006325	5.43	6.73	6.31	8.09	8.38	8.08	**	+
PLACE1006331	1.87	3.36	3.21	4.44	3.59	2.56		
PLACE1006335	1.76	3.64	2.55	4.45	2.98	2.92		
PLACE1006357	0.27	4.51	1.59	1.7	1.49	1.2		
PLACE1006360	1.1	5.11	1.79	2.46	2.74	2.62		
PLACE1006364	4.51	8.06	7.29	7.37	9.19	5.75		

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PLACE1006365	1.68	4.65	1.97	1.8	2.12	0.97		
PLACE1006368	1.53	3.11	2.57	3.01	3.04	4.27		
PLACE1006371	1.38	3.2	1.46	1.68	3.01	1.67		
PLACE1006373	2.21	5.21	5.75	7.83	8.02	7.56	*	+
PLACE1006382	0.9	4.67	2.81	3.3	1.92	2.95		
PLACE1006385	1.59	6.33	1.86	2.68	2.59	2.71		
PLACE1006391	1.19	5	1.95	1.96	2.79	1.63		
PLACE1006412	1.88	5.53	5.92	7.07	9.93	5.27		
PLACE1006414	0.63	3.42	0.95	1.22	1.87	1.6		
PLACE1006419	7.79	9.8	11.93	5.19	7.29	5.32	*	-
PLACE1006438	0.99	6.07	3.42	3.29	4.56	5.14		
PLACE1006443	2.05	5.01	5.12	5.01	5.31	6.44		
PLACE1006445	0.84	5.76	3.65	3.53	3.27	3.55		
PLACE1006447	1.34	5.81	3.28	2.95	3.26	3.96		
PLACE1006466	0.75	4.38	1.35	1.49	1.66	1.08		
PLACE1006469	0.67	4.66	2.31	1.65	2.26	1.67		
PLACE1006470	2.47	3.71	3.74	5.25	7.02	4.35		
PLACE1006472	24.4	23.44	52.17	26.23	28.52	9.36		
PLACE1006476	2.52	4.31	8.67	6.21	7.23	5.93		
PLACE1006482	1.64	3.35	4.43	4.25	4.67	4.98		
PLACE1006488	14.12	19.42	32.69	40.76	34.77	41.4	*	+
PLACE1006492	2.03	6.41	4.38	4.04	4.98	3.02		
PLACE1006506	1.78	6.67	4.04	4.41	5.71	4.17		
PLACE1006515	1.65	5.7	3.08	3.19	2.84	4.08		
PLACE1006516	1.1	7.32	7.05	4.89	5.69	7.28		
PLACE1006520	1.02	2.74	2.12	1.19	3	1.54		
PLACE1006521	2.4	3.54	6.38	6.49	6.86	5.08		
PLACE1006529	5.96	7.35	6.96	10.56	8.2	7.93		
PLACE1006531	1.01	4.31	3.33	1.84	2.05	2.43		
PLACE1006534	1.68	6.04	2.59	3.01	3.86	3.19		
PLACE1006540	2.68	9.7	7.77	8.71	11.21	4.46		
PLACE1006549	0.6	9.45	2.09	1.6	2.28	1.65		
PLACE1006550	1.76	8.82	4.07	2.77	2.94	4.14		
PLACE1006552	1.3	2.48	2.14	1.97	1.3	0.81		
PLACE1006557	2.38	4.01	3.79	2.84	2.51	2.45		
PLACE1006563	2.49	3.44	5.7	4.23	4.15	4.3		
PLACE1006579	1.53	7.5	4.82	4.88	5.38	5.78		
PLACE1006594	236.53	241.11	397.64	122.37	278.58	324.29		
PLACE1006598	0.72	8.53	2.4	1.53	1.58	2.07		

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PLACE1006607	1.47	7.69	4.18	3.45	5.86	4.29		
PLACE1006610	9.46	13.73	38.26	27.65	32.76	22.64		
PLACE1006615	6.22	9.09	18.78	20.25	15.74	15.86		
PLACE1006617	0.91	1.54	2.66	1.87	2.49	2.09		
PLACE1006618	5.42	8.01	9.24	5.33	8.59	5.76		
PLACE1006626	1.53	4.11	1.3	2.47	2.78	1.16		
PLACE1006629	0.99	5.05	1.36	2.22	2.56	1.76		
PLACE1006637	1.29	6.54	3.97	3.77	4.23	4.87		
PLACE1006640	0.59	5.14	1.17	0.85	2.54	0.94		
PLACE1006644	1.66	4.46	2.12	2.79	2.49	2.39		
PLACE1006657	1.28	2.09	2.31	4.55	3.09	2.19		
PLACE1006673	2.29	4.73	10.34	11.06	10.89	6.45		
PLACE1006678	2.54	2.98	1.44	1.37	1.96	1.39		
PLACE1006682	3.5	5.93	2.58	15.44	20.96	23.99	**	+
PLACE1006684	1.12	4.8	1.81	1.64	2.54	1.65		
PLACE1006698	1.54	5.86	4.52	2.15	3.57	1.9		
PLACE1006704	1.81	5.41	2.71	2.93	2.92	2.97		
PLACE1006708	1.69	5.07	3.49	3.46	4.11	3.7		
PLACE1006711	14.21	16.18	29.77	24.34	26.25	22.42		
PLACE1006714	2.27	3.26	4.74	4.57	5.23	3.53		
PLACE1006716	1.51	2.75	3.7	6	7.05	3.99		
PLACE1006731	1.65	3.77	2.83	2.71	4	3.09		
PLACE1006754	0.43	3.94	1.73	1.8	1.81	0.99		
PLACE1006760	7.56	10.98	10.08	8.58	8.89	11.31		
PLACE1006779	1.44	4.12	2.88	3.19	3.79	2.97		
PLACE1006782	0.44	5.17	2.42	2.95	1.57	1.15		
PLACE1006783	9.34	11.46	18.65	157.98	223.05	66.46	*	+
PLACE1006786	3.31	4.08	6.07	5.9	6.24	3.34		
PLACE1006792	1.61	3.31	5.38	5.66	3.33	4.18		
PLACE1006795	0.89	2.43	0.74	0.81	1.27	1.01		
PLACE1006800	1.62	4.94	2.53	4.7	4.56	3.93		
PLACE1006805	3.94	7.79	5.5	10.83	9.8	8.79	*	+
PLACE1006809	3.55	5.7	5.94	9.58	10.61	8.97	**	+
PLACE1006815	1.7	7.57	4.1	5.12	5.23	5.8		
PLACE1006819	0.33	0.88	0.95	0.89	1.76	0.63		
PLACE1006820	2.35	2.01	4.91	4.84	6.72	4.18		
PLACE1006826	2.28	6.22	4.84	7.68	7.62	5.58		
PLACE1006829	3.76	5.51	6.54	9.49	8.66	8.69	*	+
PLACE1006853	1.2	4.21	1.97	2.25	2.93	2.88		

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PLACE1006860	1	4.29	1.62	1.61	2.1	1	
PLACE1006867	5.65	9.36	11.34	7.04	8.33	7.63	
PLACE1006875	1.15	6.19	5.66	4.84	4.53	4.63	
PLACE1006878	1.59	2.84	3.09	2.99	3.22	2.39	
PLACE1006883	3.21	5.08	6.78	6.83	7.38	6.19	
PLACE1006898	1.67	4.23	3.67	3.54	4.77	4.59	
PLACE1006901	2.59	4.75	4.03	3.71	3.28	4.14	
PLACE1006904	0.91	3.59	2.7	3.26	2.92	2.04	
PLACE1006917	3.63	7.13	6.1	5.8	7.21	7.03	
PLACE1006932	0.54	5.85	1.29	0.92	1.34	1.19	
PLACE1006935	1.3	5.46	2.54	1.59	4.03	1.6	
PLACE1006956	0.92	2.55	3.4	2.55	2.41	2.09	
PLACE1006958	0.78	2.41	1.35	1.76	4.2	3.39	
PLACE1006959	4.97	8.48	9.98	11.46	9.58	13.62	
PLACE1006961	8.03	9.85	14.42	13.73	11.57	14.2	
PLACE1006962	2.97	7.44	6.56	5.04	7.26	6.22	
PLACE1006966	2.02	6.94	3.46	3.15	3.89	2.89	
PLACE1006979	0.95	4.44	2.03	1.46	2.64	1.77	
PLACE1006989	2.19	5.05	3.02	3.27	3.9	5.06	
PLACE1007001	4.98	6.79	10.71	4.03	7.43	7.38	
PLACE1007014	1.37	3.03	3.45	1.79	2.18	2.2	
PLACE1007021	0.74	3.03	2.11	0.75	2.2	1.73	
PLACE1007026	2.1	9.23	3.93	4.15	4.27	5.42	
PLACE1007028	4.12	8.5	10.56	7.89	8.34	9.35	
PLACE1007038	237.33	267.91	446.14	406.27	622.67	671.17	
PLACE1007040	1.55	3.14	2.85	1.57	3.31	2.45	
PLACE1007045	1.08	3.74	2.85	2.9	5.03	2.74	
PLACE1007048	147.06	149.67	259.53	121.61	211.26	109.43	
PLACE1007053	4.9	6.69	10	3.59	4.91	4.71	
PLACE1007068	7.56	10.33	62.76	39.52	45.9	36.69	
PLACE1007070	5.97	10.85	10.28	8.65	9.6	14.3	
PLACE1007076	8.22	14.4	14.19	16.53	23.62	24.67	* +
PLACE1007077	2.65	6.45	4.01	5.2	5.28	5.43	
PLACE1007081	0.36	4.47	1.94	1.92	1.92	1.37	
PLACE1007082	1.23	4.66	4.95	4.32	4.5	3.99	
PLACE1007092	2.49	4.12	7.26	4.77	5.22	4.34	
PLACE1007096	0.72	2.19	0.74	1.35	1.63	0.97	
PLACE1007097	0.54	2.49	1.35	1.61	1.28	1.04	
PLACE1007099	1.58	4.66	2.56	2.77	3.64	3.72	

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PLACE1007105	1.18	6.51	3.44	2.65	4.13	2.21		
PLACE1007108	3.55	13.02	7.41	5.03	6.87	5.75		
PLACE1007111	1.33	9.51	1.52	1.74	2.37	1.52		
PLACE1007112	1.23	7.26	1.79	2.09	3.12	2.36		
PLACE1007130	0.54	2.02	1.92	0.87	1.47	0.33		
PLACE1007132	1.46	3.32	4.63	3.58	3.38	2.88		
PLACE1007140	0.61	2.58	2.41	1.98	1.98	1.32		
PLACE1007143	2.79	6.32	4.62	4.9	5.34	5.33		
PLACE1007169	2.21	8.59	3.46	5.44	8.46	7.99		
PLACE1007178	0.82	8.66	2.48	3.28	6.28	4.1		
PLACE1007190	3.31	10.9	6.7	10.51	13.57	11.14		
PLACE1007201	0.81	5.82	1.41	1.72	3.04	2.51		
PLACE1007202	37.76	34.95	76.28	58.23	34.42	37.86		
PLACE1007226	2.01	2.39	2.73	1.89	3.14	2.29		
PLACE1007238	1.64	3.07	1.83	2.39	2.73	2.2		
PLACE1007239	1.81	3.68	2.99	1.76	2.72	2.44		
PLACE1007242	0.61	5.18	1.87	1.54	1.14	1.67		
PLACE1007243	2.21	7.36	2.29	2.24	3.27	3.31		
PLACE1007247	0.36	6.17	1.71	1.11	1.36	1.34		
PLACE1007257	1.67	5.33	3.34	3.3	5.27	4.25		
PLACE1007274	1.46	2.18	4.43	4.38	4.03	4.06		
PLACE1007276	0.93	2.02	1.1	2.13	2.1	1.74		
PLACE1007282	2.51	4.2	5.72	4.28	3.62	4.66		
PLACE1007286	2.97	4.8	7.85	10.14	12.47	8.79	*	+
PLACE1007296	10.55	19.45	24.46	31.43	17.57	27.05		
PLACE1007301	0.65	5.17	1.55	1.19	1.54	1.11		
PLACE1007314	3.11	6.61	8.64	7.98	8.96	10.24		
PLACE1007317	1.19	3.34	1.27	1.88	1.62	1.79		
PLACE1007329	0.89	0.73	1.78	2.38	2.35	2.09	*	+
PLACE1007338	3.96	6.47	9.58	11.59	8.93	2.32		
PLACE1007342	0.71	1.8	1.3	1.1	1.1	0.7		
PLACE1007345	1.72	4.57	2.54	2.72	3.6	3.29		
PLACE1007346	1.43	4.61	3.89	5.77	4.53	4.1		
PLACE1007359	0.74	4.55	2.16	2.59	2.44	3.53		
PLACE1007367	4.53	8.63	15.16	12.49	13.49	11.75		
PLACE1007375	0.36	3.24	2.02	1.75	2.56	1.59		
PLACE1007377	1.49	2.01	3.18	3.29	3.96	2.36		
PLACE1007386	1.55	1.75	1.47	2.37	1.68	1.36		
PLACE1007392	1.57	2.99	2.49	2.79	4.48	3.51		

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PLACE1007402	2.41	5.66	3.08	1.52	2.91	1.8		
PLACE1007409	1.05	4.57	1.04	2.51	2.68	2.02		
PLACE1007416	3.45	6.97	6.5	7.05	9.14	6.52		
PLACE1007420	12.12	12.66	20.8	25.26	23.9	22.88	*	+
PLACE1007431	1.87	7.4	5.51	7.17	5.28	5.91		
PLACE1007450	0.79	1.22	2.65	3	2.99	2.39		
PLACE1007452	0.42	2.36	1.76	2.09	2.98	1.45		
PLACE1007454	23.74	28.02	76.56	59.97	75.95	46.61		
PLACE1007460	0.75	3.52	2.35	2.34	1.93	2.58		
PLACE1007478	0.41	3.07	1.33	1.35	2.18	1.92		
PLACE1007484	0.6	4.8	2.57	2.56	1.45	1.69		
PLACE1007488	0.4	6.24	1.64	1.74	2.61	1.46		
PLACE1007507	2.91	6.36	4.49	5.31	8.29	8.11		
PLACE1007511	0.53	1.29	1.06	1.06	1.29	0.42		
PLACE1007513	10.57	10.43	24.05	12.24	16.88	16.9		
PLACE1007524	1.55	3.33	3.53	3.96	4.72	2.96		
PLACE1007525	1.24	2.95	3.14	2.38	2.85	2.24		
PLACE1007537	8.6	9.68	49.88	43.78	63.66	40.1		
PLACE1007544	1.55	6.45	4.97	3.2	3.92	4.61		
PLACE1007547	1.36	5.03	4.15	2.37	2.84	2.4		
PLACE1007557	1.12	3.16	3.14	3.07	3.9	3.41		
PLACE1007560	9.38	8.86	12.57	11.03	9.62	17.59		
PLACE1007565	0.37	2.27	1	1	1.16	0.91		
PLACE1007580	1.06	3.71	3.06	10.8	11.15	13.74	**	+
PLACE1007583	0.76	3.88	1.78	2.51	2.37	1.09		
PLACE1007591	0.79	4.62	1.7	2.2	2.53	2.07		
PLACE1007598	1.13	6.98	3.86	2.71	3.46	4.71		
PLACE1007610	0.41	5.63	1.28	1.33	3.18	1.5		
PLACE1007618	1.57	1.91	2.01	1.75	2.2	2.41		
PLACE1007621	1.78	2.83	3.64	3.33	3.57	4.38		
PLACE1007626	23.99	25.61	32.78	30.53	30.94	13.53		
PLACE1007632	2.03	3.26	2.52	2.65	3.81	4.63		
PLACE1007635	1.61	4.62	6.42	2.8	4.19	3.37		
PLACE1007645	10.59	11.55	15.06	9.99	11.58	11.95		
PLACE1007649	1.7	5.88	3.47	2.78	4.95	3.13		
PLACE1007659	1.33	5.85	3.61	4.88	6.22	4.9		
PLACE1007669	2.01	2.1	3.74	2.97	4.63	4.4		
PLACE1007677	1.25	2.29	2.81	2.68	3.07	2.91		
PLACE1007688	3.4	5.69	5.43	1.98	4.53	4.98		

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PLACE1007690	1.4	4.03	2.12	3.74	3.37	4.61		
PLACE1007697	0.69	7.13	1.37	1.84	2.56	1.8		
PLACE1007702	2.03	7.08	5.7	4.03	3.91	4.08		
PLACE1007705	1.38	3.93	1.59	1.74	4.45	2.75		
PLACE1007706	3.11	6.08	4.69	5.25	8.84	7.49		
PLACE1007725	3.41	4.69	6.65	5.1	3.29	5.39		
PLACE1007729	0.98	2.65	1.8	2.7	3.11	1.99		
PLACE1007730	1.25	4.29	3.07	3.66	3.75	4.32		
PLACE1007737	1.43	4.79	3.39	3.79	4.7	4.17		
PLACE1007743	1.38	4.26	2.29	2.3	2.83	2.03		
PLACE1007746	6.56	9.02	10.42	9.65	13.29	12.97		
PLACE1007753	0.53	4.48	1.71	1.35	2.86	1.94		
PLACE1007769	1.31	4.31	3.5	3.27	4.51	4.58		
PLACE1007780	5.77	4.63	7.11	6.51	3.75	2.17		
PLACE1007791	1.82	3.29	3.38	3.16	3.69	2.87		
PLACE1007807	0.67	2.79	1.72	2.33	1.76	1.29		
PLACE1007810	0.39	4.45	2.63	4.11	4.08	3.27		
PLACE1007814	3.57	5.98	5.04	4.2	4.62	6.3		
PLACE1007828	2.01	7.64	3.34	2.69	4.64	3.44		
PLACE1007829	1.32	6.9	2.88	2.87	4.87	3.06		
PLACE1007841	1.64	7.26	1.87	2.25	3.14	3.39		
PLACE1007842	1.1	3.32	2.44	2.09	3.96	1.39		
PLACE1007843	1.2	1.92	1.43	2.13	1.48	1.86		
PLACE1007845	1.76	3	4.11	3.45	3.42	2.36		
PLACE1007846	0.99	3.26	1.64	2.02	2.73	1.5		
PLACE1007848	1.09	3.51	2.23	2.39	2.62	2.25		
PLACE1007852	2.26	7.88	3.82	2.94	4.61	3.24		
PLACE1007858	3.65	11.57	5.81	61.71	80.46	57.09	**	+
PLACE1007866	19.42	25.98	40.48	43	80.39	56.73		
PLACE1007871	8.1	7.9	15.45	16.17	12.35	11.08		
PLACE1007877	1.09	2.09	1.45	1.4	2.39	1.53		
PLACE1007878	5.98	9.75	14.61	13.65	7.49	8.9		
PLACE1007881	0.43	2.66	1.34	1.59	1.94	1.93		
PLACE1007885	4.35	7.85	6.76	5.57	6.53	7.01		
PLACE1007897	0.27	6.51	1.85	1.72	1.53	1.41		
PLACE1007908	3.14	12.29	5.73	5.96	7.9	8.24		
PLACE1007922	6.08	11.75	8.75	5.24	7.15	4.54		
PLACE1007946	1.07	2.03	1.86	2.71	2.28	1.94		
PLACE1007950	6.98	7.6	18.21	16.17	19.34	12.63		

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PLACE1007954	−0.03	2.45	1.15	2.46	1.57	1.51		
PLACE1007955	0.92	4.01	2.17	2.05	2.52	3.05		
PLACE1007956	0.6	3.61	2.91	2.35	2.1	2.22		
PLACE1007958	0.75	6.31	1.34	0.79	1.21	0.8		
PLACE1007965	0.64	5.88	3.25	3.38	2.91	2.17		
PLACE1007969	1.09	6.37	3.06	2.35	3.29	2.21		
PLACE1007971	2.73	4.17	5.21	6.1	4.41	5.92		
PLACE1007990	1.95	2.33	2.31	3.22	3.09	1.88		
PLACE1008000	0.32	2.16	1.98	1.85	1.27	0.66		
PLACE1008002	0.99	3.38	1.7	1.81	2.04	0.51		
PLACE1008037	0.57	4.19	1.7	4.59	2.86	2.02		
PLACE1008044	1.42	5.81	2.46	4.18	4.93	4.16		
PLACE1008045	0.4	4.07	1.54	1.75	2	1.65		
PLACE1008080	2.05	6.08	3.22	4.23	4.03	4.78		
PLACE1008092	1.56	1.56	1.48	1.48	2.98	1.86		
PLACE1008095	0.59	2.14	1.48	2.38	2.73	1.23		
PLACE1008105	0.95	1.76	1.71	2.24	2.71	0.74		
PLACE1008107	0.27	2.33	0.7	1.72	1.44	1.68		
PLACE1008111	1.73	5.01	2.12	4.57	5.4	4.04		
PLACE1008113	5.88	9.24	12.48	16.57	20.29	19.24	*	+
PLACE1008122	1.22	5.54	2.55	1.61	1.57	1.5		
PLACE1008129	1.5	5.64	2.8	2.43	5.36	2.91		
PLACE1008132	5.51	4.47	8.34	6.61	11.2	7.63		
PLACE1008137	0.96	1.82	1.02	2.12	3.88	0.8		
PLACE1008174	0.77	3.16	2.43	5.12	4.39	2.46		
PLACE1008177	1.62	4.87	3.09	3.79	3.26	3.77		
PLACE1008181	1.76	3.87	1.6	2.06	2.43	1.43		
PLACE1008195	2.66	6.08	2.97	4.34	4.14	3.9		
PLACE1008198	1.06	5.56	2.52	2.55	3.31	1.54		
PLACE1008201	1.22	4.45	3.58	5.92	7.69	5.64	*	+
PLACE1008209	2.35	2.29	4.46	2.51	5.31	4.44		
PLACE1008226	1.8	2.35	5.25	4.72	5.68	7.08		
PLACE1008227	0.77	2.67	3.02	2.38	4.6	3.54		
PLACE1008231	1.26	3.85	1.85	1.05	1.83	0.78		
PLACE1008238	1.22	3.21	2.9	2.47	2	1.72		
PLACE1008244	1.01	4.69	1.56	1.68	3.2	1.56		
PLACE1008249	0.8	4.94	2.55	1.22	2.17	2.01		
PLACE1008266	11.31	18.61	43.04	60.04	82.48	59.04	*	+
PLACE1008273	1.47	3.95	3.81	3.53	3.8	4.47		

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PLACE1008275	1.59	3.67	2.17	2.62	2.57	2.34
PLACE1008280	0.85	2.6	1.84	2.42	2.48	2.36
PLACE1008282	4.71	8.19	6.89	7.27	9.02	6.38
PLACE1008297	2.32	4.7	3.36	2.89	3.42	3.21
PLACE1008303	1.65	6.68	1.24	4.12	3.83	2.65
PLACE1008309	0.43	6.52	0.82	1.77	1.5	1.29
PLACE1008315	5.3	5.93	8.61	4.92	4.79	9.83
PLACE1008329	0.47	2.23	2.06	2.32	2.8	2.49
PLACE1008330	0.72	4.06	3.16	2.48	3.36	2.96
PLACE1008331	0.84	5.01	2.1	4.5	2.17	2.91
PLACE1008351	4.34	8.66	7.41	7.91	7.31	7.1
PLACE1008356	1.56	8.23	1.93	2.86	4.16	3.35
PLACE1008359	1.57	4.11	2.89	2	2.97	2.94
PLACE1008368	2.27	6.38	7.43	5.72	7.33	6.95
PLACE1008369	0.57	2.46	1.45	1.12	1.59	1.68
PLACE1008392	0.8	3.09	2.54	2.44	3.22	3.24
PLACE1008394	2.08	4.84	3.75	3.98	5.03	4.76
PLACE1008398	5.32	9.36	11.44	11.36	11.3	12.33
PLACE1008401	1.19	7.06	3.21	2.82	3.43	3.33
PLACE1008402	3.21	6.45	7.2	7.23	10.15	9.26
PLACE1008405	10.3	10.95	18.42	17.17	18.82	20.4
PLACE1008409	1.88	5.19	5.69	4.97	5.41	5.65
PLACE1008420	1.4	1.87	1.96	2.67	2.69	2.27
PLACE1008424	0.88	2.69	2.54	1.69	2.34	1.71
PLACE1008426	0.98	2.58	1.58	1.7	2.66	2.32
PLACE1008429	0.92	3.17	2.14	1.91	3.4	1.84
PLACE1008430	1.63	4.85	3.04	2.93	3.52	3
PLACE1008437	0.87	3.64	3.01	2.83	1.82	1.57
PLACE1008453	1.16	4.8	1.02	1.64	2.06	1.17
PLACE1008454	2.14	6.46	9.23	5.46	9.02	5.92
PLACE1008455	2.06	4.33	7.2	5.26	6.68	4.87
PLACE1008457	0.51	2.6	2.01	2.28	2.43	2.47
PLACE1008465	0.49	2.41	1.72	1.56	2.13	0.48
PLACE1008469	2.42	4.36	5.32	5.16	4.75	7.1
PLACE1008488	0.81	5.48	1.97	2.44	2.03	1.8
PLACE1008519	1.48	10.85	6.17	4.41	4.99	4.51
PLACE1008524	1.04	11.09	1.72	2	3.22	2.02
PLACE1008531	0.64	8.37	1.92	1.33	2.05	1.72
PLACE1008532	2.12	3	5.51	5.66	4.72	4.19

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PLACE1008533	2.01	4	4.07	5.53	5.18	3.77		
PLACE1008542	1.61	2.36	0.96	2.05	2.1	1.72		
PLACE1008549	0.96	3.06	0.67	1.45	2.1	1.53		
PLACE1008560	1.18	4.23	2.28	2.29	3.93	3.47		
PLACE1008567	0.87	7.26	1.85	2.33	3.67	2.38		
PLACE1008568	2.37	10.67	5.49	2.97	7.47	4.21		
PLACE1008569	3.94	10.32	6.74	6.1	8.6	7.6		
PLACE1008584	0.88	1.4	1.58	2.86	3.38	1.31		
PLACE1008585	4.96	4.8	7.56	11.08	4.84	3.57		
PLACE1008603	5.9	7.25	31	30.55	43.67	29.76		
PLACE1008621	0.55	2.28	0.95	0.72	1.89	1.16		
PLACE1008625	0.64	4.01	0.9	1.18	1.41	2.03		
PLACE1008626	0.55	6.06	0.9	1.03	0.83	0.95		
PLACE1008627	0.46	8.32	1.86	1.87	3.34	2.7		
PLACE1008629	3.22	9.18	5.84	5.44	6.75	4.41		
PLACE1008630	1.68	3.39	4.23	4.21	3.01	3.51		
PLACE1008643	1.31	0.93	1.98	1.72	2.34	1.94		
PLACE1008650	0.25	3.05	1.62	2.23	1.63	1.24		
PLACE1008657	1.17	2.39	2.51	2.34	4.04	2.91		
PLACE1008664	0.91	5.93	2.37	2.91	2.51	1.13		
PLACE1008693	0.97	4.93	3.09	2.53	3.81	2.2		
PLACE1008696	0.88	3.84	2.21	2.26	2.11	1.47		
PLACE1008715	1.05	4.71	2.11	1.34	2.65	2.65		
PLACE1008716	2.48	3.94	4.19	5.75	6.9	7.07	*	+
PLACE1008722	3.85	4.34	7.37	7.64	7.19	3.45		
PLACE1008738	5.17	9.13	12.7	9.49	5.83	4.8		
PLACE1008742	6.57	6.87	14.66	14.94	15.06	12.41		
PLACE1008744	3.52	6.98	5.61	5.83	4.55	2.74		
PLACE1008748	0.63	4.39	2.75	2.44	1.67	1.61		
PLACE1008757	0.99	4.74	4.51	2.77	5.74	2.17		
PLACE1008766	2.66	6.75	3.77	3.51	6.47	4.06		
PLACE1008785	1.39	1.68	2.6	3.26	3.8	3.89	*	+
PLACE1008790	1.57	1.8	2.29	3.5	5.39	2.96		
PLACE1008798	1.71	3.82	4.45	6	5.93	3.32		
PLACE1008807	1.34	3.95	1.61	2.54	2.62	1.8		
PLACE1008808	1.6	4.53	3.01	4.24	3.69	5.04		
PLACE1008813	1.38	4.85	1.97	1.9	1.95	2.3		
PLACE1008836	1.34	5.81	3.68	3.89	6.17	4.1		
PLACE1008851	1.21	6.65	3.94	4.85	10.04	4.54		

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PLACE1008854	0.56	0.48	1.14	1.16	1.41	1.6		
PLACE1008864	1.98	1.92	2.96	2.73	2.65	2.49		
PLACE1008867	1.2	6.57	6.22	6.43	5.71	4.82		
PLACE1008876	11.7	16.5	27.29	26.74	20.94	23.24		
PLACE1008887	1.37	4.31	1.44	3.26	2.07	3.28		
PLACE1008902	1.33	5.62	2.93	3.17	4.58	2.06		
PLACE1008911	4.04	8.56	10.48	11.31	13.99	15.66		
PLACE1008917	0.6	4.53	2.72	1.7	2.9	1.71		
PLACE1008920	0.75	0.77	0.87	0.61	1.58	1.44		
PLACE1008925	0.25	0.9	1.04	0.94	1.91	0.84		
PLACE1008930	4.12	7.32	9.83	5.11	10.36	7.17		
PLACE1008934	0.9	3.42	2.9	2.89	2.28	1.7		
PLACE1008941	1.57	4.14	2.8	2.06	2.59	4.05		
PLACE1008947	2.3	5.41	5.51	3.96	5.84	5.16		
PLACE1008984	1.26	6.31	3.25	3.1	3.93	3.19		
PLACE1008985	0.94	2.75	2.74	2.84	2.43	2.7		
PLACE1008994	0.27	1.72	0.65	1.11	0.78	0.68		
PLACE1009020	0.46	3.49	2.42	2.49	3.1	2.16		
PLACE1009027	0.89	2.7	1.59	2.24	1.75	2.09		
PLACE1009039	−0.06	3.31	3.42	2.39	1.59	1.49		
PLACE1009045	1.53	6.33	6.05	23.13	20.76	22.2	**	+
PLACE1009048	0.41	5.97	2.3	0.61	1.04	0.54		
PLACE1009050	0.97	4.9	1.68	1.07	1.47	1.55		
PLACE1009060	5.61	8.4	9.51	10.74	8.55	11.96		
PLACE1009067	1.14	2.8	2.03	1.6	2.34	3.4		
PLACE1009071	1.44	4.05	3.9	3.79	7.24	9.82		
PLACE1009090	1.27	6.46	2.35	3.11	4.73	2.86		
PLACE1009091	5.58	10.22	38.11	38.77	49.35	36.29		
PLACE1009094	0.26	5.68	1.88	1.67	5.04	1.71		
PLACE1009099	1	5.52	3.47	3.49	3.36	3.84		
PLACE1009110	1.59	5.82	1.16	1.68	4.3	4.39		
PLACE1009111	1.88	5.24	2.65	3.95	3.77	2.88		
PLACE1009113	2.24	3.52	3.62	6.14	4.87	7.29	*	+
PLACE1009130	4.46	6.8	7.84	6.68	9.36	10.47		
PLACE1009150	0.88	3.54	1.95	3.23	3.3	3.01		
PLACE1009155	1.11	5.06	2.98	4.46	4.43	3.87		
PLACE1009158	1.06	5.77	1.95	1.77	2.35	2.88		
PLACE1009166	0.76	4.8	1.53	1.59	2.16	1.3		
PLACE1009172	1.43	3.96	2.45	2.26	5.85	2.61		

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	PLACE1009174	1.13	3.45	2.42	1.67	3.02	2.38	
	PLACE1009183	1.62	3.54	4.47	4.1	6.33	8.06	
	PLACE1009186	1.04	5.07	2.3	2.46	2.86	2.91	
	PLACE1009190	0.75	2.32	1.44	1.53	1.9	1.65	
	PLACE1009196	0.81	4.01	2.73	2.24	2.38	1.99	
	PLACE1009200	1.01	4.44	2.94	2.84	4.39	2.91	
	PLACE1009217	2.55	4.91	3.43	4.46	7.29	7.23	
	PLACE1009230	1.9	5.55	6.63	5.63	9.16	9.46	
	PLACE1009236	4.97	7.07	12.6	8.21	10.79	7.13	
	PLACE1009246	11.71	11.96	24.75	14.59	16.36	9.05	
	PLACE1009265	6.95	7.82	14.01	15.61	5.19	12.17	
	PLACE1009279	0.67	2.07	2.46	1.93	2.54	1.63	
	PLACE1009298	5.54	9.92	9.52	10.21	11.25	17.55	
	PLACE1009308	1.13	6.82	2.04	2.48	2.48	2.34	
	PLACE1009319	2.04	9.25	3.15	2.92	3.54	2.5	
	PLACE1009328	1.04	5.78	1.81	2.98	3.39	2.17	
	PLACE1009335	1.38	6.55	4.72	2.24	3.21	3.01	
	PLACE1009338	2.56	4.14	5.1	3.24	4.3	1.57	
	PLACE1009344	0.73	2.45	1.08	1.31	1.55	0.84	
	PLACE1009355	5.41	7.37	9.95	13.44	10.76	13.55	* +
	PLACE1009368	1.3	2.56	2.41	2.43	2.32	2.19	
	PLACE1009375	1.21	6.41	3.05	3.04	4.46	2.53	
	PLACE1009388	1.18	8.68	3.01	3.46	4.53	2.72	
	PLACE1009398	1.19	9.2	3.74	3.17	4.28	3.96	
	PLACE1009404	2.78	9.18	4.51	5.33	6.73	6.94	
	PLACE1009410	1.27	2.35	2.33	2.51	2.31	1.44	
	PLACE1009417	0.95	2.25	4.34	2.55	3.08	1.71	
	PLACE1009424	1.88	3.61	3.18	2.85	3.24	3.93	
	PLACE1009434	0.84	3.94	2.91	1.29	1.82	2.19	
	PLACE1009443	1.21	7.2	2.55	2.42	3.43	3.17	
	PLACE1009444	1.33	7.71	4.05	2.51	3.17	3.79	
	PLACE1009459	0.23	7.99	1.55	1.71	1.83	0.86	
	PLACE1009460	1.75	6.84	3.26	5.15	4.31	4.08	
	PLACE1009468	0.99	2.83	3.42	4.43	4.42	2.97	
	PLACE1009476	0.21	1.21	0.73	1.05	0.67	1.33	
	PLACE1009477	1.35	3.13	2.67	3.06	2.35	2.2	
	PLACE1009493	0.87	3.35	0.94	1	1.87	1.41	
	PLACE1009502	0.76	4.64	2.13	1.19	1.89	1.66	
	PLACE1009524	1.32	4.22	1.63	0.94	2.14	1.6	

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PLACE1009527	0.95	4.51	2.11	1.64	2.55	1.28		
PLACE1009531	20.82	28.24	41.52	46.25	43.25	49.96		
PLACE1009535	1.1	1.56	2.68	2.42	2.15	1.11		
PLACE1009539	2.15	3.41	4.18	3.88	2.65	2.57		
PLACE1009540	5.89	8	11.66	14.8	4.47	3.84		
PLACE1009542	1.11	3.37	1.42	1.51	2.06	1.44		
PLACE1009546	0.62	5.27	0.97	2.24	1.64	1.25		
PLACE1009556	0.35	4.46	3.46	3.36	2.86	3.16		
PLACE1009569	0.05	3.93	2.46	3.34	2.7	3.11		
PLACE1009571	1.67	4.27	2.52	3.04	2.85	2.67		
PLACE1009573	3.81	2.97	6.73	6.92	8.12	6.49		
PLACE1009576	1.92	2.51	4.3	2.73	3.66	2.08		
PLACE1009580	1.42	1.81	1.74	2.73	3.47	2.33	*	+
PLACE1009581	0.89	4.25	2.03	2.91	4.38	2.74		
PLACE1009587	0.96	4.91	2.29	2.43	3.2	1.99		
PLACE1009593	2.71	6.73	4.37	4.94	6.85	5.03		
PLACE1009595	1.81	5.44	2.66	2.67	5	2.79		
PLACE1009596	1.57	6.83	2.6	3.44	3.97	2.7		
PLACE1009600	3.03	4.27	4.48	5.48	9.14	4.42		
PLACE1009604	2.32	4.64	5.02	4.22	6.11	3.23		
PLACE1009607	1.29	2.48	3.18	3.19	4.17	3.18		
PLACE1009613	1.94	5.23	2.94	2.65	3.08	2.23		
PLACE1009621	1.66	6.72	3.32	8.21	8.67	8.06	*	+
PLACE1009622	1.78	5.93	3.78	3.9	4.1	3.9		
PLACE1009624	1.16	5.77	3.42	3.2	3.65	3.5		
PLACE1009637	2	6.88	3.36	3.07	4.59	3.91		
PLACE1009639	1.94	1.76	4.15	3.44	3.67	4.99		
PLACE1009654	20.88	17.13	34.95	14.94	24.53	20.64		
PLACE1009659	2.77	6.78	7.45	6.38	8.38	6.55		
PLACE1009665	1.04	4.21	1.93	1.19	2.72	1.93		
PLACE1009669	7.73	9.64	14.54	9.85	16.89	8.82		
PLACE1009670	1.76	5.36	2.54	2.77	4.47	4.01		
PLACE1009708	2.1	5.57	5.09	3.64	6.54	5.84		
PLACE1009721	1.34	4.28	3.56	5.78	5.81	3.01		
PLACE1009731	1.36	3.59	3	3.58	6.53	5		
PLACE1009735	1.94	3.94	3.21	5.16	7.52	4.78		
PLACE1009737	1.89	4.29	2.95	4.83	5.61	5.47	*	+
PLACE1009741	1.3	4.32	3.45	2.09	5.03	3.07		
PLACE1009752	1.34	5.64	2.65	2.3	3.33	1.68		

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PLACE1009763	3.95	9.73	6.82	7.13	7.44	8.39
PLACE1009766	1.46	6.98	3.32	3.07	5.19	3.75
PLACE1009772	0.48	5.19	0.6	1.01	2.46	0.89
PLACE1009782	0.91	2.39	2.03	2.88	2.91	3.74
PLACE1009794	2.58	4.45	5.11	3.54	3.66	5.03
PLACE1009798	1.59	5.37	4	6.26	5.57	5.67
PLACE1009845	1.05	6.02	2.92	2.79	3.39	3.92
PLACE1009849	0.96	6.61	2.35	1.79	3.41	2.59
PLACE1009857	0.79	4.86	1.45	1.19	1.27	1.56
PLACE1009861	1.43	4.67	3.87	4.1	3.47	3.11
PLACE1009872	53.53	52.43	88.5	74.95	49.47	81.73
PLACE1009877	5.45	7.59	12.08	10.03	10.3	12.32
PLACE1009879	0.82	3.28	1.59	1.55	2.99	1.34
PLACE1009886	0.68	4.04	1.53	1.62	3.04	1.72
PLACE1009888	1.03	7.4	3.23	5.34	5.84	7.94
PLACE1009908	1.56	7.63	8.64	3.37	6.71	5.9
PLACE1009919	4.5	7.53	8.26	5.84	10.72	10.15
PLACE1009921	0.96	3.94	3.32	1.63	4.28	2.47
PLACE1009923	3.82	5.56	6.85	6.32	8.13	5.57
PLACE1009924	3.01	2.49	4.53	4.43	4.31	1.04
PLACE1009925	0.61	2.77	1.84	2.51	2.2	2.5
PLACE1009931	2.78	5.21	9	8.71	6.93	8.09
PLACE1009935	0.74	3.71	2.1	1.19	1.08	1.5
PLACE1009947	0.47	3.83	1.64	1.51	2.46	2.03
PLACE1009961	0.43	4.08	1.39	1.69	2.18	1.9
PLACE1009971	0.92	4.9	1.98	1.35	1.74	1.45
PLACE1009982	40.34	48.71	89.8	53.8	57.87	66.96
PLACE1009992	0.94	1.9	2.59	1.47	2.52	0.68
PLACE1009995	6.47	10.83	15.72	7.79	9.03	11.23
PLACE1009997	0.55	3.7	3.03	2.76	3.2	2.64
PLACE1010002	1.4	4.14	2.82	2.89	3.04	3.46
PLACE1010011	2.09	8.13	3.85	4.4	5.21	4.68
PLACE1010013	0.18	12.85	1.74	0.92	1.81	0.68
PLACE1010021	3.18	11.98	5.42	4.12	4.13	6.06
PLACE1010023	2.15	8.45	5.16	5.62	6.52	6.14
PLACE1010031	4.6	4.35	7.23	6.79	4.91	1.82
PLACE1010039	1.17	3.3	1.45	1.28	1.23	1.19
PLACE1010045	1.1	2.83	3.66	2.52	3.55	2.64
PLACE1010053	1.42	3.56	1.65	2.21	2.76	2.37

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PLACE1010060	1.63	6.1	4.13	4.11	4.6	4.05		
PLACE1010069	0.41	7.96	2.32	1.48	2.91	1.3		
PLACE1010070	0.92	8.04	1.5	0.45	1.78	1.09		
PLACE1010074	5.25	11.67	11.8	12.32	9.51	11.22		
PLACE1010076	12.75	11.95	29.01	19.58	15.88	16.82		
PLACE1010078	2.96	2.42	4.36	4.64	4.39	3.85		
PLACE1010081	2.74	4.1	3.7	6.85	7.81	4.59	*	+
PLACE1010083	0.69	2.53	1.51	1.22	1.86	2.26		
PLACE1010089	1.86	4.89	3.35	3.45	3.47	3.48		
PLACE1010096	2.17	7.73	2.91	3.43	4.19	3.2		
PLACE1010102	3.89	10.9	5.33	7.1	9.64	7.57		
PLACE1010105	2.98	7.46	4.93	7.31	9.04	9.82		
PLACE1010106	2.46	2.95	4.48	5.47	4.88	5.8	*	+
PLACE1010130	0.53	1.79	1.17	2.27	2.55	1.23		
PLACE1010132	2.49	4.65	5.3	5.07	4.39	4.19		
PLACE1010134	0.8	3.32	1.15	1.97	2.31	1.67		
PLACE1010139	6.67	10.51	12.98	14.99	16.1	14.58		
PLACE1010148	0.96	5.07	1.62	1.48	1.9	1.97		
PLACE1010152	3.11	5.68	5.16	6.33	6.64	5.76		
PLACE1010155	3.8	6.17	6.52	16.85	20.56	20.32	**	+
PLACE1010156	13.71	15.43	32.21	132.45	85.59	134.99	**	+
PLACE1010161	1.9	2.81	5.05	3.29	2.92	1.97		
PLACE1010181	0.73	2.22	1.51	2.58	1.99	2.53		
PLACE1010194	0.64	3.35	1.03	2.26	2.14	1.64		
PLACE1010202	0.4	4.14	1.2	2.91	1.65	2.16		
PLACE1010231	1.1	3.78	2.39	1.31	2.99	2.73		
PLACE1010235	1.26	4.24	1.94	2.68	2.42	3.16		
PLACE1010237	1.01	3.4	2.1	1.14	1.97	0.87		
PLACE1010251	0.59	0.98	1.95	2.57	3.18	1.62		
PLACE1010261	0.97	2.63	2.07	2.69	1.69	1.55		
PLACE1010270	0.76	2.7	1.3	1.39	2.33	1.42		
PLACE1010273	0.97	3.27	0.46	1.48	2.25	1.5		
PLACE1010274	6.28	9.23	9.66	10.49	12.18	14.28		
PLACE1010277	6.03	10.14	12.68	14.6	16.06	15.84	*	+
PLACE1010293	1.8	5.68	3.55	3.65	3.37	3.96		
PLACE1010297	5.17	11.37	21	24.84	32.59	22.06		
PLACE1010300	4.18	4.78	8.22	8	9.95	6.87		
PLACE1010310	16.52	14.75	49.45	70.74	71	77.01	*	+
PLACE1010321	2.03	4.92	2.46	3.37	4.99	2.73		

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PLACE1010324	0.88	3.49	1.56	1.12	1.54	1.2		
PLACE1010329	0.73	4.64	1.95	2.56	3.37	1.96		
PLACE1010330	3.78	9.09	7.29	2.42	10.45	7.67		
PLACE1010335	6.43	11.15	7.43	13.15	17.89	19.1	*	+
PLACE1010341	0.19	4.81	1.24	1.07	3.13	1.54		
PLACE1010342	0.77	0.9	0.75	0.48	2.12	0.8		
PLACE1010346	1.47	1.73	3.61	2.96	4.47	1.71		
PLACE1010362	1.31	2.69	2.22	2.18	3.49	3.31		
PLACE1010364	0.78	2.56	1.65	1.19	2.32	1.49		
PLACE1010368	1.66	5.44	3.51	3.41	3.87	4.48		
PLACE1010373	9.05	10.48	16.82	12.13	15.45	12.28		
PLACE1010383	1.91	5.52	5.13	5.58	6.39	4.9		
PLACE1010385	0.3	3.01	1.07	0.04	0.6	0.9		
PLACE1010389	6.28	7.98	13.24	22.3	13.64	22.94	*	+
PLACE1010401	0.73	2.72	1.32	1.99	2.87	2.21		
PLACE1010410	3.15	4.83	6.71	4.78	7.55	7.32		
PLACE1010418	1.88	4.73	4.2	4.71	5.14	4.66		
PLACE1010425	0.93	4.78	1.43	1.78	1.96	2.15		
PLACE1010443	6.98	13.83	51.39	36.22	63.67	48.93		
PLACE1010445	0.95	5.02	0.68	2.69	3.81	2.44		
PLACE1010481	1.19	2.06	2.46	1.75	2	1.85		
PLACE1010482	28.99	29.39	53.06	31.75	19.63	40.44		
PLACE1010491	3.36	6.4	5.38	4.96	5.98	3.26		
PLACE1010492	4	4.75	5.95	5.57	8.15	7.77		
PLACE1010509	0.8	4.32	3.15	3.09	3.01	2.99		
PLACE1010518	3.33	6.72	6.58	7.3	8.25	8.24		
PLACE1010522	2.3	5.96	4.35	1.87	3.52	2.64		
PLACE1010529	1.8	6.5	3.84	5.43	8.44	7.2		
PLACE1010547	0.79	1.57	1.76	1.51	1.93	2.45		
PLACE1010560	0.63	2.51	2.06	3.31	2.2	2.51		
PLACE1010562	0.74	2.68	1.65	1.64	2.1	1.63		
PLACE1010579	1.11	7.13	2.63	3.45	4.67	3.26		
PLACE1010580	1.35	9.12	3.79	3.27	2.49	4.52		
PLACE1010599	3.56	6.07	7.94	8.32	9.26	8.13		
PLACE1010606	1.17	4.42	1.64	3.39	4.17	3.51		
PLACE1010616	1.84	3.72	5.49	4.09	8.09	6.81		
PLACE1010622	2.1	3.43	3.91	5.07	4.74	4.69	*	+
PLACE1010624	1.43	3.35	3.98	4.21	6.17	5.22		
PLACE1010628	1.37	3.97	2.83	2.14	3.63	4.22		

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PLACE1010629	1.08	4.64	2.24	3.01	3.3	3.5	
PLACE1010630	1.64	4.77	3.69	4.22	4.78	5.29	
PLACE1010631	0.5	5.35	2.64	1.55	1.66	2.67	
PLACE1010651	14.24	15.75	24.44	37.62	40.09	52.12	* +
PLACE1010661	1.62	4.09	2.28	3.56	6.43	3.22	
PLACE1010662	1.32	2.48	1.6	2.98	2.3	1.61	
PLACE1010668	12.87	15.91	27.82	37.63	30.53	28.75	
PLACE1010702	1.46	2.34	4.24	3.59	3.6	3.2	
PLACE1010709	79.16	78.33	115.91	107.07	96.3	133.25	
PLACE1010713	7	10.81	14.7	9.14	8.16	15.14	
PLACE1010714	0.82	7.41	1.58	1.75	2.04	1.47	
PLACE1010716	0.71	6.19	4.31	2.08	2.3	1.93	
PLACE1010717	0.9	6.49	2.13	2.17	3.9	2.61	
PLACE1010720	14.03	17.05	53.79	46.72	50.7	41.49	
PLACE1010739	0.9	1.2	1.11	1.73	1.21	1.93	
PLACE1010743	1.09	2.3	1.99	2.63	2.05	2.21	
PLACE1010752	0.87	2.92	1.85	1.76	2.05	1.53	
PLACE1010761	3.6	8.83	13.51	12.07	16.4	17.08	
PLACE1010771	1.41	6.89	5.03	6.13	10.3	5.42	
PLACE1010784	0.9	9.66	1.97	2.07	1.72	1.34	
PLACE1010786	1.21	8.77	2.83	2.91	3.68	2.21	
PLACE1010789	0.6	1.16	1.52	1.8	1.89	1.17	
PLACE1010800	2.18	2.86	3.25	3.95	3.24	2.93	
PLACE1010802	2.97	4.63	5.31	5.72	4.27	3.3	
PLACE1010811	0.89	2.19	1.96	1.83	1.75	2.18	
PLACE1010813	8.89	13.3	55.85	48.82	72.26	46.7	
PLACE1010827	1.54	6.43	3.94	4.3	5.52	4.81	
PLACE1010833	0.93	8.13	2.63	2.68	3.64	2.09	
PLACE1010839	1.57	6.22	3.21	4.22	6.72	4.13	
PLACE1010856	7.58	8.94	12.34	8.02	6.53	8.59	
PLACE1010857	3.41	3.81	7.63	8.24	5.98	4.56	
PLACE1010870	1.3	2.24	2.05	1.62	2.38	1.94	
PLACE1010877	1.67	4.66	2.69	2.77	3.92	2.62	
PLACE1010882	0.49	4.8	0.99	1.74	1.27	0.51	
PLACE1010891	1.1	7.73	1.12	1.85	1.73	0.95	
PLACE1010896	1.19	5.29	3.18	3.98	3.05	3.47	
PLACE1010900	7.41	13.29	27.9	23.88	20.99	18.85	
PLACE1010916	1.55	1.18	2.06	1.89	1.9	2.2	
PLACE1010917	-0.04	0.82	0.36	1.05	2.25	0.56	

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PLACE1010924	1.15	2.31	1.55	1.11	1.88	0.92		
PLACE1010925	2.76	5.36	2.17	4.92	6.32	4.16		
PLACE1010926	1.8	5.73	4.31	5.37	4.35	4.45		
PLACE1010942	1.7	6.25	5.63	5.53	7.88	7.69		
PLACE1010943	7.38	10.43	17.12	24.62	29.5	31.96	**	+
PLACE1010944	4.33	7.39	9.3	13.11	11.44	15.58	*	+
PLACE1010947	1.43	0.9	2.41	2.57	2.8	2.25		
PLACE1010954	3.56	2.92	7.4	7.92	8.55	7.64		
PLACE1010960	2.06	3.44	6.07	4.23	7.89	2.6		
PLACE1010965	2.33	3.81	3.54	6.09	4.92	5.03	*	+
PLACE1010968	1.55	4.69	1.38	4.95	6.51	3.68		
PLACE1010978	3.63	6.12	7.05	9	8.94	6.45		
PLACE1010982	2.23	5.77	5.6	4.74	5.66	4.88		
PLACE1010990	0.88	5.4	2.04	3.11	3.03	2.19		
PLACE1011017	5.6	3.78	22.57	25.64	35.47	20.97		
PLACE1011019	1.1	1.5	2.48	3.78	4.42	0.88		
PLACE1011026	4.17	4.93	6.23	6	5.19	2.74		
PLACE1011032	0.89	3.95	2.03	1.44	1.58	0.56		
PLACE1011041	1.07	4.13	1.03	1.69	1.22	1.43		
PLACE1011045	1.49	5.62	2.36	3.26	3.67	4.45		
PLACE1011046	0.83	5.25	1.79	2.57	3.17	1.87		
PLACE1011054	2.33	5.33	6.64	5.26	7.29	5.05		
PLACE1011056	5.78	5.43	16.22	14.56	19.78	15.67		
PLACE1011057	2	2.18	3.5	3.29	5.68	3.9		
PLACE1011059	0.93	1.37	1.56	1.74	2.96	1.79		
PLACE1011066	4.49	5.74	6.76	5.38	7.72	5.49		
PLACE1011087	7.6	7.04	16.48	12.43	17.42	9.79		
PLACE1011090	2.98	6.14	6.74	3.36	4.13	3.26		
PLACE1011109	1.99	7.29	4.29	4.08	7.96	3.83		
PLACE1011114	1.62	4.4	3.13	3.33	4.68	3.29		
PLACE1011116	4.89	5.94	6.66	7.43	6.81	8.98		
PLACE1011122	0.93	2.52	1.84	2.1	1.61	1.64		
PLACE1011133	0.83	2.22	3.03	3.48	3.52	2.77		
PLACE1011134	12.47	15.29	66.86	44.95	68.68	51.65		
PLACE1011143	0.68	4.53	1.48	1.84	2.62	1.41		
PLACE1011146	0.91	5.93	1.74	1.97	3.23	2.36		
PLACE1011160	1.67	7.36	3.81	3.42	4.53	4.24		
PLACE1011165	1.77	2.34	3.39	2.15	3.39	3.8		
PLACE1011181	5.25	8.31	37.21	29.38	38.44	30.55		

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PLACE1011185	2.47	4	3.57	4.66	5.15	4.8	*	+
PLACE1011186	13.16	12.8	16.45	21.18	25.69	28.83	*	+
PLACE1011203	1.08	4.64	2.19	1.75	2.94	1.96		
PLACE1011214	9.02	16.55	59.24	46.39	62.58	47.89		
PLACE1011219	1.41	4.91	3.6	3.26	4.96	2.9		
PLACE1011221	2.68	5.47	6.15	6.23	8.57	7.51		
PLACE1011229	1.38	4.2	2.69	2.43	2.43	3.09		
PLACE1011231	0.53	1.5	1.62	1.84	2.59	2.4		
PLACE1011236	5.69	7.9	43.53	33.48	56.77	44.25		
PLACE1011247	8.36	10.08	19.16	24.17	26.33	29.74	*	+
PLACE1011263	0.57	6.43	4.23	2.62	4.11	5.09		
PLACE1011273	0.72	3.62	1.17	2.01	1.64	1.72		
PLACE1011278	2.42	5	6.12	3.98	4.84	4.31		
PLACE1011289	2.73	5.84	7.57	6.34	6.13	6.08		
PLACE1011291	3.2	5.19	8.31	7.32	8.04	7.95		
PLACE1011296	0.93	2.45	1.94	1.76	2.63	2.05		
PLACE1011310	1.72	2.64	3.36	4.51	2.77	4.48		
PLACE1011311	1.8	3.97	6.33	7.8	9.34	6.73		
PLACE1011321	1.29	4.77	3.5	3.3	2.63	3.33		
PLACE1011325	0.63	4.2	1.84	2	2.74	1.59		
PLACE1011332	5.65	10.55	9.4	14.8	14.57	15.04	*	+
PLACE1011340	0.86	4.88	3.38	3.81	4.71	3.47		
PLACE1011353	5.39	5.53	8.39	10.06	8.58	4.43		
PLACE1011360	1.09	3.29	2.18	2.11	3.06	2.41		
PLACE1011364	4.88	5.69	7.92	6.34	4.57	4.57		
PLACE1011365	0.92	3.36	2.95	3.01	3.6	2.06		
PLACE1011371	9.37	10.69	63.06	56.51	87.51	64.33		
PLACE1011375	1.62	9.37	3.35	2.61	2.74	1.62		
PLACE1011386	3.91	12.96	4.18	6.88	5.51	5.93		
PLACE1011399	1.52	10.14	4.27	2.12	4.22	3.77		
PLACE1011406	1.25	2.05	1.81	5.03	3.26	2.38		
PLACE1011407	0.64	2.05	2.58	2.08	2.19	2.02		
PLACE1011419	2.83	3.2	6.02	6.23	4.18	3.72		
PLACE1011433	3.09	4.43	6.13	3.41	4.74	4.99		
PLACE1011440	0.77	5.81	2.48	2.1	2.24	2.27		
PLACE1011452	1.06	8.86	2.43	2.87	2.71	2.68		
PLACE1011465	0.09	8.53	1.96	1.04	1.68	0.85		
PLACE1011472	1.52	7.67	3.98	0.97	2.87	1.59		
PLACE1011477	11.18	12.29	54.35	31.86	55.86	45.67		

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PLACE1011478	1.24	1.64	3.11	5.03	3.02	3.01		
PLACE1011492	2.24	3.54	5.01	5.45	6.74	5.27		
PLACE1011498	0.57	2.77	0.98	1.18	1.69	1.15		
PLACE1011501	0.49	4.67	1.8	4.87	5.63	7.5		
PLACE1011503	0.44	5.37	0.79	0.5	0.82	0.35		
PLACE1011509	1.1	7.8	3.38	4.62	5.08	5.74		
PLACE1011514	5.86	11.61	11.98	13	17.7	13.17		
PLACE1011516	10.37	13.29	18.32	18.32	8.08	3.63		
PLACE1011520	0.34	0.95	1.34	1.3	1.73	1.01		
PLACE1011538	52.87	99.27	185.04	129.45	86.87	63.9		
PLACE1011555	0.87	2.88	2.83	1.55	2.03	1.48		
PLACE1011561	3.2	4.53	1.98	6.81	5.31	3.08		
PLACE1011563	1.35	4.74	3.49	2.52	2.64	2.87		
PLACE1011567	1.04	4.94	3.36	2.75	4.19	2.77		
PLACE1011569	0.32	4.35	2.77	2.38	2.46	2.28		
PLACE1011576	3.25	1.88	7.94	7.85	9.1	8.03		
PLACE1011586	3.24	2.5	6.22	4.43	4.35	2.94		
PLACE1011635	1.85	2.56	4.53	9.96	12.43	8.71	**	+
PLACE1011641	0.43	2.9	0.9	1.71	1.18	1.19		
PLACE1011642	5.05	6.96	10.37	12.13	10.86	10.09		
PLACE1011643	1.29	3.69	1.14	2.38	2.28	2.14		
PLACE1011646	8.68	12.8	30.53	39.05	54.16	37.76	*	+
PLACE1011649	1.35	5.7	3.88	4.5	4.61	5.46		
PLACE1011650	1.15	1.45	2.54	2.47	3.24	3.75		
PLACE1011661	1.02	2.26	2.8	3.95	5.92	3.46		
PLACE1011664	2.21	3.18	3.99	5.31	3.93	1.73		
PLACE1011672	0.88	4.14	0.72	2.69	3.57	2.04		
PLACE1011675	0.51	2.31	1.32	1.66	0.99	0.83		
PLACE1011682	2.04	4.56	2.23	2.22	4.03	2.12		
PLACE1011708	1.1	5.89	3.8	5.5	8.12	4.66		
PLACE1011719	1.07	4.58	1.66	3.55	3.88	3.03		
PLACE1011725	1.23	1.19	2.72	3.73	5.19	4.3	*	+
PLACE1011729	0.86	1.03	1.8	2.38	3.26	1.22		
PLACE1011741	2.36	3.67	3.64	4.16	2.52	4.23		
PLACE1011749	1.58	3.89	4.09	3.49	4.85	3.27		
PLACE1011757	20.92	30.53	55.88	56.6	55.88	49.59		
PLACE1011762	0.4	4.34	2.69	3.91	2.14	2.3		
PLACE1011778	0.51	4.39	1.99	1.34	2.02	1.34		
PLACE1011783	2.59	4.63	5.46	4.8	8.41	5.55		

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PLACE1011795	0. 74	1. 28	2. 24	1. 47	1. 8	1. 22		
PLACE1011810	9. 28	10. 82	19. 51	13. 32	17. 73	15. 47		
PLACE1011824	5. 38	8. 17	38. 05	25. 52	42. 89	16. 75		
PLACE1011825	10. 61	16. 39	22. 6	17. 63	18. 92	16. 07		
PLACE1011835	24. 64	32. 67	47. 67	32. 09	26. 75	37. 23		
PLACE1011836	18. 11	18. 97	31. 43	33. 14	47. 23	13. 95		
PLACE1011847	2. 67	6. 74	6. 42	5. 34	7. 18	5. 84		
PLACE1011855	0. 9	6. 06	3. 53	3. 23	4. 47	3. 49		
PLACE1011858	5. 83	7. 44	9. 37	6. 88	6. 25	8. 35		
PLACE1011874	1. 35	3. 14	3. 55	4. 18	5. 28	4. 65		
PLACE1011875	0. 57	2. 29	1. 11	2. 66	2. 48	2. 64		
PLACE1011877	3. 8	5. 03	4. 4	7. 67	6. 8	9. 97	*	+
PLACE1011891	0. 17	3. 81	1. 31	1. 13	1. 34	1. 26		
PLACE1011896	−0. 1	5. 22	1. 45	−0. 19	1. 07	0. 32		
PLACE1011920	0. 21	5. 87	1. 04	1. 1	1. 92	1. 76		
PLACE1011922	2. 4	4. 18	4. 72	3. 72	2. 88	3. 98		
PLACE1011923	3. 42	4. 82	7. 51	8. 09	5. 38	12. 28		
PLACE1011937	3. 16	2. 24	3. 76	3. 81	5. 58	4. 64		
PLACE1011939	14. 93	17. 81	26. 01	41. 75	45. 05	47. 88	**	+
PLACE1011940	6. 13	7. 58	12. 68	5. 73	7	7. 23		
PLACE1011962	3. 28	7. 83	7. 35	6. 39	8. 38	8. 01		
PLACE1011964	0. 39	5. 05	1. 66	1. 04	1. 95	1. 46		
PLACE1011978	1. 55	4. 65	3. 35	4. 48	5. 91	5. 14		
PLACE1011980	2. 1	4. 62	6. 07	3. 95	4. 91	5. 35		
PLACE1011981	5. 77	7. 28	38. 2	27. 22	35. 24	34. 99		
PLACE1011982	0. 83	3. 1	2. 23	1. 82	2. 59	1. 57		
PLACE1011995	0. 81	3. 4	3. 73	2. 51	3. 59	2. 86		
PLACE1012023	1. 38	5. 37	1. 87	2. 09	2. 46	1. 91		
PLACE1012026	1. 95	5. 72	4. 23	6. 08	9. 51	9. 8		
PLACE1012031	2. 49	5. 81	4. 54	4. 34	6. 35	4. 03		
PLACE2000003	1. 18	3. 64	6. 86	7. 38	8. 12	8. 92		
PLACE2000005	1. 16	2. 41	2. 16	2. 76	2. 03	1. 89		
PLACE2000006	2. 52	4. 13	15. 6	11. 34	16. 58	13. 4		
PLACE2000007	0. 96	4. 85	4. 24	3. 94	5. 13	3. 33		
PLACE2000011	1. 72	3. 27	3. 34	4. 3	5. 06	3. 62		
PLACE2000014	4. 04	5. 93	23. 94	27. 19	30. 87	30. 97	*	+
PLACE2000015	1. 27	4. 79	3. 52	2. 77	3. 31	2. 69		
PLACE2000017	0. 48	4. 78	2. 15	2. 65	2. 56	2. 45		
PLACE2000021	1. 99	5. 06	4. 09	3. 72	6. 24	5. 61		

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PLACE2000022	1.8	2.8	4.31	3.35	4.64	2.71
PLACE2000030	9.37	11.08	71.38	55.43	60.32	35.97
PLACE2000032	1.23	2.89	3.51	3.53	3.24	2.32
PLACE2000033	3.29	6.3	12.11	12.49	14.25	9.37
PLACE2000034	0.6	4.3	1.92	1.79	2.19	2.44
PLACE2000039	2.75	8.06	3.92	6.27	8.01	4.81
PLACE2000043	7	11.08	22.94	19.27	26.58	17.38
PLACE2000044	0.63	6.92	1.12	1.8	1.71	1.29
PLACE2000047	0.84	5.25	5.15	5.4	6.46	7.32
PLACE2000050	1.48	2.68	4.78	2.92	2.98	1.2
PLACE2000061	0.47	2.07	1.17	0.95	1.34	0.25
PLACE2000062	1.99	2.83	4.12	4.89	4.4	3.09
PLACE2000072	0.78	2.45	1.57	1.85	1.62	1.69
PLACE2000073	0.89	5.86	2.86	2.8	2.61	3.07
PLACE2000097	8.54	19.93	23.93	27.69	35.36	26.36
PLACE2000100	1.87	7.79	3.53	4.23	6.29	4.22
PLACE2000103	1.03	7.44	2.25	3.51	5.17	4.38
PLACE2000106	1.53	2.42	4.19	5.71	3.29	4.01
PLACE2000111	2.05	3.17	4.37	4.07	6.6	4.75
PLACE2000115	0.3	2.06	0.75	0.31	1.29	0.97
PLACE2000118	10.15	17.04	21.09	13.73	15.21	22.01
PLACE2000124	10.14	17.83	62.13	53.2	98.37	62.96
PLACE2000132	0.06	6.26	1.48	0.99	1.5	1.56
PLACE2000136	0.55	7.94	0.91	1.47	1.37	1.02
PLACE2000137	0.96	4.46	2.4	2.65	4.12	3.14
PLACE2000140	2.91	5.24	14.34	13.2	12.08	9.43
PLACE2000147	1.49	1.52	2.83	1.06	0.97	1.12
PLACE2000153	0.3	3.44	2.15	1.69	2.45	1.95
PLACE2000164	0.66	2.78	1.13	2.66	1.62	1.62
PLACE2000170	1.54	6.18	4.69	5.26	9.09	6.24
PLACE2000172	0.33	4.34	2.15	1.25	1.93	2.43
PLACE2000173	0.92	4.97	3.37	3.33	3.71	2.74
PLACE2000174	1.17	4.68	2.43	1.85	2.89	2.05
PLACE2000176	1.22	1.57	2.58	3.28	2.27	1.42
PLACE2000187	1.01	2.08	2.55	3.45	3.66	2.19
PLACE2000216	7.03	9.28	11.47	14.09	9.13	3.68
PLACE2000219	0.69	4.02	2.72	3.55	3.58	2.3
PLACE2000221	2.49	6.81	6.53	7.22	9.33	8.56
PLACE2000223	0.72	3.2	1.71	1.16	1.05	0.48

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PLACE2000231	1.02	3.97	3.11	3.43	2.61	2.47		
PLACE2000235	1.82	5.27	6.17	6.02	7.45	6.97		
PLACE2000246	1.93	2	6.06	4.58	5.09	3.93		
PLACE2000264	0.67	1.39	1.85	2.45	3.74	3	*	+
PLACE2000274	0.65	2.4	2.12	3.09	4.11	2.1		
PLACE2000287	0.81	4.44	1.49	2	2.59	1.34		
PLACE2000296	1.01	4.56	1.55	2.5	3.16	1.69		
PLACE2000302	1.34	4.67	2.86	3.52	3.35	3.45		
PLACE2000305	3.09	6.65	5.42	6.3	7.15	5.02		
PLACE2000317	0.92	6.34	2.26	3.15	2.95	2.4		
PLACE2000324	1.19	1.25	3.09	4.2	5.84	3.3		
PLACE2000334	3.52	5	6.6	7.33	8.12	5.88		
PLACE2000335	1.47	4.35	4.24	5.68	6.25	4.76		
PLACE2000340	0.64	3.47	1.63	1.58	1.52	1.65		
PLACE2000341	4.21	7.87	28.81	18.94	32.45	19.16		
PLACE2000342	2.07	5.11	4.32	4.84	5.82	4.49		
PLACE2000347	1.24	5.26	5.58	7.83	6.22	7.55		
PLACE2000357	8.49	13.56	15.35	17.83	18.98	21.24	*	+
PLACE2000358	2.87	3.65	8.67	4.88	7.63	4.37		
PLACE2000359	1.27	1.79	4.45	3.28	6.65	3.61		
PLACE2000366	1.93	3.14	3.22	3.99	5.6	4.17		
PLACE2000371	4.29	5.2	6.08	5.95	9.06	7.32		
PLACE2000373	1.91	4.8	5.98	5.69	6.29	4.19		
PLACE2000374	1.86	5.17	2.78	1.62	2.79	1.49		
PLACE2000379	0.34	4.85	1.32	1.28	0.92	0.04		
PLACE2000386	39.29	43.92	84.66	87.53	104.55	76.56		
PLACE2000388	1.96	3.35	3.89	2.78	3.48	3.49		
PLACE2000392	33.29	39.2	59.56	42.5	52.12	58.24		
PLACE2000394	1.26	3.27	3.01	5.69	4.35	4.34	*	+
PLACE2000398	0.73	3.88	2.36	2.03	3.59	1.35		
PLACE2000399	3.7	6.82	7.01	7.15	7	6.79		
PLACE2000402	2.15	6.88	3.84	2.86	3.68	3.9		
PLACE2000404	5.2	9.96	10.67	10.03	11.04	6.47		
PLACE2000411	3.21	7.2	5.21	5.27	5.73	6.68		
PLACE2000418	0.73	2.28	2.41	2.22	3.07	2.37		
PLACE2000419	0.99	2.32	2.54	4.95	4.55	3.29	*	+
PLACE2000425	1.26	3.98	3.11	4.28	4.81	5.2		
PLACE2000427	0.7	5.13	3.27	2.54	3.04	2.47		
PLACE2000433	0.77	7.05	2.6	2.33	3.09	2.46		

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PLACE2000435	0.48	5.19	1.49	1.69	1.63	1.5		
PLACE2000438	1.61	4.74	3.66	2.33	2.81	3.15		
PLACE2000450	3.01	4.38	5.67	6.51	7.39	5.63		
PLACE2000455	0.24	2.62	1.24	1.65	2	1.82		
PLACE2000458	0.38	3.3	1.81	1.06	2.7	1.24		
PLACE2000464	2.15	4.91	5.3	7.43	9.68	8.83	*	+
PLACE2000465	1.43	6.72	6	6.51	8.27	6.31		
PLACE2000473	120.94	179.35	328.3	214.7	297.75	279.74		
PLACE2000477	0.43	3.87	1.34	1.13	2.22	0.97		
PLACE3000004	2.22	4.63	6.39	5.27	7.51	5.2		
PLACE3000009	19.91	19.71	105.63	77.3	140.99	92.95		
PLACE3000020	10.03	9.03	49.6	36.74	46.52	23.82		
PLACE3000029	6.59	9.63	24.88	14.88	18.47	20.04		
PLACE3000038	0.52	2.37	2.47	1.44	2.4	2.05		
PLACE3000052	5.13	7.95	23.92	25.01	29.61	24.94		
PLACE3000059	0.57	5	2.42	0.75	2.8	1.27		
PLACE3000067	2.51	5.79	7.44	5.66	8.53	7.75		
PLACE3000069	1.95	5.61	3.58	5.24	3.79	4.55		
PLACE3000070	2.57	5.57	9.04	9.5	10.42	10.57		
PLACE3000103	3.85	7.84	11.87	6.6	8.32	4.37		
PLACE3000119	1.59	2.74	3.15	3.24	3.67	2.95		
PLACE3000121	7.58	8.44	38.1	30.63	42.28	32.64		
PLACE3000124	1.53	4.54	5.95	6.35	7.75	7.18		
PLACE3000135	0.69	5.46	1.1	0.76	0.9	0.59		
PLACE3000136	0.77	10.46	4.46	2.12	2.77	2.01		
PLACE3000142	0.7	9.94	1.75	1.53	2.76	1.13		
PLACE3000145	8.69	17.55	55.33	42.85	49.12	39.96		
PLACE3000147	15.7	12.92	39.97	64.96	54.76	30.34		
PLACE3000148	0.7	2.08	1.48	0.82	1.4	1.38		
PLACE3000154	0.48	1.86	0.67	1.5	0.87	0.44		
PLACE3000155	1.28	4.26	2.53	3.97	4.76	3.04		
PLACE3000156	1.11	7.96	2.07	1.96	3.4	2.81		
PLACE3000157	0.92	8.37	1.75	2.06	3.02	2.72		
PLACE3000158	1.73	8.82	5.05	3.81	5.63	4.77		
PLACE3000160	8.11	15.22	19.5	33.66	34.71	33.78	**	+
PLACE3000169	2.15	2.65	6.87	4.3	5.11	5.12		
PLACE3000181	1.06	2.14	3.94	3.22	2.62	3		
PLACE3000194	0.31	2.83	1.77	1.89	2.58	2.42		
PLACE3000197	1.18	2.66	2.09	2.42	2.46	2.21		

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PLACE3000199	0.22	4.8	1.63	0.55	0.86	0.43		
PLACE3000205	11.79	17.95	57.49	51.4	63.83	42.63		
PLACE3000207	3.37	6.91	7.13	6.7	8.92	6.23		
PLACE3000208	2.26	4.96	2.66	5.28	5.97	5.84		
PLACE3000213	4.79	5.55	10.8	5.12	5.16	5.05		
PLACE3000215	1.88	5.02	5.71	4.74	5	3.03		
PLACE3000218	0	1.63	1.18	0.97	0.62	0.31		
PLACE3000220	1.96	3.55	4.58	6.74	7.52	6.69	*	+
PLACE3000221	14.42	25.34	40.15	43.8	51.16	36.99		
PLACE3000225	1.15	4.68	3.11	2.11	2.67	1.28		
PLACE3000226	1.37	5.65	5.16	3.78	7.42	3.68		
PLACE3000230	0.83	3.46	1.36	2	2.8	1.73		
PLACE3000231	1.31	1.97	2.37	4.86	3.95	4.12	**	+
PLACE3000235	1.12	1.75	3.89	3.95	4.21	3.39		
PLACE3000242	2.6	5.11	9.24	9.46	10.97	8.29		
PLACE3000244	1.05	3.2	1.81	1.85	1.81	0.64		
PLACE3000253	0.7	3.75	1.64	2.67	2.11	1.27		
PLACE3000254	2.5	4.75	4.04	6.19	6.09	5.75	*	+
PLACE3000271	2.67	6.06	6.81	10.96	10.99	9.5	*	+
PLACE3000276	1.1	5.78	2.27	1.48	1.9	1.78		
PLACE3000304	5.55	4.69	10.81	11.19	11.49	10.5		
PLACE3000309	0.43	1.67	1.87	2.43	2.94	2.78	*	+
PLACE3000310	2.19	2.19	3.73	4.84	4.81	3.4		
PLACE3000320	1.02	3.65	1.8	2.54	2.37	2.32		
PLACE3000322	1.31	4.23	6.63	7.5	7.8	6.09		
PLACE3000330	24.05	24.44	41.08	31.87	35.83	29.17		
PLACE3000331	1.21	5.86	4.14	4.34	5.7	4.31		
PLACE3000336	2.61	6.99	4.42	4.24	5.72	5.11		
PLACE3000339	7.36	5.1	11.41	16.25	18.28	17.37	**	+
PLACE3000341	1.65	1.32	2.41	4.08	4.35	3.65	**	+
PLACE3000350	5.88	6.4	12.86	15.45	18.5	15.41	*	+
PLACE3000352	1.54	3.88	2.13	2.37	2.25	1.71		
PLACE3000353	5.38	9.72	11.8	19.12	22.98	15.5	*	+
PLACE3000362	0.62	4.92	4.72	3.61	5.33	3.39		
PLACE3000363	2.19	5.13	2.32	1.89	3.28	2.07		
PLACE3000365	1.34	6.11	3.37	3.34	4.05	2.12		
PLACE3000373	0.89	1.52	3.66	2.93	6.08	2.3		
PLACE3000374	1.07	1.85	2.91	2.72	2.99	2.15		
PLACE3000387	0.31	3.32	1.04	1.24	1.65	1.29		

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PLACE3000388	1.18	3.22	1.94	2.76	3.49	2.22		
PLACE3000399	2.12	4.66	6.28	7.42	9.84	6.05		
PLACE3000400	3.08	5.44	11.87	7.97	10.77	7.82		
PLACE3000401	7.52	11.42	18.59	22.61	29.55	23.4	*	+
PLACE3000402	1.79	3.21	3.4	2.19	1.74	1.79		
PLACE3000405	3.37	3.74	5.82	5.54	7.22	6.01		
PLACE3000406	2.1	2.91	3.11	3.48	3.68	2.42		
PLACE3000413	1.18	2.72	2.69	1.71	2.06	1.52		
PLACE3000416	1.05	4.03	4.04	3.43	2.67	2.72		
PLACE3000425	1.21	6.27	4.33	3.98	6.36	3.92		
PLACE3000437	4.79	10.85	29.89	16.69	25.26	19.14		
PLACE3000455	2.97	8.07	10.62	8.97	10.39	7.91		
PLACE3000475	16.52	19.2	47.35	40.22	39.77	34.21		
PLACE3000477	5.44	4.79	5.56	8.05	5.52	8.42		
PLACE4000003	0.38	2.97	1.61	3.14	2.33	2.31		
PLACE4000008	15.19	11.38	16.76	13.05	14.26	8.84		
PLACE4000009	1.17	6.19	3.39	3.93	3.37	1.82		
PLACE4000014	1.31	5.12	1.77	2.16	3.03	2.19		
PLACE4000029	6.33	8.48	35.37	23.93	32.21	24.25		
PLACE4000034	2.27	6.24	5.22	6.46	6.52	4.91		
PLACE4000049	3.39	3.35	5.21	3.85	5.82	4.86		
PLACE4000052	1.41	3.36	2.2	2.62	2.64	2.02		
PLACE4000062	1.6	4.94	5.06	4.25	5.06	3.71		
PLACE4000063	2.59	6.87	5.19	4.86	4.81	3.73		
PLACE4000089	1.52	6.31	3.35	2.81	3.91	2.84		
PLACE4000093	0.44	5.6	1.61	1.28	1.65	1.98		
PLACE4000100	2.72	6.13	4.75	4.33	3.62	3.94		
PLACE4000103	0.63	4.48	5.64	4.4	5.67	2.9		
PLACE4000106	3.2	5.33	6.63	7.1	5.13	7.21		
PLACE4000128	1.93	3.97	4.88	4.15	4.96	4.4		
PLACE4000129	0.74	3.26	1.64	1.57	2.11	1.78		
PLACE4000131	7.14	10.85	41.43	32.45	41.08	31.22		
PLACE4000147	0.34	3.65	0.54	0.45	0.93	0.61		
PLACE4000156	2.47	6.08	8.06	7.83	13.47	9.07		
PLACE4000175	0.72	4.08	1.48	0.98	0.91	0.84		
PLACE4000190	14.55	18.47	70.34	49.15	74.82	60.76		
PLACE4000192	1.3	2.27	3.6	2.36	2	1.25		
PLACE4000206	5.35	6.65	12.44	7.13	7.1	6.02		
PLACE4000211	3.34	4.64	22.23	11.68	12.35	13.44		

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PLACE4000214	0. 86	3. 61	2. 68	2. 08	2. 53	1. 69		
PLACE4000222	0. 93	5. 28	4. 36	4. 13	4. 75	3. 5		
PLACE4000223	0. 46	4. 51	1. 79	1. 37	1. 22	0. 38		
PLACE4000229	1. 9	5. 79	2. 11	2. 81	3. 36	3. 48		
PLACE4000230	1. 11	5. 89	6. 51	3. 61	6. 81	5. 15		
PLACE4000233	1. 26	3. 02	5. 66	2. 92	2. 98	3. 51		
PLACE4000239	2. 35	3. 68	4. 17	4. 19	3. 97	3. 35		
PLACE4000247	0. 52	2. 37	3. 38	2. 64	3. 1	2. 35		
PLACE4000250	1. 18	3. 24	2. 35	3. 33	3. 68	2. 8		
PLACE4000252	1. 06	4. 99	2. 25	1. 92	1. 75	1. 64		
PLACE4000259	4. 42	11. 95	18. 1	14. 47	22. 09	14. 02		
PLACE4000261	0. 87	10. 29	1. 07	2. 03	1. 9	1. 12		
PLACE4000264	15. 86	24. 96	36. 9	11. 96	21. 82	22. 51		
PLACE4000269	3. 48	3. 71	7. 95	4. 62	4. 55	2. 85		
PLACE4000270	0. 43	1. 42	1. 87	1. 75	1. 83	0. 59		
PLACE4000281	17. 84	20. 97	44. 05	32. 93	28. 37	28. 87		
PLACE4000300	0. 67	2. 06	2. 04	3. 21	2. 88	3. 58	*	+
PLACE4000320	1. 33	5. 86	3. 1	2. 84	5. 32	3. 21		
PLACE4000323	1. 63	7. 43	5. 13	4. 03	4. 65	4. 82		
PLACE4000326	1. 8	10. 98	5. 67	5. 72	8. 73	5. 59		
PLACE4000344	0. 22	5. 75	2. 62	1. 66	1. 6	1. 18		
PLACE4000347	4. 7	3. 82	13. 93	16. 83	16. 75	17. 36	*	+
PLACE4000354	3. 18	6. 29	10. 68	5. 17	2. 81	2. 79		
PLACE4000367	0. 79	2. 97	1. 71	0. 87	1. 3	1. 38		
PLACE4000369	1. 35	3. 97	2. 36	1. 99	1. 96	0. 82		
PLACE4000379	2. 44	6. 66	5. 44	5. 94	7. 55	5. 07		
PLACE4000387	0. 88	5. 86	2. 11	1. 28	0. 84	1. 12		
PLACE4000392	0. 42	5. 58	1. 32	1. 81	1. 02	1. 63		
PLACE4000399	10. 99	17. 08	75. 17	59. 11	80. 22	58		
PLACE4000401	0. 72	0. 7	1. 53	1. 17	0. 83	1. 4		
PLACE4000403	3. 15	4. 13	8. 51	5. 29	6. 38	5. 87		
PLACE4000411	2. 22	2. 28	4	2. 27	2. 6	1. 82		
PLACE4000415	0. 7	3. 55	2. 8	1. 16	1. 86	0. 78		
PLACE4000416	25. 49	29. 13	33. 54	23. 65	21. 92	24. 83		
PLACE4000424	1. 61	5. 59	3. 33	3. 27	3. 92	2. 51		
PLACE4000431	3. 89	7. 39	21. 01	17. 68	28. 21	16. 79		
PLACE4000443	0. 07	4. 33	2. 15	1. 52	2. 83	1. 14		
PLACE4000445	3. 94	5. 43	9. 98	7. 62	6. 99	6. 27		
PLACE4000450	2. 99	3. 65	23. 28	15. 51	24. 53	16. 04		

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PLACE4000455	5.18	7.39	9.55	8	7.21	4.63		
PLACE4000465	1.39	4.34	3.26	4.15	6.07	4.34		
PLACE4000466	120.96	98.04	201.25	113.83	170.96	145.31		
PLACE4000472	3.12	9.6	10.17	10.92	13.21	9.22		
PLACE4000487	3.18	7.83	16.5	14.66	16.62	15.05		
PLACE4000489	0.93	4.69	3.41	1.95	3.88	1.69		
PLACE4000494	1.15	1.6	4.07	2.74	3.1	2.08		
PLACE4000502	6.3	5.39	10.92	11.65	15.08	6.37		
PLACE4000521	2.5	3.44	16.06	12.78	20.63	11.2		
PLACE4000522	5.07	6.17	9.07	12.43	8.68	14.11		
PLACE4000537	0.98	4.28	1.27	1.67	1.61	1.22		
PLACE4000548	1.99	5.69	2.46	3.04	3.68	2.32		
PLACE4000558	0.87	6.72	1.97	3.15	2.41	2.15		
PLACE4000581	2.1	7.22	7.04	3.9	5.96	5.44		
PLACE4000590	0.4	0.61	0.15	0.4	0.81	−0.25		
PLACE4000593	2.94	2.98	5.22	4.44	5.82	3.83		
PLACE4000612	0.68	3.33	3.33	1.5	3.02	2.74		
PLACE4000638	1.25	4.24	0.84	1.2	1.44	1.58		
PLACE4000650	0.82	4.67	1.02	1.43	1.11	1.16		
PLACE4000651	2.42	6.4	7.48	5	7.01	6.07		
PLACE4000654	0.98	5.7	2.47	1.35	2.48	1.47		
PLACE4000670	0.5	4.06	2.92	0.76	1.29	0.67		
PLACE4000685	6.35	8.68	13.83	13.46	14.26	13.77		
PLACE4000687	0.37	3.02	1.11	2.2	1.4	1.12		
PLACE5000003	1.1	2.74	3.31	3.21	3.55	3.07		
PLACE5000005	12.43	16.53	27.36	24.54	24.57	24.76		
PLACE5000019	0.4	4.15	1.13	0.59	1.89	0.79		
PLACE5000021	0.74	4.59	1.61	0.39	0.93	0.32		
PLACE5000022	1.2	6.11	2.25	3.17	2.76	2.09		
PLACE5000024	1.77	2.58	2.27	2.92	3.39	3.84	*	+
PLACE5000036	1.81	3.24	3.11	2.41	3.19	2.84		
PLACE5000059	14.41	17.79	26.55	25.98	30.03	34.87		
PLACE5000076	1.41	3.61	2.22	4.04	3.96	2.54		
PLACE5000117	7.44	12.48	15.66	16.87	18.78	20.64		
PLACE5000143	0.85	6.45	2.11	1.67	2.85	2.73		
PLACE5000152	0.42	4.49	1.23	1.61	1.95	1.57		
PLACE5000154	18.23	23.5	45.06	21.81	25.65	31.8		
PLACE5000155	3.35	2.81	5.51	3.94	2.78	4.87		
PLACE5000165	3.78	4.4	6.67	4.51	5.99	5.82		

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SKNMC1000004	9.7	11.62	16.77	10.19	12.16	13.96		
SKNMC1000011	1.82	8.58	4.12	5.89	3.95	6.77		
SKNMC1000013	0.51	6.69	1.13	1.21	2.14	1.44		
SKNMC1000014	1.28	4.18	3.22	3.77	6.37	3.96		
SKNMC1000018	3.42	5.19	5.25	5.51	5.68	3.44		
SKNMC1000020	0.95	4.03	3.46	3.6	4.68	4.56		
SKNMC1000046	2	3.17	3.48	3.95	3.26	2.55		
SKNMC1000050	4.99	8.04	10.32	5.4	6.28	6.12		
SKNMC1000062	9.79	12.6	20.18	19.2	15.42	18.73		
SKNMC1000075	1.45	4.3	2.01	1.98	1.89	2.92		
SKNMC1000082	1.12	4.39	2.13	1.85	1.78	2.39		
SKNMC1000091	4.54	7.52	7.95	11.74	12.86	12.77	**	+
SKNMC1000099	0.33	4.29	1.98	1.32	0.65	1.18		
SKNMC1000104	1.13	4.24	3.45	1.47	3.14	2.43		
SKNMC1000113	0.97	1.83	1.2	1.74	2.63	0.89		
SKNMC1000119	1.73	2.64	5.07	4.48	5.34	4.67		
SKNMC1000142	0.04	2.87	0.99	1.27	0.75	1		
SKNMC1000170	0.91	4.75	2.34	1.71	1.49	1.11		
SKNMC1000178	3.02	8.39	7.08	5.77	9.65	9.02		
SKNMC1000194	0.63	9.82	1.51	0.61	1.73	1.3		
SKNMC1000198	1.35	11.01	3.33	2.65	2.1	2.88		
SKNMC1000225	1.35	6.44	2.97	2.39	3.4	3.26		
SKNMC1000249	0.49	2.14	0.75	0.57	0.51	0.52		
SPLEN1000007	0.74	2.15	2.11	1.7	2.26	1.99		
SPLEN1000012	0.39	1.9	1.72	1.19	0.8	0.84		
SPLEN1000014	1.78	4.4	4.9	5.75	4.33	3.99		
SPLEN1000036	4.95	11.64	24.32	20.56	27.73	21.68		
SPLEN1000059	0.04	6.69	1.06	0.91	1.79	1.47		
SPLEN1000068	1.68	10.81	5.71	5.79	5.17	5.64		
SPLEN1000072	1	8.5	4.7	2.82	3	2.21		
SPLEN1000101	20.01	18.4	45.64	29.93	25.24	12.63		
SPLEN1000108	0.56	1.54	0.98	0.75	1.11	0.76		
SPLEN1000113	1.33	2.27	3.04	2.72	4.13	3.04		
SPLEN1000114	2.97	4.19	6.03	3.59	4.76	6.32		
SPLEN1000132	0.85	4	1.72	2.25	2.67	1.99		
SPLEN1000135	3.13	8.76	14.93	11.12	15.28	10.52		
SPLEN1000136	12.41	21.47	15.14	20.24	27.48	21.8		
SPLEN1000141	2.26	7.07	10.79	4.03	5.41	4.51		
SPLEN1000164	2.49	3.79	8.58	3.98	5.88	7.61		

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SPLEN1000166	0.4	2.9	2.96	1.67	1.19	1.68		
SPLEN1000175	2.16	4.48	6.1	5.65	4.12	4.15		
SPLEN1000182	0.98	2.66	-0.23	0.83	0.6	0.67		
SPLEN1000185	3.41	8.49	8.54	11.38	10.43	11.95		
THYMU1000004	10.22	14.07	20.43	22.34	22.76	23.6		
THYMU1000009	9.48	10.13	14.9	13.48	23.86	22.1		
THYMU1000015	8.87	10.42	16.18	19.25	22.21	20.8	*	+
THYMU1000016	6.24	5.96	13.03	10.3	8.45	9.38		
THYMU1000023	0.77	1.86	3.6	5.22	3.68	3.6		
THYMU1000034	0.16	1.77	1.8	0.79	0.88	0.14		
THYMU1000035	0.62	2.8	0.97	1.17	0.95	1.31		
THYMU1000037	1.53	4.15	2.11	2.06	2.81	1.45		
THYMU1000042	5.97	10.24	12.23	12.03	13.98	13.28		
THYMU1000047	2.72	6.03	6.72	6.04	7.77	7.23		
THYMU1000080	0.56	4.31	2.6	3.26	1.85	2.11		
THYMU1000094	2.77	3.47	7.91	9.17	8.35	4.55		
THYMU1000109	17.28	14.34	111.37	98.05	142.29	93.04		
THYMU1000127	2.75	5.95	10.76	8.18	9.98	6.74		
THYMU1000130	2.5	4.4	4.55	6.69	6.07	4.94		
THYMU1000137	3.53	7.18	10.26	12.67	18.55	13.05	*	+
THYMU1000146	4.37	8.38	6.52	8.29	7.46	7.74		
THYMU1000159	5.43	9.51	16.37	12.4	15.15	13.27		
THYMU1000163	5.85	12.26	37.58	45.53	58.37	36.93		
THYMU1000167	2.39	3.02	4.73	4.89	6.79	3.97		
THYMU1000186	0.69	1.05	1.45	1.31	2.45	0.66		
THYRO1000017	0.94	3.45	2.54	2.02	3.54	2.11		
THYRO1000026	1.56	5.63	4.02	3.96	4.82	3.36		
THYRO1000034	0.49	4.16	1.59	1.99	2	1.82		
THYRO1000035	0.86	4.84	1.34	2.29	2.48	2.11		
THYRO1000036	0.93	8.32	4	3.08	4.36	5.59		
THYRO1000040	2.58	7.02	4.76	4.66	4.83	4.93		
THYRO1000061	2.01	1.91	3.07	3.53	3.8	2.61		
THYRO1000067	1.98	2.8	5.12	3.37	4.14	3.3		
THYRO1000070	1.26	2.09	3.59	2.65	3.85	3.45		
THYRO1000072	1.33	3.37	4.22	2.54	4.08	2.06		
THYRO1000084	8.07	12.69	22.39	2.99	5.61	4.42		
THYRO1000085	1.44	5.66	3.99	2.42	3.86	2.85		
THYRO1000086	-0.05	5.46	1.74	0.89	1.18	1.15		
THYRO1000087	0.72	3.86	1.01	0	0.58	0.17		

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THYR01000092	2. 32	5. 1	4. 66	3. 75	4. 43	4. 5		
THYR01000093	0. 35	3. 24	0. 83	1. 54	1. 27	0. 95		
THYR01000099	0. 45	2. 53	2. 73	2. 8	1. 67	2. 39		
THYR01000107	0. 5	2. 95	2. 7	2. 86	3. 22	2		
THYR01000111	0. 85	4. 58	1. 78	1. 4	2. 06	2. 36		
THYR01000121	1. 33	5. 72	2. 52	1. 94	2. 4	2. 95		
THYR01000124	0. 27	5. 55	0. 64	0. 86	0. 89	0. 64		
THYR01000129	0. 36	2. 1	0. 11	0. 94	1. 11	0. 92		
THYR01000130	1. 82	3. 11	3. 13	3. 85	3. 01	2. 39		
THYR01000132	2. 4	3. 62	9. 43	11. 14	6. 99	6. 26		
THYR01000134	1. 5	4. 07	3. 22	4. 06	3. 65	3. 73		
THYR01000144	1. 72	4. 78	3. 15	7. 87	7. 09	2. 33		
THYR01000155	1. 6	4. 1	1. 45	1. 77	1. 9	2. 23		
THYR01000156	1. 13	6. 53	3. 62	2. 45	4. 29	2. 58		
THYR01000163	3. 62	8. 42	5. 28	4. 76	6. 63	2. 24		
THYR01000173	1. 19	4. 45	2. 26	3. 33	1. 36	2. 75		
THYR01000186	1. 98	3. 24	7. 86	6. 91	6. 84	6. 35		
THYR01000187	2. 7	3. 58	5. 3	4. 92	6. 24	5. 22		
THYR01000190	1. 12	3. 32	2. 94	3. 73	4. 55	2. 71		
THYR01000196	0. 3	5. 28	0. 81	0. 66	1. 21	0. 52		
THYR01000197	2. 05	7. 28	4. 69	4. 08	6. 24	3. 89		
THYR01000199	0. 76	6. 28	4. 13	1. 93	2. 08	1. 98		
THYR01000206	8. 47	6. 92	9. 25	8. 44	11. 6	7. 5		
THYR01000221	1. 9	3. 17	4. 42	4. 02	5. 87	4. 54		
THYR01000222	3. 65	4. 26	4. 23	4. 68	4. 96	4. 93	*	+
THYR01000228	0. 81	3. 67	2. 85	2. 24	3. 04	2. 94		
THYR01000241	1. 76	3. 7	6. 29	4. 62	5. 54	4. 01		
THYR01000242	0. 63	4. 16	4. 46	2. 49	2. 56	2. 62		
THYR01000246	1. 61	5. 5	3. 9	3. 43	4. 7	3. 91		
THYR01000253	1. 07	4. 05	1. 73	1. 99	3. 35	2. 31		
THYR01000270	1. 15	5. 12	1. 39	1. 22	2. 5	1. 26		
THYR01000279	0. 42	2. 84	0. 25	0. 65	1. 01	0. 58		
THYR01000285	2. 75	4. 65	7. 31	7. 03	7. 75	4. 88		
THYR01000288	7. 76	7. 59	11. 77	5. 68	5. 07	7. 22		
THYR01000296	4. 18	6. 04	6. 22	7. 4	11. 24	8. 96	*	+
THYR01000320	1. 54	5. 83	4. 97	3. 65	4. 45	3. 34		
THYR01000322	1. 1	5. 48	2. 48	1. 76	3. 93	1. 76		
THYR01000327	1. 75	7. 69	4. 77	6. 21	5. 23	4. 41		
THYR01000343	2. 5	6. 12	5. 35	5. 06	5. 04	6. 13		

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THYR01000345	1.36	7.34	11.92	7.82	5.84	9.49		
THYR01000358	1.82	3.39	3.08	1.92	2.32	1.54		
THYR01000368	0.76	2.39	2.73	1.43	2.82	0.58		
THYR01000375	3.2	7.03	4.79	7.38	6.09	9.77		
THYR01000381	0.92	2.88	2.19	3.87	3.11	2.74		
THYR01000387	0.98	6.66	3.22	2.53	3.56	2.51		
THYR01000394	1.31	9.88	4.59	4.29	5.19	2.61		
THYR01000395	0.8	10.44	2.26	1.97	2.07	2.02		
THYR01000400	0.57	8.1	2.82	2.35	2.96	2.52		
THYR01000401	0.86	1.94	2.5	1.87	1.16	1.57		
THYR01000407	1.97	2.3	1.36	1.37	1.58	0.55		
THYR01000420	1.8	2.67	4.46	3.52	3.53	3.39		
THYR01000438	1.78	4.37	3.26	2.94	3.33	3.15		
THYR01000452	2.62	7.99	6.45	3.71	5.75	4.38		
THYR01000455	0.32	6.67	2.31	0.25	0.97	0.87		
THYR01000471	0.99	8.03	2.05	1.11	2.08	1.02		
THYR01000481	1.33	6.23	4.68	3.79	3.45	4.55		
THYR01000484	1.2	1.42	2.41	2.35	3	2.21		
THYR01000488	1.18	2.64	2.44	1.49	2.02	1.7		
THYR01000501	1.12	4.01	2.78	3	1.92	1.82		
THYR01000502	0.34	3.7	1.69	1.79	1.44	1.2		
THYR01000505	0.13	4.64	1.19	1.14	1.02	0.6		
THYR01000535	11.1	20.54	39.24	54.13	69.59	62.96	*	+
THYR01000556	1.89	6.36	4.13	3.77	5.17	3.69		
THYR01000558	0.25	2.82	1.12	1.16	0.81	0.61		
THYR01000569	2.88	4.12	6.05	5.78	4.46	4.88		
THYR01000570	2.31	3.28	8.46	8.53	6.04	3.49		
THYR01000572	0.43	2.04	1.11	0.17	0.97	−0.42		
THYR01000573	0.69	4.02	1.73	2.02	2.2	1.78		
THYR01000577	1.06	5	1.34	0.96	1.22	0.71		
THYR01000580	0.79	3.72	3.01	2.82	2.2	1.79		
THYR01000584	2.18	6.88	8.8	7.57	6.61	7.58		
THYR01000585	4.83	9.37	9.83	5.76	6.27	9.52		
THYR01000596	0.22	0.93	1.19	0.44	1.36	0.21		
THYR01000602	2.08	2.95	4.01	4.05	4.65	4.97		
THYR01000605	0.37	3.01	0.98	2.13	2.14	1.56		
THYR01000615	1.02	3.62	1.24	1.55	1.36	1.29		
THYR01000625	0.71	5.48	2.28	2.46	2.9	1.78		
THYR01000636	3.67	5.65	6.9	6.53	7.84	6.67		

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THYR01000637	0.91	3.96	1.71	1.18	2.03	1.54
THYR01000641	0.38	4.19	2.49	1.36	1.67	1.64
THYR01000657	2.99	3.69	5.42	7.67	12.28	3.86
THYR01000658	2.68	3.62	5.39	5.4	5.55	6.09
THYR01000662	1.1	3.19	2.09	2.42	2.69	1.66
THYR01000666	0.57	3.19	2.28	1.63	1.48	1.43
THYR01000676	1.37	4.53	2.01	1.75	1.83	1.56
THYR01000678	0.52	5.86	0.99	1.29	1.4	0.53
THYR01000684	0.95	4.98	2.94	1.92	2.65	1.47
THYR01000694	2.08	6.64	4.65	2.8	2.48	3.59
THYR01000699	2.98	2.14	5.55	4.86	7.08	7.12
THYR01000712	1.88	4.25	5.9	6.25	6.75	7.78
THYR01000715	5.74	5.67	27.37	21.74	28.63	16.99
THYR01000716	0.92	3.26	3.2	1.88	1.78	1.35
THYR01000717	1.58	5	4.36	2.98	4.63	1.91
THYR01000723	0.6	4.54	1.6	0.55	1.06	0.85
THYR01000734	−0.01	4.81	1.89	1.49	1.73	1.07
THYR01000748	0.98	5.51	5.23	2.35	3.85	3.18
THYR01000755	1.74	3.26	4.32	4.33	3.47	4.38
THYR01000756	2.79	4.24	3.24	3.46	4.2	3.41
THYR01000776	0.48	2.17	3.02	3.36	3.99	3.34
THYR01000777	1.81	3.39	4.54	4.99	2.05	2.37
THYR01000779	1.45	3.55	0.88	0.18	1.01	−0.26
THYR01000782	3.92	10.13	12.52	10.76	15.05	14.05
THYR01000783	0.12	5.51	1.2	1.11	1.41	0.92
THYR01000786	6.65	9.54	19.71	15.74	7.92	13.7
THYR01000787	0.23	1.88	1.67	1.31	1.54	0.78
THYR01000792	1.51	3.13	2.29	3.09	3.13	2.11
THYR01000793	0.11	3.13	0.84	1.51	1.86	1.16
THYR01000795	1.23	6.03	3.54	2.76	3.1	3.05
THYR01000796	0.6	7.73	2.44	2.26	2.95	1.66
THYR01000798	1.89	5.82	2.51	2.59	3.57	3.53
THYR01000800	9.26	17.2	24.74	17.74	20.68	21.06
THYR01000805	0.49	3.04	1.08	0.72	2.66	1.38
THYR01000815	2.54	3.49	9.48	7.61	5.47	7.87
THYR01000829	5.55	7.83	10.57	3.78	8.32	10.01
THYR01000835	0.96	3.2	1.93	1.07	2.36	1.8
THYR01000843	1.09	11.48	3.56	3.69	4.41	3.62
THYR01000846	0.76	5.71	1.32	2.67	1.62	1.26

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THYR01000852	1.59	6.02	5.63	2.8	4.7	3.32		
THYR01000855	3.14	5.02	6.63	9.03	15.1	10.07	*	+
THYR01000865	1.86	4.3	11.97	10.01	11.47	8.95		
THYR01000866	7.47	6.29	12.66	4.49	7.87	6.01		
THYR01000881	5.62	7.3	10.93	15.65	26.64	29.58	*	+
THYR01000894	0.33	3.95	1.36	1.75	1.48	1		
THYR01000895	0.58	4.43	1.42	1.62	1.46	0.82		
THYR01000916	1.22	5.49	3.43	2.43	3.13	2.29		
THYR01000917	16.19	25.26	34.11	30.37	37.42	35.89		
THYR01000926	0.78	3.13	1.27	1.76	1.57	0.82		
THYR01000934	0.08	3.1	1.34	0.43	1.38	1.46		
THYR01000951	0.52	2.46	1.26	2.33	2.11	1.9		
THYR01000952	2.25	3.81	6.01	2.38	2.53	2.24		
THYR01000956	0.06	2.55	1.81	1.16	1.5	0.87		
THYR01000960	0.5	6.72	2.89	1.85	2.79	1.48		
THYR01000961	1.67	7.77	3.56	4.73	5.26	4.64		
THYR01000964	0.42	11.59	0.76	1	1.27	1.06		
THYR01000971	1.82	9.9	3.56	3.29	3.33	2.19		
THYR01000974	2.87	8.83	7.53	9.87	11.79	8.71		
THYR01000975	1.5	2.19	3.8	4.02	3.68	3.68		
THYR01000983	6.42	8.31	11.63	12.67	8.49	7.12		
THYR01000984	2.4	2.83	3.03	3.29	2.98	3.26		
THYR01000988	1.36	4.14	3.23	3.48	3.68	2.67		
THYR01000991	1.22	4.71	2.05	1.76	2.22	3.2		
THYR01000999	0.87	9.64	3.26	1.96	3.14	2.26		
THYR01001003	2.97	8.43	4.42	3.1	4.52	3.56		
THYR01001015	0.6	6.29	2.04	2.22	1.79	1.66		
THYR01001016	1.73	2.26	3.34	2.06	1.85	1.24		
THYR01001022	0.9	1.86	0.86	1.68	1.25	1.41		
THYR01001031	4.65	3.97	4.55	5.03	7.03	6.16		
THYR01001033	1.18	3.34	2.46	2.86	3.45	2.02		
THYR01001062	1.21	5.4	4.14	2.9	4.31	2.62		
THYR01001063	0.5	8.74	2.38	2.37	2.09	2.84		
THYR01001071	0.12	7.45	0.88	1.33	0.68	0.76		
THYR01001080	2.56	6.75	5.11	4.96	4.31	4.78		
THYR01001093	0.77	1.63	3.24	5.11	1.74	1.5		
THYR01001100	0.52	1.89	2.05	1.89	1.21	0.78		
THYR01001102	2.61	3.6	5.7	4.4	4.95	6.93		
THYR01001104	3.67	6.54	6.55	8.77	8.01	11.18		

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THYR01001109	1.81	6.02	2.68	3.06	2.58	1.99	
THYR01001113	11.41	17.42	32	21.81	26.65	18.72	
THYR01001120	1.65	6.22	5.27	4.78	5.8	3.72	
THYR01001121	1.57	4.28	4.19	3.92	2.72	3	
THYR01001128	1.64	2.77	5.86	3.52	3.19	5.09	
THYR01001133	1.14	3.02	7.23	6.54	4.54	4.12	
THYR01001134	2.97	4.78	1.63	3.14	2.83	1.38	
THYR01001142	0.3	2.69	0.63	1.3	1.71	0.22	
THYR01001173	8.37	12.87	7.72	11.14	9.92	10.62	
THYR01001175	3.26	6.63	5.51	3.46	4.62	3.52	
THYR01001177	1.36	5.85	5.93	4.66	7.27	7.97	
THYR01001189	2.74	6.93	11.42	7.84	7.27	9.94	
THYR01001194	1.05	2.62	4.96	4.89	4.57	2.31	
THYR01001204	2.17	3.58	4.27	4.03	4.74	4	
THYR01001205	5.76	10.65	20.23	18.54	19.57	20.9	
THYR01001213	1.21	4.69	4.44	3.12	3.21	2.33	
THYR01001224	3.59	8.25	6.37	9.92	12.69	10.55	* +
THYR01001237	2.82	6.25	4.99	3.61	4.53	4.46	
THYR01001242	9.74	11.65	19.04	20.02	19.98	20.46	
THYR01001258	2.08	5.45	3.58	3.33	2.05	2.66	
THYR01001262	0.86	2.64	3.38	2.36	3.61	2.69	
THYR01001266	0.15	2.39	1.02	0.97	1.64	0.66	
THYR01001271	1.85	4.12	4.12	2.46	2.77	2.97	
THYR01001287	7.3	8.3	39.26	30.14	43.68	26.2	
THYR01001290	0.38	3.25	1.14	1.15	1.35	0.36	
THYR01001291	0.96	7.17	4.38	4.31	4.97	3.5	
THYR01001297	3.05	8.04	6.14	6.85	7.47	9.18	
THYR01001302	1.72	5.59	5.17	3.8	3.71	3.5	
THYR01001313	1.61	2.33	2.91	2.91	2.62	1.48	
THYR01001320	1.76	2.52	5.31	5.07	5.74	4.83	
THYR01001321	2.25	2.65	4.3	2.48	4.23	4.23	
THYR01001322	1.34	3.93	3.34	1.75	2.67	2.01	
THYR01001327	1.29	6.01	4.18	1.4	3.89	2.49	
THYR01001336	1.89	6.84	6.72	4.62	4.43	4.18	
THYR01001347	0.43	4.12	3.35	1.85	2.81	0.65	
THYR01001358	2.57	5.74	4.52	4.3	5.75	5.1	
THYR01001363	0.8	2.15	1.52	2.09	2.24	2.28	
THYR01001365	0.86	3	1.6	2.19	2.6	1.96	
THYR01001374	1.85	4.45	12.86	9.4	13.01	6.21	

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	THYR01001401	1.76	5.33	4.89	5.39	7.86	6.29	
	THYR01001403	1.26	5.15	3.22	3.22	4.42	3.94	
	THYR01001405	6.99	12.5	10.86	6.69	8.56	10.63	
	THYR01001406	15.73	14.87	27.69	21.36	22.77	21.36	
	THYR01001411	4.49	5.46	10.08	8.93	12.44	8.12	
	THYR01001420	11.55	15.25	47.52	42.01	44.49	49.87	
	THYR01001426	3.42	5.56	8.83	9.32	12.77	11.18	
	THYR01001430	6.97	6.54	10.84	11.13	11.7	13.81	
	THYR01001434	0.68	5.19	2.11	2.08	4.23	1.73	
	THYR01001456	1.74	6.05	2.63	2.89	2.66	2.4	
	THYR01001457	1.71	4.72	2.04	2.95	4.7	2.67	
	THYR01001458	0.95	5.44	6.11	6.13	9.17	7.23	
	THYR01001459	4.54	5.07	9.42	7.18	9.87	14.21	
	THYR01001471	0.91	2.07	1.93	2.36	2.91	1.64	
	THYR01001478	0.58	3.09	1.34	0.95	2.61	2.75	
	THYR01001480	5.4	10.53	13.62	14.79	15.94	15.57	
	THYR01001481	2.95	8.64	7.24	4.91	7.76	7.13	
	THYR01001487	1.36	5.51	3.52	4.1	2.67	3.48	
	THYR01001495	2.06	5.57	5.43	5.06	9.4	7.55	
	THYR01001498	5.39	8.08	13.42	11.59	16.38	19.6	
	THYR01001510	1.67	2.88	1.59	1.65	2.57	3.35	
	THYR01001512	26.7	26.97	110.28	56.03	90.95	68.54	
	THYR01001519	5.92	7.77	11.05	8.91	5.75	10.38	
	THYR01001522	2.02	4.7	5.79	4.15	4.69	5.51	
	THYR01001523	1.83	4.92	3.73	4.38	4.07	4.26	
	THYR01001526	26.21	28.22	44.73	34.28	47.64	46.52	
	THYR01001529	1.64	5.27	2.8	2.32	2.42	2.98	
	THYR01001534	1.41	4.01	4.96	5.1	5.9	4.54	
	THYR01001537	7.4	5.17	12.33	5.97	7.42	7.23	
	THYR01001541	2.14	3.88	8.27	7.76	8.7	6.73	
	THYR01001545	1.26	3.84	2.9	4.95	3.57	3.16	
	THYR01001559	4.52	6.34	8.04	9.06	10.5	10.54	* +
	THYR01001563	9.49	14.06	15.89	10	15.49	22.09	
	THYR01001570	2.01	8.2	3.85	4.25	5.17	3.41	
	THYR01001573	1.15	5.77	2.22	1.47	2.87	2.67	
	THYR01001584	2.47	8.54	8.38	5.14	7.81	7.29	
	THYR01001593	4.27	5.67	11.17	9.5	10.93	9.52	
	THYR01001595	3.14	4.53	7.06	5.97	6.35	7.29	
	THYR01001596	4.71	5.48	7.44	6.45	5.86	2.51	

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THYR01001602	1.49	3.26	3.52	4.95	5.22	3.41		
THYR01001605	1.58	4.48	3.22	3.2	3.43	2.42		
THYR01001608	1.87	9.45	5.1	5.04	8.23	4.7		
THYR01001617	6.06	13.68	11.47	9.75	10.87	9.61		
THYR01001634	1.87	9.08	3.46	2.93	5.59	2.05		
THYR01001637	3.51	3.13	9.65	8.72	7.94	9.07		
THYR01001641	2.57	3.73	5.09	4.03	3.08	2.94		
THYR01001656	1.59	2.94	4.16	2.82	5.36	2.33		
THYR01001658	22.34	29.19	40.11	34.98	33.16	42.01		
THYR01001661	1.4	5.83	2.31	2.93	3.31	2.05		
THYR01001671	0.67	7.36	2.68	1.89	1.34	1.8		
THYR01001672	1.1	9.24	2.1	1.14	1.52	1.66		
THYR01001673	1.59	7.6	3.49	2.86	4.74	2.16		
THYR01001677	1.6	2.27	3.87	3.03	3.54	3.36		
THYR01001683	12.71	17.66	29.06	24.4	15.4	16.72		
THYR01001700	1.39	2.52	2.67	2.09	1.58	1.37		
THYR01001702	11.83	15.98	16.19	15.63	14.35	14.29		
THYR01001703	1.63	6.74	4.25	4.72	3.27	4.21		
THYR01001706	1.7	6.47	3.01	2.96	5.6	3.53		
THYR01001721	1.84	5.66	3.2	2.73	6.37	2.77		
THYR01001725	5.3	6.55	9.69	8.97	8.65	8.29		
THYR01001730	17.72	20.4	40.1	30.61	26.56	34.8		
THYR01001738	1.35	3.18	4.65	3.52	2.82	1.78		
THYR01001743	0.19	2.13	1.85	1.8	1.64	1.06		
THYR01001745	0.47	2.88	1.55	1.05	1.2	1.27		
THYR01001746	1.9	6.25	4.04	6.12	4.01	3.88		
THYR01001770	15.49	20.38	35.39	41.65	44.42	40.17	*	+
THYR01001772	1.12	4.88	3.64	4.78	4.24	3.06		
THYR01001778	3.89	6.68	9.89	14.67	13.47	14.25	*	+
THYR01001793	3.85	3.77	9.43	10.3	10.42	4.92		
THYR01001796	1.35	2.28	2.28	3.45	4.22	3.24	*	+
THYR01001800	1.82	2.99	2.75	4.17	5.12	2.09		
THYR01001803	3.42	6.03	5.21	4.31	4.14	3.42		
THYR01001809	1.6	4.26	3.4	5.9	4.23	3.39		
THYR01001817	8.69	18.33	24.88	22.11	22.77	25.27		
THYR01001819	4.68	8.46	9.01	7.84	10.46	6.77		
THYR01001828	21.89	24.53	104.32	106.68	121.95	68.55		
THYR01001854	6.67	6.12	12.45	13.43	15.86	13.31		
THYR01001895	0.85	1.31	2.52	3.54	4.31	1.28		

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THYR01001907	2.16	3.08	3.37	3.9	4.53	2.74		
TRACH1000006	2.51	5.87	6.63	4.34	3.46	3.22		
TRACH1000013	1.53	4.65	3.68	2.55	3.33	2.65		
TRACH1000074	2.65	6.75	6.09	7.5	7.26	4.77		
TRACH1000095	0.28	5.66	2.23	2.46	1.48	1.11		
TRACH1000102	2.42	6.66	4.09	5.79	5.04	3.65		
TRACH1000108	1.1	1.01	2.05	1.75	2.49	1.09		
TRACH1000126	0.96	1.75	2.71	1.82	3.79	2.54		
TRACH1000146	1.3	2.67	2.31	3.02	5.18	3.75		
TRACH1000160	0.61	4.06	1.5	1.47	1.76	0.72		
TRACH1000184	4.45	7.16	10.16	7.47	8.73	5.69		
VESEN1000004	0.69	5.55	3.19	2.56	2.95	2.02		
VESEN1000007	0.93	5.32	2.94	2.38	3.45	2.94		
VESEN1000013	5.96	10.11	16.78	10.76	11.25	13.88		
VESEN1000028	5.2	7.5	9.88	13.18	11.71	14.08	*	+
VESEN1000059	1.55	2.88	2.1	3.38	2.82	2.27		
VESEN1000100	1.96	3.22	3.35	3.49	4.58	3.59		
VESEN1000107	0.88	4.84	2.88	3.12	2.9	2.48		
VESEN1000117	1.63	6.43	2.46	2.16	2.7	1.79		
VESEN1000122	1.52	5.34	1.24	4.79	4.51	4.5		
VESEN1000137	0.76	5.47	1.92	1.75	3.33	1.65		
VESEN1000195	7.79	7.93	11.67	8.42	7.51	10.27		
VESEN1000215	1.48	3.03	2.06	2.67	3.84	1.87		
VESEN1000279	8.71	11.32	18.49	22.93	23.38	34.68	*	+
VESEN1000363	3.52	6.07	9.99	7.2	9.06	4.59		
VESEN1000388	2.55	6.48	3.31	4.17	3.75	6.7		
VESEN1000394	0.44	7.11	2.33	2.37	2.55	2.36		
VESEN1000410	1.11	5	1.78	2.36	2.71	3.69		
VESEN1000411	2.37	4.95	5.08	6.76	7.55	9	*	+
VESEN1000415	1.54	2.64	4.03	5.57	3.92	5.29		
VESEN1000440	7	5.53	7.81	3.79	9.4	12.22		
VESEN1000452	1.22	3.65	2.33	2.91	3.97	4.11		
VESEN1000539	191.54	185.28	334.6	389.84	403.89	547.31	*	+
VESEN1000554	0.67	6.47	1.43	1.47	2.55	1.58		
VESEN1000557	4.22	7.94	7.73	6.55	9.07	10		
VESEN1000575	7.49	9.75	16.33	11.95	11.73	14.8		
VESEN1000585	1.69	4.49	3.37	2.53	2.93	3.08		
VESEN1000592	1.58	2.31	1.58	2.02	1.83	1.46		
VESEN1000658	1.96	3.56	4.45	5.86	3.91	4.91		

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VESEN1000669	8.43	10.02	16.35	15.06	14.17	15.51		
VESEN1000743	0.97	3.3	2.52	1.99	3.37	3.21		
VESEN1000752	37.43	51.51	72.35	49.32	57.03	57.96		
VESEN1000761	13.48	18.17	19.37	24.6	33.21	31.28	*	+
VESEN2000039	10.45	15.98	15.56	13.56	18.3	20.1		
VESEN2000102	0.4	3.99	1.6	1.21	1.51	1.61		
VESEN2000164	2.45	3.52	4.8	5.55	4.36	3.66		
VESEN2000175	0.57	2.64	1.94	3.03	2.05	2.59		
VESEN2000186	3.77	5.53	6.53	6.68	3.87	2.47		
VESEN2000199	8.94	13.26	21.75	19.58	24.45	24.12		
VESEN2000200	0.5	4.97	2.78	3.03	3.1	1.6		
VESEN2000204	0.48	12.7	1.02	0.98	1.2	0.33		
VESEN2000218	6.66	20.26	19.48	21.37	20.75	18.86		
VESEN2000230	0.84	7.4	1.45	2.74	1.7	2.41		
VESEN2000272	2.29	4	8.92	7	8.31	5.88		
VESEN2000299	1.99	2.97	3.2	3.3	3.77	3.31		
VESEN2000323	4.51	8.12	8.37	8.91	9.5	9.36		
VESEN2000327	3.16	5.8	4.42	3.62	7.66	5.07		
VESEN2000328	5.44	8.02	11.88	8.73	15.35	14.36		
VESEN2000330	6.39	15.42	14.7	14.59	27.73	18.86		
VESEN2000336	0.82	8.97	2.54	3.46	3.83	2.88		
VESEN2000354	1.56	8.24	2.48	1.53	2.71	2.1		
VESEN2000378	7.17	8.87	14.57	13.23	11.14	10.3		
VESEN2000379	19.87	23.02	44.55	49.13	42.81	32.61		
VESEN2000397	0.72	2.38	1.24	1.36	2.06	1.54		
VESEN2000416	2.83	3.88	4.41	5.74	5.31	5.71	*	+
VESEN2000420	1.08	3.58	1.94	0.95	1.21	1.13		
VESEN2000430	0.51	6.68	1.53	2.06	1.79	1.8		
VESEN2000448	0.51	6.87	1.73	2.12	2.69	1.5		
VESEN2000449	2.43	8.07	6.59	8.3	11.31	8.21		
VESEN2000456	0.74	0.87	2.11	1.54	1.22	0.87		
VESEN2000562	4.07	3.42	17.42	13.67	22.82	14.47		
VESEN2000573	0.18	1.75	1.75	1.04	1.21	1.13		
VESEN2000604	1.73	3.44	2.24	2.04	1.67	2.15		
VESEN2000614	4.16	9.02	14.64	13.54	16.27	12.27		
VESEN2000638	0.48	5.92	1.98	1.33	1.91	1.68		
VESEN2000641	0.83	3.69	1.34	1.95	2.21	1.43		
VESEN2000645	2.18	5.29	5.38	5.91	5.73	5.5		
Y79AA1000013	2.57	2.7	4.33	3.45	3.8	3.94		

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Y79AA1000030	1.79	4.06	4.52	3.24	3.85	2.47		
Y79AA1000033	2.87	6	8.4	8.37	10.17	5.83		
Y79AA1000037	1.38	3.36	5.71	4.84	6.82	4.49		
Y79AA1000041	1.05	5.16	3.79	4.73	3.65	2.06		
Y79AA1000059	1.69	5	4.09	3.88	4.51	2.82		
Y79AA1000065	24.06	28.99	52.25	82.48	101.48	98.73	**	+
Y79AA1000081	39.47	49.78	73.62	113.19	114.49	98.22	**	+
Y79AA1000127	4.08	4.21	5.8	8.42	10.03	7.39	*	+
Y79AA1000130	2.24	2.48	5.76	6.61	8.1	8.03	*	+
Y79AA1000131	507.64	569.21	946.04	769.75	725.35	342.07		
Y79AA1000134	1.99	4.93	4.21	5.63	4.75	5.38		
Y79AA1000143	3.58	8.79	4.83	9.98	10.98	11.04	*	+
Y79AA1000144	4.63	10.79	10.59	11.02	11.62	11		
Y79AA1000150	18.39	22.18	84.69	93.5	117.62	78.89		
Y79AA1000153	183.67	191.4	436.64	423.46	442.52	386.45		
Y79AA1000166	2.13	2.25	4.15	3.52	4.97	3.6		
Y79AA1000179	2.58	3.76	4.2	6.85	7.58	3.89		
Y79AA1000181	1.96	3.92	4.2	4.82	5.66	3.79		
Y79AA1000202	22.93	24.47	55.57	91.68	86.86	83.22	**	+
Y79AA1000207	5.22	7.51	9.82	14.95	16.24	12.62	*	+
Y79AA1000214	14.94	22.18	33.76	50.43	60.78	41.96	*	+
Y79AA1000222	11.8	14.89	21.69	49.21	58.01	68.86	**	+
Y79AA1000226	11.04	14.94	34.41	22.86	33.54	30.03		
Y79AA1000227	5.95	4.52	7.25	8.98	9.51	9.62	*	+
Y79AA1000230	1.09	1.49	2.02	2.07	2.88	2.59		
Y79AA1000231	5.99	9.04	15.81	14.63	23.77	17.1		
Y79AA1000239	15.47	20.55	25.65	18.95	24.01	22.11		
Y79AA1000258	2.64	5.17	6.72	5.87	4.95	5.84		
Y79AA1000268	2.65	5.48	5.09	4.33	5.76	4.01		
Y79AA1000269	4.32	7.88	7.86	8	6.86	8.24		
Y79AA1000270	5.28	8.35	11.58	13.17	17.58	16.23	*	+
Y79AA1000280	1.74	4.17	4.9	5.29	3.1	5.27		
Y79AA1000285	3.44	4.21	5.91	4.01	6.86	5.22		
Y79AA1000295	0.75	3.06	4.85	4.32	4.23	4.45		
Y79AA1000307	2.88	3.91	5.06	9.35	7.58	11.25	*	+
Y79AA1000313	3.11	9.02	9.85	10.61	12.84	13.36		
Y79AA1000314	4.23	10.74	9.19	6.93	6.53	7.51		
Y79AA1000328	4.65	10.05	2.64	7.73	9.28	8.68		
Y79AA1000334	1.43	4.22	3.55	2.68	2.81	3.46		

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Y79AA1000342	10.65	10.05	26.47	23.7	19.13	28.35		
Y79AA1000346	7.61	8.17	7.9	20.1	22.06	20.18	**	+
Y79AA1000347	6.94	7.96	12.42	18.78	16.47	18.48	**	+
Y79AA1000349	6.93	9.63	12.67	12.31	11.96	14.75		
Y79AA1000355	3.17	8.28	8.94	8.84	13.55	8.77		
Y79AA1000368	5.24	8.39	24.43	22.48	35.67	22.55		
Y79AA1000388	22.9	32.66	62.37	94.17	128.35	109.08	**	+
Y79AA1000392	3.02	6.81	3.76	3.42	2.73	3.78		
Y79AA1000405	3.98	5.97	8.25	7.14	8.17	9.32		
Y79AA1000410	6.01	7.87	15.72	13.79	17.05	14.95		
Y79AA1000420	1.54	4.78	3.13	3.32	3.95	5.1		
Y79AA1000423	1.38	7.08	5.59	5.22	6.04	10.27		
Y79AA1000426	3.61	9.44	8.66	4.24	4.43	5.22		
Y79AA1000432	0.8	4.79	2.16	1.91	2.01	2.34		
Y79AA1000453	23.94	30.67	47.79	39.74	50.65	58.24		
Y79AA1000465	4.12	6.02	6.65	4.77	4.14	7.69		
Y79AA1000469	11.59	9.61	18.04	13.82	16.21	17.18		
Y79AA1000480	1.24	4.37	2.78	3.33	3.57	2.79		
Y79AA1000502	5.31	7.97	12.58	10.49	11.35	15.26		
Y79AA1000521	1.24	4.4	4.13	2.51	3.61	2.7		
Y79AA1000534	3.22	8.13	8.92	11.97	14.41	13.46	*	+
Y79AA1000538	3.58	6.95	8.79	9.52	12.12	8.41		
Y79AA1000539	12.76	14.96	53.11	42.61	68.56	50.97		
Y79AA1000540	1.32	3.59	1.61	2.54	2.97	3.21		
Y79AA1000560	160.46	140.99	339.33	380.8	313.21	220.43		
Y79AA1000574	1	2.92	1.65	1.98	2.04	1.59		
Y79AA1000584	2.07	4.55	4.97	4.62	5.39	4.04		
Y79AA1000589	10.74	13.67	81.43	59.09	95.35	68.5		
Y79AA1000598	1.43	7.64	2.17	1.85	3.88	3.18		
Y79AA1000600	2.7	10.02	7.93	13.64	15.64	12.84	*	+
Y79AA1000609	1.18	5.16	1.44	2.28	2.77	1.55		
Y79AA1000618	1.85	10.59	5.76	7.4	9.5	9.37		
Y79AA1000627	1.91	3.93	4.57	3.27	3.02	2.43		
Y79AA1000636	5.16	5.7	9.9	15.57	11.52	5.38		
Y79AA1000649	9.45	10.97	12.73	18.7	11.56	20.54		
Y79AA1000656	15.32	20.21	96.75	80.17	115.97	82.61		
Y79AA1000673	1.02	5.86	2.14	1.39	3.13	2.4		
Y79AA1000674	11.88	21.96	78.28	59.4	98.22	62.67		
Y79AA1000678	2.48	8.91	3.88	3.01	4.15	2.45		

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Y79AA1000682	17.99	53.99	93.7	102.53	110.87	118.22		
Y79AA1000683	1.87	2.66	3.21	4.27	2.59	2.17		
Y79AA1000697	21.76	27.52	43.01	21.93	24.76	27.31		
Y79AA1000700	5.07	7.1	7.08	7.51	6.93	9.97		
Y79AA1000702	5.13	14.57	13.31	41.48	56.57	63.15	**	+
Y79AA1000704	1.34	5.24	1.14	1.5	2.1	1.18		
Y79AA1000705	1.86	9.7	6.24	6.06	7.98	6.45		
Y79AA1000717	6.18	12.39	9.42	9.73	11.1	8.7		
Y79AA1000722	5.61	8.6	8.65	26.26	34.81	34.31	**	+
Y79AA1000724	6.42	9.77	18.55	26.57	21.7	11.95		
Y79AA1000726	0.77	1.24	0.83	1.46	2.01	0.71		
Y79AA1000734	2.05	4.46	4.92	3.57	3.3	2.94		
Y79AA1000748	0.88	4.38	1.77	2.14	2.99	1.56		
Y79AA1000750	4.17	8.47	20.58	18.11	20.02	18.62		
Y79AA1000752	1.25	5.13	2.33	2.23	3.38	3.38		
Y79AA1000774	2.11	6.23	4.24	4.28	5.79	4.21		
Y79AA1000776	1.2	4.37	1.9	2.13	1.83	2.11		
Y79AA1000777	4.36	5.84	9.63	10.05	6.99	6.01		
Y79AA1000778	1.72	3.77	3.79	3.87	4.19	1.44		
Y79AA1000782	2.08	4.18	3.72	3.53	2.89	2.96		
Y79AA1000784	7.04	10.01	7.78	13.87	15.58	14.26	**	+
Y79AA1000794	0.61	5.21	1.88	2.92	1.69	1.23		
Y79AA1000800	1.59	5.44	3.82	3.38	2.97	3.39		
Y79AA1000802	0.64	4.18	1.15	2.52	1.77	2.1		
Y79AA1000805	2.29	4.03	2.63	2.43	2.11	2.6		
Y79AA1000814	2.73	3.9	4.14	4.98	7.09	6.76	*	+
Y79AA1000823	7.91	9.99	12.07	12.02	12.42	6.56		
Y79AA1000824	0.98	2.47	1.84	2.75	2.26	0.79		
Y79AA1000827	1.6	4.02	7.27	6.71	8.91	6.14		
Y79AA1000831	7.04	10.49	17.32	26.61	30.43	27.82	**	+
Y79AA1000833	62.14	67.46	191.76	270.42	308.16	248.21	*	+
Y79AA1000850	1.69	5.68	2.72	4.92	4.59	4.21		
Y79AA1000856	3.49	6.78	6.31	9.28	6.01	8.51		
Y79AA1000862	2.22	2.76	2.44	3.08	2.87	2.59		
Y79AA1000876	7.46	10.04	17.91	27.36	27.61	25.46	**	+
Y79AA1000888	4.59	5.07	28.1	24.51	38.78	22.48		
Y79AA1000902	4.65	5.74	8.44	12.18	12.32	7.68		
Y79AA1000935	3.53	5.99	6.69	8.28	10.07	9.18	*	+
Y79AA1000959	0.74	6.29	4.35	6.71	5.77	6.07		

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Y79AA1000962	1.22	4.45	3.18	2.9	2.41	1.79		
Y79AA1000963	18.6	26.86	35.93	31.61	42.17	49.13		
Y79AA1000966	18.52	19.25	98.18	77.47	116.12	61.1		
Y79AA1000967	8.62	8.82	33.82	34.47	40.36	29.3		
Y79AA1000968	3.32	5.67	6.89	8.86	9.4	7.96	*	+
Y79AA1000969	0.91	3.18	3.04	2.66	2.91	1.41		
Y79AA1000976	1.43	4.72	3.02	2.55	3.51	1.43		
Y79AA1000978	1.99	5.6	7.26	6.9	10.54	5.56		
Y79AA1000985	9.39	12.84	40.49	38.26	44.3	27.89		
Y79AA1000989	21.59	22.49	46.19	51.84	58.65	55.19	*	+
Y79AA1000991	22.11	22.21	110.42	72.46	96.96	82.23		
Y79AA1001013	59.2	62.64	140.9	174.85	214.13	201.9	*	+
Y79AA1001014	2.27	4.16	4.1	4.8	5.2	6.55		
Y79AA1001019	3.37	5.89	7.74	9.24	9.02	9.43	*	+
Y79AA1001020	5.37	7.82	9.43	12.31	11.11	10.86	*	+
Y79AA1001023	0.83	6.11	2.29	1.22	1.95	1.54		
Y79AA1001030	4.23	8.79	10.87	11.14	10.72	12.43		
Y79AA1001035	0.19	2.88	0.03	14.44	8.19	17.16	*	+
Y79AA1001041	1.78	2.46	2.36	2.93	2.45	2.78		
Y79AA1001043	11.65	12.62	15.22	8.64	12.01	14.71		
Y79AA1001048	1.1	4.78	3.73	4.05	4.52	4.21		
Y79AA1001056	4.56	7.82	11.04	8.27	7.11	9.94		
Y79AA1001061	1.53	7.79	5.28	6.13	7.46	6.66		
Y79AA1001062	2.62	6.14	5.02	4.44	6.01	4.67		
Y79AA1001068	3.46	6.39	7.29	6.61	8.69	7.05		
Y79AA1001073	8.19	13.08	17.46	24.14	22.1	29.81	*	+
Y79AA1001077	7.1	7.08	17.15	14.69	14.74	17.08		
Y79AA1001078	3.11	8.34	11.07	5.01	12.15	12.92		
Y79AA1001081	3.59	5.61	4.94	9.62	9.98	10.5	**	+
Y79AA1001088	27.75	38.61	69.33	93.1	88.97	113.04	*	+
Y79AA1001089	4.64	7.8	11.92	22.67	22.6	27.73	**	+
Y79AA1001090	1.38	4.15	2.2	3.58	2.83	2.35		
Y79AA1001105	3.7	5.23	15.81	12.52	22.1	13.35		
Y79AA1001142	8.53	13.38	15.85	14.28	11.42	22.32		
Y79AA1001145	2.22	4.68	5.13	4.97	6.26	5.87		
Y79AA1001162	2.27	2.91	1.62	1.62	4.56	4		
Y79AA1001167	0.86	2.76	2.38	1.12	2.35	0.77		
Y79AA1001176	0.57	3.33	1.14	2.02	1.68	0.88		
Y79AA1001177	1.21	5.5	2.22	2.35	3.01	1.99		

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Y79AA1001179	6.81	8.66	16.73	22.82	22.64	20.07	*	+
Y79AA1001185	1.33	5.3	4.55	3.65	4.49	5.8		
Y79AA1001201	5.69	11.3	16.13	14.57	15.21	19.38		
Y79AA1001205	1.87	3.28	2.85	5.87	4.85	4.09	*	+
Y79AA1001211	1.64	4.75	6.93	4.83	4.36	4.15		
Y79AA1001212	3.55	6.93	15.91	13.74	15	11.65		
Y79AA1001216	52.59	51.46	93.73	76.52	97.53	109.55		
Y79AA1001228	6.1	11.21	9.34	8.99	12.19	10.24		
Y79AA1001233	0.68	11.46	2.39	0.92	1.66	1.09		
Y79AA1001236	4.46	12.86	9.25	11.4	10.66	13.08		
Y79AA1001239	4.62	13.93	9.94	11.53	12.15	12.94		
Y79AA1001240	8.74	8.6	13.75	9.13	6.68	3.01		
Y79AA1001255	10.37	12.22	22.61	12.47	7.51	6.57		
Y79AA1001264	3.63	5.15	4.49	7.73	8.59	8.75	**	+
Y79AA1001272	10.81	13.63	17.47	21.56	20.67	21.32	*	+
Y79AA1001281	0.45	4.95	1.89	1.42	1.81	0.95		
Y79AA1001299	2.49	11.34	9.06	9.9	9.26	9.81		
Y79AA1001312	2.49	10.36	5.17	2.15	4.77	4.14		
Y79AA1001319	3.34	11.88	5.27	7.23	6.05	7.15		
Y79AA1001323	1.22	1.16	2.09	1.11	1.55	0.89		
Y79AA1001328	2.04	3.18	3.62	4.66	4.48	4.05	*	+
Y79AA1001343	154.19	151.55	345.05	304.88	394.54	265.65		
Y79AA1001351	0.81	2.77	1.67	0.03	1.26	0.96		
Y79AA1001364	1.65	6.07	4.03	3.39	4.43	3.6		
Y79AA1001367	2.16	7.41	2.93	3.09	5.34	3.19		
Y79AA1001384	0.5	5.14	1.98	0.73	1.15	0.94		
Y79AA1001391	0.59	3.73	2.88	1.35	1.65	1.2		
Y79AA1001394	3.12	4.66	12.92	10.94	9.56	10.94		
Y79AA1001402	2.77	3.7	5.95	5.65	5.09	4.14		
Y79AA1001410	0.82	2.78	2.33	2.06	2.31	2.25		
Y79AA1001414	2.76	7.5	7.59	11.08	10.73	10.06	*	+
Y79AA1001426	0.61	4.36	2.61	1.5	1.43	1.82		
Y79AA1001427	14.22	13.44	86.36	59.92	88.36	63.53		
Y79AA1001430	11.28	16.98	20.98	29.04	34.03	34.38	**	+
Y79AA1001439	16.22	21.53	33.42	45.02	43.74	43.1	*	+
Y79AA1001485	1.65	2.51	4.38	4.85	3.88	3.57		
Y79AA1001493	1.29	2.3	3.43	2.43	2.35	2.46		
Y79AA1001511	4.79	8.57	11.05	9.39	9.11	6.47		
Y79AA1001523	2.64	6.57	5.08	8.74	7.37	6.1		

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Y79AA1001530	7.46	11.69	22	41.43	36.37	36.07	**	+
Y79AA1001532	5.12	7.35	6.69	10.49	14.82	12.9	*	+
Y79AA1001533	1.84	4.89	2.53	4.15	4	4.19		
Y79AA1001541	2.82	5.89	7.54	7.23	5.08	7.34		
Y79AA1001548	4.25	4.84	9.82	10.46	7.37	7.1		
Y79AA1001555	2	2.55	3.65	4.7	5.28	4.25	*	+
Y79AA1001562	7.76	10.11	17.15	14.07	16.16	10.83		
Y79AA1001581	2	5.05	4.47	5.1	7.01	3.54		
Y79AA1001585	3.18	7.38	10.96	9.72	10.93	8.05		
Y79AA1001592	2.61	7.38	5.97	8.15	8	7.02		
Y79AA1001594	0.76	4.73	3.85	1.96	3.24	1.73		
Y79AA1001603	56.74	70.81	153.14	131.56	112.16	107.66		
Y79AA1001613	3.74	3.52	14.81	13.12	15.36	10.66		
Y79AA1001630	0.71	2.36	1.73	1.14	2.64	0.67		
Y79AA1001647	1.96	3.57	2.47	4.14	4.32	2.65		
Y79AA1001664	4.67	8.39	11.43	8.96	10.01	8.73		
Y79AA1001665	1.39	6.4	3.73	4.67	4.71	3.75		
Y79AA1001679	8.92	15.94	20.71	20.53	26.67	25.35		
Y79AA1001692	1.87	5.55	3.95	3.99	3.95	3.51		
Y79AA1001696	1.97	6.49	2.77	1.83	2.63	2.55		
Y79AA1001705	6.09	6.44	10.39	7.62	7.92	7.85		
Y79AA1001711	16.17	12.34	29.74	13.73	23.83	21		
Y79AA1001717	0.72	2.99	1.29	1.68	3.13	1.14		
Y79AA1001719	2.5	5.79	6.44	6.15	6.07	6.43		
Y79AA1001727	6.87	12.13	14.99	8.73	14.71	8.77		
Y79AA1001750	10.21	13.63	21.67	21.92	32.29	24.33		
Y79AA1001760	25.24	27.31	122.97	113.56	155.17	83.24		
Y79AA1001777	1.17	3.59	1.6	2.49	1.75	1.28		
Y79AA1001781	0.31	2.3	0.42	1.62	1.84	1.42		
Y79AA1001787	1	3.94	3.54	5.51	5.18	5.15		
Y79AA1001793	16.23	15.19	91.7	60.44	87.21	75.35		
Y79AA1001795	1.23	3.84	2.24	2.05	2.45	2.8		
Y79AA1001799	4.9	8.35	6.99	10.7	10.72	11.26	*	+
Y79AA1001800	2.25	8.3	10.1	8.49	10.51	9.9		
Y79AA1001801	1.77	6.44	4.87	7.67	5.91	7.33		
Y79AA1001803	0.74	2.15	1.72	1.85	1.68	1.17		
Y79AA1001805	6.05	6.88	12.15	10.21	8.32	11.15		
Y79AA1001807	3.37	6.33	12.56	11.76	17.8	16.79		
Y79AA1001827	1.7	4.41	3.12	3.43	3.6	2.52		

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Y79AA1001846	1.82	6.52	5.51	6.52	5.09	5.07		
Y79AA1001848	0.86	5.57	2.75	5.98	4.78	5.14		
Y79AA1001853	1.38	6.16	2.76	3.24	4.56	3.63		
Y79AA1001863	0.86	5	2.53	2.93	3.83	3.85		
Y79AA1001866	2.29	3.2	5.81	3.53	3.98	3.46		
Y79AA1001874	0.12	2.18	−0.21	1.17	0.75	0.51		
Y79AA1001875	9.33	12.67	13.09	11.05	17.79	18.63		
Y79AA1001907	68.02	70.94	96.4	118.34	86.75	104.86		
Y79AA1001908	0.64	8.4	2.29	1.92	2.59	2.31		
Y79AA1001923	1.61	6.64	3.03	3.86	3.76	3.35		
Y79AA1001927	19.1	22.05	36.94	42.46	45.29	48.81	*	+
Y79AA1001930	4.07	6.65	8.07	7.92	12.42	12.21		
Y79AA1001932	2.84	4.41	8.47	11.51	9.1	8.57		
Y79AA1001933	2.14	3.27	3.69	4.34	7.99	6.65	*	+
Y79AA1001942	1.58	3.45	2.69	2.94	2.13	2.41		
Y79AA1001963	9.6	9.37	46.06	38.48	49.64	47.27		
Y79AA1001968	18.61	27.73	37.44	42.93	44.16	55.23	*	+
Y79AA1001983	1.81	6.35	4.28	3.97	5.86	4.47		
Y79AA1002000	2.55	5.35	4.55	4.42	3.21	2.83		
Y79AA1002004	13.1	18.87	27.47	23.72	29.45	40.93		
Y79AA1002008	2.51	3.73	3.79	4.54	2.19	2.85		
Y79AA1002012	1.37	3.22	2.81	3.22	2.29	2.87		
Y79AA1002017	1.34	2.53	2.46	3.51	3.07	2.82		
Y79AA1002022	2.99	4.94	5.93	7.32	7.51	6.01		
Y79AA1002027	2.02	6.33	2.67	2.69	4.03	4.09		
Y79AA1002050	2.53	8.12	4.22	6.68	6.91	5.11		
Y79AA1002058	13.69	21.8	70.12	59.07	70.89	55.33		
Y79AA1002060	6.38	13.17	20.54	17.14	21.12	24.23		
Y79AA1002062	4.33	5.18	8.15	8.54	6.66	5.51		
Y79AA1002065	33.54	39.97	72.6	49.46	30.04	41.81		
Y79AA1002067	10.11	11.64	17.24	16.25	9.42	8.13		
Y79AA1002069	0.97	1.79	0.54	1.55	1.44	0.66		
Y79AA1002070	10.16	33.47	44.36	52.16	71.15	73.35	*	+
Y79AA1002074	38.55	74.38	179.6	165.55	282.48	224.96		
Y79AA1002076	0.48	9.71	2.89	2.86	3.34	1.91		
Y79AA1002083	1.2	7.48	2.03	2.73	1.75	2.06		
Y79AA1002084	1.79	2.59	4.54	3.73	3.73	2.98		
Y79AA1002086	0.96	1.78	1.71	2.77	1.88	1.43		
Y79AA1002087	11.18	14.9	27.67	33.34	30.01	23.08		

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Y79AA1002089	1.18	3.46	2.13	1.46	2.92	3.26		
Y79AA1002093	2.19	5.48	5.25	5.28	5.68	6.17		
Y79AA1002101	1.11	8.58	2.98	6.54	5.58	6.6		
Y79AA1002103	1.47	10.22	3.39	4.43	6.49	4.7		
Y79AA1002115	4.34	9.78	7.37	7.45	7.03	6.95		
Y79AA1002121	1.55	2.16	2.18	1.67	2.55	2.31		
Y79AA1002125	6.67	7.08	9.29	8.81	6.4	7.6		
Y79AA1002129	1.64	6.23	7.84	5.41	2.2	4.93		
Y79AA1002131	0.9	3.25	0.78	0.77	1.29	1.15		
Y79AA1002139	0.69	5.02	1.04	1.83	1.53	1.34		
Y79AA1002144	25.99	29.62	51.01	42.61	51.16	43.17		
Y79AA1002177	1.72	5.97	4.33	4.79	3.09	4.73		
Y79AA1002183	10.44	13.89	17.69	27.61	29.67	28.92	**	+
Y79AA1002202	3.97	7.15	8.34	18.27	10.12	17.85	*	+
Y79AA1002204	0.53	0.99	1.56	1.7	2.2	1.54		
Y79AA1002206	2.63	5.36	7.28	4.35	2.95	1.49		
Y79AA1002208	4.26	6.54	3.94	6.88	6.3	3.96		
Y79AA1002209	1.8	6.34	2.88	4.38	3.74	4.57		
Y79AA1002210	0.41	4.14	2.09	1.8	2.24	1.65		
Y79AA1002211	2.25	5.39	3.85	5.71	5.3	4.5		
Y79AA1002213	1.15	4.13	6.53	7.38	7.54	7.43		
Y79AA1002215	18.7	18.69	26.61	17.72	15.59	9.62		
Y79AA1002220	3.78	3.38	2.87	4.89	4.19	4.14	*	+
Y79AA1002226	8.54	8.9	9.75	13.06	14.2	4.41		
Y79AA1002229	1.35	3.88	3.38	2.95	2.79	2.67		
Y79AA1002234	3.24	6.82	3.94	4.29	7.74	6.88		
Y79AA1002235	5.6	7.55	6.43	8.78	9.74	9.47	*	+
Y79AA1002246	0.59	5.06	2.41	3.94	2.54	4.27		
Y79AA1002258	0.72	7.26	2.92	3.99	4.19	2.7		
Y79AA1002279	17.79	19.12	27.8	16.52	19.13	11.5		
Y79AA1002292	1.68	2.1	3.22	2.96	3.91	2.73		
Y79AA1002298	0.76	2.52	1.32	2.03	2.77	1.06		
Y79AA1002307	1.05	4.35	1.79	0.76	1.05	1.2		
Y79AA1002309	1.15	4.19	2.3	2.21	1.78	2.55		
Y79AA1002311	2.84	7.35	3.43	5.71	6.04	5.45		
Y79AA1002334	1.72	6.54	2.95	4.77	4.19	3.35		
Y79AA1002351	1.27	5.5	2.89	3.5	3.38	3.06		
Y79AA1002355	12.83	12.25	28.96	22.94	22.07	21.02		
Y79AA1002361	2.22	2.27	3.26	2.47	4.54	1.55		

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Y79AA1002365	0. 66	2. 04	2. 26	1. 97	3. 51	2. 25		
Y79AA1002373	1. 17	3. 93	2. 42	1. 59	1. 97	1. 43		
Y79AA1002376	110. 81	135. 82	249. 8	205. 99	213. 25	191. 69		
Y79AA1002378	1. 9	4. 8	4. 91	2. 2	3. 6	3		
Y79AA1002381	8. 65	14. 11	19. 19	18. 84	21. 52	17. 97		
Y79AA1002388	7. 05	9. 99	18. 24	15. 88	21. 51	19. 99		
Y79AA1002399	1. 79	4. 25	3. 74	4. 62	4. 08	3. 47		
Y79AA1002407	3. 05	4. 16	3. 13	4. 66	5. 77	4. 5	*	+
Y79AA1002413	3. 21	6. 78	8. 05	6. 46	8. 32	6. 87		
Y79AA1002416	1. 46	5	2. 74	2. 49	3. 44	3. 55		
Y79AA1002429	5. 5	8. 15	7. 27	8	11. 11	8. 01		
Y79AA1002431	0. 92	4. 43	0. 48	0. 79	1. 78	0. 89		
Y79AA1002433	1. 27	5. 9	3. 24	4. 8	3. 84	5. 58		
Y79AA1002445	4. 01	5. 34	5. 76	3. 1	4. 89	5. 41		
Y79AA1002461	0. 63	2. 45	1. 79	1. 19	2. 71	1. 41		
Y79AA1002466	39. 02	70. 71	94. 5	91. 12	82. 27	94. 71		
Y79AA1002471	4. 44	6. 67	6. 08	7. 43	8. 06	10. 49		
Y79AA1002472	2. 41	6. 16	5. 99	6. 8	8. 39	4. 06		
Y79AA1002474	1. 93	8. 27	4. 31	4. 89	6. 52	7. 13		
Y79AA1002482	3. 52	6. 66	10. 37	9. 02	11. 81	8. 69		
Y79AA1002487	1. 38	4. 12	2. 46	1. 96	3. 01	2. 56		
Y79AA1002490	10. 37	9. 91	16. 35	11. 11	12. 88	16. 86		
Y79AA1002493	1. 96	4. 07	6. 14	6. 5	8. 9	4. 1		
ZRV6C1006278	0. 61	4. 08	2. 22	1. 81	1. 58	2. 11		

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Table 353

Expression of each cDNA in skin-derived fibroblast cells exposed and unexposed to ultraviolet light (the table also includes clones that are not described in Examples)

In the table, UV_0h represents skin-derived fibroblast cells without ultraviolet irradiation; UV_4h and UV_24h represent skin-derived fibroblast cells 4 and 24 hours, respectively, after the irradiation. The assay was performed in triplicate (n=3) and each result is shown in the column of Exp1, Exp2, or Exp3. "t-test 0/4" and "t-test 0/24" represent the results of the test for significant difference between the unexposed cells and the cells 4 hours after the irradiation, and between the unexposed cells and the cells 24 hours after the irradiation, respectively. The table also includes the information on an increase (+) or decrease (-) in the expression level of the gene in the exposed cells 4 hours or 24 hours after the ultraviolet light irradiation. The results of the test for significant difference are shown in the columns of *p<0.05 and **p<0.01.

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Clone	UV 0h			UV 4h			UV 24h			t test		4h 24h	
	Exp. 1	Exp. 2	Exp. 3	Exp. 1	Exp. 2	Exp. 3	Exp. 1	Exp. 2	Exp. 3	0/4	0/24	+/-	+/-
GAPDH(Cr1)	0	1.29	0.1	0.9	0.06	1.18	1.49	0.47	0				
β actin(Cr2)	256.82	283.53	414.29	388.38	117.29	329.8	189.18	190.26	157.87		*		-
ADRGL1000005	15.9	10.68	19.67	3.3	6.44	12.69	6	3.06	5		*		-
ADRGL1000007	47.47	31.62	85.7	41.54	41.35	40.62	31.64	14.77	31.5				
ADRGL1000009	3.97	2.45	8.72	6.06	2.65	3.32	3.72	1.8	2.91				
ADRGL1000011	21.55	13.26	21.8	18.36	12.63	13.95	15.62	6.5	14.45				
ADRGL1000027	2.4	1.68	5.6	4.02	2.48	2.04	3.18	0.81	3.55				
ADRGL1000058	84.24	29.04	76.55	95.27	68.98	72.58	39.84	22.31	39.98				
ADRGL1000069	7.61	6.31	10.67	3.58	5.86	4.59	2.92	1.14	2.62		*		-
ADRGL1000077	4.08	5.99	6.34	5.76	3.87	4.68	4.23	2	3.08				
ADRGL1000092	41.45	38.57	55.77	73.06	40.91	54.59	24.67	18.9	27.36		*		-
ADRGL1000099	43.57	33.01	48.6	56.04	29.24	45.47	24.87	18.08	20.27		*		-
ADRGL1000136	52.22	43.6	70.27	58.84	40.95	44.91	35.09	21.07	29.76		*		-
ADRGL1000147	6.66	6.78	11.64	6.52	5.38	7	5.38	2.59	5.89				
ADRGL1000159	7.28	7.31	7.55	10.23	10.38	9.89	7.3	4.68	8.62	**		+	
ADRGL1000160	11.62	12.89	8.28	9.39	13.77	23.6	7.39	5.18	9.59				
ADRGL1000171	4.47	4.72	5.01	4.83	6.43	4.19	3.69	1.77	4.29				
ADRGL1000181	9.73	12.6	18.02	18.65	11.48	13.93	9.96	11.18	7.77				
BGGI11000015	25.13	21.03	22.91	10.68	12.73	20.09	10.32	15.5	18.5		*		-
BGGI11000016	63.98	55.25	74.82	18.05	36.94	8.26	17.67	40.65	37.24	*	*	-	-
BGGI11000017	8.13	6.51	11.46	3.65	5.27	5.54	2.72	4.69	3.8		*		-
BGGI11000022	12.98	14.45	15.11	7.84	9.62	8.77	7.97	8.92	10.08	**	**	-	-
BGGI11000031	13.67	9.32	14.45	9.12	13.53	12.58	6.75	10.28	15.5				
BGGI11000042	78.81	92.28	77.71	51.19	53.47	19.5	23.41	16.53	22.63	*	**	-	-
BGGI11000046	59.14	59.17	43.06	30.88	42.51	35.11	16	15.29	7.23		**		-
BNGH41000025	34.23	58.36	71.87	11.96	22.6	19.45	12.51	15.56	19.08	*	*	-	-
BNGH41000026	8.61	10.35	11.92	5.79	4.65	4.41	2.7	3.65	4.11	**	**	-	-
BNGH41000027	36.04	26.15	57.91	21.21	34.28	46.33	28.86	28.53	19.37				
BNGH41000035	71.93	95.4	103.3	77.48	91.38	82.2	85.4	91.4	89.21				
BNGH41000037	11.37	8.43	18.43	4.88	12.04	10.79	4.26	3.88	5.78				
BNGH41000042	153.34	222.69	94.88	128.41	120.85	102.56	66.52	26.75	52.39		*		-
BNGH41000048	115.13	80.94	131.08	158.03	99.22	95.02	70.52	58.67	62.66		*		-
BNGH41000056	6.81	7.33	32.46	17.81	11.49	11.22	6.84	4.36	6.34				
BNGH41000087	7.57	4.78	6.77	6.26	6.74	6.12	2.23	3.11	5.45				
BNGH41000091	5.88	4.66	7.21	3.92	3.81	2.29	2.51	1.95	5.23	*		-	
BNGH41000157	24.78	9.57	39.68	15.95	28.36	14.05	14.96	12.43	25.4				
BNGH41000169	4.77	2.7	8.76	3.03	4.07	2.47	2.48	1.85	2.4				
BNGH41000181	15.03	14.16	15.82	9.14	8.43	9.02	9.57	5.48	4.7	**	**	-	-
BNGH41000198	5.23	7.17	13.44	2.81	5.92	4	2.64	2.63	2.78				
BNGH41000219	55.36	63.96	42.98	30.63	34.86	27.19	11.04	4.75	5.11	*	**	-	-
BNGH41000229	41.48	41.07	32.45	12.86	20.86	15.06	12.11	29.5	42.2	**		-	
BNGH41000237	30.57	28.92	29.88	23.95	17.14	16.36	7.62	11.39	18.2	*	**	-	-
BNGH41000238	12.97	6.92	11.13	3.1	5.96	5.05	3.21	2.99	4.83	*	*	-	-
BNGH41000243	37.29	22.23	38.12	21.69	20.76	22.29	17.48	13.04	12		*		-
BNGH41000270	7.24	2.74	13.66	5.03	4.81	3.91	2.55	1.06	3.15				
BRAWH1000004	26.05	12.1	22.36	14.77	13.7	15.56	10.21	9.28	9.3				
BRAWH1000018	16.02	18.04	23.1	10.35	11.87	13.62	8.4	6.81	8.26	*	**	-	-
BRAWH1000021	13.77	12.07	18.61	14.58	14.48	10.65	13.45	8.59	11.48				
BRAWH1000027	4.8	4.82	5.71	4.63	4.59	5.52	2.19	2.04	7.42				
BRAWH1000029	7.2	4.85	5.05	4.67	2.83	2.65	2.93	2.18	1.97		*		-
BRAWH1000040	20.85	33.58	27.15	16.04	13.44	12.14	8.98	5.99	6.77	*	**	-	-
BRAWH1000050	86.78	63.26	107.91	121.47	88.32	92.39	77.36	45.55	64.9				
BRAWH1000051	3.25	3.15	8.62	2.34	1.27	1.81	2.29	1.14	1.52				
BRAWH1000060	103.56	87.24	102.14	122.05	99.97	107.12	58.34	59.07	66.98		**		-
BRAWH1000075	6.97	6.63	15	3.29	4.01	3.69	3.52	2.95	3.34				
BRAWH1000081	23.41	12.71	28.79	20.72	20.86	22.65	19.13	9.85	15.04				
BRAWH1000084	219.94	140.27	3.27	8.21	5.55	1.75	106.89	121.2	155.45				
BRAWH1000095	6.67	5.04	6.84	7.47	5.22	4.62	3.81	0.91	1.79		*		-

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Table 354

BRAWH1000096	5.38	6.14	9.95	5.23	5.99	6.41	5.29	2.17	4.29				
BRAWH1000097	32.73	36.25	38.91	16.1	26.45	25.46	34.97	22.26	21.98	*		-	
BRAWH1000100	3.44	3.77	6.36	1.33	1.79	1.51	2.06	0.88	1.83	*	*	-	-
BRAWH1000101	151.17	188.03	182.43	124.31	137.07	112.48	156.93	114.91	72.6	*		-	
BRAWH1000104	3.11	5.16	13	2.27	6.18	12.04	5.42	9.52	5.16				
BRAWH1000107	4.13	9.11	10.29	5.8	8.93	4.46	6.91	1.75	1.45				
BRAWH1000110	63.35	48.25	85.05	53.28	34.71	42.03	42.56	51.83	49.06				
BRAWH1000111	17.89	14.24	19.42	6.38	13.57	14.32	11.88	11.36	7.34		*		-
BRAWH1000135	7.97	7.93	10.18	6.35	4.56	3.75	5.18	4.92	2.5	*	*	-	-
BRAWH1000190	13.15	11.52	18.33	11.13	9.11	7.4	12.15	9.59	8.37				
HEMBA1000005	35.95	34.82	38.35	20.64	26.11	18.05	30.81	17.47	24.15	**	*	-	-
HEMBA1000006	9.78	9.8	11.36	1.4	5.53	2.46	3.8	1.71	7.12	**	*	-	-
HEMBA1000012	142.4	148.44	163.52	136.28	167.18	112.45	92.75	76.02	85.25		**		-
HEMBA1000020	190.7	248.05	252	200.63	259.1	183.87	186.01	114.55	161.9				
HEMBA1000030	20.38	15.29	27.68	14.24	16.3	11.52	9.94	9.08	14.21				
HEMBA1000034	15.22	17.47	15.15	7.36	10.81	14.4	7.69	4.87	8.91		**		-
HEMBA1000042	22.23	17.73	35.18	17.22	20.39	12.68	19.66	13.46	21.05				
HEMBA1000045	12.71	14.02	2.46	0.7	7.88	1.39	4.27	2.85	2.17				
HEMBA1000046	10.19	13.7	20.59	6.92	10.64	7.67	13.72	12.92	11.87				
HEMBA1000047	4.05	7.12	13.48	2.54	4.15	2.97	2.37	0.81	3.55				
HEMBA1000048	10.63	14.86	15.51	2.18	6.64	3.23	4.43	0.94	3.67	**	**	-	-
HEMBA1000050	3.15	3.21	10.5	2.13	3.59	2.35	2.36	0.05	2.24				
HEMBA1000053	5.98	3.98	9.78	8.93	5.91	6.48	2.35	1.85	5.68				
HEMBA1000060	10.62	11.2	18.18	10.13	8.71	11.8	7.34	2.99	9.16				
HEMBA1000072	530.32	492.25	767.01	366.98	521.7	354.83	288.04	399.85	194.47		*		-
HEMBA1000073	26.51	17.12	39.76	19.17	28.84	19.97	20.8	18.82	12.3				
HEMBA1000076	30.89	23.42	46.09	20.74	16.14	16.31	22.31	20.51	20.54				
HEMBA1000084	46.03	48.38	54.47	61.64	67.48	73.34	43.23	26.25	43.33	*		+	
HEMBA1000087	2.35	3.13	9.77	1.66	2.08	0.86	1.69	0.8	1.37				
HEMBA1000088	3.05	3.73	12.72	2.97	3.67	2.66	4.68	0.94	2.56				
HEMBA1000091	38.82	23.63	75.02	58.3	74.93	71.96	24.1	16.38	30.08				
HEMBA1000111	21.39	20.11	44.78	24.89	20.7	26.97	20.62	12.93	18.49				
HEMBA1000121	18.15	14.06	45.72	26.38	18.11	19.11	16.09	9.88	11.04				
HEMBA1000128	6.74	4.73	14.38	8.16	5.93	6.25	3.31	1.93	2.79				
HEMBA1000129	6.94	5.68	13.44	7.51	6.89	6.55	4.13	5.51	3.96				
HEMBA1000141	12.4	7.44	22.8	8.83	6.54	5.23	5.19	3.51	3.66				
HEMBA1000146	6.55	7.84	15.71	4.62	7.62	7.46	5.3	2.57	3.09				
HEMBA1000150	28.41	41.35	48.05	22.83	16.47	23.82	28.66	15.99	24.53	*		-	
HEMBA1000154	717.61	696.56	881.96	454.74	531.19	670.47	527.79	542.09	612.33		*		-
HEMBA1000156	10.8	18.5	21	9.98	4.23	6.43	3.69	3.2	3.36	*	*	-	-
HEMBA1000158	18.74	13.45	14.16	7.7	2.81	4.64	5.39	2.06	3.26	**	**	-	-
HEMBA1000168	8.01	6.75	7.08	5.88	4.99	5.86	6.83	2.42	4.44	*		-	
HEMBA1000180	3.02	3.26	4.77	4.2	2.93	2.73	2.69	1.65	3.39				
HEMBA1000185	19.4	18.46	23.05	27.72	15.45	13.55	13.51	10.97	19.3				
HEMBA1000188	6.28	5.61	7.48	5.62	6.91	3.78	3.34	2.85	4.56		*		-
HEMBA1000193	7.66	7.79	11.97	13.74	5.68	7.85	5.99	5.1	6.65				
HEMBA1000194	31.21	25.82	29.1	20.52	12.15	13.24	9	11.15	12.72	*	**	-	-
HEMBA1000201	13.81	8.63	14.31	11.15	8.36	7.64	5.43	4.05	4.24		*		-
HEMBA1000213	2.97	4.59	8.02	5.36	2.78	4.45	3.2	1.24	3.2				
HEMBA1000216	7.62	8.45	11.73	6.7	6.96	6.62	6.13	4.35	5.56		*		-
HEMBA1000227	2.73	4.56	8.5	4.18	3.58	2.84	3.35	1.71	2.27				
HEMBA1000231	24.52	27.31	24.37	15.72	17.43	21.38	21.29	12.5	20.49	*		-	
HEMBA1000237	76.81	74.32	83.86	66.84	59.97	42.93	44.61	22.46	38.37		**		-
HEMBA1000243	13.82	10.47	25.88	21.77	11.3	17.41	12.09	8.84	11.38				
HEMBA1000244	9	7.04	9.25	7.59	2.86	4.81	3.47	4.91	3.18		**		-
HEMBA1000251	4.62	4.41	5.87	4.22	1.63	3.25	2.37	2.22	2.32		**		-
HEMBA1000254	10.09	13.73	13.57	7.22	5.82	7.35	8.91	6.98	9.5	*	*	-	-
HEMBA1000264	5.1	3.56	11.16	4.22	2.15	2.47	2.98	1.73	5.35				
HEMBA1000269	4.34	6.24	5.63	3.94	4.73	5.35	3.13	1.23	3.19		*		-
HEMBA1000275	22.4	40.99	22.83	21.15	22.57	23.38	10.3	5.45	12.41		*		-
HEMBA1000280	6.51	8.26	15.12	7.28	7.37	8.84	7.59	2.9	7.78				
HEMBA1000282	18.71	16.98	38.85	19.86	12.71	13.67	18.74	14.02	21.9				
HEMBA1000287	10.5	12.84	12.5	3.76	7.11	6.81	3.4	8.14	8.93	**		-	
HEMBA1000288	14.15	21.12	36.73	13.92	11.11	18.3	14.48	11.79	19.51				

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Table 355

HEMBA1000290	5.54	5.24	10.06	5.33	1.73	3.05	3.54	2.47	2.22				
HEMBA1000296	9.5	13.84	20.76	5.15	12.54	6.86	5.85	5.2	3.4		*		-
HEMBA1000300	35.72	34.39	45.53	27	31.39	25.7	26.91	18.61	28.62		*		-
HEMBA1000302	3.92	5.7	9.9	1.71	5.14	2.38	3.51	1.14	3.24				
HEMBA1000303	7.88	7.6	13.76	3.6	4.76	4.02	4.64	2.88	3.92		*		-
HEMBA1000304	20.77	16.02	19.73	12.6	11.48	11.65	12.2	13.31	13.14	**	*	-	-
HEMBA1000307	7.67	8.03	6.72	5.49	4.16	4.06	1.61	1.51	3.67	**	**	-	-
HEMBA1000312	26.83	27.01	36.09	21.32	17.54	18.68	18.71	13.82	23.54	*		-	
HEMBA1000318	14.81	10.63	16.92	6.25	7.77	8.66	2.82	1.83	3.66	*	**	-	-
HEMBA1000327	16.1	19.56	31.73	13.19	19.56	35.1	16.48	11.24	13.77				
HEMBA1000333	4.8	4.82	8.3	2.23	3.1	2.42	2.41	0.71	1.87	*	*	-	-
HEMBA1000338	14.85	18.8	25.1	10	13.67	12.74	13.23	10.79	10.59				
HEMBA1000343	9.76	12.6	14.72	7.21	10.87	8.74	6.58	5.91	8.76		*		-
HEMBA1000349	7.48	9.48	16.3	4.37	4.58	5.11	3.79	2.9	11.15				
HEMBA1000351	16.95	12.69	26.79	18.1	17.55	14.44	11.22	7.92	17.2				
HEMBA1000355	11.99	7.36	8.03	7.48	3.22	2.44	1.27	2.39	3.56		*		-
HEMBA1000356	34.47	36.59	32.24	39.62	29.15	32.82	22.27	24.67	20.29		**		-
HEMBA1000357	16.16	16.75	30.37	11.91	12.99	11.46	14.62	9.28	12.57				
HEMBA1000366	10.73	7.46	15.42	5.17	5.07	3.55	5.42	3.22	6.53	*		-	
HEMBA1000369	10.72	11.69	16.34	4.55	5.5	4.39	6.76	3.13	5.67	*	*	-	-
HEMBA1000370	9	13.55	13.78	4.72	8.24	7.37	5.92	3.13	3.05	*	*	-	-
HEMBA1000376	90.99	73.26	0.51	1.99	5.8	2.22	56.72	52.09	77.09				
HEMBA1000387	26.37	30.02	2.06	0.67	28.79	0	22.74	18.21	26.75				
HEMBA1000389	16.44	15.64	23.44	8.78	10.05	15.24	16.41	8.42	9.96				
HEMBA1000390	10	6.3	9.6	4.59	5.15	2.55	7.47	3.11	6.96	*		-	
HEMBA1000392	7.7	8.4	14.19	5.19	4.42	2.87	4.91	3.87	4.75				
HEMBA1000396	9.8	6.67	9.18	1.73	1.25	0.34	3.88	1.99	4.11	**	*	-	-
HEMBA1000411	4.32	4.84	13.72	2.13	3.17	1.91	3.36	1.45	2.17				
HEMBA1000418	10.46	14.65	17.48	5.45	8.2	5.71	4.56	2.35	3.71	*	**	-	-
HEMBA1000422	9.96	6.26	0	0.69	0.58	0.28	3.62	3.45	7.58				
HEMBA1000428	8.49	7.69	1.25	0.25	8.33	0	5.22	5.3	9.15				
HEMBA1000434	6.78	3.73	4.63	2.97	2.1	1.84	5.95	1.48	3.75	*		-	
HEMBA1000442	3.73	3.34	8.65	2.11	3.23	1.05	2.87	2.62	6.58				
HEMBA1000443	6.03	7.17	14.31	3.08	6.26	3.05	8.49	4.27	7.22				
HEMBA1000446	56.88	47.2	7.47	1.38	1.35	0.83	46.56	24.3	38.67				
HEMBA1000456	14.88	20.85	28.05	5.95	15.86	10.1	10.12	2.72	7.69		*		-
HEMBA1000459	15.34	18.32	27.74	11	17.98	14.9	11.74	7.37	11.06				
HEMBA1000460	23.55	16.11	28.93	19.24	20.63	19.37	10.12	7.72	17.35				
HEMBA1000462	25.82	7.48	2.26	1.21	3.05	10.25	13.12	8.17	7.37				
HEMBA1000464	7.56	4.51	6.06	3.68	3.64	2.38	3.55	1.26	2.53	*	*	-	-
HEMBA1000468	3	4	6.33	1.85	2.29	0.39	1.45	0.17	1.64		*		-
HEMBA1000469	22.54	28.03	34.83	17.42	17.27	14.02	27.65	14.61	18.23	*		-	
HEMBA1000477	17.38	15.06	7.59	1.07	12.5	0.35	11.11	7.11	9.19				
HEMBA1000481	63.47	80.18	49.05	5.51	28	7.01	17.9	5.67	5.55	*	**	-	-
HEMBA1000488	14.11	13.36	8.09	0.4	9.3	4.86	6.34	1.81	3.54		*		-
HEMBA1000490	9	6.13	11.44	3.85	4.12	5.04	6.84	2.63	7.56	*		-	
HEMBA1000491	5.32	6.61	17.42	8.34	8.06	9.74	6.93	4.28	9.22				
HEMBA1000498	14.5	18.25	24.06	10.95	15.11	14.4	16.82	10.93	14.38				
HEMBA1000501	7.87	9.11	2.74	0.21	2.74	4.51	6.04	4.62	6.97				
HEMBA1000504	12.54	5.58	11.75	3.41	4.13	2.59	2.67	4.18	4.58	*		-	
HEMBA1000505	6.92	8.54	7.08	0	1.28	0.84	5.6	2.13	4.7	**	*	-	-
HEMBA1000507	0.45	1.56	8.28	0	1.2	0.18	0.77	0	0.38				
HEMBA1000508	26.91	34.97	50.59	22.03	32.11	27.29	38.18	21.05	20.98				
HEMBA1000518	3.76	3.28	6.48	5.32	4.44	6.01	3.59	1.86	3.38				
HEMBA1000519	85.07	91.86	141.09	42.18	50.11	71.14	47.48	35.9	57.59		*		-
HEMBA1000520	6.49	7.75	13.06	6.32	6.26	4.22	5.77	4.5	4.14				
HEMBA1000523	11.85	6.14	1.44	0	1.42	0.29	4.15	3.58	2.35				
HEMBA1000531	8.26	6.64	16	4.73	9.37	11.46	9.54	4.57	6.14				
HEMBA1000534	28.94	37.16	55.86	24.81	22.76	20.48	41.37	29.08	32.84				
HEMBA1000538	14.97	19.18	30.49	12.11	14.95	11.04	13.25	9.03	10.27				
HEMBA1000540	18.41	10.82	26.42	7.05	8.02	12.43	11.49	5.58	4.88				
HEMBA1000542	68.21	65.66	96.9	105.13	126.6	107.62	49.4	38.5	50.6	*	*	+	-
HEMBA1000545	10.72	9.72	19.53	13.15	9.91	10.84	7.59	4.75	4.2				
HEMBA1000547	16.09	12.61	26.19	11.54	11.54	13.04	5.83	5.77	5.14		*		-

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Table 356

HEMBA1000551	31.43	29.13	74.52	42.08	38.34	36.48	27.97	18.18	17.63				
HEMBA1000555	23.07	51.65	28.63	16.75	19.18	84.47	21.47	21.24	16.53				
HEMBA1000557	20.2	22.07	26.42	16.84	15.85	18.08	21.6	11.99	15.53	*		-	
HEMBA1000561	6.79	6.3	13.7	3.18	1.89	4.15	4.27	2.09	3.68				
HEMBA1000563	5.71	6.02	9.65	3.7	5.59	3.42	4.89	1.86	4.27				
HEMBA1000567	2.91	1.55	3.34	2.35	0.99	3.67	2.89	1.41	2.17				
HEMBA1000568	8.19	5.62	14.84	8.57	7.03	7.81	7.88	3.61	9.31				
HEMBA1000569	2.57	3.31	7.08	4.64	2.77	3.17	2.3	1.18	2.24				
HEMBA1000575	24.44	15.32	39.5	24.17	18.92	19.53	17.36	14	17.06				
HEMBA1000588	7.1	5.81	8.91	7.39	8.88	8.85	8.33	2.25	5.9				
HEMBA1000590	5.23	6.06	5.7	5.36	6.93	6.66	4.07	2.31	4.39		*		-
HEMBA1000591	24.12	22.46	26.56	10.74	18.87	21.61	11.03	5.76	13.01		**		-
HEMBA1000592	30.95	41.43	24.53	10.67	31.41	23.82	10.57	11.36	12.37		*		-
HEMBA1000594	5.11	7.29	6.57	8.37	4.71	6.68	5.32	3.27	3.89				
HEMBA1000604	21.62	17.48	22.7	28.09	18.45	20.99	13.92	9.43	17.25				
HEMBA1000607	59.03	59	91.06	71.67	51.82	56.83	60.28	42.6	51.42				
HEMBA1000608	9.41	4.42	6.41	8.42	5.12	4.07	7.92	3.99	8.94				
HEMBA1000622	7.92	7.76	16.15	9.11	9.27	13.89	9.94	3.81	11.14				
HEMBA1000634	52.78	74.71	70.68	39.88	65.82	64.7	32.15	24.17	25.34		**		-
HEMBA1000636	27.22	28.11	25.27	25.4	22.96	20.49	9.12	9.28	12.36		**		-
HEMBA1000637	8.86	11.75	7.97	5.21	9.26	6.88	4.93	3.34	3.68		*		-
HEMBA1000655	30.73	31.69	54.9	27.54	16.27	22.75	21.5	18.39	24.41				
HEMBA1000657	14.08	9.28	10.28	5.96	7.53	6.3	3.93	18.82	5.24	*		-	
HEMBA1000662	6.27	5.79	10.27	3.02	6.27	5.29	2.93	4.16	3.38				
HEMBA1000664	6.29	6.77	9.71	5.57	5.25	9.62	2.22	2.8	4.62		*		-
HEMBA1000671	30.41	19.43	27.86	31.58	22.01	24.63	20.58	14.98	15.56				
HEMBA1000673	24.11	24.74	28.83	18.72	18.93	18.52	21.96	17.14	28.31	**		-	
HEMBA1000675	11.22	13.93	16.24	11.01	14.94	12.36	11.46	6.91	7.33				
HEMBA1000678	5.24	8.15	11.3	5.35	7.05	6.17	5.02	1.55	1.87				
HEMBA1000682	34.57	35.39	53.17	14.17	19.8	19.96	13.73	23.76	33.18	*		-	
HEMBA1000686	21.71	40.16	35.85	10.91	16.11	14.54	4.3	11.52	5.8	*	*	-	-
HEMBA1000702	10.84	17.35	25.73	7.39	11.25	13.13	7.56	7.08	9.42				
HEMBA1000705	4.6	3.75	8.97	3.21	1.09	3.11	3.08	4.72	3.61				
HEMBA1000713	10.43	11	19.66	5.79	9.41	8.35	11.72	6.95	13.37				
HEMBA1000718	27.65	31.72	34.47	19.34	17.98	21.82	22.89	15.55	26.61	**		-	
HEMBA1000719	21.36	28.6	18.8	18.63	23.29	31.74	21.77	16.83	13.89				
HEMBA1000722	10.72	14.07	15.25	12.4	11.9	8.36	7.24	4.41	3.46		**		-
HEMBA1000726	32.15	32.06	69.89	34.36	26.18	30.36	36.32	22.04	41.04				
HEMBA1000727	16.97	26.82	19.68	5.88	11.41	11.31	4.45	8.11	7.29	*	**	-	-
HEMBA1000732	8.15	9.73	16.83	6.74	7.08	9.59	5.57	4.8	5.38				
HEMBA1000736	9.38	7.92	11.45	7.38	12.77	8.49	9.33	6.94	12.57				
HEMBA1000743	6.76	5.78	11.72	5.12	7.77	27.92	5.16	3.39	8.47				
HEMBA1000745	7.61	8.54	13.88	4.04	5.82	4.46	4.98	2.87	5.45				
HEMBA1000747	5.32	4.72	12.62	2.69	5.68	3.35	3.85	2.1	3.4				
HEMBA1000748	7.08	6.97	13.44	6.2	9.91	9.41	8.23	3.96	6.55				
HEMBA1000749	18.03	20.17	33.28	13.55	12.82	15.47	12.43	12.59	18.76				
HEMBA1000752	9.61	11.01	10.43	7	5.98	6.12	4.8	4.54	8.58	**	*	-	-
HEMBA1000753	14.73	8.44	14.96	4.78	5.04	11.61	5.39	6.35	8.17				
HEMBA1000757	11.82	6.81	16.04	4.91	5.14	4.63	2.56	3.42	2.84		*		-
HEMBA1000760	13.51	13.09	20.98	7.09	10.48	10.58	5.68	4.5	6.77		*		-
HEMBA1000769	7.76	13.89	13.94	4.47	6.26	7.04	9.68	6.14	7.78				
HEMBA1000773	3.65	4.13	15.13	0.99	5.68	8.11	2.71	1.47	3.38				
HEMBA1000774	21.34	27.53	42.71	22.13	28.3	22.38	30.47	15.88	17.88				
HEMBA1000780	6.15	5.35	9.22	6.03	4.9	4.38	2.5	2.74	2.78		*		-
HEMBA1000783	8.54	7.55	8.23	4.94	5.39	5.68	3.76	3.66	3.46	**	**	-	-
HEMBA1000791	29.92	28.02	44.77	28.48	22.57	21.5	32.85	19.21	32.35				
HEMBA1000793	30.39	19.19	19.38	8.64	16.27	16.1	13.32	16.07	12.64				
HEMBA1000802	4.74	2.72	8.7	3.43	2.84	2.21	2.09	1.11	2.74				
HEMBA1000813	46.62	47.69	50.56	27.4	35.01	30.28	30.89	15.81	34.56	**	*	-	-
HEMBA1000817	12.55	12.98	16.93	6.72	11.22	3.95	2.79	1.89	3.94		**		-
HEMBA1000822	6.54	19.54	13.74	4.86	7.54	6.86	4.29	1.48	3.36				
HEMBA1000827	13.88	14.84	28.11	13.31	20.08	16.37	7.68	5.83	12.73				
HEMBA1000833	12.7	15.8	16.64	5.65	5.56	4.66	3.19	1.79	1.87	**	**	-	-
HEMBA1000835	118.36	117.03	136.17	175.69	117.43	151.33	112.03	74.79	83.7				

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Table 357

HEMBA1000843	12.55	15.69	27.26	12.49	12.36	9.92	12.67	6.01	13.01				
HEMBA1000851	7.99	8.88	11.08	3.31	3.75	3.94	6.33	2.77	2.83	**	*	-	-
HEMBA1000852	16.57	13.81	23	7.9	10.22	6.68	11.13	8.47	9.44	*	*	-	-
HEMBA1000867	6.41	40.09	21.59	7.82	12.17	12.73	16.16	8.86	5.82				
HEMBA1000869	6.66	6.92	14.84	4.94	6.58	4.87	5.66	1.59	2.82				
HEMBA1000870	16.63	14.8	15.74	6.74	7.25	8.9	6.35	3.09	4.06	**	**	-	-
HEMBA1000872	19	16.2	19.95	12.25	11.2	8.26	7.42	4.77	5.4	**	**	-	-
HEMBA1000875	7.38	6.41	11.16	2.07	4.19	4.92	3.96	2.9	2.7		*		-
HEMBA1000876	12.29	12.13	19.01	9.58	10.69	6.67	12.67	6.89	9.73				
HEMBA1000907	4.99	12.04	11.83	5.83	7.88	10.61	8.24	2.82	6.62				
HEMBA1000908	7.89	3.64	11.79	2.7	10.96	1.89	2.83	0.62	3.13				
HEMBA1000910	4.91	8.05	12.14	3.81	5.91	4.56	6.84	3.7	4.74				
HEMBA1000918	21.04	31.68	45	25.17	23.52	19.82	25.88	9.86	18.68				
HEMBA1000919	4.44	2.5	5.8	3.35	2.86	3.17	3.08	0.43	2.37				
HEMBA1000934	4.04	4.57	5.7	3.99	3.21	2.45	2.55	1.54	2.64		*		-
HEMBA1000935	4.4	5.61	6.39	3.11	4.92	2.1	3.77	2.49	2.75		*		-
HEMBA1000940	8.69	8.39	12.11	6.45	5.94	4.28	6.33	4.58	4.22	*	*	-	-
HEMBA1000942	12.05	15.91	20.05	9.92	11.92	8.31	14.27	9.3	8.99				
HEMBA1000943	2.61	3.51	9.04	0.06	1.63	0.43	1.65	0.02	0.85				
HEMBA1000946	5.48	9.79	16.74	3.82	4.51	6.06	3.38	0.73	4.11				
HEMBA1000960	30.15	53.34	82.32	44.07	41.58	37.38	55.19	30.36	32.98				
HEMBA1000962	10.91	13.68	14.99	4.87	9.87	8.15	6	5.38	7.85	*	**	-	-
HEMBA1000968	9.18	5.88	12.53	7.34	5.67	5.5	4.92	3.16	5.55				
HEMBA1000971	12.8	9.28	22.24	4.73	7.24	3.99	4.56	3.74	2.56		*		-
HEMBA1000972	8.17	5.02	15.62	6.78	5.58	5.96	5.46	4.31	5.77				
HEMBA1000974	17.96	18.06	33.14	22.9	19.86	19.01	13.64	8.08	13.41				
HEMBA1000975	8.54	6.18	15.36	5.78	4.48	4.06	6.6	5	4.55				
HEMBA1000979	12.05	14.89	32.47	11.86	10.02	10.56	16.5	7.76	11.37				
HEMBA1000981	31.09	24.35	60.14	12.11	16.96	23.49	26.22	14.59	14.47				
HEMBA1000983	16.01	16.07	24.38	8.83	12.27	20.3	15.26	9.78	16.85				
HEMBA1000985	7.28	3.65	6.98	4.91	4.64	4.99	4.05	3.11	1.91				
HEMBA1000986	13.51	10.48	26.88	15.8	12.5	15.39	12.22	6.19	7.06				
HEMBA1000991	15.73	13.96	24.7	13.38	13.44	8.96	12.92	7.37	7.9				
HEMBA1001007	6.2	4.4	10.1	3.64	3.96	2.18	2.52	1.45	2.54				
HEMBA1001008	5.26	4.15	10.22	2.95	3.18	4.11	4.27	1.48	2.86				
HEMBA1001009	2.98	2.47	7.99	2.44	3.53	2.07	2.05	0.9	2.84				
HEMBA1001014	36.78	43.69	57.32	33.05	32.39	34.29	37.95	15.24	32.56				
HEMBA1001017	7.14	5.71	12.9	9.32	5.72	6.57	4.21	2.97	4.79				
HEMBA1001019	6.35	3.7	5.48	7.22	3.14	5.53	3.87	2.27	2.61				
HEMBA1001020	9.13	7.41	10.99	8.19	4.18	5.07	8.01	5.07	4.27				
HEMBA1001021	4.2	4.32	9.05	3.87	3.59	5.86	6.3	1.95	6.15				
HEMBA1001022	10.5	4.41	10.29	9.91	9.22	14.59	10.15	4.7	6.8				
HEMBA1001024	1.82	2.83	6.27	3.68	2.95	3.77	2.92	1.3	2.29				
HEMBA1001026	3.74	3.71	5.2	2.99	4.11	4.69	3.01	1.9	3.66				
HEMBA1001043	6.37	5.28	6.61	4.42	5.68	7.08	4.73	0.86	3.01				
HEMBA1001051	120.57	138.21	211.05	111.88	82.79	99.92	82.72	88.42	94.95				
HEMBA1001052	6.69	6.44	5.5	6.15	5.41	3.95	3.07	3.55	4.05		**		-
HEMBA1001059	56.7	56.44	76.92	96.6	52.77	73	38.68	40.32	41.94		*		-
HEMBA1001060	22.93	14.44	26.88	16.88	16.28	14.69	14.87	11.27	12.22				
HEMBA1001064	7.94	5.9	11.63	5.61	6.84	7.38	5.01	1.85	2.88				
HEMBA1001071	2.97	5.22	8.35	8.63	6.39	5.39	3.26	1.85	3.81				
HEMBA1001077	6.95	10.47	5.65	10.99	11.81	13.69	3.82	3.2	5.87				
HEMBA1001078	13.55	16.29	18.17	15.7	24.22	16.62	14.25	7.88	7.1				
HEMBA1001080	18.26	14.99	25.65	14.28	9.2	7.86	14.01	11.12	10.13				
HEMBA1001084	10.12	12.02	19.64	11.43	8.23	10.4	8.52	5.91	8.47				
HEMBA1001085	12.67	14.13	17.46	10.37	7.16	7.36	9.72	8.19	7.2	*	*	-	-
HEMBA1001088	3.47	2.77	6.21	3.04	2.22	2.64	4.71	4.47	2.67				
HEMBA1001093	5.99	7.48	12.08	5.52	4.12	4.26	4.75	3.73	5.78				
HEMBA1001094	3.87	3.67	7.3	1.83	2.98	1.32	1.79	1.61	3.04				
HEMBA1001099	4.27	4.88	10.87	6.66	5.88	4.18	3.44	1.48	3.72				
HEMBA1001104	3.23	5.58	9.6	7.66	21.55	10.79	5.83	1.68	4.13				
HEMBA1001109	55.09	49.61	96.04	54.26	41.61	45.47	44.91	34.62	57.09				
HEMBA1001114	101.03	160.97	118.61	64.42	78.99	99.5	43.15	105.03	85.05				
HEMBA1001121	8.11	7.04	9.73	5.44	4.04	4.32	4.43	2.6	4.72	*	*	-	-

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Table 358

HEMBA1001122	9.39	9.29	17.71	6.58	5.73	6.53	2.46	3.1	3.26		*		-
HEMBA1001123	17.13	17.37	24.47	15.29	11.78	13.71	12.33	9.75	10.61		*		-
HEMBA1001133	8.92	6.97	12.93	3.69	4.11	4.57	3.05	2.9	3.3	*	*	-	-
HEMBA1001137	6.57	7.37	12.88	4.24	4.79	2.86	4.1	2.06	3.89				
HEMBA1001140	9.64	11.4	16.66	10.87	12.26	10.82	8.45	8.07	5.83				
HEMBA1001144	75.62	79.41	130.35	64.7	57.88	71.91	43.23	38.45	52.04		*		-
HEMBA1001145	228.88	419.26	297.93	34.88	83.53	106.81	28.23	79.02	93.39	*	*	-	-
HEMBA1001158	11.25	10.45	12.32	5.71	7.87	10.11	6.5	4.55	5.45		**		-
HEMBA1001172	13.23	15.14	21.25	10.8	9.67	9.91	10.54	8.89	11.23				
HEMBA1001174	4.77	4.96	13.93	3.36	4.72	5.71	5.53	3.53	3.57				
HEMBA1001175	25.64	49.85	37.18	5.53	36.99	18.9	6.53	8.52	5.43		*		-
HEMBA1001182	253.75	199.19	217.61	213.83	179.06	196.11	166.5	128.3	113.47		*		-
HEMBA1001184	2.72	5.66	6.46	2.92	7.84	3.84	2.54	1.64	3.55				
HEMBA1001192	7.71	9.61	13.89	5.11	4.84	2.98	2.49	2.97	4.44	*	*	-	-
HEMBA1001196	20.51	33.03	45	22.81	18.19	24.13	7.47	12.08	16.7				
HEMBA1001197	377.82	621.74	482.95	613.89	355.35	492.48	223.5	509.73	494.09				
HEMBA1001208	6.77	4.91	9.09	4.11	4.25	4.69	3.47	2.44	4.54				
HEMBA1001213	162.45	150.13	151.88	224.78	129.48	188.61	135.18	97.08	115.8		*		-
HEMBA1001214	10.4	15.18	18.46	6.51	7.45	6.56	4.99	3.77	6.34	*	*	-	-
HEMBA1001221	12.82	12.25	13.21	2.1	6.95	5.45	2.31	0.75	2.8	**	**	-	-
HEMBA1001225	4.23	4.43	8.6	1.43	2.73	4.08	2.02	0.94	2.52				
HEMBA1001226	43.15	51.42	64.65	33.28	48.87	38.83	29.67	18.32	24.38		*		-
HEMBA1001228	5.8	4.52	8.07	5.69	4.51	3.32	3.32	1.37	1.24		*		-
HEMBA1001229	171.43	141.71	227.65	215.79	153.09	225.88	105.81	85.9	109.68		*		-
HEMBA1001235	51.44	62.4	68.51	46.01	34.3	36.55	26.86	20.23	22.59	*	**	-	-
HEMBA1001238	19.14	19.72	19.8	10.86	15.88	9.5	15.04	10.36	16.33	*	*	-	-
HEMBA1001242	153.09	161.43	160.67	152.69	145.07	151.85	99.19	75.76	86.89		**		-
HEMBA1001247	33.3	29.15	48.14	21.32	32.34	22.28	34.27	20.52	27.05				
HEMBA1001253	159.45	91.8	142.61	116.02	138.28	127.87	95.67	74.41	74.86				
HEMBA1001257	10.7	11.57	12.78	5.67	10.33	4.37	9.19	6.06	4.62		*		-
HEMBA1001261	6.83	4.18	8.42	7.74	2.14	4.76	3.41	1.78	5.45				
HEMBA1001262	12	7.56	5.09	4.62	4.49	6.27	3.32	1.44	4.7				
HEMBA1001265	15.44	18.41	25	9.71	8.97	12.14	13.41	14.3	11.72	*		-	
HEMBA1001266	22.75	26.99	30.66	16.84	17.03	12.35	18.86	10.28	14.84	*	*	-	-
HEMBA1001269	62.54	134.76	5.56	0.22	1.58	0.07	24.28	23.59	16.64				
HEMBA1001272	5.33	4.56	13.33	2.87	3.94	3.83	3.1	1.67	1.95				
HEMBA1001279	26.1	31.13	42.25	28.49	33.02	28.73	22.53	17.36	24.84				
HEMBA1001281	43.22	55.66	55.89	31.39	34.2	26.87	21.08	11.24	15.62	*	**	-	-
HEMBA1001286	42.89	33.78	59.69	41.46	36.64	48.02	50.11	34.66	41.6				
HEMBA1001289	4.71	4.83	5.28	3.13	4.27	3.23	3.56	1.6	3.12	*	*	-	-
HEMBA1001291	36.57	24.72	38.55	19.37	18.57	13.13	19.39	15.96	11.69	*	*	-	-
HEMBA1001294	8.41	15.41	16.09	9.8	8.09	6.28	18.25	5.05	15.73				
HEMBA1001296	7.97	20.06	12.99	5.33	6.56	3.52	5.19	2.03	4.63				
HEMBA1001297	10.62	19.22	19.19	4.41	7.4	5.61	6.49	1.83	3.17	*	*	-	-
HEMBA1001299	34.22	39.68	53.21	25.14	29.23	20.66	39.68	22.86	32.79	*		-	
HEMBA1001302	25.32	40.78	38.96	17.94	26.15	22.11	18.04	11.91	7.95		*		-
HEMBA1001303	10.97	8.86	13.92	4.53	5.04	4.42	4.71	4.03	7.45	*	*	-	-
HEMBA1001306	14.82	11.94	17.26	5.51	7.45	6.38	3.83	5.28	4.41	**	**	-	-
HEMBA1001308	44.73	35.49	88.39	29.14	49.52	28	40.25	28.31	38				
HEMBA1001310	8.14	6.04	8.8	2.67	3.81	3.08	5.37	3.64	2.99	**	*	-	-
HEMBA1001312	42.22	39.35	44.87	10.33	40.14	18.42	38.81	18.56	13.38				
HEMBA1001319	3.83	6.75	12.77	3	5.03	13.5	4.72	0.95	4.62				
HEMBA1001322	10.16	10.91	17.38	3.57	7.15	4.09	5.93	2.59	3.36	*	*	-	-
HEMBA1001323	41.14	36.93	47.79	17.38	18.24	15.31	13.85	10.42	3.9	**	**	-	-
HEMBA1001326	38.26	32.16	36.43	4.89	17.62	29.01	7.49	3.64	9.8		**		-
HEMBA1001327	22.04	9.71	15.11	7.86	12.59	16.77	4.84	4.12	2.75		*		-
HEMBA1001330	29.76	31.78	64.11	34.57	26.99	26.81	34.76	20.01	20.9				
HEMBA1001348	8.77	6.35	12.87	5.62	7.19	5.23	5.41	4.95	2.78				
HEMBA1001350	11.78	12.52	19.81	3.72	3.89	6.89	7.45	5.17	4.88	*	*	-	-
HEMBA1001351	31.73	33.01	83.64	16.41	14.04	17.67	14.45	12.88	6.51				
HEMBA1001352	16.11	10.31	24.58	3.9	5.27	4.13	8.48	3.75	2.44	*		-	
HEMBA1001353	239.33	87.11	196.31	30.75	66.77	70.17	148.92	56.48	39.11				
HEMBA1001358	74.35	56.7	93	21.23	34.67	61.64	20.12	9.88	14.9		**		-
HEMBA1001361	9.19	10.7	19.27	11.26	10.32	15.03	5.68	3.47	4.41				

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Table 359

HEMBA1001364	5.59	5.71	8.25	5.34	8.32	6.23	4.19	2.87	3.41		*		-
HEMBA1001375	10.82	8.04	9.96	6.56	6.52	8.55	3.93	8.03	4.02				
HEMBA1001377	30.09	30.45	47.44	34.01	31.38	34.79	26.34	19.08	22.43				
HEMBA1001383	3.91	6.12	10.35	4.08	4.49	3.29	3.04	1.16	2.13				
HEMBA1001387	4.6	4.17	9.82	4.35	3.61	5.27	5	2.3	4.29				
HEMBA1001388	3.38	12.99	10.77	8.84	13.96	11.27	14.15	2.79	4.79				
HEMBA1001390	16.62	20.96	41.58	20.9	20.32	29.35	22.75	17.7	27.56				
HEMBA1001391	2.64	5.63	6.55	6.35	4.1	4.57	3.4	1.38	3.14				
HEMBA1001398	7.95	9	20.79	14.55	10.11	10.1	9.09	3.86	9.96				
HEMBA1001405	12.88	15.37	29.38	17.27	15.08	16.39	13.42	7.68	15.76				
HEMBA1001406	1.07	1.48	6.07	4.64	2.23	2.45	3.84	0.53	2.8				
HEMBA1001407	26.07	42.46	69.39	34.3	28.94	28.07	26.15	15.14	21.96				
HEMBA1001411	12.19	10.95	23.76	12.34	12.91	16.6	13.01	4.8	11.91				
HEMBA1001413	3.96	7.52	13.68	7.68	4.74	6.7	4.77	2.46	3.91				
HEMBA1001414	10.32	10.99	22.49	13.09	11.95	9.01	7.42	9.57	11.87				
HEMBA1001415	108.07	112.24	218.31	263.58	139.52	200.62	94.4	74.64	97.27				
HEMBA1001416	5.94	4.6	7.89	5.06	3.57	4.15	3.74	1.73	3.21		*		-
HEMBA1001432	3.3	3.49	7.34	4.93	5.95	7.57	4.22	3.23	2.6				
HEMBA1001433	5.11	5.55	7.48	5.92	7.1	6.22	4.04	2.29	5.52				
HEMBA1001435	448.61	559.24	661.15	777.73	679.52	650.29	640.12	377.73	869.06				
HEMBA1001442	5.84	10.08	7.28	7.83	12.04	8.46	5.85	1.96	2.4				
HEMBA1001446	3.77	5.34	6.49	8.2	4.64	4.7	3.45	2.22	3.65				
HEMBA1001450	87.92	103.44	150.5	232.41	124.8	175.34	89.47	74.72	92.31				
HEMBA1001454	32.58	33.13	59.47	19.79	12.7	25.66	18.88	24.9	33.22				
HEMBA1001455	4.27	6.3	7.42	3.13	5.27	4.96	6.16	1.51	6.96				
HEMBA1001459	13.66	26.28	34.13	12.19	9.69	14.19	9.18	11.22	13.6				
HEMBA1001461	30.98	26.88	43.29	63.45	32.06	36.73	26.62	18.12	23.29				
HEMBA1001462	9.43	9.05	11.64	4.2	7.04	5.63	4.19	2.77	3.22	*	**	-	-
HEMBA1001463	1.15	4.7	4.74	4.99	6.6	4.02	4.68	1.57	3.46				
HEMBA1001469	23.94	42.87	64.76	64.17	33.38	52.34	14.36	18.57	20.01				
HEMBA1001473	7.37	9.89	11.35	4.59	3.3	4.44	2.71	5.14	2.51	*	*	-	-
HEMBA1001477	143.72	139.98	283.29	91.65	145.02	139.05	125.85	114.31	63.92				
HEMBA1001478	3.38	2.99	11.83	2.63	2.55	3.35	2.27	2.13	2.08				
HEMBA1001480	12.29	13.63	23.93	4.88	9.2	12.63	3.97	2.72	4.12		*		-
HEMBA1001483	20.97	27.37	23.32	22.22	18.94	28.05	14.33	10.01	19.51		*		-
HEMBA1001490	14.01	20.37	28.13	15.26	17.45	15.48	22.44	13.02	12.6				
HEMBA1001495	29.87	31.18	55.68	75.52	52.85	69.44	21.73	15.8	24.63				
HEMBA1001497	50.34	63.13	114.17	128.19	117.69	137.5	43.07	37.4	51.44				
HEMBA1001510	6.77	7.43	13.73	8.69	8.1	7.82	5.34	3.9	10.87				
HEMBA1001515	4.96	2.98	9.2	1.95	4	3.02	1.96	0.89	7.49				
HEMBA1001517	8.97	7.98	15.08	6.1	6.94	5.43	7.39	5.25	8.47				
HEMBA1001522	12.78	16.29	21.22	10.39	13.01	11	10.54	9.25	10.66				
HEMBA1001526	8.05	10.86	20.31	6.19	10.35	7.24	6.93	4.75	7.32				
HEMBA1001533	10.67	13.52	23.12	12.09	16.84	9.55	9.42	6.16	11.58				
HEMBA1001547	5.91	8.31	10.54	8.17	5.66	9.57	6.23	2.5	7.38				
HEMBA1001552	2.97	4.72	5.75	6.36	5.56	2.49	2.68	1	5.09				
HEMBA1001553	11.17	10.19	22.05	10.98	12.27	11.05	5.91	7.82	10.68				
HEMBA1001557	7.49	2.45	11.09	3.83	4.84	5.27	3.14	6.97	8.01				
HEMBA1001563	6.6	2.01	15.37	5.55	6.29	6.53	4.15	2	6.53				
HEMBA1001566	4.27	3.01	8.62	2.13	3.6	3.87	2.2	1.62	3.88				
HEMBA1001569	9.15	15.35	27.87	11.41	11.78	14.08	8.02	5.27	11.03				
HEMBA1001570	10.89	22.06	19.57	12.99	13.03	16.53	9.14	4.13	3.81		*		-
HEMBA1001579	95.92	121.26	222.36	134.48	102.06	70.96	25.6	43.38	73.16				
HEMBA1001581	4.11	4.25	7.71	3.25	2.45	2.33	0.91	1.64	3.55				
HEMBA1001582	12.19	16.67	20.04	15.87	10.82	11.89	13.98	8.69	21.33				
HEMBA1001585	6.81	4.99	13.1	7.76	5	7.16	4.04	1.85	5.57				
HEMBA1001589	7.95	8.96	19.02	7.86	6.17	6	7.81	5.42	8.45				
HEMBA1001595	152.72	179.08	178.84	145.86	142.24	141.98	126.66	83.83	110.77	*	*	-	-
HEMBA1001604	23.66	24.89	37.02	23.72	21.32	19.26	15.97	14.33	15.78		*		-
HEMBA1001608	43.55	20.96	66.71	67.7	43.63	57.55	24.58	18.07	23.43				
HEMBA1001615	5.42	4.63	6.98	6.61	4.72	4.09	3.11	2.02	10.18				
HEMBA1001620	30.69	48.66	53.49	25.04	17.81	22.67	7.35	9.47	10.42	*	**	-	-
HEMBA1001621	8.82	12.26	20.39	18.14	12.47	10.32	10.67	8.68	14.11				
HEMBA1001635	3.29	3.32	8.82	2.2	2.68	3.13	2.05	0.94	1.44				

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Table 360

HEMBA1001636	3.01	3.66	7.63	2.63	2.16	1.96	2	2.43	2.09					
HEMBA1001640	29.8	43.06	50.77	23.27	24.57	21.36	34.37	24.57	21.57	*		-		
HEMBA1001647	5.45	3.94	16.28	4.05	6.97	2.61	5.21	2.15	4.19					
HEMBA1001651	40.26	49.2	70.61	64.68	55.88	51.2	30.59	17.33	15.12		*		-	
HEMBA1001655	10.17	9.88	20.1	6.79	14.34	13.87	15	5.01	12.4					
HEMBA1001658	5.48	21.34	12.68	3.21	27.79	21.94	17.32	4.91	4.48					
HEMBA1001661	1.92	2.27	3.66	1.72	2.22	1.93	2.04	0.71	3.46					
HEMBA1001665	5.27	5.54	9.55	3.17	2.96	2.46	2.94	1.87	2.02	*	*	-	-	
HEMBA1001670	14.59	18.93	22.5	10.01	11.18	7.78	13.23	9.01	14.55	*		-		
HEMBA1001672	5.67	6.19	14.07	4.38	5.16	2.99	5.11	2.78	4.53					
HEMBA1001673	67.5	83.13	100.8	79.52	76.6	62.66	79.54	46.76	80.49					
HEMBA1001675	11.65	14.39	26.02	11.92	12.54	11.44	8.96	6.24	12.74					
HEMBA1001676	5.94	6.55	16.33	9.03	9.2	9.7	5.97	3.49	7.17					
HEMBA1001678	408.84	460.84	545.99	212.4	385.11	245.37	243.82	358.42	324.52	*	*	-	-	
HEMBA1001680	17.81	21.9	34.13	4.77	16.15	9.85	5.24	7.39	4.29		*		-	
HEMBA1001681	4.07	7.09	7.63	4.19	6.03	3.95	5.56	3.95	9.27					
HEMBA1001684	9.98	10.79	18.76	5.52	7.17	3.85	8.63	7.5	7.69					
HEMBA1001695	6.3	10.78	12.26	4.59	5.86	5.01	6.15	3.07	8.56					
HEMBA1001702	4.21	4.98	12.28	2.87	3.73	2.48	2.67	0.5	1.76					
HEMBA1001709	2.14	4.26	13.24	2.55	2.4	2.49	3	0.8	2.49					
HEMBA1001711	4.46	2.9	7.77	4.65	5.15	6.37	2.22	1.03	3.22					
HEMBA1001712	17.3	21.73	24.38	4.68	4.43	7.93	6.13	3.94	7.49	**	**	-	-	—
HEMBA1001714	5.44	5.05	12.26	3.87	6.98	3.98	4.35	1.76	2.27					
HEMBA1001717	12.02	13.24	20.14	10.04	12.58	8.86	8.97	5.33	8.75					
HEMBA1001718	6.01	7.09	16.45	6.91	7.4	6.4	6.45	5.23	4.35					
HEMBA1001723	4.38	5.84	13.91	3.89	3.74	3.51	3.82	2.36	1.25					
HEMBA1001731	2.72	5.88	12.37	2.09	2.33	1.98	2.59	1.24	1.73					
HEMBA1001734	3.48	4.86	15.18	4.34	3.76	3.13	3.75	1.03	2.79					
HEMBA1001736	7.38	10.86	24.38	12.76	10.32	13.2	4.98	2.9	5.27					
HEMBA1001741	15.06	22.96	34.81	18.57	17.99	31.53	19.64	14.22	21.03					
HEMBA1001744	3.63	4.77	7.03	5.75	5.45	4.88	3.08	0.38	1.67					
HEMBA1001745	6.61	5.99	11.87	4.17	5.23	3.45	2.53	2.9	1.77		*		-	
HEMBA1001746	10	14.3	20.05	11.55	8.04	11.63	7.31	4.66	10.54					
HEMBA1001761	4.09	4.47	15.81	2.95	5.47	4.97	4.55	2.51	3.77					
HEMBA1001762	12.27	16.22	31.71	11.79	12.77	9.07	10.3	5.04	7.64					
HEMBA1001781	15.21	11.25	22.91	6.13	9.86	7.74	12.65	6.92	10.68					
HEMBA1001784	7.14	8.4	14.02	11.89	8.86	32.45	4.84	4.18	5.94					
HEMBA1001791	5.49	5.04	11.37	7.91	5.03	6.87	4.96	3.16	6.54					
HEMBA1001794	20.29	19.03	24.02	20.07	12.65	17.58	18.71	4.14	12.87					
HEMBA1001800	3.21	4.6	6.87	7.34	5.09	5.03	5.14	1.64	4.39					
HEMBA1001803	13.17	17	29.4	25.23	15.99	17.41	14	9.49	14.18					
HEMBA1001804	10.28	12.82	18.21	18.52	13.37	6.76	5.06	3.75	9.33					
HEMBA1001808	1.39	1.46	0.57	2.77	3.18	1.86	0.98	1.2	0.86	*		+		
HEMBA1001809	10.03	14.07	29.16	27.06	14.98	19.9	10.22	6.76	12.88					
HEMBA1001811	4.85	4.27	3.18	10.29	3.63	4.31	3.6	2.84	5.25					
HEMBA1001815	12.35	11.27	24.93	14.76	10.57	16.04	11.75	6.51	11.06					
HEMBA1001816	15.52	16.02	31.22	15.84	13.09	17.05	15.48	10.68	15.2					
HEMBA1001819	6.04	14.01	18.63	8.04	9.05	17.69	7.85	3.75	9.93					
HEMBA1001820	1.8	2.22	6.75	3.5	2.81	3.45	1.98	0.63	2.02					
HEMBA1001822	10	12.84	23.21	14.57	16.12	12.64	12.36	6.85	15.78					
HEMBA1001824	5.2	8.63	7.51	6.46	8.51	5.78	4.67	0.98	4.7					
HEMBA1001835	9.56	9.62	14.11	4.64	5.39	6.11	3.44	4.66	3.04	*	**	-	-	
HEMBA1001844	8.02	10.52	19.05	12.42	10.73	9.57	5.22	6.54	4.99					
HEMBA1001847	5.48	6.03	7.01	5.38	4.93	4.88	3.96	3.19	3.69		**		-	
HEMBA1001849	6.93	9.14	14.78	5.03	7.86	7.21	7.8	8.87	10.07					
HEMBA1001850	16.31	17.09	25.61	18.6	20.16	20.58	11.51	7.47	10.97		*		-	
HEMBA1001861	2.36	3.42	4.47	4.07	3.37	3.99	2	1.11	3.64					
HEMBA1001862	13.85	31.74	17.1	16.22	16.82	16.11	10.11	2.6	10.67					
HEMBA1001864	2.79	3.87	7.65	5.32	5.64	4.4	3.29	2.25	6.43					
HEMBA1001866	5.87	7.28	17.71	11.53	8.34	6.62	3.42	4.81	5.52					
HEMBA1001869	12.96	19.53	27.66	23.68	16.72	23.14	5.91	10.06	12.62					
HEMBA1001871	3.56	6.35	8.61	4.54	2.2	3.49	3.21	1.17	2.75					
HEMBA1001876	4.6	3.93	8.22	5.16	4.46	4.33	3.76	4.15	6.11					
HEMBA1001878	8.8	14.72	27.92	7.18	13.52	10.62	6.43	4.37	4.82					

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Table 361

HEMBA1001879	23.8	24.57	36.17	27.25	30.71	21.12	18.92	12.59	21.51					
HEMBA1001884	22.79	25.41	39.57	18.36	21.7	20.15	24.74	18.16	27.02					
HEMBA1001886	2.49	3.21	10.85	4.21	4.2	3.06	3.99	2.94	2.81					
HEMBA1001888	5.93	5.79	13.13	8.79	5.21	8.71	5.32	6.52	7.9					
HEMBA1001890	12.55	17.2	16.26	7.93	7.84	9.91	5.34	7.04	9.79	*	*	-	-	
HEMBA1001896	8.62	13.4	18.92	9.94	9.97	13.19	7.37	7.12	11.57					
HEMBA1001899	9.63	9.32	14.65	9.07	9.12	9.82	4.74	3.78	7.78					
HEMBA1001904	17.69	9.43	25.81	8.49	15.82	16.23	7.42	3.21	4					
HEMBA1001910	13.84	17.03	18.88	10.76	16.22	11.5	15.72	11.44	11.3					
HEMBA1001911	84.18	136.96	104.54	60.48	92.99	36.82	38.97	44.93	16.51		*		-	
HEMBA1001912	8.8	18.15	15.1	11.38	13.1	11.76	6.02	5.45	6.48		*		-	
HEMBA1001913	63.5	67.85	178.77	91.97	76.48	71.89	38.1	40.9	79.58					
HEMBA1001915	9.95	12.39	24.42	17.53	14.5	13	8.17	4.57	10.88					
HEMBA1001918	5.57	6.46	12.5	8.11	6.81	8.09	4.3	2.18	7.19					
HEMBA1001921	8.68	9.91	12.62	8.57	8.25	7.86	5.28	3.66	4.78		**		-	
HEMBA1001931	9.24	10.47	21.38	7.16	7.58	6.86	8.41	6.87	7.96					
HEMBA1001939	3.59	7.32	15.17	1.25	16.55	5.08	4.84	5.03	14.82					
HEMBA1001940	11.2	9.93	21.45	9.87	12.2	10.55	7.02	5.09	7.03					
HEMBA1001942	22.25	36.8	27.34	8.22	35.32	31.27	17.26	9.8	12.44		*		-	
HEMBA1001944	14.23	17.39	30.07	21.25	14.66	13.47	4.56	8.32	14.97					
HEMBA1001945	8.53	9.04	18.07	9.58	9.66	6.81	6.7	4.7	10.21					
HEMBA1001950	35.24	36.06	25.81	22.39	20.56	21.76	31.55	22.6	14.77	*		-		-
HEMBA1001951	39.37	38.17	52.67	44.58	33.39	34.05	41.69	23.81	45.03					
HEMBA1001958	3.68	3.88	9.13	1.87	2.36	1.68	2.36	1.43	3.59					
HEMBA1001960	11.92	13.79	24.84	7.91	13.38	11.06	7.97	3.56	9.09					
HEMBA1001962	10.82	11.31	28.75	9.3	13.76	9.37	10.95	7.24	13.69					
HEMBA1001964	11.99	14.1	28.18	9.47	13.95	12.22	12.21	4.77	10.5					
HEMBA1001967	33.16	31.11	63.39	22.3	13.19	20.77	8.29	10.21	24.27					
HEMBA1001979	6.77	6.74	6.61	3.38	4.61	6.79	4.27	2.37	4.75		*		-	
HEMBA1001987	6.84	5.64	7.7	5.03	3.79	3.32	4.73	5.25	2.63	*		-		
HEMBA1001991	4.14	2.8	6.6	1.78	2.7	1.18	2.19	1.73	1.57					
HEMBA1002003	3.19	3.64	8.31	2.58	2.51	1.13	4.14	2.93	2.53					
HEMBA1002005	21.43	25.67	43.64	22.86	20.88	16.44	24.76	11.27	20.55					
HEMBA1002008	15.2	19.08	39.6	14.05	18.61	13.62	20.77	11.98	21.03					
HEMBA1002018	4.58	11.59	12.53	3.51	5.86	20.49	4.43	1.81	2.74					
HEMBA1002022	29.07	36.45	75.11	52.83	42.93	48.33	30.25	25.12	55.78					
HEMBA1002029	19.99	24.25	30.34	10.7	17.32	16.65	10.55	13.15	11.59		*		-	
HEMBA1002030	11.06	12.89	19.22	8.24	7.3	5.76	8	6.82	6.24	*	*	-	-	
HEMBA1002035	3.07	17.04	7.87	2.25	5.11	2.16	4.64	3.69	6.06					
HEMBA1002037	95.17	141.19	140.82	59.83	84.82	73.74	61.45	42.2	28.14	*	*	-	-	
HEMBA1002038	11.96	19.11	18.49	6.44	9.02	6.74	4.63	2.27	2.59	*	**	-	-	
HEMBA1002039	6.42	7.41	13.48	2.37	5.91	2.48	3.27	1.37	3.16		*		-	
HEMBA1002042	3.25	8.61	11.52	6.6	6.65	6.58	7.97	0.75	4.67					
HEMBA1002043	13.24	16.58	22.47	5.13	6.87	6.08	5.01	5.72	8.43	*	*	-	-	
HEMBA1002048	25.65	31.58	36.46	5.14	12.63	17.17	11.27	12.56	24.5	*	*	-	-	
HEMBA1002049	431.22	564.03	858.02	234.02	525.06	482.28	304.41	585.23	233.29					
HEMBA1002053	66.35	61.58	114.43	104.42	98.85	104.79	56.5	40.65	69.44					
HEMBA1002055	19.16	20.77	33.11	22.38	16.8	17.16	15.07	11.5	15.77					
HEMBA1002056	5.26	6.55	10.96	2.52	2.93	4.72	5.3	2.16	5.03					
HEMBA1002061	3.02	4.19	9.86	2.45	3.45	0.92	2.37	0	1.82					
HEMBA1002080	2.59	8.96	20.11	3.27	8.34	5.7	6.09	2.76	4.82					
HEMBA1002084	7.01	3.85	10.52	5.96	3.47	4.97	2.69	1.31	2.02					
HEMBA1002085	3.68	5.88	10.92	2.9	5.24	7.31	3.65	1.95	5					
HEMBA1002092	18.94	17.76	38.17	14.49	14.47	17.01	14.19	7.25	10.23					
HEMBA1002098	8.74	16.29	15.2	3.59	8.82	8.02	9.31	14.32	5.83					
HEMBA1002100	13.69	10.18	19.02	11.56	6.49	4.52	8.34	7.69	7.11					
HEMBA1002101	12.62	14.09	31.93	14.79	12.76	11.05	16.17	8.68	13.96					
HEMBA1002102	4.18	7.54	13.28	4.1	4.71	4.56	3.77	3.14	3.09					
HEMBA1002105	5.07	7.15	15.22	5.77	3.71	9.62	4.21	1.98	2.79					
HEMBA1002107	7.22	7.4	21.27	9.53	10.18	12.18	2.67	2.93	5.58					
HEMBA1002113	5.14	7.17	14.68	10.73	7.63	8.56	6.5	2.35	7.99					
HEMBA1002119	24.1	26.96	60	38.03	31.14	26.41	31.91	16.47	21.72					
HEMBA1002125	4.31	5.62	9.66	11.65	3.83	5.15	2.02	2.4	2.97					
HEMBA1002131	2612	1876.5	3959.7	1306.5	2879.6	1519.6	1255.8	1936.4	1651.4					

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Table 362

HEMBA1002133	29.03	35.39	76.13	107.6	70.61	84.67	29.03	14.5	31.23					
HEMBA1002139	11.59	23.7	52.84	28.04	21.84	20.31	32.1	12.89	25.76					
HEMBA1002141	3.72	5.77	10.55	5.21	5.75	3.18	3.83	1.34	5.31					
HEMBA1002144	2.85	4.6	6.42	4.94	2.2	5.21	1.49	2.58	2.66					
HEMBA1002147	10.27	15.44	23.81	11.25	8.38	13.35	8.76	6.54	9.55					
HEMBA1002150	1.33	1.23	3.53	2.46	2.28	2.8	1.93	0.73	2.03					
HEMBA1002151	6.03	4.63	11.41	5.99	5.56	6.68	5.34	2.78	4.91					
HEMBA1002153	0.77	2.83	4.03	3.46	4.19	3.78	2.71	1.39	3.61					
HEMBA1002156	2.06	3.91	4.83	5.6	4.46	2.69	2.87	0.76	2.49					
HEMBA1002160	56.44	32.19	84.15	108.2	70.78	79.86	43.2	16.4	44.96					
HEMBA1002161	44.7	21.27	41.93	61.65	56.83	51.89	26.74	12.83	24.21					
HEMBA1002162	89.86	103.46	226.68	313.25	143.99	221.76	91.22	73.96	98.59					
HEMBA1002163	40.99	33.35	79.59	79.2	53.49	69.59	30.86	22.17	36.21					
HEMBA1002164	5.75	8.38	13.54	8.04	3.83	5.52	3.45	2.03	3.62					
HEMBA1002166	15.02	15.38	25.99	20.34	17.99	15.76	15	11.24	18.28		-			
HEMBA1002167	11.24	16.13	23.3	10.71	13.78	13.32	12.46	7.17	15.43					
HEMBA1002173	2.74	4.74	7.08	7.8	4.98	8.26	4.32	0.11	6.96					
HEMBA1002177	3.19	7.92	6.73	9.46	13.68	11.32	3.6	0.89	5.89	*		+		
HEMBA1002178	3.07	3.14	5.24	4.35	5.65	4.54	2.7	1.64	3.18					
HEMBA1002179	4.9	4.72	9.91	6.66	4.93	4.53	2.62	2.86	3.55					
HEMBA1002185	24.67	32.27	51.89	14.08	21.43	18.77	8.38	11.95	12.92		*		-	
HEMBA1002188	5.88	6.14	7.11	2.97	4.39	3.33	2.27	4.54	2.68	**	*	-	-	-
HEMBA1002189	69.59	81.69	157.25	233.85	141.07	152.77	75.89	48.73	66.24					
HEMBA1002191	4.08	3	7.66	6.05	7	4.24	3.01	1.76	4.2					
HEMBA1002192	5.95	7	11.91	7.01	6.79	6.52	4.64	2.39	5.33					
HEMBA1002195	4.46	6.6	10.03	6.4	6.23	6.42	6.4	2.77	4.74					
HEMBA1002196	11.48	14.42	16.69	14.62	12.56	12.05	7.65	1.78	5.06		*		-	
HEMBA1002199	17.19	29.45	44.34	8.12	15.7	10.6	4.22	6.56	8.91		*		-	
HEMBA1002204	12.36	17.29	25.36	18.54	15.65	13.06	6.95	7.55	12.67					
HEMBA1002208	4.42	3.1	8.67	2.76	2.3	3.61	1.67	2.17	2.81					
HEMBA1002212	8.54	9.41	18.06	5.8	6.49	9.16	8.07	6.31	7.72					
HEMBA1002215	3.77	4.75	11.1	3.82	3.64	4.93	3.19	2.31	3.82					
HEMBA1002217	3.21	2.97	8.05	1.88	2.5	3.26	2.77	1.7	3.42					
HEMBA1002220	40.07	58.29	38.41	33.44	37.1	26.5	27.12	21.87	26.71		*		-	
HEMBA1002226	3.86	6.37	9.01	5.94	8.12	6.13	6.11	1.94	2.28					
HEMBA1002227	29.2	48.92	80.06	21.26	24.93	28.49	9.06	21.04	35.76					
HEMBA1002229	33.53	65.16	51.1	12.99	38.46	30.19	10.92	21.02	13.32		*		-	
HEMBA1002237	5.24	7.25	13.43	6.25	5.49	6.14	5.27	3.9	7.13					
HEMBA1002239	4.63	2.53	7.61	2.56	2.45	2.52	2.39	1.83	5.54					
HEMBA1002241	106.58	86.21	101.41	191.32	99.49	119.15	95.67	52.74	66.24					
HEMBA1002253	12.22	17.16	20.51	2.71	7.33	6.42	3.87	2.39	2.33	*	**	-	-	
HEMBA1002257	7.54	10.24	15.29	4.58	6.87	7.36	4.9	4.18	3.85		*		-	
HEMBA1002259	13.5	22.26	29.8	14.68	19.62	16.23	17.99	11.27	18.91					
HEMBA1002262	15.09	23.24	29.3	18.72	15.42	11.55	9.03	9.95	14.69					
HEMBA1002265	14.18	19.86	21.44	12.15	13.48	12.48	8.23	10.18	13.41		*		-	
HEMBA1002267	27.68	15.47	50.07	10.16	19.76	26.78	8.51	9.81	8.8					
HEMBA1002270	6.74	5	13	3.57	4.76	3.79	3.06	1.88	3.1					
HEMBA1002286	3.26	3.45	8.41	1.32	1.98	2.17	2.49	0.44	3.13					
HEMBA1002290	13.88	14.35	29.79	17.54	14.92	16.25	8.98	7.54	11.64					
HEMBA1002302	2.59	3.21	9.4	1.67	2.25	2.2	2.59	2.03	2.91					
HEMBA1002304	28.75	42.22	44.71	47.37	56.93	39.52	32.89	19.02	22.8					
HEMBA1002307	11.61	12.1	29.02	16.8	17.52	14.8	7.63	7.75	11.14					
HEMBA1002316	59.64	53.59	76.81	100.13	70.41	86.41	40.44	34.11	39.43		*		-	
HEMBA1002319	5.85	6.03	12.11	6.62	5.15	5.86	4.45	4.18	4.84					
HEMBA1002320	5.15	6.41	11.19	4.43	3.26	5.68	2.72	1.07	1.82		*		-	
HEMBA1002321	26.14	32.72	45.81	15.36	15.91	12.15	25.74	14.29	26.13	*		-		
HEMBA1002328	3.49	3.33	9.66	1.53	2.94	1.89	1.67	1.15	3.51					
HEMBA1002333	14.03	17.53	33.87	10.39	17.53	10.54	14.85	12.2	18.17					
HEMBA1002337	74.1	90.11	104.64	39.01	88.83	67.57	65.51	46.31	39.48		*		-	
HEMBA1002339	7.99	5.95	12.61	11.75	8.3	7.98	3.81	2.17	4.39					
HEMBA1002341	10.07	14.65	15.74	8.32	6.89	8.79	4.57	2.09	3.76	*	**	-	-	
HEMBA1002348	59.9	42.49	67.67	22.81	39.26	47.94	42.75	47.55	14.2					
HEMBA1002349	3.79	4.77	8.57	3.9	2.41	2.17	3.1	1.47	1.4					
HEMBA1002353	16.84	19.17	38.76	16.44	19.61	18.36	31.34	14.04	19.17					

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Table 363

HEMBA1002356	36	42.3	70.07	29.6	29.36	25.6	38.93	22.92	26.48				
HEMBA1002357	5.52	13.1	13.45	6.21	11.96	5.72	6.55	2.43	6.78				
HEMBA1002360	7.18	14.99	31.64	16.74	12.78	10.39	10.06	6.73	9.23				
HEMBA1002363	7.21	6.56	15.23	7.32	10.07	12.95	6.94	4.08	5.41				
HEMBA1002365	5.13	6.37	6.27	3.06	3.21	2.92	4.54	1.5	1.04	**	*	-	-
HEMBA1002370	2.68	3.2	4.12	1.48	1.53	1.16	1.82	1.08	0.59	*	*	-	-
HEMBA1002374	7.98	8.73	12.15	4.74	5.3	4.18	4.71	3.04	5.14	*	*	-	-
HEMBA1002376	3.93	7.64	11.22	5.3	5.08	2.77	3.34	1	2.5				
HEMBA1002377	9.59	9.89	16.96	5.63	7.09	6.15	6.12	1.21	4.87		*		-
HEMBA1002380	10.33	16.4	28.08	14.11	13.73	11.4	15.31	7.9	14.99				
HEMBA1002381	4.05	9.29	15.58	7.37	6.4	6.25	6.86	1.71	6.19				
HEMBA1002384	8.47	11.56	16.49	7.99	8.37	10.32	10.3	5.34	12.08				
HEMBA1002389	11.42	20.29	29.05	5.75	14.68	8.45	8.49	15.83	6.08				
HEMBA1002396	12.69	16.26	27.27	7.41	9.5	6.56	5.14	3.17	3.81		*		-
HEMBA1002402	11.74	16.83	21.99	13.15	10.97	7.11	8.38	8.96	10.5				
HEMBA1002417	16.84	19.38	28.25	14.12	13.6	10.71	18.74	11.52	12.94				
HEMBA1002419	5.76	8.38	11.36	2.24	4.5	1.91	3.6	1.74	2.93	*	*	-	-
HEMBA1002420	19.24	23.07	51.09	26.34	25.11	18.31	20.11	12.19	18.92				
HEMBA1002421	18.39	32.76	48.68	28.36	38.24	25	28.96	7.94	14.32				
HEMBA1002423	22.61	32.68	44.06	7.09	7.86	5.55	4.56	5.5	6.54	*	*	-	-
HEMBA1002424	10.97	10.88	26.72	15.1	10.87	9.61	12.1	6.14	11.48				
HEMBA1002426	7.39	16.83	33.68	10.19	19.75	11.23	14.09	9.36	9.51				
HEMBA1002430	3.4	2.99	7.25	1.05	5.01	3.49	1.89	3.82	1.55				
HEMBA1002439	16.88	14.68	38.41	5.15	12.09	6.57	10.43	3.04	5.71				
HEMBA1002441	6.85	11.02	20	8.08	6.54	5.94	8.36	4.52	6.62				
HEMBA1002454	12.57	18.57	41.83	19.84	16.12	15.91	15.68	8.28	16.15				
HEMBA1002458	18.76	29.12	42.05	23.99	29.98	19.78	21.68	9.8	15.93				
HEMBA1002460	17.05	22.65	60.16	30.55	31.36	38.17	25.74	12.29	25.18				
HEMBA1002462	4.29	4.96	6.67	4.04	2.82	5.54	6.09	4.59	1.34				
HEMBA1002465	18.46	17.14	33.42	10.69	9.15	14.44	4.41	4.25	2.08		*		-
HEMBA1002469	5.68	18.77	19	7.83	8.55	8.09	9.48	5.61	6.29				
HEMBA1002475	4.8	4.95	7.67	3.53	3.61	2.82	2.16	0.66	3.66		*		-
HEMBA1002477	14.5	19.14	47.19	10.6	19.29	17.91	11.51	6.53	9.54				
HEMBA1002480	3.04	4.91	11.31	4.99	4.91	2.26	3.45	1.28	2.5				
HEMBA1002481	3.73	5.8	10.36	6.68	9.38	9.35	6.55	0.82	5.73				
HEMBA1002486	14.96	20.73	36.85	17.9	13.84	17.9	9.8	9.17	15.34				
HEMBA1002490	32.89	43.68	75.36	48.87	29.68	38.22	19.18	16.64	20.65				
HEMBA1002495	43.66	58.23	82.55	111.1	32.51	41.26	76.83	29.1	14.88				
HEMBA1002498	3.78	6.46	9.54	6.71	5.27	12.7	10.64	3.53	6.2				
HEMBA1002501	7.77	5.26	15.06	10.61	8.44	10.8	6.66	2.76	7.39				
HEMBA1002503	1.3	3.76	4.26	11.14	4.16	3.06	2.94	0.74	2.46				
HEMBA1002504	11.32	6.35	15.09	5.12	7.76	6.01	3.02	1.3	4.4		*		-
HEMBA1002508	5.06	9.32	4.01	3.71	7.02	5.17	4.27	2.18	3.39				
HEMBA1002513	9.71	15.43	17.71	11.5	8.94	8.42	3.65	5.7	5.29		*		-
HEMBA1002515	22.59	29.58	33.08	19.66	17.58	7.29	3.31	4.58	5.25		**		-
HEMBA1002524	2.52	5.5	6.81	5.24	5.07	5.47	3.51	2.04	6.31				
HEMBA1002536	4.86	8.27	13.28	5.54	6.86	8.78	7.76	3.44	3.36				
HEMBA1002542	14.29	22.48	34.17	23.25	22.99	20.23	26.21	13.64	24.16				
HEMBA1002544	80.29	71.81	142.33	191.63	103.72	120.69	75.35	42.62	73.64				
HEMBA1002546	16.49	22.78	27.12	14.78	15.43	17.06	9.62	3.52	9.44		*		-
HEMBA1002547	3.95	4.98	8.23	6.73	9.06	6.15	8.5	2.36	7.03				
HEMBA1002550	49.15	78.71	90.52	40.75	20.92	26.29	11.49	22.91	24.84	*	*	-	-
HEMBA1002551	21.39	26.41	43.07	27.63	15.98	20.86	15.81	13.41	19.29				
HEMBA1002552	2.51	5.57	9.92	2.51	4.26	4.71	1.72	3.19	4.1				
HEMBA1002555	22.2	20.07	42.05	23.19	22.23	22.76	15.94	12.91	13.98				
HEMBA1002558	12.09	15.97	19.47	12.44	11.51	11.85	16.99	12.78	19.34				
HEMBA1002561	5.12	5.08	10.95	9.59	4.94	7.59	3.52	2.9	5.93				
HEMBA1002562	11.02	16.11	24.74	19.26	26.78	27.85	11.51	7.07	19.83				
HEMBA1002568	196.94	317.85	248.99	300.72	297.51	250.18	199.37	60.64	136.04				
HEMBA1002569	23.5	41.31	56.08	12.56	22.81	12.46	7.29	13.02	18.03				
HEMBA1002570	30.8	40.14	52.73	26.65	25.92	32.98	19.03	21.81	22.76		*		-
HEMBA1002574	18.81	25.29	36.64	14.11	18.09	18.3	12.06	11.37	15.9				
HEMBA1002583	7.94	6.71	16.38	5.31	5.66	5.07	2.73	4.44	3.12				
HEMBA1002587	2.94	4.41	12.22	7.72	5.53	9.69	4.6	2.49	5.42				

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Table 364

HEMBA1002590	5.95	11.3	17.91	3.86	9.68	7.63	4.92	3.2	3.29				
HEMBA1002592	24.56	35.63	62.38	31.85	31.39	28.3	31.44	17.58	25.5				
HEMBA1002595	18.13	24.94	28.1	20.67	22.43	16.85	23.31	9.38	10.88				
HEMBA1002609	10.62	12.63	20.23	14.42	14.63	14.25	5.32	5.93	14.35				
HEMBA1002617	4.27	5.73	7.4	1.57	2.4	3.96	1.42	3.15	4.02				
HEMBA1002619	2.85	2.62	7.5	3.1	2.95	3.67	1.94	0.73	2.61				
HEMBA1002621	8.59	8.17	23.61	10.11	9.98	16.3	7.86	5.88	9.09				
HEMBA1002624	27.35	35.73	38.2	18.75	33.76	30.42	15.63	13.42	13.94		**		-
HEMBA1002628	9.91	18.29	22.67	1.48	9.73	6.58	2.84	2.68	1.86		*		-
HEMBA1002629	17.6	28.89	36.07	15.14	20.64	15.47	19.33	12.69	24.63				
HEMBA1002632	12.9	25.94	21.19	10.8	16.54	18.64	7.96	5.15	6.22		*		-
HEMBA1002645	10.16	17.89	28.87	12.29	14.08	14.33	9.35	8.1	11.96				
HEMBA1002651	13.26	18.44	26.72	15.43	10.74	15.26	12.68	8.84	17.98				
HEMBA1002652	38.73	48.42	65.53	46.16	37.25	33.78	28.26	20.1	36.36				
HEMBA1002659	9.03	11.88	19.16	8.75	10.05	12.88	11.02	6.8	9.75				
HEMBA1002661	5.06	3.99	9.25	2.67	2.42	2.71	2.5	0.54	3.81				
HEMBA1002666	4.98	2.76	10.31	1.02	2.15	2.47	1.95	1.39	2.97				
HEMBA1002667	66.26	92.17	95.25	40.2	49.75	38.64	17.08	15.46	18.87	*	**	-	-
HEMBA1002673	10.24	11.61	24.1	10.91	20.39	11.76	14.29	6.19	10.4				
HEMBA1002678	13.62	19.9	33.62	20.45	17.4	13.57	11.46	10.78	12.98				
HEMBA1002679	13.69	14.71	16.04	4.7	9.65	9.85	3.39	2.88	4.57	*	**	-	-
HEMBA1002688	5.6	5.12	9.48	4.59	5.44	5.04	4.69	4.1	9.84				
HEMBA1002696	59.06	73.44	43.41	32.21	38.96	30.65	22.83	22.73	43.71				
HEMBA1002703	7.17	12.58	16.11	7.07	6.09	6.51	6.44	2.28	5.09				
HEMBA1002706	6.13	6.22	16.32	2.59	4.89	3.24	4.44	2.11	3.85				
HEMBA1002712	11.08	15.22	21.38	7.53	9.92	6.72	6.23	2.15	5.09		*		-
HEMBA1002715	7.25	9.24	15.63	3.34	13.16	4.85	8.59	3.19	5.46				
HEMBA1002716	10.24	5.79	8.57	7.72	6.63	11.75	6.68	8.82	8.25				
HEMBA1002718	5.54	9.62	8.18	5.1	4.05	3.87	4.38	2.74	1.77		*		-
HEMBA1002728	12.44	14.25	13.51	6.78	9.73	5.54	5.16	3.78	4.32	*	**	-	-
HEMBA1002730	18.89	21.85	36.97	19.48	14.69	13.56	21.24	13.64	21.33				
HEMBA1002734	18.2	30.15	26.54	25.61	18.78	20.96	17.72	11.44	17.14				
HEMBA1002742	3.87	2.34	11.09	2.03	2.86	2.81	1.76	0.66	1.41				
HEMBA1002746	22.55	32.65	52.23	26.89	25.86	22.2	22.76	13.04	18.94				
HEMBA1002748	9.65	15.62	22.06	9.53	12.94	6.47	8.64	2.48	4.44				
HEMBA1002750	4.66	4.65	9.25	7.27	4.67	4.79	3.27	2.62	3.14				
HEMBA1002755	6.97	7.74	9.25	6.37	7.77	4.16	3.95	4.22	4.36		**		-
HEMBA1002759	16.7	17.27	27.62	16.79	11.68	13.5	9.91	9.05	10.68		*		-
HEMBA1002763	47.58	57.94	56.78	54.23	36.74	38.37	36.64	19.12	21.65		*		-
HEMBA1002767	8.72	14.41	17.03	5.04	11.17	4.96	8.31	3.05	8.44				
HEMBA1002768	5.52	5.94	12.79	2.88	4.3	2.49	2.51	1.17	1.65				
HEMBA1002769	17.19	27.21	15.86	8.55	10.83	3.03	6.22	1.99	5.25	*	*	-	-
HEMBA1002770	2.13	4.12	10.85	3.83	4.73	3.88	2.44	1.5	3.81				
HEMBA1002777	6.28	5.97	10	5.84	6.03	4.58	3.3	3.36	7.09				
HEMBA1002779	4.32	3.05	9.05	3.43	3.09	3.54	2.97	2.09	4.26				
HEMBA1002780	18.15	7.73	29.43	3.93	22.04	8.61	11.74	14.31	4.26				
HEMBA1002790	44.22	50.48	73.09	31.77	35.83	33.38	43.74	34.78	30.04				
HEMBA1002794	7.76	9.01	14.22	4.88	6.33	4.1	3.98	2.38	3.09		*		-
HEMBA1002798	58.19	53	86.62	94.91	76.86	71.68	49.35	25.85	43.83				
HEMBA1002801	3.51	8.44	16.4	3.59	4.66	6.72	3.9	1.17	4.1				
HEMBA1002810	3.05	9.57	15.59	8.92	5.81	6.43	5.04	3.55	5.63				
HEMBA1002816	33.54	55.39	45.57	5.42	16.08	37.06	10.38	10.74	17.79		**		-
HEMBA1002818	13.01	14.09	20.64	7.78	6.78	5.49	5.04	2.96	3.82	*	**	-	-
HEMBA1002820	27.01	29.21	56.88	35.9	30.38	30.6	30.02	21.79	27.81				
HEMBA1002826	19.2	24.63	59.75	28.13	24.2	21.9	24.8	13.89	24.13				
HEMBA1002833	63.25	54.77	137.72	30.62	26.06	40.67	37.5	33.73	24.96				
HEMBA1002850	32.24	50.44	106.97	13.72	14.84	20.17	21.65	20.43	7.04				
HEMBA1002862	2.91	4.02	13.2	2.77	4.61	2.19	2.67	1.11	1.52				
HEMBA1002863	5.54	4.99	10.17	2.83	5.36	5.71	5.41	0.6	2.81				
HEMBA1002867	12.64	16.67	40.23	22.98	17.46	25	12.79	7.67	12.95				
HEMBA1002876	33.33	40.68	56.24	16.95	25.21	41.71	19.36	18.11	7.35		*		-
HEMBA1002886	38.07	46.59	100.23	134.31	130.1	87.32	31.47	23.92	40.5				
HEMBA1002896	373.7	87.77	442.56	153.27	289.24	233.48	153.73	231.71	129.4				
HEMBA1002913	5.91	13.06	17.5	7.91	16.67	18.64	16.24	3.53	12.2				

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Table 365

HEMBA1002921	10.08	17.69	26.78	4.57	11.52	17.13	10.57	6.89	8.36				
HEMBA1002924	16.52	23.06	41.44	17.55	21.51	18.51	16.69	6.29	12.01				
HEMBA1002934	7.43	7.93	15.24	8.33	19.71	10.41	9.2	4.34	7.83				
HEMBA1002935	44.38	58.85	52.49	15.89	32.69	26.1	15.32	13.88	12.84	*	**	-	-
HEMBA1002937	2.13	5.21	6.49	6.16	3.25	2.49	3.22	1.79	2.68				
HEMBA1002939	6.4	9.23	9.9	6.39	7.51	3.18	2.69	1.8	1.53		**		-
HEMBA1002944	6.74	7.31	12.98	7.18	6.53	7.34	7.96	2.7	9.59				
HEMBA1002951	2.29	3.34	4.29	3.26	3.2	3.99	3	1.79	2.41				
HEMBA1002954	17.42	19.44	25.7	12.87	16.68	13.48	13.76	7.82	14.9				
HEMBA1002962	8.79	11.09	12.46	11.77	11.02	6.43	11.04	6.23	10.79				
HEMBA1002968	7.03	12.43	15.52	4.99	4.92	6.17	4.89	4.54	3.33		*		-
HEMBA1002970	3.97	3.94	8.85	9.45	5.39	4.2	3.04	1.94	3.66				
HEMBA1002971	46.35	65.62	65.66	55.83	32.32	29.43	18.21	22.18	16.03		**		-
HEMBA1002973	19.1	22.88	32.02	18.54	14.79	14.79	14.19	10.32	16.42				
HEMBA1002978	9.61	14.49	12.56	9.49	10.35	10.49	8.97	6.63	9.32				
HEMBA1002981	7.62	7.65	10.48	7.25	7.54	7.91	5.93	4.75	6.33				
HEMBA1002985	117.94	141.29	115.79	100.57	91.73	67.47	36.07	32.99	67.86	*	**	-	-
HEMBA1002986	1.09	4.19	2.41	1.9	4.92	2.49	2.41	1.95	2.68				
HEMBA1002988	6.76	12.45	10.76	6.53	13.58	5.88	8.35	4.66	5.88				
HEMBA1002992	6.35	10.06	11.88	10.23	8.86	4.79	4.31	25.89	6.31				
HEMBA1002995	4.3	8.89	7.73	5.51	4.55	4.85	3.59	3.01	4.66				
HEMBA1002997	107.63	114.87	183.64	177.35	156.59	181.54	82.75	91.36	112.69				
HEMBA1002999	53.34	68.01	72.24	37.39	47.67	41.25	62.98	43.59	63.81	*		-	
HEMBA1003004	3.64	4.33	7.42	2.58	3.67	3.65	3	1.57	3.06				
HEMBA1003006	4.28	5.05	7.7	1.79	6.77	4.05	4.37	2.61	3.52				
HEMBA1003008	27.15	36.55	38.8	26.92	32.63	23.56	33.58	25.15	30.26				
HEMBA1003021	5.81	12.5	13.45	11.13	6.12	5.84	7.32	6.94	6.02				
HEMBA1003027	18.79	26.5	31.66	21.25	18.71	19.18	16.11	14.87	19.02				
HEMBA1003029	19.01	29.05	31.26	23.38	17.83	18.43	16.34	15.3	19.09				
HEMBA1003031	23.27	32.76	35.52	18.12	20.06	19.05	22.57	22.89	27.58	*		-	
HEMBA1003032	10.51	18.48	23.57	10.46	10.87	8.93	13.71	10.94	13.4				
HEMBA1003033	3.28	3.5	9.21	2.58	2.99	3.45	2.32	2.32	3.69				
HEMBA1003034	32.22	43.17	44.46	25.3	23.69	20.88	30.34	23.98	27.83	*	*	-	-
HEMBA1003035	6.89	6.34	9.49	7.01	5.99	4.57	6.73	1.95	2.1				
HEMBA1003037	3.15	4.76	8.43	6.95	3.5	6.33	1.17	2.19	4.48				
HEMBA1003041	5.81	4.77	6.88	6.46	7.11	3.98	3.65	3.49	6.68				
HEMBA1003045	3.59	5.57	7.67	2.55	3.97	2.74	1.99	1	3.62				
HEMBA1003047	2.75	3.6	7.28	2.24	3.39	2.22	1.7	2.72	4.34				
HEMBA1003048	7.72	9.91	17.38	5.16	6.98	5.24	7.18	5.24	6.81				
HEMBA1003064	7.42	7.15	11.39	6.45	5.86	2.65	4.01	3.53	5.26		*		-
HEMBA1003067	3.5	4.14	10.69	1.88	3.75	2.7	1.84	2.09	2.56				
HEMBA1003071	4.3	6.5	8.99	2.07	3.4	1.57	3.49	0.09	2.65	*		-	
HEMBA1003072	22.65	30.56	72.67	40.85	32.84	36.51	17.64	22.4	33.19				
HEMBA1003076	10.41	7.13	12.54	12.87	5.59	14.57	5.56	3.38	7.99				
HEMBA1003077	57.77	42.56	38.04	15.22	22.46	42.9	9.06	21.41	25.7		*		-
HEMBA1003078	5.9	3.99	8.44	5.05	5.47	3.08	3.19	1.13	4				
HEMBA1003079	2.67	1.28	11.95	1.19	1.44	0	1.26	1.15	2.5				
HEMBA1003083	17.29	19.57	26.48	12.28	16.41	11.4	17.96	11.77	14.23				
HEMBA1003086	66.37	81.42	75.05	81.77	61.06	81.5	45.88	45.17	41.59		**		-
HEMBA1003090	27.88	31.13	33.36	17.15	38.66	20.27	13.44	24.06	7.13		*		-
HEMBA1003094	7.62	15.14	35.58	19.46	14.45	10.58	6.94	6.32	13.5				
HEMBA1003096	5.15	5.97	7.99	4.67	5.25	3.62	2.44	1.23	5.06				
HEMBA1003098	51.24	56.94	73.88	44.19	37.83	35.41	49.21	42.96	49.32	*		-	
HEMBA1003101	55.72	62.33	39.5	28.21	27.13	36.8	19.35	33.07	15.18	*	*	-	-
HEMBA1003109	21.19	29.16	38.82	18.38	20.48	14.86	17.89	17.36	21.07				
HEMBA1003114	16.2	22.18	27.85	11.32	13.05	11.32	15.03	12.24	12.98	*		-	
HEMBA1003117	4.55	5.29	16.23	3.16	6.98	2.06	3.55	1.47	2.05				
HEMBA1003120	26.44	23.65	42.74	11.15	27.45	17.66	13.62	6.31	12.11		*		-
HEMBA1003129	13.18	14.01	38.23	23.62	19.83	17.41	9	7.3	18.68				
HEMBA1003133	18.25	22.53	34.22	24.55	19.61	15.34	21.94	16.17	21.16				
HEMBA1003136	16.39	19.51	25.59	18.11	18.16	15.75	14.64	13.22	14.96				
HEMBA1003142	14.56	16.27	15.48	9.65	8.16	8.79	8.14	5.26	6.82	**	**	-	-
HEMBA1003148	16.81	26.84	29.42	16.45	16.92	11.14	21.43	11.51	11.59				
HEMBA1003151	8.82	10.43	18.65	5.42	8.75	3.56	10.89	7.34	8.14				

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Table 366

HEMBA1003152	4.25	6.9	16.54	3.43	9.18	3.49	6.82	2.75	2.37				
HEMBA1003157	16.47	20.65	36.14	14.57	15.21	12.8	18.89	12.37	10.25				
HEMBA1003166	6.07	8.14	15.45	9.26	7.78	7.15	6.88	3	7.14				
HEMBA1003171	4.76	6.01	1.83	0.22	9.4	0.95	4.99	3.3	4.74				
HEMBA1003175	9.06	9.36	15.39	5.94	5.41	4.09	8.31	5.54	6.76	*		-	
HEMBA1003179	11.74	19.14	23.08	11.43	19.69	16.88	15.24	11.13	8.75				
HEMBA1003186	32.34	34.21	53.13	30.02	30.6	23.62	32.72	27.67	23.79				
HEMBA1003196	4.93	5.75	11.29	1.52	4.36	1.61	2.88	1.66	1.27				
HEMBA1003197	11.79	16.34	26.33	10.88	17.37	11.43	13.65	9.71	13.56				
HEMBA1003199	23.1	49.93	40.51	25.63	28.94	20.25	30.98	8.01	23.38				
HEMBA1003202	23.9	28.7	33.49	4.92	13.85	16.67	6.88	7.46	15.28	*	**	-	-
HEMBA1003204	4.47	10.56	14.07	5.38	6.97	3.66	4.1	2.93	5.45				
HEMBA1003210	26.93	30.85	39.03	16.12	18.97	10.78	20.75	18.2	19.07	*	*	-	-
HEMBA1003212	25.47	38.89	40.06	19.34	20.63	15.78	34.72	24.84	21.07	*		-	
HEMBA1003218	4.32	4.85	11.19	2.63	4.58	1.07	3.74	6.58	2.3				
HEMBA1003220	35.02	49.9	56.61	20.36	27.56	20.54	37.25	33.59	30.02	*		-	
HEMBA1003222	6.38	11.47	27.57	6.14	9.88	5.85	9.63	5.71	6.41				
HEMBA1003225	1.99	5.89	11.4	3.67	2.98	2	2.78	0.36	1.82				
HEMBA1003229	4.11	5.35	10.53	5.06	6.91	5.05	3.62	3.37	4.28				
HEMBA1003230	19	22.89	41.86	21.05	18.18	18.78	15.9	9.68	15.54				
HEMBA1003235	6.36	6.82	18.89	3.6	5.78	3.31	5.14	2.94	2.76				
HEMBA1003236	28.57	38.02	51.11	22.25	24.92	17.63	25.41	23	19.94				
HEMBA1003250	3.88	5.03	10.29	3.12	4.49	3.35	3.78	2.8	3.87				
HEMBA1003252	10.38	11.26	18.86	6.09	9.53	8.62	8.03	4.87	3.9				
HEMBA1003257	4.81	5.23	14.11	3.29	4.4	2.15	4.08	0.86	2.62				
HEMBA1003268	4.15	9.87	10.08	10.51	3.68	3.28	8.7	2.22	2.32				
HEMBA1003273	11.8	16.03	28.72	15.07	19.11	17.4	12.91	12.48	21.18				
HEMBA1003276	149.48	149.2	143.91	64.58	44.3	74.17	103.96	79.83	39.01	**	*	-	-
HEMBA1003277	46.25	23.14	67.56	22.07	19.01	38.9	14.72	11.37	3.34				
HEMBA1003278	4.71	4.24	12.6	4.3	4.28	2.48	2.75	2.48	1.06				
HEMBA1003280	129.77	109.77	149.42	22.66	42.91	45.72	29.75	44.29	19.43	**	**	-	-
HEMBA1003281	66.35	33.44	113.06	20.36	31.97	38.12	40.97	35.41	13.12				
HEMBA1003284	4.17	19.37	13.16	7.85	6.12	2.69	7.14	1.71	3.34				
HEMBA1003286	19.63	12.62	36.72	8.93	14.12	12.7	52.4	15.77	35.62				
HEMBA1003291	72.44	65.02	121.3	168.07	81.81	87.09	38.11	45.46	43.73				
HEMBA1003294	2.81	2.31	6.5	6.68	2.5	2.72	2.16	1.36	1.58				
HEMBA1003296	44.35	42.6	76.86	89.38	53.17	64.95	32.4	28.59	38.37				
HEMBA1003304	9.89	11.83	11.34	8.37	7.94	10.02	7.8	7.09	8.26		**		-
HEMBA1003306	13.02	19.68	19.63	24.93	17.19	18.48	10.47	8.08	13.83				
HEMBA1003309	1.78	3.09	6.44	4.38	2.65	4.86	2.49	0.95	2.26				
HEMBA1003314	2.38	3.32	2.13	4.26	4.38	3.35	2.15	1.3	2.04	*		+	
HEMBA1003315	4.7	9	9.09	4.13	2.95	4.64	2.23	3.29	3.07		*		-
HEMBA1003322	21.51	21.29	36.71	38.62	23.41	31.81	14.65	15.44	16.23				
HEMBA1003326	6.02	5.69	11.31	6.59	5.79	5.51	2.11	1.05	2.65		*		-
HEMBA1003327	7.54	6.06	15.43	8.47	7.53	8.8	4.99	4.52	3.75				
HEMBA1003328	105.65	106.38	147.91	165.04	127.51	111.83	74.7	76.39	78.34		*		-
HEMBA1003330	6.01	12.33	12.91	7.65	8.96	7.41	6.19	2.7	6.56				
HEMBA1003348	3.04	4.46	6.33	4.48	9.58	12.27	5.11	0.11	2.09				
HEMBA1003369	4.61	6.54	9.12	7.83	6.84	2.91	5.15	1.7	5.2				
HEMBA1003370	3.59	5.98	8.58	5.67	3.43	4.27	2.86	5.19	3.68				
HEMBA1003373	11.8	17.95	18.19	5.05	9.3	7.7	3.82	6.22	4.16	*	**	-	-
HEMBA1003376	3.97	3.38	4.86	3.82	1.97	2.14	1.54	0.79	1.25		**		-
HEMBA1003380	1.93	2.67	5.1	1.31	0.26	1.37	0.83	1.72	0.69				
HEMBA1003384	26.49	38.34	57.87	29.22	29.1	27.24	18.27	17.42	21.24				
HEMBA1003387	16.13	19.1	24.1	17.73	14.37	13.92	9.34	7.52	11.3		*		-
HEMBA1003392	2.68	3.97	8.74	2.76	4.49	2.32	2.44	0.39	3.04				
HEMBA1003395	2.69	3.42	9.32	1.54	4.93	3.86	3.02	1.02	1.64				
HEMBA1003399	20.63	29.8	52.54	29.45	22.45	24.07	12.86	13.2	21.21				
HEMBA1003400	3.56	5.58	6.33	3.88	4.46	4.23	1.87	2.25	1.87		*		-
HEMBA1003402	38.86	90.8	85.59	22.6	36.87	47.3	19.41	16.83	28.09		*		-
HEMBA1003403	4.18	3.19	7.45	2.51	2.47	2.16	1.4	2.51	3.27				
HEMBA1003408	25.83	33.63	38.04	42.18	33.38	41.52	23.7	19.86	28.4				
HEMBA1003412	5.21	6.25	13.71	2.82	5	4.22	2.53	1.53	2.45				
HEMBA1003417	21.02	35.52	34.24	13.8	14.17	10.79	5.28	6.88	9.43	*	**	-	-

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Table 367

HEMBA1003418	9.46	10.25	16.29	13.88	11.67	7.88	6.52	7.48	6.95				
HEMBA1003420	15.13	21.37	34.54	8.98	7.12	8.99	3.93	4.32	8.36		*		-
HEMBA1003425	3.65	4.02	7.55	3.03	3.24	2.46	1.29	1.12	2.83				
HEMBA1003433	12.41	15.45	35.09	18.37	16.85	15.26	10.85	5.12	17.58				
HEMBA1003440	22.95	34.38	33.51	20.78	28.45	21.36	23.78	22.34	28.46				
HEMBA1003442	12.86	16.85	24.45	11.09	13.33	10.29	12.08	9.47	11.31				
HEMBA1003447	27.49	33.89	33.23	17.4	23.73	18.49	24	17.15	19.81	*	*	-	-
HEMBA1003453	4.92	6.64	13.34	4.01	5.69	5.13	2.36	4.48	3.86				
HEMBA1003461	31.42	55.4	52.29	25.16	39.67	29.85	35.26	26.74	37.73				
HEMBA1003463	20.03	30.11	90.85	47.21	1.41	0.3	30.58	24.08	33.93				
HEMBA1003465	4.42	6.66	9.68	7.8	5.17	6.44	3.4	2.84	6.1				
HEMBA1003480	8.18	9.01	15.32	7.58	7.38	7.85	10.22	6.26	8.1				
HEMBA1003485	8.87	6.95	9.95	4.15	3.42	4.03	5.45	1.61	3.1	**	*	-	-
HEMBA1003487	40.56	64.18	72.24	34.53	33.37	41.02	45.43	44.42	46.48				
HEMBA1003492	47.07	69.63	47.91	15.87	60.76	43.2	54.01	24.37	34.94				
HEMBA1003494	8.97	13.82	17.09	5.4	7.03	7.86	9.14	5.83	9.54				
HEMBA1003497	27.59	34.3	36.93	14.93	24.2	20.37	27.68	19.83	25.35	*		-	
HEMBA1003503	17.58	24.95	1.06	0.82	1.26	0.04	6.53	10.32	21.23				
HEMBA1003511	10.13	12.6	23.58	12.03	11.2	10.45	9.65	8.73	14.36				
HEMBA1003528	10.75	13.6	9.55	5.22	4.34	5.54	2.88	3.04	2.97	**	**	-	-
HEMBA1003530	6.02	6.59	12.41	4.68	4.85	4.75	5.24	2.55	3.96				
HEMBA1003531	12.73	22.2	30.65	9.86	14.37	9.03	13.96	8.06	18.14				
HEMBA1003532	13.65	14.91	22.65	8.4	21.22	7.2	8.43	8.83	11.91				
HEMBA1003538	10.23	12.68	27.62	8.9	13.63	10.34	9.68	5.53	8.3				
HEMBA1003545	4.35	9.29	13.49	7.12	6.86	6.1	7.44	2.65	6.35				
HEMBA1003546	6.53	3.47	17.38	20.26	8.26	12.59	2.96	5.15	4.61				
HEMBA1003548	2.71	6.58	8.78	3.2	9.19	3.14	6.24	4.03	2.98				
HEMBA1003553	4	4.81	7.29	3.53	3.84	2.73	2.82	2.01	2.64		*		-
HEMBA1003555	8.02	14.32	16.54	7.4	9.1	7.1	7.78	7.09	7.03				
HEMBA1003556	5	8.35	8.92	2.85	4.91	3.37	2.9	2.25	2.94		*		-
HEMBA1003550	11.54	14.47	20.06	8.38	13.16	7.52	7.48	5.19	5.3		*		-
HEMBA1003565	12.47	6.48	14.4	4.78	7.63	5.19	7.77	3.47	4.1				
HEMBA1003558	167.82	373.84	257.14	82.85	193.26	96.08	64.68	26.85	13.07		*		-
HEMBA1003569	19.02	23.29	63.64	40.15	29.03	28.36	20	16.6	26.95				
HEMBA1003571	8.12	11.43	9.83	5.26	10.52	5.78	8.95	5.27	5.01				
HEMBA1003578	22.13	20.38	39.63	17.94	15.09	12.56	17.53	15.68	17.94				
HEMBA1003580	18.63	22.77	31.1	30.35	20	21.57	12.72	8.11	11.25		*		-
HEMBA1003581	4.54	7.44	11.51	2.94	2.83	4.01	3.4	1.33	1.8				
HEMBA1003591	9.77	30.24	25.57	6.75	16.55	5.72	11.87	5.17	9.69				
HEMBA1003595	11.6	18.67	39.48	13.28	20.4	12.94	13.52	5.6	8.35				
HEMBA1003597	34.44	63.26	65.19	37.08	35.21	30.06	23.33	8.38	16.41		*		-
HEMBA1003598	2.25	2.74	3.02	2.41	2.07	1.24	1.39	0.6	1.38		*		-
HEMBA1003600	21.91	26.66	48.26	21.72	21.86	19.48	19.9	18.88	27.46				
HEMBA1003602	5.44	4.97	13.36	4.53	6.21	5.48	3.61	3.19	3.61				
HEMBA1003604	4.52	2.99	9.05	3.91	3.29	1.56	2.58	2.5	3.04				
HEMBA1003610	13.16	15.85	27.61	10.3	9.81	5.68	10.32	8.77	8.07				
HEMBA1003615	14.12	19.51	37.31	8.32	15.31	10.64	25.53	7.2	9.53				
HEMBA1003617	2.15	10.76	12.38	1.63	5.11	1.57	4.87	0.26	2.23				
HEMBA1003620	1.75	4.53	12.78	1.34	3.78	1.52	1.5	0.27	0.68				
HEMBA1003621	12.05	16.03	37.29	21.96	16.06	15.37	10.98	5.36	14.36				
HEMBA1003622	7.66	5.59	10	3.27	5.47	4.78	6.97	4.55	2.99				
HEMBA1003630	43.11	47.17	86.26	32.33	46.01	44.24	29.63	21.05	20.55				
HEMBA1003637	920.66	472.86	680.3	365.52	904.5	411.7	621.11	976.32	238.58				
HEMBA1003640	62.65	69.86	125.99	45.58	48.68	42	65.31	45.48	45.21				
HEMBA1003645	15.97	22.75	34.7	19.9	17.55	14.87	21.4	9.64	18.1				
HEMBA1003646	6.76	13.27	28.86	11.35	10.28	4.41	12.2	6.62	10.03				
HEMBA1003647	68.54	91.82	142.01	91.35	74.78	80.66	83.06	37.92	60.33				
HEMBA1003656	41.62	46.94	78.5	39.66	28.08	37.31	18.6	12.53	17.55		*		-
HEMBA1003662	9.43	10.68	20.41	19.54	13.88	13.03	9.65	4.93	11.88				
HEMBA1003666	8.44	8.9	21.02	18.11	19.64	14.87	11.75	6.74	12.93				
HEMBA1003667	27	32.49	46.33	29.7	40.13	34.43	25.82	21.77	25.87				
HEMBA1003670	16.71	15.12	35.71	10.11	19.12	14.79	10.97	18.94	10.06				
HEMBA1003674	3.06	3.93	11.38	12.14	7.69	5.61	4.08	1.48	5.42				
HEMBA1003677	3.52	4.3	9.92	2.94	5.26	2.08	4.03	0.72	1.84				

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Table 368

HEMBA1003679	15.99	25.43	34.72	23.29	23.03	14.07	32.67	15.26	20.68					
HEMBA1003680	2.36	1.32	3.39	2.39	1.66	4.26	2	1.23	1.59					
HEMBA1003684	27.44	32.04	37.17	24.58	15.64	21.48	12.03	9.61	13.69	*	**	-	-	
HEMBA1003690	26.36	32.22	54.74	28.94	29.04	32.33	34.36	26.69	39.53					
HEMBA1003692	6.49	10.11	9.34	7.04	5.15	6.04	7.51	6.23	5.84					
HEMBA1003702	8.56	9.3	12.43	12.4	14.68	13.17	6.17	5.02	7.69					
HEMBA1003711	8.11	10.45	15.16	11.96	9.29	6.3	7.03	5.46	7.91					
HEMBA1003714	6.44	11.03	12.83	2.97	13.46	9.98	7.86	7.19	9.67					
HEMBA1003715	14.81	13.59	14.56	12.43	13.78	10.5	10.14	8.94	12.29		*		-	
HEMBA1003717	42.45	55.77	82.27	41.74	41.39	40.14	43.46	40.44	41.87					
HEMBA1003720	6.21	6.28	13.24	9.93	12.72	5.69	6.86	5.05	6.12					
HEMBA1003725	3.95	3.77	7.26	6.08	3.65	3.36	2.76	2.23	2.52					
HEMBA1003728	4.28	12.26	8.88	10.99	2.88	4.38	6.4	1.69	3.67					
HEMBA1003729	12.13	13.18	16.13	8.92	13.67	11.13	18.08	6.56	14.8					
HEMBA1003732	30.17	53.31	40.17	33.85	38.01	30.07	19.05	11.75	17.73		*		-	
HEMBA1003733	3.45	4.52	4.35	2.89	6.7	2.94	3.18	1.76	2.64		*		-	
HEMBA1003742	9.01	9.99	10.98	9.56	10.71	5.69	9.3	5.6	9.68					
HEMBA1003743	9.87	14.77	20.42	19.53	13.74	11.37	9.02	7.5	9.36					
HEMBA1003758	14.27	20.31	26.23	15.6	15.1	13.01	12.22	13.09	13.08					
HEMBA1003760	19.21	17.1	29.51	6.01	14.54	12.36	3.4	6.9	5.12		*		-	
HEMBA1003764	14.01	17.88	25.76	13.37	20.5	16.53	15.36	15.5	19.31					
HEMBA1003769	38.51	54.43	53.66	30.93	34.09	32.37	42.08	31.8	46.8	*		-		
HEMBA1003773	6.19	9.28	8.37	4.69	7.62	4.92	2.95	1.6	4.58		*		-	
HEMBA1003783	2.33	2.73	7.18	6	7.98	9.31	5.24	2.04	3.66					
HEMBA1003784	24.68	20.11	23.17	22.69	20.46	14.65	16.36	8.3	11.94		*		-	
HEMBA1003794	35.77	59.53	74.01	32.36	32.73	29.52	23.99	30.47	35.64					
HEMBA1003799	28.51	43.08	44.43	24.39	25.46	22.11	20.76	21.74	26.31	*	*	-	-	
HEMBA1003803	6.9	7.98	12.5	2.71	3.98	5.61	1.91	2.94	2.14		*		-	
HEMBA1003804	12.17	15.5	24.58	5.01	10.25	5.91	7.51	11.06	8.61					
HEMBA1003805	15.63	21.11	29.95	13.7	15.15	11.89	15.1	12.06	15.76					
HEMBA1003807	12.24	15.49	18.72	15.37	14.25	10.11	18.36	12.3	19.08					
HEMBA1003810	4.78	6.92	11.21	4.53	9.91	7.45	6.79	2.53	4.42					
HEMBA1003827	10.51	13.97	18.38	12.97	15	8.61	18.16	7.58	9.11					
HEMBA1003836	4.91	7.17	10.85	4.73	8.8	6.53	3.27	4.61	5.48					
HEMBA1003838	48.74	66.87	76.01	40.91	58.53	48.34	31.6	26.6	30.51		*		-	
HEMBA1003843	23.09	39.55	55.11	24.97	26.61	27.21	27.17	12.95	30.84					
HEMBA1003846	18.74	19.56	28.45	26.4	19.75	21.25	14.77	12.94	15.9					
HEMBA1003856	31.17	48.34	48.82	28.74	30.87	25.87	49.83	42.07	42.91					
HEMBA1003857	3.66	4.84	10.52	2.38	4.43	1.85	3.66	2.4	2.28					
HEMBA1003864	24.35	38.16	29.59	24.03	32.07	18.61	15.17	4.79	6.89		*		-	
HEMBA1003866	15.55	24.7	24.92	21.6	24.17	13.88	22.15	14.95	14.16					
HEMBA1003868	3.42	4.24	4.55	5.4	4.56	2.52	1.88	2.32	3.07		*		-	
HEMBA1003879	54.55	71.41	99.07	52.85	60.23	59.91	38.15	32.08	50.85					
HEMBA1003880	26.75	40.67	50.47	32.31	30.57	23.71	28.74	17.94	31.69					
HEMBA1003884	3.51	2.7	10.4	2.34	3.19	1.65	5.36	1.65	2.02					
HEMBA1003885	15.83	16.07	23.65	9.67	12.61	9.91	13.22	10.04	13.72	*		-		
HEMBA1003887	8.92	10.53	15.63	3.65	12.51	2.64	7.43	4.94	3.2					
HEMBA1003890	5.77	11.6	13.5	3.76	5.14	4.95	4.38	2.61	3.42		*		-	
HEMBA1003893	2.5	2.24	6.97	3.71	6.34	3.91	2.06	0.55	2.76					
HEMBA1003896	13.16	13.74	38.07	17.77	20.7	14.83	10.45	11	13.75					
HEMBA1003902	6.09	5.71	13.87	4.58	5.68	4.39	3.52	2.56	5.08					
HEMBA1003904	41	55.7	67.32	43.67	30.73	35.35	31.08	26.57	32.22		*		-	
HEMBA1003908	27.42	42.25	49.6	27.37	22.92	19.91	28.26	21.38	25.22					
HEMBA1003926	35.54	56.96	89.19	56.48	59.31	44	48.79	37.72	50.83					
HEMBA1003937	14.37	14.68	20.38	10.43	17.34	12.15	14.47	8.13	15.59					
HEMBA1003939	3.4	3.02	10.99	1.88	5.36	0.25	1.12	0.35	2.25					
HEMBA1003940	6.76	11.65	10.45	4.59	10.56	5.86	9.9	2.16	3.94					
HEMBA1003941	31.48	46.87	93.42	56.75	59.75	51.31	23.68	24.05	38.11					
HEMBA1003942	3.19	4.4	9.44	4.64	4.07	4.72	1.95	2.11	3.24					
HEMBA1003945	59.01	80.97	80.84	37.7	37.04	46.98	37.87	33.83	28.54	*	**	-	-	
HEMBA1003949	12.02	16.53	20.22	10.36	8.89	9.69	11.57	6.85	10.8					
HEMBA1003950	27.53	47.63	43.7	25.53	28.11	14.15	20.64	11.67	12.95		*		-	
HEMBA1003953	10.33	12.12	25.01	8.15	9.43	6.53	13.65	9.93	7.98					
HEMBA1003958	4.65	6.88	15.41	6.73	7.93	3.72	5.9	3.43	4.74					

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Table 369

HEMBA1003959	14.89	19.53	30.66	18.5	16.34	12.43	19.48	10.78	14.94					
HEMBA1003960	6.1	5.31	11.07	8.55	9.98	6.62	4.38	4.38	3.84					
HEMBA1003966	4.32	4.36	6.33	4.53	3.74	1.94	2.49	2.11	0.85		*		-	
HEMBA1003967	11.38	13.34	19.36	11.07	6.9	6.77	8.93	7.19	5.9		*		-	
HEMBA1003968	52.83	102.28	87.2	14.25	26.41	16.31	15.76	9.02	11.36	*	**	-	-	
HEMBA1003974	4.37	4.4	7.25	2.02	4.53	1.13	3.82	0.89	2.56					
HEMBA1003976	15.15	20.18	27.02	12.74	18.84	11.73	18.38	14.83	18					
HEMBA1003977	8.76	9.42	22.28	9.64	11.17	3.97	8.14	5.18	9.28					
HEMBA1003978	9.01	16.51	20.07	10.86	6.71	7.75	11.84	5.73	13.48					
HEMBA1003981	68.06	77.17	117.23	62.61	51.44	47.41	51.47	46.06	74.31					
HEMBA1003982	5.4	13.31	18.21	3.94	11.62	6.14	3.92	4.82	3.97					
HEMBA1003985	7.59	8.14	15.01	6.55	7.27	6.74	5.12	5.29	7.02					
HEMBA1003987	10.14	14.01	20.78	6.87	9.2	5.37	6.58	6.5	8.96					
HEMBA1003989	10.11	15.44	20.52	5.53	5.4	4.86	8.66	4.07	5.03	*	*	-	-	
HEMBA1004000	2.93	4.96	11.45	2.25	2.97	1.76	2.52	0.75	2.54					
HEMBA1004006	18.54	20.18	42.2	18.19	19.39	15.33	18.84	12.3	17.01					
HEMBA1004007	19.65	39.73	40.28	26.62	20.72	17.41	38.95	21.37	27.19					
HEMBA1004010	67.05	91.68	2.46	0.19	0.95	0.35	50.08	44.9	72.79					
HEMBA1004011	10.54	11.89	17.43	5.17	7.46	5.81	5.72	5.31	4.01	*	*	-	-	
HEMBA1004012	20.42	22.3	36.75	7.27	17.23	8.75	11.84	7.16	6.96		*		-	
HEMBA1004015	4.26	3.69	8.92	3.2	3.73	2.56	1.97	1.37	3.1					
HEMBA1004024	7.24	8.25	20.14	4.09	6.96	4.29	7.49	2.93	4.36					
HEMBA1004029	3.05	5.65	11.19	0.74	1.77	1.68	2.55	0.21	0.47					
HEMBA1004038	30.88	38.16	65.02	18.09	23.34	18.57	34.1	18.52	13.77					
HEMBA1004042	0.37	2.38	5.48	0.32	1.77	1.14	0.62	0	0.22					
HEMBA1004045	20.4	33.53	50.23	28.78	29.43	29.29	14.02	11.2	16.1					
HEMBA1004048	37.85	38.8	52.99	50.26	40.74	37.18	34.52	20.41	13.02					
HEMBA1004049	21.46	22.41	47.43	24.15	22.42	24.41	19.84	20.47	15.98					
HEMBA1004051	9.9	8.46	21.25	12.84	10.63	10.43	12.39	7.87	8.34					
HEMBA1004053	15.29	25.2	37.82	19.98	13.35	13.99	21.18	11.93	18.89					
HEMBA1004055	5.25	11.05	5.64	0.16	1.02	0	9.11	3.17	5.22	*		-		
HEMBA1004056	2.41	5.85	10.01	3.45	3.17	2.37	4.07	0.71	2.14					
HEMBA1004060	6.43	8.34	15.71	14.49	7.75	6	14.41	5.93	6.72					
HEMBA1004061	7.43	8.52	15.21	11.54	9.65	13.29	5.83	3.71	5.22					
HEMBA1004067	8.97	11.51	14.78	16.09	9.22	11.3	7.43	5.81	9.07					
HEMBA1004071	2.92	2.4	5.93	4.14	2.31	3.09	3.1	0.97	2.2					
HEMBA1004074	126.78	177.45	131.41	229.36	160.88	89.6	187.87	113.1	134.85					
HEMBA1004078	20.55	20.84	34.63	28.09	31.27	21.15	16.53	16.06	27.35					
HEMBA1004085	20.65	31.8	30.03	32.27	21.47	13.85	11.87	12.81	9.59		*		-	
HEMBA1004086	2.06	3.76	5.23	2.03	3.33	2.95	2.57	0.6	1.89					
HEMBA1004097	1.94	3.31	1.59	1.13	4.7	3.06	2.83	1.2	1.23					
HEMBA1004100	14.77	24.96	29.01	20.87	18.7	13.96	10.94	12.24	15.57					
HEMBA1004103	7.32	13.02	15.94	12.18	10.65	9.17	7.19	6.37	7.49					
HEMBA1004110	19.03	26.3	37.33	22.14	20.14	20.02	18.64	15.91	19.14					
HEMBA1004111	24.42	41.97	41.29	22.57	21.56	20.91	28.72	16.68	19.6					
HEMBA1004124	10.47	10.61	15.29	11.7	10.51	11.56	7.45	6.39	9.02					
HEMBA1004130	6.32	9.6	13.12	7.07	7.66	3.98	10.02	6.52	8.94					
HEMBA1004131	11.62	15.68	22.49	12.3	15.58	10.2	7.69	8.91	12.88					
HEMBA1004132	1.7	3.66	8.07	2.75	4.82	2.5	5.8	1.43	6.28					
HEMBA1004133	61.09	100.97	106.22	48.94	25.58	18.64	11.83	36.24	13.37	*	*	-	-	
HEMBA1004138	8.15	8.84	9.84	8.72	6.31	5.94	4.18	4.48	5.03		**		-	
HEMBA1004143	6.39	11.32	13.28	4.24	5.74	4.33	4.63	4.09	3.58		*		-	
HEMBA1004146	12.23	19.23	24.6	16.14	12.69	10.61	14.04	14.11	16.75					
HEMBA1004148	5.02	6.85	14.92	7.36	6.63	8.78	2.34	5.06	6.01					
HEMBA1004149	13.01	27.48	21.59	12.24	21.36	25.46	6.33	6.45	12.24					
HEMBA1004150	162.3	225.69	242.62	246.24	265.35	201.29	161.22	151.68	209.57					
HEMBA1004154	54.95	73.81	77.08	67.59	61.25	43.45	53.14	36.47	45.58		*		-	
HEMBA1004164	27.89	39.95	75.25	53.13	38	41.78	27.04	21.48	32.66					
HEMBA1004168	27.29	41.16	48.5	30.28	31.63	25.87	20.87	19.25	25.4					
HEMBA1004199	11.53	17.04	30.46	12.77	16.45	14.72	15.81	10.26	14.34					
HEMBA1004200	10.21	15.6	23.4	12.76	12.18	11.22	9.51	9.03	10.57					
HEMBA1004201	27.51	39.39	51.71	29.35	27.61	28.68	24.64	21.71	24.17					
HEMBA1004202	18.3	30.46	37.1	17.92	20.38	16.33	20.83	15.59	21.86					
HEMBA1004203	11.35	16.48	25.18	12.27	10.37	8.08	12.69	8.41	9.37					

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Table 370

HEMBA1004207	5.23	7	7.18	5.06	6.93	4.27	6.27	2.78	3.75				
HEMBA1004210	4.96	5.53	8.99	5.1	8.24	7.88	8.78	4.25	6.82				
HEMBA1004225	11.76	16.11	15.08	1.96	9.21	5.85	1.74	2.95	4.57	*	**	-	-
HEMBA1004227	5.13	5	14.56	6.73	5.83	3.8	3.56	2.92	3.47				
HEMBA1004235	55.87	67.36	100.86	60.82	63.74	64.98	56.93	44.28	61.25				
HEMBA1004237	63.06	67.44	67.86	54.44	56.68	54.92	61.37	42.55	49.6	**		-	
HEMBA1004238	5.4	9.74	19.37	3.19	7.79	5.08	4.55	3.62	5.8				
HEMBA1004241	58.53	94.19	86.84	45.42	61.25	30.71	41.3	31.18	35.09		*		-
HEMBA1004242	95.96	94.64	132.52	129.29	124.32	88.47	86.26	40.26	43.03				
HEMBA1004243	7.18	9.59	11.11	5.01	7.55	7.79	4.07	6.19	8.9				
HEMBA1004246	3.92	5.45	6.92	3.64	1.73	7.61	2.23	1.7	3.01		*		-
HEMBA1004247	36.08	39.65	23.46	13.27	21.43	17.87	8.15	9.3	7.87	*	**	-	-
HEMBA1004248	60.7	102.92	68.75	40.08	49.28	54.01	55.12	49.8	49.38				
HEMBA1004250	6.46	7.1	17.92	5.92	8.57	3.92	3.52	3.06	5.66				
HEMBA1004252	9.76	13.49	18.16	5.3	8	5.39	8.18	4.43	8.93	*		-	
HEMBA1004260	3.71	7.97	10.5	2.84	9.75	1.75	6.82	1.55	1.83				
HEMBA1004264	4.86	4.92	5.04	3.34	5.85	4	4.03	2.37	1.97		*		-
HEMBA1004267	14.31	26.05	30.36	19.35	16.25	13.91	15.22	15.98	20.33				
HEMBA1004272	7.23	8.73	9.64	3.95	3.4	3.74	3.02	1.81	2.67	**	**	-	-
HEMBA1004274	3.8	4.23	13.32	4.59	3.82	2.88	5.15	2.11	5.65				
HEMBA1004275	6.92	5.28	11.01	3.44	3.27	3.1	4.62	3.75	4.56				
HEMBA1004276	53.98	104.51	88.12	40.54	57.2	47.57	40.16	23.52	29.44		*		-
HEMBA1004279	3.9	4.4	11.72	1.47	4.01	1.18	2.34	1.51	2.01				
HEMBA1004284	15.6	17.68	32.1	11.85	15.45	12.29	19.44	11.68	15.92				
HEMBA1004286	1.1	4.52	5.35	1.91	3.11	0	3.7	0.1	2.34				
HEMBA1004289	4.33	10.31	14.89	4.93	9.21	6.85	5.43	4.43	9.27				
HEMBA1004293	14.22	23.33	31.53	19.23	14.77	12.78	16.77	15.46	15.6				
HEMBA1004295	5.99	9.65	12.39	6.69	4.97	4.03	6.51	6.63	6.32				
HEMBA1004302	27.72	69.78	67.78	35.38	30.81	31.86	31.74	25.34	24.05				
HEMBA1004306	22.59	41.69	39.11	30.27	34.77	20.17	21.64	11.35	18.3				
HEMBA1004312	8.29	12	23.23	5.76	9.79	3.74	7.73	4.58	8.66				
HEMBA1004314	17.03	23.79	39.64	14.71	20.95	13.02	20.7	16.59	24.72				
HEMBA1004321	2.16	4.06	8.11	3.21	4	1.12	2.54	0	3.38				
HEMBA1004323	4.43	3.01	0.68	0.1	10.07	1.6	2.71	1.11	0.96				
HEMBA1004327	3.2	5.57	7.13	3.58	3.76	2.03	3.61	2.13	4.27				
HEMBA1004329	47.09	53.32	108.52	56.12	44.95	40.88	71.49	47.58	48.41				
HEMBA1004330	7.28	14.18	16.85	8.09	8.07	7.74	11.04	9.62	5.53				
HEMBA1004334	6.28	6.86	13.5	5.07	6.47	3.23	5.33	2.42	4.72				
HEMBA1004335	2.77	3.49	11.65	1.67	3.64	0.75	1.36	0.2	2				
HEMBA1004341	4.79	7.07	13.59	3.55	3.83	2.11	5.23	1.8	5.75				
HEMBA1004344	5.88	15.53	22.36	10.54	9.43	7.32	16.14	4.47	6.61				
HEMBA1004347	8.48	17.07	21.37	11.69	14.36	7.58	5.26	6.18	12.85				
HEMBA1004349	19.03	22.2	39.78	17.07	23.84	11.42	16.44	11.72	16.17				
HEMBA1004352	30.36	31.05	54.47	23.2	27.22	18.91	26.94	20.35	19.47				
HEMBA1004353	65.35	90.37	111.41	40.12	57.25	44.69	62.88	49.41	51.19	*		-	
HEMBA1004354	31.04	48.91	55.45	29.8	26.92	23.18	26.7	16	25		*		-
HEMBA1004356	36.8	69.45	87.9	42.77	38.63	30.42	48.78	31.27	34.28				
HEMBA1004360	21.37	39.1	60.88	24.3	25.32	19.97	35.28	18.19	17.1				
HEMBA1004366	3.36	19.8	13.89	9.13	8.25	3.58	5.88	3.78	6.29				
HEMBA1004372	25.71	35.24	61.82	27.78	27.66	28.9	23.52	16.32	31.11				
HEMBA1004377	57.43	64.54	125.12	52.77	52.36	39.76	63.76	39.09	45.41				
HEMBA1004389	26.6	23.69	56.36	35.4	23.53	18.76	21.22	13.56	17.27				
HEMBA1004391	15.02	20.13	38.52	17.1	15.91	14.1	20.59	16.16	16.69				
HEMBA1004393	6.23	8.43	14.77	10.01	2.68	5.81	6.08	4.76	4.24				
HEMBA1004394	6.59	9.68	22.73	7.13	7.36	4.87	8.86	2.4	3.32				
HEMBA1004396	6.98	7.79	21.04	5.3	10.85	6.63	4.46	2.99	4.78				
HEMBA1004401	25.42	37.64	61.19	35.6	34.11	30.34	50.39	18.9	33.72				
HEMBA1004405	12.61	20.04	37.41	22.75	14.99	14.73	15.19	9.3	13.54				
HEMBA1004408	33.43	47.3	70.7	34.73	36.57	32.16	33.47	25.45	21.56				
HEMBA1004414	11.75	12.41	34.08	20.66	20.73	15.48	9.96	9.26	12.21				
HEMBA1004429	11.38	11.1	25.62	16.77	12.96	11.07	10.66	8.23	8.04				
HEMBA1004433	4.53	4.23	9.92	6.93	6.74	8.36	4.52	0.98	3.02				
HEMBA1004440	12.02	23.81	31.06	19.67	29.44	19.7	15.12	10.66	15.31				
HEMBA1004444	18.31	24.79	46.54	21.84	22.35	18.04	25.64	13.85	21.08				

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Table 371

HEMBA1004446	1.03	3.03	4.89	2.99	6.41	1.96	3.37	0.17	1.81				
HEMBA1004451	47.91	49.66	86.71	31.61	23.94	40.91	29.4	25.22	31.73				
HEMBA1004452	7.95	9.5	12.93	8.01	5.07	6.5	4.65	4.16	4.59		*		-
HEMBA1004454	21.61	21.48	36.91	22.76	21.2	22.64	20.66	13.58	20.72				
HEMBA1004460	3.23	5	9.05	6.23	2.51	4.45	3.96	1.85	1.76				
HEMBA1004461	9.82	11.87	18.26	13.46	12.46	12.25	11.75	5.13	11.97				
HEMBA1004468	5.97	8.24	11.49	13.09	9.63	6.4	4.93	3.14	5.27				
HEMBA1004479	7.22	6.26	11.32	4.91	8.01	9.21	5.84	3.77	4.35				
HEMBA1004482	5.37	8.99	11.74	7.23	3.06	5.24	4.77	2.99	3.49				
HEMBA1004491	7.67	10.41	13.9	11.84	11.35	7.74	9.41	6.84	7.99				
HEMBA1004499	7.91	12.25	21.91	14.4	10.84	11.41	12.99	9.9	12.88				
HEMBA1004502	28.69	31.67	44.53	24.39	21.51	21.75	15.45	9.07	14.65		*		-
HEMBA1004505	9.98	9.29	16.72	11.78	9.95	10.23	12.78	4.69	8.35				
HEMBA1004506	10.31	10.67	16.69	10.45	12.56	11.51	11.7	4.59	11.13				
HEMBA1004507	21.1	25.48	30.3	21.45	19.73	18.7	29.74	17.59	32.44				
HEMBA1004509	2.41	4.16	3.19	4.33	6.97	5.13	3.86	1.09	3.24				
HEMBA1004523	16.14	17.44	35.11	23.55	14.39	18.02	17.09	11.42	16.4				
HEMBA1004528	10.51	13.24	19.75	9.57	16.03	13.29	6.5	10.38	8.52				
HEMBA1004534	15.22	16.88	30.37	16.94	14.03	18.54	14.2	7.84	17.61				
HEMBA1004536	6.18	6.2	10.88	7.97	5.18	6.58	4.33	4.17	3.26				
HEMBA1004538	9.62	8.85	16.21	10.28	7.48	8.38	4.46	3.25	4.87		*		-
HEMBA1004542	7.28	10.06	13.56	7.76	7.83	8.12	4.06	4.75	6.69				
HEMBA1004552	3.25	4.65	8.61	4.79	5	6.2	4.33	0.53	3.64				
HEMBA1004554	8.19	11.95	16.92	9.57	13.98	10.14	9	4.19	10.81				
HEMBA1004558	12.36	17.94	21.39	13.09	11.7	13.96	9.64	9.22	10.83				
HEMBA1004560	4.66	8.68	10.86	4.85	5.89	4.95	2.86	5.27	5.83				
HEMBA1004564	9.73	17.48	27.36	16.06	14.28	12.2	13.33	10.15	10.66				
HEMBA1004565	3.56	3.98	12.25	2.36	4.04	2.92	3.05	2.38	2.63				
HEMBA1004573	4.48	3.98	12.03	4.58	4.29	4.64	2.63	3.89	4.83				
HEMBA1004576	18.09	17.62	32.93	24.33	34.17	25.83	17	11.99	13.66				
HEMBA1004577	3.54	7.83	16.24	7.08	11.02	14.75	9.75	3.87	4.69				
HEMBA1004586	4.65	5.81	14.36	5.07	7.86	5.89	6.37	2	4.74				
HEMBA1004596	284.44	249.12	425.92	413.25	261.05	315.49	139.33	269.7	335.01				
HEMBA1004604	11.58	13.47	19.78	11.02	11.29	12.05	9.52	8.82	11.26				
HEMBA1004607	44.74	50.81	86.88	51.55	56.7	51.72	48.7	32.51	56.83				
HEMBA1004610	6.05	7.49	14.69	9.25	6.9	7.29	6.72	4.7	9.16				
HEMBA1004617	12.1	9.56	20.48	8.02	10.16	8.41	9.52	5.32	9.98				
HEMBA1004622	5.16	6.28	10.24	4.13	6.32	4.27	7.06	2.49	4.07				
HEMBA1004626	5.67	7.39	15	4.2	9.2	4.95	4.59	5.59	4.31				
HEMBA1004629	13.02	21.22	41.46	19.54	21.07	18.99	20.74	13.12	14.82				
HEMBA1004631	73.82	82.05	86.06	51.43	26.56	15.5	10.72	28.9	42.6	*	**	-	-
HEMBA1004632	24.68	42.63	52.95	37.34	39.22	29.39	26.96	22.05	34.67				
HEMBA1004633	38.98	38.11	53.52	17.86	40.68	39.12	15.84	33.55	35.48				
HEMBA1004636	16.64	14.75	24.41	11.5	12.22	12.63	6.1	4.97	7.02		*		-
HEMBA1004637	10.33	12.11	26.18	5.02	9.26	11.39	12.44	6.08	12.85				
HEMBA1004638	17.07	21.26	52.09	19.97	27.34	24.5	24.76	14.24	22.8				
HEMBA1004645	41.39	65.54	74.75	36.73	58.32	57.87	35.72	21.96	40.06				
HEMBA1004656	33.89	50.4	80.19	35.73	46.51	37.77	45.77	32.71	37.95				
HEMBA1004657	8.65	8.21	14.8	8.65	5.01	4.76	2.7	2.34	16.46				
HEMBA1004666	18.27	17.29	28.67	14.15	16.19	11.73	13.41	11.89	17.32				
HEMBA1004669	9.31	10.17	13.58	7.96	6.32	5.8	4.8	3.37	4.51	*	**	-	-
HEMBA1004670	6.26	8.23	12.51	5.31	4.65	7.13	5.07	1.93	2.73		*		-
HEMBA1004672	7.49	5.42	13.8	6.32	5.91	7.14	7.17	3.42	6.19				
HEMBA1004689	18.06	37.4	36.02	13.85	14.84	13.32	10.59	5.45	12.39		*		-
HEMBA1004690	8.71	10.59	14.84	3.74	5.26	4.9	4.08	1.25	4.02	*	*	-	-
HEMBA1004693	54.63	51.62	109.86	81.26	86.47	81.99	74.06	35.68	58.9				
HEMBA1004697	107.99	90.54	174.23	129.1	114.25	71.95	45.98	67.21	100.42				
HEMBA1004702	17.82	20.4	33.62	24.43	14.82	19.64	15.1	13.79	12.53				
HEMBA1004704	4.12	4.28	3.95	3.01	2.64	2.5	2.6	1.84	1.67	**	**	-	-
HEMBA1004705	8.53	8.58	10.66	4.87	5.69	4.53	7.25	3.35	5.23	**	*	-	-
HEMBA1004706	4.44	4.15	10.51	3.36	3.58	2.66	4.3	1.58	2.61				
HEMBA1004709	17.24	19.06	37.36	23.46	18.59	23.59	17.98	10.66	14.19				
HEMBA1004711	162.08	157.26	293.47	260.03	204.86	251.04	138.17	104.82	96.04				
HEMBA1004723	8.81	12.37	23.58	15.07	18	14.65	13.5	4.03	7.35				

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Table 372

HEMBA1004725	8.16	9.51	14.17	11.97	14.28	12.46	9.22	7.11	10.71				
HEMBA1004730	9.5	30.77	15.01	11.4	24.39	8.96	5.69	6.95	7.79				
HEMBA1004733	4.35	1.94	6.11	2.44	2.1	1.31	3.15	0.66	3.23				
HEMBA1004734	6.35	4.56	8.84	3.47	5.46	3.65	7.89	2.85	5.88				
HEMBA1004736	16.7	24.9	39.79	8.08	17.63	7.89	15.58	8.45	13.06				
HEMBA1004748	7.15	9.02	16.19	2.15	7.19	3.48	6.72	4.3	8.2				
HEMBA1004749	24.36	23.03	33.63	4.23	9.92	4.61	5.83	2.01	3.6	**	**	-	-
HEMBA1004751	2.98	5.64	15.55	3.81	7.93	4.03	5.96	2.05	2.94				
HEMBA1004752	114.05	106.99	178.16	68.94	72.11	86.46	30.58	32.81	51.61		*		-
HEMBA1004753	63.77	72.42	98.61	28.89	47.7	46.76	41.95	35	54.38	*	*	-	-
HEMBA1004755	14.23	13.71	21.59	11.51	11.62	10.29	10.53	11.28	11.46				
HEMBA1004756	8	8.06	13.16	9.58	10.37	12.14	11.47	5.24	11.51				
HEMBA1004758	28.52	33.28	46.67	20.49	28.34	19.64	31.58	21.06	23.78				
HEMBA1004763	5.65	6.08	11.46	2.37	10.09	17.67	15.26	61.35	5.43				
HEMBA1004768	3.64	9.18	17.67	4.3	5.33	4.44	3.13	1.14	2.86				
HEMBA1004770	3.52	3.97	15.56	4.59	3.64	3.31	3.4	1.61	4.49				
HEMBA1004771	9.14	8.57	13.33	7.83	4.73	6.17	4.13	3.12	6.19		*		-
HEMBA1004775	4.31	4.72	7.01	2.54	3.11	3.68	4.57	1.14	2.99				
HEMBA1004776	24.15	24.27	34.07	11	13.72	16.67	11.79	13.87	5.14	*	*	-	-
HEMBA1004778	7.73	3.98	15.13	3.29	12.02	3.24	6.23	3.84	2.81				
HEMBA1004784	24.44	36.5	43.33	23.54	19.27	15.1	33.56	28.4	19.49				
HEMBA1004785	13.67	18.37	27.67	13.73	15.71	13.71	15.09	7.19	15.39				
HEMBA1004789	4.14	8.07	13.1	2.66	4.24	5.12	10.75	3.53	4.53				
HEMBA1004795	7.33	8.35	20.46	14.48	8.52	7.53	6.22	3.52	6.52				
HEMBA1004797	7.1	4.75	10.25	8.19	4.85	5.24	4.01	3.13	5.6				
HEMBA1004803	8.6	9.94	11.36	7.93	6.31	7.52	6.11	2.35	5.54	*	*	-	-
HEMBA1004806	3.19	2.79	8.69	6.88	5.26	4.11	3.33	0.92	0.9				
HEMBA1004807	4.03	3.35	11.54	5.63	6	7.16	2.01	2.6	2.3				
HEMBA1004816	15.48	10.97	19.39	6.27	7.54	6.26	5.63	8.15	5.23	*	*	-	-
HEMBA1004820	7.87	10.12	20.63	12.23	11.52	10.1	9.12	3.16	8.37				
HEMBA1004833	4.21	6.73	18.25	5.9	8.04	9.77	5.85	1.98	3.49				
HEMBA1004847	3.02	6.46	11.24	4.65	7.78	8.66	8.67	2.5	5.11				
HEMBA1004850	4.4	5.74	10.78	6.32	4.58	7.77	3.54	4.67	2.65				
HEMBA1004863	17.31	15.86	32.11	21.23	15.33	16.21	14.88	9.41	17.84				
HEMBA1004864	17.46	20.24	32.03	15.36	13.18	16.06	19.67	7.45	13.87				
HEMBA1004865	113.3	61.73	148.7	148.79	88.87	115.94	64.71	39.42	63.09				
HEMBA1004880	8.83	11.17	12.28	9.73	8.92	10.05	5.47	2.68	3.9		**		-
HEMBA1004882	141.61	124.12	179	131.9	123.22	118.49	123.09	86.3	152.75				
HEMBA1004885	7.94	7.93	12.26	7.41	11.08	9.32	5.37	3.13	5.59		*		-
HEMBA1004889	35.77	44.93	60.57	51.03	25.98	30.7	17.41	45.83	36.11				
HEMBA1004900	52.96	49.82	61.95	21.61	27.4	15.4	7.06	13.28	12.57	**	**	-	-
HEMBA1004909	14.18	13.16	28.88	16.89	11.25	13.43	12.38	9.23	13.02				
HEMBA1004918	6.03	4.11	8.13	4.43	3.46	3.67	3.79	1.63	1.47				
HEMBA1004923	9.64	9.9	14.09	8.35	13.9	10.52	5.58	4.15	7.26		*		-
HEMBA1004929	3.15	3.03	7.44	3.03	3.95	3.22	2.76	0.8	3.27				
HEMBA1004930	4.7	7.7	9.9	4.33	7.94	6.01	5.83	3.66	7.33				
HEMBA1004933	48.9	58.84	65.65	52.38	60.44	49.38	52.85	24.83	54.95				
HEMBA1004934	3.85	4.55	8.24	5.31	3.47	5.34	6.35	6.72	5.35				
HEMBA1004937	12.55	13.42	25.29	16.02	10.93	15.03	11.34	9.36	13.16				
HEMBA1004943	6.33	9.2	8.01	2.75	3.28	2.19	4.11	2.61	3.13	**	**	-	-
HEMBA1004944	19.58	19.31	31.82	17.17	17.7	18.72	15.62	10.66	19.2				
HEMBA1004946	12.19	9.84	23.87	11.5	9.34	11.54	7.67	6.35	7.52				
HEMBA1004952	5.52	5.6	7.61	2.28	4.07	4.82	1.95	1.52	2.27		**		-
HEMBA1004954	95.41	161.15	61.32	125.56	130.49	124.27	79.29	36.2	131.05				
HEMBA1004956	3.34	5.15	10.1	3.76	7.59	6.47	4.82	2.29	4.38				
HEMBA1004960	18.1	21	43	23.94	15.38	19.28	12.99	14.78	18.5				
HEMBA1004971	17.31	26.71	28.24	5.08	6.02	5.94	4.63	4.75	6.7	**	**	-	-
HEMBA1004972	122.03	238.04	172.22	44.53	137.98	72.83	61.38	80.13	88.64		*		-
HEMBA1004973	3.44	2.83	7.72	3.58	1.82	6.46	2.6	2.06	3.24				
HEMBA1004977	14	10.09	24.08	10.99	9.73	9.85	6.91	5.11	5.98				
HEMBA1004978	11.81	9.75	18.48	9.66	9.26	8.27	8.68	4.77	8.65				
HEMBA1004980	6.76	8.63	15.4	3.58	6.32	6.19	5.45	3.4	4.05				
HEMBA1004982	6.24	8	15.9	4.68	8.72	7.61	5.71	2.32	4.42				
HEMBA1004983	27.66	31.4	50.17	31.75	22.28	27.83	26.75	25.03	37.28				

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Table 373

HEMBA1004895	13.04	8.58	10.13	7.12	8.06	6.92	2.73	3.68	5.31		*		-
HEMBA1005004	4.77	5.36	6.34	4.11	3.26	3.94	3.94	3.84	5.52	*		-	
HEMBA1005008	57.09	40.78	98.86	67.53	69.03	54.32	23.5	39.71	21.46				
HEMBA1005009	1057.6	723.08	1508	886.08	1346.5	1172.9	1256.5	763.02	961.92				
HEMBA1005019	4.41	3.37	12.38	2.48	5.05	3.17	5.8	3.17	5.15				
HEMBA1005021	20.78	39.68	34.72	6.67	27.86	14.2	11.45	16.23	4.97		*		-
HEMBA1005029	70.74	90.66	114.47	109.76	103.35	90.04	59.53	40.06	53.52		*		-
HEMBA1005035	18.47	18.85	35.14	26.8	19.92	22.3	9.64	15.48	14.58				
HEMBA1005036	6.46	8.45	12.94	4.31	7.1	4.1	3.99	2.47	4.91				
HEMBA1005039	30.97	34.92	39.63	34.24	27.86	28.36	12.93	8.11	16.92		**		-
HEMBA1005047	8.28	10.14	13.81	4.91	5.09	5.36	2.77	2.57	2.31	*	**	-	-
HEMBA1005050	3.68	2.17	10.81	2.45	2.33	1.31	2.32	1.28	0.56				
HEMBA1005062	4.16	12.91	14.13	4.05	8.34	22.08	6.52	3.12	5.74				
HEMBA1005066	10.67	14.99	36.8	11.75	15.95	10.56	12.8	8.39	12.44				
HEMBA1005067	4.44	5.11	10.87	2.4	4.78	3.11	2.95	0.22	2.1				
HEMBA1005070	52.72	54.64	132.49	164.51	146.19	162.23	48.46	33.29	55.3	*		+	
HEMBA1005075	3.89	4.62	7.08	4.3	4.86	3.7	4.12	2.52	4.18				
HEMBA1005078	9.47	16.56	13.83	7.13	9.41	6.63	4.44	6.27	3.76		*		-
HEMBA1005079	31.02	35.09	45.38	24.46	22.17	19.63	32.37	21.21	24.67	*		-	
HEMBA1005083	6.87	5.26	12.68	2.37	3.44	3.16	3.82	1.83	4.73				
HEMBA1005084	14.72	21.03	25.93	7.18	18.88	15.76	10.99	5.75	6.49		*		-
HEMBA1005088	4.46	4.67	12.93	1.85	3.81	2.49	3.1	1.87	2.53				
HEMBA1005089	4.71	9.88	14.88	4.89	6.06	3.51	4.1	0.92	1.92				
HEMBA1005090	25.03	17.55	31.81	18.25	14.13	11.76	5.18	6.32	11.92		*		-
HEMBA1005096	5.89	3.91	4.65	4.65	2.95	3.34	2.39	2.2	2.94		*		-
HEMBA1005101	39.08	41.35	50.86	29.48	23.15	20.02	33.26	32.78	29.58	*	*	-	-
HEMBA1005107	40	41.43	50.54	29.82	24.91	24.18	41.74	30.86	33.12	**		-	
HEMBA1005113	113.11	107.38	156.04	92.91	86.12	76.09	106.26	47.64	78.36				
HEMBA1005123	10.25	18.19	27.19	10.94	11.91	8.06	14	8.52	9.01				
HEMBA1005133	17.82	23.43	41.02	14.36	24.16	22.06	27.83	16.74	25.23				
HEMBA1005135	5.59	8.93	15.2	4.63	7.32	4.29	4.52	1.48	2.68				
HEMBA1005145	4.53	2.71	8.45	5.36	4.35	4.23	3.05	2.29	4.35				
HEMBA1005149	378.91	317.95	317.16	22.18	181	208.94	102.53	216.46	124.98	*	**	-	-
HEMBA1005152	6.82	9.2	10.54	4.39	6.2	1.79	3.59	2.97	2.92	*	**	-	-
HEMBA1005159	7.43	8	10.73	4.97	6.07	2.08	4.16	3.29	1.57		*		-
HEMBA1005172	7.45	10.34	13.12	4.47	4.62	4.49	4.3	1.57	2.99	*	*	-	-
HEMBA1005185	22.87	28.13	43.59	20.68	28.1	16.31	27.6	18.57	18.78				
HEMBA1005186	8.26	12.01	22.97	7.71	9.71	6.32	6.15	2.19	5.11				
HEMBA1005195	21.01	45.46	54.34	19.83	21.77	13.25	11.91	3.42	10.22		*		-
HEMBA1005201	30.23	25.81	53.48	38.66	31.34	27.12	18.26	15.51	22.99				
HEMBA1005202	5.59	7.98	9.58	3.99	3.6	4.2	6.81	2.2	7.96	*		-	
HEMBA1005204	16.46	12.78	28.18	11.48	14.05	9.97	14.37	10.45	14.76				
HEMBA1005206	23.26	6.89	27.27	4.57	14.1	5.14	8.86	8.11	3.99				
HEMBA1005219	46.02	33.86	64.57	13.22	55.15	17.76	33.33	34.4	11.24				
HEMBA1005223	6.35	5.89	13.54	0.44	2.75	4.32	3.73	1.82	1.78				
HEMBA1005229	6.79	9.67	19.26	5.01	5.11	5.18	4.75	0.62	2.59				
HEMBA1005230	211.84	132.19	314.59	37.27	92.19	87.58	104.99	40.98	12.2		*		-
HEMBA1005232	5.02	3.23	8	4.94	3.86	4.85	3.42	2.21	2.54				
HEMBA1005238	4.01	4.87	12.04	12.05	4.27	6.06	2.73	1.86	3.31				
HEMBA1005241	4.78	4.02	12.24	4.12	3.03	3.52	2.77	1.9	3.08				
HEMBA1005244	7.96	6.13	14.8	5.66	6.64	4.51	3.63	3.58	2.47				
HEMBA1005246	144.3	160.26	353.25	249	171.68	181.26	165.76	91.77	157.68				
HEMBA1005251	11.91	8.98	32.78	5.64	10.3	10.41	18.87	11.34	4.1				
HEMBA1005252	12.16	18.12	37.6	17.48	16.35	13.11	14.26	8.12	11.62				
HEMBA1005267	41.28	35.46	59.97	65.43	48.12	53.65	34.92	15.48	29.09				
HEMBA1005274	146.06	122.53	200.33	113.76	78.58	123.13	106.12	95.92	123.47				
HEMBA1005275	50.96	52.4	71.8	62.52	44.67	45.43	64.52	35.24	52.21				
HEMBA1005288	36.19	33.62	70.75	88.7	68.37	56.26	25.84	20.1	22.79				
HEMBA1005293	11.95	9.22	34.15	19.57	13.03	24.04	13.57	18.82	7.5				
HEMBA1005296	17.02	8.96	24.16	11.91	18.13	12.63	5.55	16.37	7.9				
HEMBA1005301	7.64	4.4	12.18	6.44	7.08	7.49	6.66	3.04	4.73				
HEMBA1005304	3.18	4.74	9.81	5.51	5.89	5.14	6.35	2.58	2.92				
HEMBA1005305	4.23	5.99	12.03	5.04	5.33	5.38	6.54	0.53	2.54				
HEMBA1005311	11.53	9.17	14.37	12.69	6.17	11	10.14	6.62	9.41				

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Table 374

HEMBA1005313	33.27	32.37	38.89	32.29	19.06	24.67	17.8	16.01	18.82		**		-
HEMBA1005314	24.58	33.06	42.65	21.87	11.43	15.5	9.92	9.33	8.85	*	*	-	-
HEMBA1005315	12.58	12.96	19.94	17.38	10.31	13.36	9.94	6.48	5.8		*		-
HEMBA1005317	4.9	4.68	7.03	6.55	5.75	6.41	3.83	2.01	4.66				
HEMBA1005318	2.91	3.45	4.86	4.07	3.07	4.69	2.08	0.38	2.27				
HEMBA1005324	11.54	12.46	27.19	15.78	17.61	18.74	11.73	1.86	14.23				
HEMBA1005331	43.61	41.81	60.5	40.68	48.26	41.6	45.76	21.6	43.46				
HEMBA1005337	20.3	20.66	34.16	18.47	13.27	15.91	13.2	7.95	13.16		*		-
HEMBA1005338	37.76	51.08	62.83	38.86	14.3	16.63	9.18	11.59	18.35		**		-
HEMBA1005344	58.27	53.4	127.13	158.88	86.48	122.88	43.73	24.53	36.87				
HEMBA1005353	291.67	197.22	329.41	381.89	358.33	324.87	364.08	232.83	294.3				
HEMBA1005359	3.54	4.47	8.65	4.81	7.38	8.25	4.29	2.88	3.92				
HEMBA1005362	14.29	12.72	20.99	11.94	11.74	13.92	13.73	6.82	10.98				
HEMBA1005364	3.08	8.57	11.19	9.32	9.41	5.54	6.78	3.23	3.82				
HEMBA1005367	9.52	14.36	9.74	11.62	16.31	12.41	12.24	9.27	3.86				
HEMBA1005372	309.34	404.59	430.49	84.13	123.69	78.11	25.56	68.19	97.12	**	**	-	-
HEMBA1005374	36.56	51.63	69.8	44.44	39.19	38.53	36.51	36.03	34.64				
HEMBA1005379	33.5	27	43.36	22.13	30.26	17.05	21.18	29.05	27.22				
HEMBA1005382	15.49	19.66	32.8	16.35	15.89	24.51	20.76	15.49	21.41				
HEMBA1005384	6.36	8.47	15.31	11.14	12.78	12.49	8.42	6.41	12.29				
HEMBA1005386	7.43	7.3	12.47	6.27	5.44	7.51	3.39	1.08	4.63		*		-
HEMBA1005389	18.61	20.29	18.71	13.6	21.69	22.09	19.9	13.97	9.2				
HEMBA1005394	12.89	8.67	16.27	12.3	14.5	11.32	10.11	3.58	3.69				
HEMBA1005403	4.34	4.47	10.77	7.65	8.37	7.4	6.03	4.21	5.27				
HEMBA1005408	5.14	5.28	8.12	4.84	5.38	6.7	5.4	4.72	1.33				
HEMBA1005410	147.8	198.98	244.61	96.9	175.54	169.68	68.34	63.45	81.73		*		-
HEMBA1005411	3.94	4.86	10.62	4.18	2.45	4.02	1.07	3.25	2.19				
HEMBA1005423	7.19	6.73	19.41	6.38	7.84	8.58	6.14	3.21	5.83				
HEMBA1005426	95.36	92.66	185.58	213.51	144.79	175.18	76.93	45.72	96.01				
HEMBA1005427	3.18	3.68	9.55	2.9	4.08	4.42	2.98	1.86	3.96				
HEMBA1005430	38.92	50.77	66.51	41.28	49.27	33.43	51.65	28.88	24.29				
HEMBA1005438	85.73	96.52	156.38	59.22	45.51	57.38	12.76	14.31	32.68		*		-
HEMBA1005443	15.2	22.18	31.05	12.38	21.42	15.9	15.18	10.34	15.89				
HEMBA1005447	7.4	8.91	13.83	6.04	6.83	6.51	4.71	3.18	4.95		*		-
HEMBA1005449	188.67	185.78	227.88	315.2	205.18	189.94	184.99	92.08	155.69				
HEMBA1005452	87.1	82.51	97.54	153.23	76.5	106.72	73.14	41.42	77.58				
HEMBA1005454	4.07	5.62	12.12	2.12	9.94	2.42	3.66	2.56	2.8				
HEMBA1005468	3.12	5.06	12.85	2.9	5.78	4.72	3.8	1.69	1.54				
HEMBA1005469	4.06	5.82	14.74	4.56	9.66	7.3	4.34	3.61	3.19				
HEMBA1005472	48.84	68.93	98.37	43.92	45.45	42.16	48.44	44.29	63.31				
HEMBA1005474	3.81	5.4	6.23	3.61	6.81	3.03	3.23	2.83	4.47				
HEMBA1005475	18.35	13.18	29.74	13.69	11.52	8.61	14	8.86	16.92				
HEMBA1005489	11.24	6.84	19.41	11.32	8.2	10.15	7.69	4.76	6.72				
HEMBA1005497	3.55	3.84	13.2	3.87	5.02	4.47	2.68	1.54	6.08				
HEMBA1005500	9.06	12.27	15.75	5.67	8.54	10.09	5.5	7.58	6.57		*		-
HEMBA1005506	66.72	77.27	99.37	69.96	83.48	86.85	48.45	36.29	43.04		*		-
HEMBA1005508	10.52	16.74	23.57	15.52	16.57	19.17	24.35	7.4	7.32				
HEMBA1005511	106.43	145.35	110.4	50.22	49.21	46.23	5.8	10.19	8.56	**	**	-	-
HEMBA1005513	13.22	13.61	12.43	5.61	8.6	9.42	6.36	6.5	6.97	*	**	-	-
HEMBA1005517	8.83	13.8	21.17	12.19	9.09	9.65	12.06	10.72	8.14				
HEMBA1005518	6.15	6.12	10.29	3.31	2.65	3.34	2.82	2.51	2.48	*	*	-	-
HEMBA1005520	4.72	5.27	15.66	1.8	9.96	5.07	11.44	4.1	6.1				
HEMBA1005522	7.43	6.22	15.1	2.69	4.51	4.56	4.2	1.89	5.13				
HEMBA1005526	12.95	11.98	23.79	6.97	14.67	6.23	7.41	3.51	8.41				
HEMBA1005528	20.88	31.78	47.82	17.24	26.35	20.12	19.44	10.67	18.86				
HEMBA1005530	155.03	123.7	313.84	376.32	270.85	265.42	127.01	98.49	126.67				
HEMBA1005538	4.22	2.81	4.67	3.91	2.23	1.75	0.82	1.49	1.34		*		-
HEMBA1005539	7.37	8.42	11.33	9.56	8.07	5.43	6.22	7.08	3.71				
HEMBA1005545	6.67	6.11	9.83	3.2	2.97	2.68	4.51	2.07	2.36	*	*	-	-
HEMBA1005548	9.67	16.77	17.36	7.24	13.44	14.5	10.18	7.2	5.13				
HEMBA1005552	51.47	60.33	76.88	44.85	67.33	45.49	61.05	38.5	41.19				
HEMBA1005558	1303.4	1695.5	2079.7	1863.4	2100.7	1420	1688.2	1099.2	644.47				
HEMBA1005568	18.05	24.94	43.8	19.93	30.36	19.35	24.29	10.08	5.54				
HEMBA1005570	9.18	10.68	10.58	5.69	4.61	5.33	3.91	1.39	3.62	**	**	-	-

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Table 375

HEMBA1005576	3.76	5.34	5.63	3.54	6.15	2.3	3.82	3.83	3.35				
HEMBA1005577	3.45	4.03	5.12	2.3	2.95	1.9	2.63	1.06	1.56	*	*	-	-
HEMBA1005581	17.34	15.11	23.24	3.89	10.6	7.1	4.64	4.62	3.74	*	**	-	-
HEMBA1005582	240.9	356.29	365.46	317.4	608.67	346.15	243.13	155.96	316.09				
HEMBA1005583	56.28	75.41	54.74	36.66	53.45	30.25	44.93	12.37	20.67		*		-
HEMBA1005588	48.19	61.31	71.13	27.32	36.77	18.93	99.81	56.7	45.14	*		-	
HEMBA1005593	8.46	13.58	28.24	14.33	10.97	7.86	11.3	3.59	6.67				
HEMBA1005595	5.4	4.89	14.77	3.77	3.53	5.64	3.73	2.81	4.24				
HEMBA1005597	4.61	6.07	5.65	4.04	20.76	7.93	6.41	5.62	16.69				
HEMBA1005606	10.57	19.2	23.77	3.86	10.94	4.17	5.54	1.39	3.32		*		-
HEMBA1005609	15.17	18.03	17.77	3.19	7.05	3.09	3.33	3.84	3.16	**	**	-	-
HEMBA1005616	3.29	3.65	8.89	1.88	4.28	2.06	3.75	2.04	3.26				
HEMBA1005621	2.8	5.27	13.13	1.63	2.71	2.81	4.45	1.3	2.19				
HEMBA1005627	26.17	45.68	60.66	11.35	32.13	15.73	25.61	10.31	7.56				
HEMBA1005628	4.16	6.62	18.11	5.71	6.97	5.93	6.45	1.4	3.09				
HEMBA1005631	2.97	2.99	6.58	2.7	2.52	4.68	1.93	1.12	1.83				
HEMBA1005632	8.75	7.76	13.3	5.6	4.94	4.75	6.21	2.5	5.1	*		-	
HEMBA1005634	13.26	27.71	36.18	8.65	7.52	11.69	10.2	6.61	5.28				
HEMBA1005662	5.49	5.63	8.59	1.07	4.9	3.69	4.47	3.62	2.83				
HEMBA1005666	4.1	8.92	17.42	4.51	5.05	7.36	8.37	3.56	4.18				
HEMBA1005670	19.65	25.57	58.84	10.77	25.74	28.55	25.33	19.21	13.78				
HEMBA1005671	3.25	3.78	12.05	4.13	4.03	2.36	2.63	0.58	1.59				
HEMBA1005679	30.48	23.92	60.53	11.99	24.03	21.81	34.62	12.99	24.28				
HEMBA1005680	5.31	5.25	11.55	7.98	6.67	8.25	4.31	2.95	4.88				
HEMBA1005685	10.54	10.31	19.75	6.25	14.08	11.58	12.25	7.49	2.77				
HEMBA1005698	3.05	4.09	5.98	5.75	3.35	4.26	2.89	1.71	1.85				
HEMBA1005699	81.55	73.56	131.24	173.55	121.01	131.74	58.39	29.63	52.24				
HEMBA1005703	8.7	6.7	19.33	15.32	12.15	10.29	11.29	5.53	9.29				
HEMBA1005705	10.69	16.62	28.52	12.65	15.48	9.89	13.24	7.86	8.73				
HEMBA1005712	14.41	9.07	21.89	4.52	12.06	8.24	12.54	7.16	9.37				
HEMBA1005717	9.58	15.11	28.28	15.34	17.37	16.39	10.48	4.92	9.53				
HEMBA1005718	14.72	17.46	32.28	23.31	13	19.82	12.33	8.89	13.45				
HEMBA1005721	7.61	8.19	16.43	10.15	9	9.16	5.24	3.31	7.52				
HEMBA1005722	8.96	8.38	15.56	10.88	5.15	8.22	6.16	2.61	4.2				
HEMBA1005724	3.21	3.63	9.19	3.08	3.41	4.96	4.32	2.79	3.41				
HEMBA1005732	26.35	14.39	37.65	46.13	33.11	35.41	27.65	13.58	24.67				
HEMBA1005737	10.7	10.58	19.74	12.96	11.14	14.53	14.77	5.18	11.46				
HEMBA1005742	24.19	21.22	31.29	17.65	22.38	19.25	19.89	11.57	20.16				
HEMBA1005746	16.18	18.76	28.18	19.8	21.24	20.22	17.64	16.51	21.84				
HEMBA1005747	4.59	6.97	9.33	5.84	4.66	4.23	3.4	2.42	2.9		*		-
HEMBA1005749	4.06	4.65	5.89	4.59	4.51	2.42	4.14	4.65	3.14				
HEMBA1005755	6.51	5.76	10.77	4.34	2.96	3.2	3.26	2.6	1.41		*		-
HEMBA1005760	8.14	6.09	21.23	11.82	15.12	18.05	5.99	3.99	9.09				
HEMBA1005765	16.17	18.36	30.68	12.16	17.74	19.5	18.91	12.07	18.52				
HEMBA1005766	4.59	6.7	11.4	6.4	6.48	7.14	3.63	2.36	6.46				
HEMBA1005780	66.74	88.34	50.49	70.57	83.73	79.9	51.01	23.87	50.17				
HEMBA1005795	12.49	13.53	22.26	21.04	27.08	17.3	17.89	8.53	16.93				
HEMBA1005809	27.58	28.57	37.75	10.82	11.75	10.76	7.41	20.02	13.83	**	*	-	-
HEMBA1005813	11.01	13.12	21.07	10.05	5.62	7.48	3.75	4.75	2.72		*		-
HEMBA1005815	13.88	21.46	26.3	18.7	15.38	15.54	15.88	14.09	23.04				
HEMBA1005822	2.32	4.46	5.72	1.33	1.78	1.99	1.83	4.15	2.65				
HEMBA1005829	11.63	17.29	26.15	14.23	14.49	18.69	18.12	8.68	16.12				
HEMBA1005833	7.51	11.08	19.55	8.36	9.46	9.74	7.13	4.47	9.24				
HEMBA1005834	2.53	4.28	9.15	2.39	5.2	3.43	3.05	1.57	2.22				
HEMBA1005844	5.49	8.18	12.47	6.96	9.74	5.87	6.18	2.19	5.4				
HEMBA1005852	9.05	12.52	17.23	5.22	7.99	5.59	7.73	5.09	7.72				
HEMBA1005853	12.09	27.26	20.62	6.51	8.22	6.09	4.4	8.87	5.67	*	*	-	-
HEMBA1005878	16.48	26.29	29.76	6.78	14.33	12.64	11.87	13.79	15.64	*		-	
HEMBA1005883	10.6	8.45	21.85	5.18	5.86	5.16	3.04	2.55	2.52				
HEMBA1005884	18.4	17.45	38.78	13.72	28.17	26.47	16.14	9.17	16.98				
HEMBA1005891	14.35	23.5	28.7	12.96	17.06	15.29	15.47	12.21	17.4				
HEMBA1005894	20.76	25	45.44	20.3	23.59	18.03	21.15	9.72	19.92				
HEMBA1005898	6.21	7.33	9.72	7.72	7.66	5.64	3.86	1.59	3.36		*		-
HEMBA1005902	52.63	54.98	95.93	140.97	103.88	141.36	40.77	40.69	57.15	*		+	

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Table 376

HEMBA1005907	11.51	24.95	21.68	5.18	12.96	7.51	14.52	20.83	32.4				
HEMBA1005909	12.54	10.65	15.16	9.37	9.7	8.92	5.33	5.2	5.61		**		-
HEMBA1005911	4.25	2.94	8.69	4.53	4.07	3.47	3.19	0.81	2.14				
HEMBA1005912	35.05	30.41	48.44	55.56	35.89	54.16	35.55	16.99	36.27				
HEMBA1005913	8.07	12.66	17.16	3.35	11.55	8.12	4.56	4.08	5.57		*		-
HEMBA1005921	8.39	17.95	29.27	13.5	18.47	18.42	20.02	11.79	13.13				
HEMBA1005922	10.23	12.69	22.71	8.62	19.47	16.43	10.1	8.02	9.98				
HEMBA1005929	14.03	14.99	35	19.43	15.07	16.06	12.42	10.95	15.92				
HEMBA1005931	6.92	7.45	8.96	7.96	7.11	4.38	5.8	5.53	5.56		*		-
HEMBA1005934	9.15	11.61	14.52	6.47	9.42	7.17	6.06	6.07	3.78		*		-
HEMBA1005945	13.18	17.17	24.76	14.61	10.38	10.87	14.78	9.7	14.04				
HEMBA1005962	8.03	8.91	21.61	8.95	9.17	9.16	8.64	3.56	9.28				
HEMBA1005963	7.03	8.04	15.69	2.68	5.58	6.69	5.62	2.88	7				
HEMBA1005990	1.77	6.11	10.33	2.7	4.79	2.9	2.4	1.78	3.08				
HEMBA1005991	64.98	101.38	91.59	21.08	89.91	49.01	45.05	21.27	28.13		*		-
HEMBA1005999	10.77	8.18	14.85	9.74	9.96	11.62	9.75	7.35	11.3				
HEMBA1006002	4.73	10.03	9.92	4.44	5.47	3.19	2.29	3.3	1.96		*		-
HEMBA1006005	11.33	12.26	21.89	15.72	14.29	10.03	11.77	7.68	11.25				
HEMBA1006011	7.74	6.02	9.99	4.17	3.85	3.65	4.89	1.78	2.14	*	*	-	-
HEMBA1006013	15.75	24.43	27.02	14.33	11.65	10.41	12.44	6.76	8.78	*	*	-	-
HEMBA1006016	12.67	16.72	32.68	4.67	8.33	5.18	11.34	2.62	5.66				
HEMBA1006019	39.35	43.51	94.43	41.01	47.95	33.8	48.65	20.74	35.48				
HEMBA1006021	100.18	64.95	186.84	161.47	154.88	173.68	76.07	51.55	67.34				
HEMBA1006022	4.41	4.65	8.97	5.98	4.93	5.29	5.93	2.38	6.8				
HEMBA1006031	54.5	55.09	63.41	23.75	30.34	33.23	14.55	24.74	14.18	**	**	-	-
HEMBA1006035	26.81	26.57	28.41	13.64	17.75	10.2	23.49	16.85	24.27	**		-	
HEMBA1006036	30.41	35.58	51.17	28.85	21.84	21.47	22.61	12.69	16.92		*		-
HEMBA1006042	14.78	15.89	30.2	21.62	13.62	17.35	12.05	7.06	10.83				
HEMBA1006044	6.37	6.38	15.67	2.89	5.13	3.3	5.6	2.77	4.16				
HEMBA1006045	5.05	5.98	16.26	5.37	6.51	3.98	4.26	3.34	4.33				
HEMBA1006048	5.66	8.21	17.12	5.57	7.7	7.23	7.81	2.07	6.93				
HEMBA1006053	9.91	12.14	22.17	11.19	10.11	10.25	6.6	4.29	8.53				
HEMBA1006055	18.11	16.89	29.58	15.19	13.98	12.78	12.35	11.58	12.66				
HEMBA1006058	12.02	10.46	14.6	9.27	7.95	6.43	9.22	7.8	6.16	*	*	-	-
HEMBA1006063	115.82	107.87	141.14	161.05	129.88	130.01	94.43	64.84	83.98		*		-
HEMBA1006067	14.46	16.19	18.97	8.28	13.91	5.01	10.46	4.28	4.98		*		-
HEMBA1006081	3.95	8.3	15.7	2.09	6.94	3.38	3.92	1.35	3.37				
HEMBA1006089	4.09	6.69	17.6	2.93	4.85	1.66	3.54	1.57	3.85				
HEMBA1006090	16.61	33.98	39.21	14.19	23.81	18.25	18.94	5.99	5.67				
HEMBA1006091	6.4	6.94	10.5	5.04	5.34	5.02	4.02	3.3	3.85		*		-
HEMBA1006093	24.23	35.95	33.59	5.11	7.76	13.97	5.79	10.1	7.62	**	**	-	-
HEMBA1006099	23.7	22.12	46.77	18.77	21.87	13.39	21.06	17.59	21.54				
HEMBA1006100	15.19	17.46	28.4	13.14	14.55	10.6	18.9	11.15	17.08				
HEMBA1006108	9.23	5.57	12.26	4.66	7.02	4.99	4.59	2.55	4.37				
HEMBA1006114	6.24	4.2	16.8	2.53	7.16	4.48	5.37	0.85	3.06				
HEMBA1006121	4.96	7.47	17.94	3.37	6.22	2.88	5.11	1.02	2.9				
HEMBA1006124	23.37	10.77	43.63	10.18	13.13	12.16	9.91	5.78	5.28				
HEMBA1006125	5.3	5.09	9.35	4.55	4.9	6.58	2.71	1.37	4.21				
HEMBA1006130	81.41	100.18	218.91	239.88	178.96	190.17	100.6	68.45	89.08				
HEMBA1006138	16.78	21.47	42.54	20.91	18.85	14.71	18.67	11.93	13.92				
HEMBA1006142	6.25	5.14	9.74	3.49	5.53	4.08	2.75	2.92	2.44		*		-
HEMBA1006150	20.94	16.77	47.47	16.05	12.94	20.13	22.73	16.22	18.83				
HEMBA1006151	3.81	3.62	12.07	4.06	2.71	3.79	4.85	1.6	3.25				
HEMBA1006155	51.87	36.97	81.85	14.8	33.19	24.55	29.86	21.38	8.77				
HEMBA1006158	7.8	6.18	16.28	4	7.84	5.44	10.27	1.55	3.09				
HEMBA1006164	7.41	4.45	10.51	11.19	6.62	6.2	5.41	2.39	2.71				
HEMBA1006171	11.38	13.76	11.95	10	9.74	12.84	7.5	4.2	3.45		**		-
HEMBA1006173	5.77	5.17	5.55	5.75	11.01	7.35	5.28	2.14	3.83				
HEMBA1006176	10.21	6.39	20.68	12.36	13.62	14.28	6.26	8.81	6.76				
HEMBA1006182	6.52	8.53	12.82	8.56	9.55	11.37	5.71	3.32	5.23				
HEMBA1006197	4.36	5.59	8.45	4.07	4.78	4.63	3.18	1.47	2.61		*		-
HEMBA1006198	6.83	8.29	18.43	9.27	9.93	14.63	6.95	4.93	6.04				
HEMBA1006213	46.5	59.16	87.76	45.37	52.9	41.61	64.69	38.82	49.81				
HEMBA1006217	77.53	104.19	150.86	44.45	56.82	81.63	56.2	53.63	65.92				

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HEMBA1006226	60.66	89.4	128.3	98.59	21.45	56.73	34.83	42.34	47.3		
HEMBA1006235	7.29	6.42	9.51	4.4	5.83	6.34	4	1.9	2.78	*	-
HEMBA1006248	8.59	14.3	12.76	17.84	10.1	10.62	14.29	11.1	13.06		
HEMBA1006251	15.98	24.11	24.67	22.82	19.08	21.09	16.03	3.32	8.44		
HEMBA1006252	6.29	11.35	24.58	17.83	5.75	7.22	9.32	6.16	9.75		
HEMBA1006253	6.65	9.14	20.63	14.78	17.19	22.49	8.79	1.77	6.4		
HEMBA1006259	11.81	21.15	28.91	16.9	10.94	16.19	15.68	14.83	17.05		
HEMBA1006261	25.45	37.82	48.94	33.85	29.71	14.07	18.76	15.97	24.68		
HEMBA1006268	4.53	5.62	11.14	5.03	3.83	5.91	4.8	2.63	2.52		
HEMBA1006271	27.87	48.98	84.46	39.21	39.6	40.82	30.74	14.23	28.33		
HEMBA1006272	3.48	5.09	12.53	3.82	7.27	10.33	8.77	2.68	5.16		
HEMBA1006273	4.26	5.62	9.16	7.22	6.74	6.25	4.33	1.91	3.78		
HEMBA1006276	8	7.56	13.01	10.92	8.88	11.33	8.59	5.55	8.36		
HEMBA1006278	3.56	6.86	4.87	4.56	7.03	4.18	3.68	1.91	2.81		
HEMBA1006283	21.61	22.15	38.14	17.11	13.97	13.64	11.04	8.54	8.53	*	-
HEMBA1006284	9.77	12.43	9.21	7.3	6.48	8.65	4.11	16.95	4.13		
HEMBA1006291	7.57	5.98	8.47	4.12	5.97	5.86	4.51	2.35	4.32	*	-
HEMBA1006292	28.37	23.25	41.05	49.83	29.24	37.1	21.69	20.86	21.95		
HEMBA1006293	3.75	5.49	8.43	3.08	2.38	10.01	0.91	2.39	2.11	*	-
HEMBA1006298	20.83	28.58	31.92	37.12	28.94	29.71	18.96	13.53	20.58		
HEMBA1006309	12.21	13.85	16.63	10.12	12.48	15.92	14.59	3.8	13.91		
HEMBA1006310	10.98	14.98	14.35	11.71	17.38	10.36	10.75	8.47	4.15		
HEMBA1006311	7.24	7.64	16.35	13.11	5.74	8	7.15	4.03	4.85		
HEMBA1006313	3.22	8.11	10.2	4.45	3.61	3.07	2.82	2.44	2.58		
HEMBA1006316	7.65	12.92	15.52	10.38	5.11	11.89	7.9	6.94	9.74		
HEMBA1006328	21.63	21.11	38.33	32.37	21.64	26.1	17.68	13.27	19.36		
HEMBA1006334	3.37	3.68	14.62	4.58	3.28	2.72	2.89	4.86	1.73		
HEMBA1006335	17.68	32.85	46.47	23.14	32.25	24.21	26.2	15.13	17.28		
HEMBA1006344	55.44	64.87	82.83	51.59	45.13	40.79	32.94	23.43	27.33	**	-
HEMBA1006347	7.7	7.61	11.32	7.96	6.93	5.21	8.91	1.81	2.49		
HEMBA1006349	5.12	7.39	13.08	11.96	7.92	10.21	7.73	3.41	9.88		
HEMBA1006352	4.71	5.44	5.8	3.17	4.05	6.34	3.53	2.18	6.11		
HEMBA1006357	21.84	30.15	32.51	16.24	19.4	20.03	17.68	17.67	25.75	*	-
HEMBA1006358	9.29	7.19	14.9	8.1	8.4	7.37	7.12	3.93	6.97		
HEMBA1006359	5.5	5.93	13.36	4.55	6.66	5.77	4.91	2.59	3.15		
HEMBA1006360	4.46	4.17	9.74	2.49	4.18	4.08	2.89	1.16	2.66		
HEMBA1006364	4.83	5.25	14.76	2.78	4.9	3.21	2.71	2.21	3.79		
HEMBA1006377	80.85	114.32	105.84	75.76	102.36	58.33	93.99	60.04	78.87		
HEMBA1006380	20.03	20.23	49.46	23.06	19.66	23.19	14.68	15.28	25.75		
HEMBA1006381	21.8	26.78	34.04	28.98	18.12	16.56	28.76	15.54	19.65		
HEMBA1006385	26.15	27.47	48.23	21.69	21.93	26.5	17.06	11.15	26.66		
HEMBA1006390	66.76	79.54	86.03	47.23	63.78	61.2	79.04	51.69	65.97		
HEMBA1006391	9.83	7.54	21.2	5.37	10.85	8.66	7.1	4.25	6.66		
HEMBA1006398	7.74	10.16	17.94	6.15	8.15	10.18	5.31	3.87	6.36		
HEMBA1006405	17.21	30.3	36.97	11.67	17.28	9.3	9.52	5.99	10.52	*	-
HEMBA1006410	12.29	24.19	20.82	11.01	22.54	19.08	10.32	24.08	7.5		
HEMBA1006416	13.77	16.34	35.1	20.2	19.08	14.96	13.83	12.25	17.9		
HEMBA1006418	14.88	14.23	12.55	8.74	10.37	7.82	5.57	12.05	3.94	**	-
HEMBA1006419	30.32	26.38	45.23	21.57	20.76	20.5	35.29	23.16	35.95		
HEMBA1006421	6.94	7.3	14.62	4.48	5.03	4.44	5.76	2.74	5.79		
HEMBA1006424	6.59	5.16	10.86	2.39	3.13	4.03	3.8	3.29	5.21		
HEMBA1006426	16.94	21.77	35.51	13.82	15.6	11.92	15.06	10.89	16.55		
HEMBA1006430	21.51	23.1	52.14	21.8	26.01	14.55	25.55	15.62	24.71		
HEMBA1006438	7.39	9.88	27.72	9.7	12.86	10.02	7.77	3.89	8.06		
HEMBA1006445	5.97	4.62	11.24	6.9	4.18	5.84	3.07	2.65	7.57		
HEMBA1006446	10.44	29.9	25.23	12.03	4.68	7.84	2.86	8.87	4.65		
HEMBA1006456	20.27	20.9	27.71	19.85	19.2	23.69	16.72	10.9	15.13	*	-
HEMBA1006461	10.85	13.87	19.86	8.91	8.16	8.85	10.75	7.35	8.75		
HEMBA1006467	2.98	4.33	9.77	4.94	3.17	2.56	4.06	1.76	2.14		
HEMBA1006470	34.3	38.7	56.67	41.16	36.04	29.19	28.2	24.42	29.45		
HEMBA1006471	8.92	14.85	23.43	12.81	12.27	40.2	16.21	5.14	6.51		
HEMBA1006474	80.88	55.42	113.87	93.82	77.51	77.92	59.58	47.32	61.33		
HEMBA1006476	124.18	126.67	311.61	282.54	252.79	111.47	88.12	112.31	128.83		
HEMBA1006482	750.18	800.51	717.99	555.6	740.67	596.85	785.76	753.48	372.51		

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Table 378

HEMBA1006483	10.38	11.79	17.97	10.54	8.06	5.41	9.39	6.26	10.8				
HEMBA1006485	14.11	21.34	22.05	9.66	9.42	6.66	9.41	4.35	6.34	*	*	-	-
HEMBA1006486	25.6	38.65	46.49	15.25	21.42	18.99	28.29	12.46	17.42	*		-	
HEMBA1006489	4.69	5.66	11.99	2.16	3.64	2.6	4.74	2.19	2.49				
HEMBA1006492	21.26	21.32	31.79	8.11	21.1	11.99	16.25	6.33	8.98		*		-
HEMBA1006494	3.73	5.82	13.17	4.37	5.86	3.22	4.57	1.78	4.99				
HEMBA1006497	9.48	5.39	9.72	6.41	4.7	6.22	4.84	2.41	5.11				
HEMBA1006501	70.71	74.3	109	137.89	121.18	132.43	56.47	47.55	54.22	*		†	
HEMBA1006502	26	37.84	37.28	17.65	19.66	21.79	14.53	13.47	14.09	*	**	-	-
HEMBA1006507	74.35	71.35	93.56	76.72	76.19	89.01	54.44	45.62	81.01				
HEMBA1006517	10.15	13.34	25.2	8.05	9.91	8.2	9.98	8.78	9.53				
HEMBA1006521	4.71	7.89	15.55	2.17	4.99	3.48	4.73	1.47	4.08				
HEMBA1006529	20.44	40.14	54.85	11.1	18.97	9.04	8.44	3.17	5.16		*		-
HEMBA1006530	2.11	3.93	16.06	3.3	3.94	2.97	2.36	0.8	2.85				
HEMBA1006535	4.76	6.35	8.43	4.93	4.07	4.99	1.52	1.3	3.36		*		-
HEMBA1006536	7.73	9.35	15.74	6.97	6.8	8.19	6.06	4.78	7.71				
HEMBA1006540	4.89	5.07	10.1	3.8	4.1	3.21	4.5	0.57	2.57				
HEMBA1006544	9.55	9.44	12.65	5.51	6.6	3.64	6.81	6.28	5.66	*	*	-	-
HEMBA1006546	13.83	18.34	35.37	18.49	13.07	8.02	20.42	13.65	12.24				
HEMBA1006549	3.69	4.64	10.47	3.5	3.22	3.38	4.38	1.91	2.6				
HEMBA1006559	5.63	7.78	15.93	4.1	5.24	3.33	4.33	1.27	1.6				
HEMBA1006562	4.46	7.73	13.41	4.81	4.36	7.66	6.04	1.8	5.11				
HEMBA1006566	1.97	2.79	6.04	4.85	3.75	3.09	2.63	0.98	3.24				
HEMBA1006569	9.03	13.38	17.77	8.08	5.02	11.82	6.18	3.56	5.28		*		-
HEMBA1006572	4.01	5.33	6.28	3.85	4.61	4.82	3.06	1.11	1.97		*		-
HEMBA1006579	48.81	48.67	106.01	77.85	58.85	72	32.03	38.94	29.18				
HEMBA1006583	21.83	28.38	52.62	37.84	32.54	33.86	32.6	18.06	30.33				
HEMBA1006595	9.39	11.2	24.82	12.48	12.13	12.39	11.97	4.53	9.41				
HEMBA1006597	10.74	17.9	34.13	14.71	18.52	13.99	17.64	9.01	20.29				
HEMBA1006606	9.14	17.8	25.4	12.84	13.75	11.34	17.49	5.73	12.78				
HEMBA1006612	16.16	16.45	27.36	16.16	10.37	13.84	7.68	7.75	9.58		*		-
HEMBA1006617	8.08	9.55	19.24	13.65	9.22	10.71	8.25	4.71	9.91				
HEMBA1006624	62.58	66.3	115.43	55.71	47.06	62.71	45.87	24.82	44.31				
HEMBA1006631	23.12	25.87	43.15	23.48	22.27	20.06	24.55	15.53	27.45				
HEMBA1006635	7.91	10.88	14.85	9.02	10.78	9.39	11.43	5.66	11.05				
HEMBA1006639	10.04	12.39	17.07	18.66	19.19	12.58	8.27	4.47	14.67				
HEMBA1006643	1.84	4.34	3.2	4.98	3.53	3.26	2.93	0.82	1.75				
HEMBA1006648	15.53	17.03	27.49	19.15	15.29	16.67	5.29	8.82	12.26				
HEMBA1006652	26.71	34.75	50.3	32.97	21.76	18.68	16.24	13.51	23.67				
HEMBA1006653	7.56	6.61	17.15	7.18	4.77	7.22	2.33	2.95	3.74				
HEMBA1006658	19.91	14.88	49.21	18.71	18.4	21.38	11.54	8.35	7.4				
HEMBA1006659	58.61	60.76	125.49	159.5	103.52	108.54	57.82	49.19	67.43				
HEMBA1006665	2.46	4.7	11.42	4.57	4.2	3.45	4.37	1.96	4.61				
HEMBA1006666	3.78	4.89	6.54	3.83	3.74	5.58	5.07	2.85	4.33				
HEMBA1006671	29.88	46.04	31.81	11.03	10.78	7.48	20.4	8.57	17.2	**	*	-	-
HEMBA1006674	17.95	21.64	48.41	21.77	17.05	22.65	20.34	20.43	18.22				
HEMBA1006676	8.33	14.71	17.2	11.8	6.88	5.97	6.74	4.48	6.11		*		-
HEMBA1006682	5.28	7.81	6.48	5.22	3.34	3.44	5.44	2.35	3.91				
HEMBA1006688	8.06	7.99	15.76	5.58	7.11	7.53	6.82	4.86	5.53				
HEMBA1006695	11.68	16.81	23.72	8.98	10.42	13.13	10.55	9	11.41				
HEMBA1006696	12.25	15.75	12.83	8.51	9.6	6.76	4.49	2.19	4.51	*	**	-	-
HEMBA1006702	6.88	9.14	9.5	5.54	6.34	5.86	4.33	1.73	4.63	*	*	-	-
HEMBA1006707	12.13	15.02	19.11	19.48	16.83	14.64	14.25	5.63	13.01				
HEMBA1006708	7.17	12.19	21.37	12.13	8.06	8.49	3.77	4.26	7.59				
HEMBA1006709	13.09	19.04	28.5	14.85	14.05	15.86	11.87	11.01	16.42				
HEMBA1006717	5.25	5.26	12.53	4.74	4.01	3.68	7.38	2.38	6.67				
HEMBA1006724	12.11	8.3	19.78	5.53	10.32	5.8	9.44	6.24	6.16				
HEMBA1006731	7.48	7.6	18.92	6.67	8.76	6.75	5.19	3.77	3.96				
HEMBA1006737	6.06	6.19	10.33	4.37	4.14	4.69	4.38	0.91	4.4				
HEMBA1006742	8.98	8.7	24.13	7.5	9.95	8.07	10.84	6.04	17.08				
HEMBA1006743	14.91	22.66	22.54	17.15	17.28	14.05	13.93	8.87	7.89		*		-
HEMBA1006744	17.72	19.61	39.58	28.17	20.27	23.33	18.16	15.95	23.07				
HEMBA1006749	4.84	4.51	4.65	3.84	2.79	5.06	3.99	2.53	5.17				
HEMBA1006752	74.49	114.01	106.5	80.8	62.77	63.46	56.97	93.88	63.11				

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Table 379

HEMBA1006754	10.3	5.77	11.65	6.17	5.72	5.75	6.13	5.01	8.39				
HEMBA1006758	7.27	4.9	12.62	10.94	5.09	5.73	5.5	2.15	4.84				
HEMBA1006767	5.55	6.53	9.74	2.73	5.09	3.33	3.97	3.29	3.02		*		-
HEMBA1006770	10.91	18.24	23.01	9.34	17.17	9.49	6.46	5.37	4.52		*		-
HEMBA1006779	21.14	29.08	46.61	19.18	32.07	21.74	27.02	14.11	23.35				
HEMBA1006780	31.66	41.91	71.99	39.02	25.6	33.44	20.75	21.87	35.28				
HEMBA1006789	11.15	8.92	10.14	6.24	5.48	5.24	3.29	3.78	6.02	**	**	-	-
HEMBA1006795	13.29	18.12	23.2	10.87	8.5	11.23	14.12	7.4	15.69				
HEMBA1006796	8.15	7.65	12.79	2.99	3.39	3.14	3.97	0.85	2.9	*	*	-	-
HEMBA1006805	10.17	13.14	20.22	7.25	5.84	4.86	8.13	5.47	7.83	*		-	
HEMBA1006807	358.41	425.1	450.14	425.56	524.37	388.31	479.65	356.88	266.31				
HEMBA1006813	3.32	4.75	8.38	0.01	2.65	1.47	2.36	0.6	1.87				
HEMBA1006819	11.44	14.72	25.12	8.56	18.43	11.48	10.78	2.32	9.36				
HEMBA1006821	15.76	14.89	42.37	23.12	22.95	19.27	10.56	11	21.11				
HEMBA1006824	31.97	30.86	49.16	24.26	23.62	19.71	31.05	26.34	34.02				
HEMBA1006832	259.36	308.26	291.59	339.91	237.21	321.61	326.22	280.59	176.89				
HEMBA1006834	46.64	65.27	67.81	62.09	43.11	55.61	73	47.8	42.25				
HEMBA1006835	8.46	14.27	21.58	9.55	10.78	10.45	9.6	6.1	8.18				
HEMBA1006843	18.15	18.91	28.2	12.23	21.78	20.94	21.53	7.17	5.58				
HEMBA1006849	26.18	26.08	44.03	23.34	31.15	21.57	33.36	14.9	24.69				
HEMBA1006850	16.77	33.56	37.75	10.59	18.63	8	9.03	3.5	6.56		*		-
HEMBA1006861	14.67	13.53	34.61	20.34	16.15	19.04	12.38	6.63	17.89				
HEMBA1006865	39.2	38.77	61.65	71.58	60.52	57.06	33.27	28.86	36.65				
HEMBA1006867	18.5	15.53	22.34	9.22	8.88	9.34	9.42	6.3	3	**	**	-	-
HEMBA1006873	17.71	23.93	26.16	14.12	11.71	14.57	15.58	7.18	17.11	*		-	
HEMBA1006877	7.4	13.49	15.12	6.73	6.6	3.67	5.7	2.95	4.47		*		-
HEMBA1006878	10.48	14.11	25.64	11.23	13.75	11.88	9.01	2.84	7.36				
HEMBA1006879	12.94	16.27	24.73	12.26	12.67	8.96	12.1	3.4	9.76				
HEMBA1006884	16.51	27.4	33.59	6.17	20.26	51.39	18.62	5.59	4.55				
HEMBA1006885	29.88	29.68	41.54	20.77	25.78	20.37	13.71	10.53	21.42		*		-
HEMBA1006886	94.54	114.96	86.8	8.15	45.42	40.45	16.06	32.92	14.53	**	**	-	-
HEMBA1006889	11.07	12.36	15.21	4.3	6.85	5.29	4.87	2.48	1.64	**	**	-	-
HEMBA1006896	72.84	75.71	95.1	25.42	32.71	26.4	32.9	16.88	9.13	**	**	-	-
HEMBA1006900	25.47	32.8	47.12	42.47	30.76	32.5	22.96	11.97	13.31				
HEMBA1006902	4.95	12.4	20.5	3.65	6.21	3.85	6.17	0.96	2.8				
HEMBA1006912	17.87	28.61	49.99	20.94	22.1	17.02	26.3	12.33	21.55				
HEMBA1006914	76.35	138.05	152.36	81.86	82.01	60.45	85.41	43.28	74.2				
HEMBA1006916	15.23	15.18	19.35	6.9	10.02	9.36	4.27	4.91	5.74	**	**	-	-
HEMBA1006921	5.69	9.45	11.27	4.84	7.39	7.2	5.96	4.4	4.47				
HEMBA1006926	14.39	14.83	25.68	4.9	10.25	8.6	7.17	9.16	6.2		*		-
HEMBA1006927	8.1	6.16	12.12	3.55	6.9	3.55	4.27	4.44	3.56				
HEMBA1006929	20.15	20.6	39.98	22.07	23.94	22.4	25.87	18.49	21.97				
HEMBA1006936	9.54	10.99	23.15	1.82	9.22	9.34	13.47	4.19	5.58				
HEMBA1006938	3.12	8.25	12.19	4.54	5.27	8.96	3.85	0.26	1.77				
HEMBA1006941	38.07	33.9	81.07	14.16	37.03	19.11	37.54	10.57	9.16				
HEMBA1006942	17.04	18.44	31.05	13.54	11.67	15.34	9.95	7.49	11.08				
HEMBA1006945	67.94	90.41	117.96	45.68	44.82	62.84	58.07	38.55	55.06				
HEMBA1006949	5.04	6.37	14.93	11.38	7.05	7.71	7.34	3.55	6.74				
HEMBA1006952	4.19	5.26	9.54	3.87	5.23	3.34	4.22	1.4	1.92				
HEMBA1006960	34.21	40.14	82.69	40.95	44.04	37.38	52.24	36.27	39.73				
HEMBA1006973	11.14	12.47	24.84	14.07	12.49	8.94	10.47	5.46	6.01				
HEMBA1006974	9.69	21.72	26.59	5.58	10.54	8	10.23	6.86	3.65				
HEMBA1006976	5.49	4.82	13.28	5.67	2.91	2.68	2.79	1.22	3.42				
HEMBA1006989	5.64	5.97	15.87	14.35	9.67	15.25	5.09	3.23	6.48				
HEMBA1006993	22.88	33.04	62.59	43.82	36.96	35.47	29.4	20.95	25.28				
HEMBA1006996	6.77	6.15	10.45	9.29	8.92	7.56	4.85	2.62	3.17		*		-
HEMBA1007001	13.6	18.68	46.24	26.01	27.9	24.22	17.93	11.6	13.83				
HEMBA1007002	38.2	51.66	86.51	157.46	90.61	115.16	37.83	43.86	26.69				
HEMBA1007013	4.23	5.6	9.85	5.49	4.83	5.04	4.32	1.34	5.39				
HEMBA1007016	13.73	18.8	46.37	32.25	24.75	25.55	26.93	13.32	18.08				
HEMBA1007017	1.76	2.36	7.34	5.45	3.5	5.8	4.75	0.45	2.16				
HEMBA1007018	12.78	19.44	26.15	6.88	7.17	10.67	5.95	5.18	4.75		*		-
HEMBA1007044	4.27	3.89	8.13	7.26	4.08	4.08	4.49	2.95	4.25				
HEMBA1007045	3.76	6.62	12.6	6.66	6.82	7.16	7.91	2.23	5.58				

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Table 380

HEMBA1007051	8.21	9.64	21.16	10.38	7.94	9.6	8.59	4.82	5.46				
HEMBA1007052	0.84	3.34	5.89	3.8	5.54	5	4.04	2.23	3.75				
HEMBA1007053	13.43	20.61	15.83	23.76	9.7	6.82	3.37	2.88	5.47		**		-
HEMBA1007057	6.84	7.67	12.49	5.42	9.68	14.27	10.77	4.02	8.83				
HEMBA1007062	5.25	11.04	5.4	4.94	7.78	6.88	7.11	2.74	5.57				
HEMBA1007063	19.82	23.76	40.56	22.16	18.37	20.33	18.69	15.25	20.25				
HEMBA1007066	7.17	6.3	7.54	7.55	3.16	6.35	4.34	2.31	5.66		*		-
HEMBA1007069	6.08	6.94	13.93	10.41	5.55	7.88	5.56	3.75	4.11				
HEMBA1007073	5	7.14	13.19	9.06	6.96	8.85	10.68	5.02	4.92				
HEMBA1007076	9.13	8.92	19.82	9.03	17.18	17.73	15.84	7.01	8.52				
HEMBA1007078	47.57	62.26	92.7	36.29	60.73	51.72	32.07	18.35	34.97				
HEMBA1007080	86	60.21	81.69	89.81	65.76	74.19	50.6	40.71	38.08		*		-
HEMBA1007084	10.6	15.68	20.31	13.17	16.74	11.58	13.37	8.47	13.17				
HEMBA1007085	27.29	31.32	26.53	13.81	11.35	9.85	7.06	8.85	9.17	**	**	-	-
HEMBA1007087	17.6	23.13	29.36	17.3	13.84	15.36	6.49	22.47	10.72				
HEMBA1007089	21.17	21.1	33.63	20.7	38.69	28.03	18.24	32.57	32.51				
HEMBA1007095	201.88	116.22	315.3	326.58	303	223.56	75.5	112.08	127.01				
HEMBA1007101	27.84	40.49	45.85	23.93	27.74	34.28	41.09	23.85	46.77				
HEMBA1007104	4.09	6	7.77	5.68	5.26	4.31	5.49	1.3	6.52				
HEMBA1007106	21.73	33.28	23.78	16.4	24.34	20.37	10.72	5.09	4.25		**		-
HEMBA1007112	9.74	14.28	16.52	10.26	12.13	8.53	8.39	3.2	3.6		*		-
HEMBA1007113	21.85	25.07	43.45	24.93	19.55	20.96	26.57	21.39	27.54				
HEMBA1007121	143.44	168.43	201.05	310.6	189.7	223.39	139.17	100.56	162.13				
HEMBA1007129	6.41	8.28	18.59	3.42	2.84	6.23	5.66	3.45	4.93				
HEMBA1007147	12.43	15.07	27.38	13.28	12.69	11.69	10.77	9.49	8.81				
HEMBA1007149	15.43	22.2	36.85	20.24	33.61	28.67	16.97	12.22	16.92				
HEMBA1007151	6.66	4.91	10.19	4.89	4.76	3.64	3.37	0.61	3.29				
HEMBA1007172	5.54	5.79	15.25	6.45	6.57	4.48	5.2	2.26	4.93				
HEMBA1007174	5.55	6.74	11.4	7.96	7.31	3.31	8.36	1.4	3.1				
HEMBA1007176	10.89	13.76	22.08	12.85	11.37	10.5	5.77	8.47	15.97				
HEMBA1007178	12.93	22.04	21.56	10.13	15.89	11.16	5.44	5.45	3.49		**		-
HEMBA1007185	12.08	13.89	28.24	5.12	12.57	13.87	7.15	7.65	10.67				
HEMBA1007186	7.21	3.2	19.91	4.57	4.73	5.62	4.03	0.89	3.73				
HEMBA1007194	17.48	18.75	30.8	17.47	18.26	18.1	18.81	10.34	19.89				
HEMBA1007200	4.21	4.82	12.05	2.35	4.05	3.94	2.19	1.93	1.96				
HEMBA1007203	17.41	23.17	30.14	16.76	21.31	8.75	11.68	7.36	6.25		*		-
HEMBA1007206	25.5	42.75	37.89	30.71	35.28	24.97	38.96	21.71	36.83				
HEMBA1007224	24.39	40.17	34.49	15.91	19.51	9.53	6.52	8.53	10.32	*	**	-	-
HEMBA1007226	89.72	73.23	108.85	134.34	88.67	116.09	67.3	41.82	79.65				
HEMBA1007240	13.54	17.35	25.69	5.08	7.14	11.16	4.24	5.15	6.41		*		-
HEMBA1007241	5.35	7.7	9.62	3.24	3.12	3.91	4.59	2.56	3.21	*	*	-	-
HEMBA1007242	4.41	5.32	8.31	2.05	4.24	3.88	2.68	0.75	5.03				
HEMBA1007243	111.71	101.13	126.82	187.45	120.72	165.9	80.87	65.01	83.79		*		-
HEMBA1007251	4.65	5.56	13.42	3.87	5.2	4.27	3.75	1.77	3.34				
HEMBA1007256	7.71	17.43	18.8	11.41	15.37	11.45	13.72	5.68	6.36				
HEMBA1007267	27.14	33.68	57.79	28.23	30.36	27.93	22.24	21.62	27.1				
HEMBA1007273	5.82	10.89	12.53	5.12	4.08	4.32	3.9	1.99	5.52				
HEMBA1007279	8.03	6.83	14.11	6.96	6.78	5.74	5.78	2.58	3.49				
HEMBA1007281	4.41	6.17	11.59	1.95	1.64	1.99	3.42	2.15	2.75				
HEMBA1007283	10.13	14.5	18.59	11.27	10.46	9.5	8.86	8.35	11.65				
HEMBA1007288	10	10.12	23.07	7.39	8.9	6.31	9.07	7.22	9.19				
HEMBA1007291	3.94	6.53	14.21	2.35	5.74	4.15	6.79	3.29	5.42				
HEMBA1007299	60.36	57.45	88.44	47.01	83.94	54.92	41.98	17.99	24.76		*		-
HEMBA1007300	10.43	10.11	14.15	17.47	5.8	7.61	10.92	2.6	3.93				
HEMBA1007301	10.28	11.15	10.5	7.08	5.07	5.8	3.91	4.02	3.67	**	**	-	-
HEMBA1007319	7.15	12.6	10.93	3.57	6.52	4.89	3.16	3.33	2.24	*	*	-	-
HEMBA1007320	6.22	6.62	11.18	5.17	5.74	4.76	5.15	2.1	2.94				
HEMBA1007322	281.14	504.93	265.82	479.23	433.13	233.63	384.76	246.29	107.4				
HEMBA1007323	3.87	5.98	13.69	3.16	3.64	1.67	4.69	0.43	1.85				
HEMBA1007326	33.32	37.02	90.88	53.8	48.19	37.22	52.37	23.73	38.43				
HEMBA1007327	14.51	15.7	50.08	17.82	23.55	19.83	20.48	9.78	17.51				
HEMBA1007332	15.93	13.1	23.53	14.44	19.66	12.93	14.13	7.11	7.2				
HEMBA1007341	8.96	9.53	11.63	7.92	6.35	6.27	7.48	4.06	5.93	*	*	-	-
HEMBA1007342	5.2	5.9	6.99	1.75	3.52	2.76	4.48	1.49	2.47	*	*	-	-

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Table 381

HEMBA1007347	16.98	22.65	29.56	14.57	13.83	11.3	16.82	11.86	19.8				
HEMBA1007353	5.79	10.55	11.68	3.83	9.63	8.03	10.26	4.85	8.24				
HEMBB1000005	12.22	17.75	30.52	11.82	12.78	11.43	13.73	6.39	17.44				
HEMBB1000008	18.71	35.13	41.01	19.83	22.41	13.75	23.85	15.07	25.11				
HEMBB1000018	26.09	49.37	73.92	38.01	40.34	30.35	46.13	23.51	34.37				
HEMBB1000024	16.68	21.57	43.98	24.42	20.7	22.54	19.03	14.92	22.2				
HEMBB1000025	4.76	6.51	12.97	5.38	4.72	5.89	4.38	2.53	3.35				
HEMBB1000030	20.29	17.68	33.24	12.16	16.77	10.61	16.77	10.43	14.37				
HEMBB1000036	14.36	14.21	18.16	2.88	10.75	5.3	7.22	6.69	3.23	*	**	-	-
HEMBB1000037	11.11	16.21	12.93	4.27	8.42	4.3	6.83	2.67	4.79	*	*	-	-
HEMBB1000039	8.22	15.6	26.39	9.92	10.66	6.88	12.98	7.81	13.65				
HEMBB1000044	11.18	16.44	31.14	11.2	12.12	8.02	10.52	6.21	8.17				
HEMBB1000048	8.23	14.79	19.17	7.61	10.2	7.2	15.14	3.23	4.66				
HEMBB1000050	12.03	11.84	30.06	14.4	13.92	13.02	11.35	6.38	12.59				
HEMBB1000054	10.07	11.4	26.35	13.58	11.4	7.91	11.76	6.55	12.26				
HEMBB1000055	458.88	310.46	850.13	127.99	485.16	208.47	362.27	384.63	141.27				
HEMBB1000059	37.26	47.72	97.02	40.48	50.48	36.83	47.77	33.17	34.67				
HEMBB1000072	84.93	93.08	177.56	168.05	149.4	148.43	84.23	55.56	75.03				
HEMBB1000081	14.03	23.77	42.88	15.97	19.18	19.43	14.35	5.64	10.31				
HEMBB1000083	11.03	18.35	42.57	17.47	14.86	14.26	18.14	9.46	16.73				
HEMBB1000089	12.54	18.95	30.4	15.64	14.81	12.6	22.7	8.13	18.39				
HEMBB1000094	10.67	10.41	27.93	13.66	21.42	16.12	14.95	8.63	10.48				
HEMBB1000097	6.26	10.91	14.76	6.71	9.5	4.54	15.21	6.91	3.77				
HEMBB1000099	14.89	12.94	32.83	17.41	17.02	13.25	13.99	10.91	12				
HEMBB1000103	79.17	84.17	154.39	129.48	133.3	142.91	117.04	80.44	93.95				
HEMBB1000106	13.4	15.97	19.47	7.19	4.59	5.52	5.12	3.42	4.98	**	**	-	-
HEMBB1000113	4.8	10.67	20.57	6.45	7.88	9.01	9.02	3.11	6.76				
HEMBB1000119	3.97	10.01	14.45	4.41	4.33	3.8	9.37	5.02	5.7				
HEMBB1000133	88.66	47.28	101.21	23.18	118.13	70.04	134.7	41.76	81.57				
HEMBB1000134	13.38	15.77	31.72	20.8	11.19	14.5	6.59	5.64	9.53				
HEMBB1000136	34.17	26.36	69.3	67.42	34.73	49.05	25.95	21.33	26.27				
HEMBB1000141	7.91	11.34	20.35	10.92	8.05	11.46	11.73	5.94	9.7				
HEMBB1000144	8.4	6.34	18.36	7.4	9.42	9.69	10.21	5.05	11.22				
HEMBB1000147	3.5	3.8	22	5.61	6.52	8.28	7.06	1.83	3.83				
HEMBB1000152	1.94	5.3	5.59	10.75	5.38	4.1	5.98	1.86	3.56				
HEMBB1000154	7.08	8.64	11.01	9.8	10.82	8.45	9.52	5.05	11.09				
HEMBB1000155	7.22	13.83	13.07	9.95	12.99	12.51	9.62	5.43	10.29				
HEMBB1000173	36.12	47.88	77.86	40.67	28.34	43.42	25.94	23.15	34.58				
HEMBB1000175	4.3	6.41	7.7	6	3.69	3.11	3.98	4.45	4.04				
HEMBB1000176	23.34	24.4	50.1	18.86	26.55	28.15	17.6	14.1	16.3				
HEMBB1000198	1.73	5.17	9.68	5.19	3.63	4.66	4.31	1.03	3.4				
HEMBB1000208	2.42	2.22	6.16	4.71	3	3.25	2.71	1.91	2.68				
HEMBB1000209	4.99	7.73	19.16	5.65	5.94	7.5	3.72	1.31	4.4				
HEMBB1000212	4.66	5.69	7.88	3.69	6.97	3.08	4.71	1.75	3.95				
HEMBB1000215	16.57	20.63	27.19	17.82	25.31	15.88	26.39	12.95	25.36				
HEMBB1000217	25.38	37.33	52.96	16.88	15.01	12.09	9.3	23.54	15.2	*		-	
HEMBB1000218	31.37	54.57	73.09	37.79	38.52	34.06	37.08	24.06	36.49				
HEMBB1000226	12.28	16.29	20.13	10.11	7.98	11.16	5.4	9.82	9.11		*		-
HEMBB1000230	5.26	3.6	7.07	0.71	2.52	2.36	2.7	2.25	2.54	*	*	-	-
HEMBB1000240	5.06	6.06	9.84	4.39	4.5	5.46	2.75	2.24	3.3		*		-
HEMBB1000244	7.48	12.78	15.39	11.19	10.98	11.37	6.63	4.57	10.35				
HEMBB1000250	1.27	3.14	7.4	1.44	3.59	2.75	1.47	0.52	2.71				
HEMBB1000258	10.17	16.3	24.98	15.18	17.62	13.97	14.16	8.49	16.99				
HEMBB1000264	26.46	35.45	52.88	26.93	18.98	21.08	16.44	18.13	29.32				
HEMBB1000266	12	14.67	15.28	5.33	5.8	4.87	9.31	5.79	7.42	**	*	-	-
HEMBB1000272	8.27	9.13	14.25	3.35	4.95	7.95	4.41	2.77	4.49		*		-
HEMBB1000274	6.98	5.53	13.54	4.71	5.52	4.64	3.24	3.87	5.65				
HEMBB1000276	5.09	3.14	11.53	3.19	3.43	4.43	2.41	0.94	4.11				
HEMBB1000284	6.8	5.53	21.28	3.19	4.36	4.46	4.47	2.08	4.87				
HEMBB1000307	8.46	14.9	24.21	13.5	12.6	8.38	8.3	4.98	7.88				
HEMBB1000309	5.61	8.47	14.17	8.25	9.84	9.39	9.88	4.06	6.44				
HEMBB1000312	6.97	8.62	14.26	14.76	8.04	11.17	5.36	4.07	7.05				
HEMBB1000317	7.52	4.64	7.99	3.4	3.92	3.39	4.7	5.98	4.31	*		-	
HEMBB1000318	6.93	8.7	14.09	8.17	6.23	6.97	7.59	3.11	9.29				

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Table 382

HEMBB1000332	4.52	4.05	10.22	2.71	3.85	3.38	4.09	2.98	4.92				
HEMBB1000335	4.77	4.71	13.27	5.2	6.34	6.3	5.06	1.38	4.17				
HEMBB1000336	4.61	9.32	11.37	1.79	3.32	1.88	2.23	1.53	1.7	*	*	-	-
HEMBB1000337	29.33	35.43	67.58	48.11	46.55	55.37	21.92	22.71	26.93				
HEMBB1000338	34.7	54.08	50.89	33.23	39.29	35.27	51.12	24.63	33.57				
HEMBB1000339	10.36	11.59	21.89	13.7	11	9.9	8.4	6.43	14.47				
HEMBB1000341	7.15	6.94	11.5	5.95	5.91	6.13	8.18	5.44	9.71				
HEMBB1000343	22.54	22.93	36.07	24.96	20.99	25.34	24.47	20.51	25.26				
HEMBB1000354	24.93	29.93	37.49	16.95	17.28	19.25	24.74	17.57	19.26	*		-	
HEMBB1000358	4.2	3.56	9.08	2.24	3.75	2.51	2.41	0	3.07				
HEMBB1000369	7.77	9.59	8.26	0	3.16	0.74	4.97	3.09	8.59	**		-	
HEMBB1000373	4.9	5.6	9.86	3.73	5.67	3.02	3.88	2	4.12				
HEMBB1000374	33.91	39.77	79.58	37.61	43.98	33.27	46.4	29.37	24.06				
HEMBB1000376	23.61	37.46	51.78	28.25	29.92	24.65	24.75	22.13	31.75				
HEMBB1000383	18.87	23.34	28.75	7.22	8.14	5.48	8.08	3.98	4.53	**	**	-	-
HEMBB1000391	18.94	23.82	39.78	18.85	17.85	18.64	26.87	13.66	21.63				
HEMBB1000399	7.91	9.01	13.97	2.99	3.3	3.33	3.37	1.8	1.69	*	*	-	-
HEMBB1000402	5.66	7.15	13.91	3.49	5.23	2.79	6.8	2.16	2.32				
HEMBB1000404	4.49	5.13	14.15	2.37	3.5	4.1	3.34	1.25	1.09				
HEMBB1000407	10.22	16.01	27.46	10.21	12.59	7.8	5.46	2.69	5.89				
HEMBB1000420	8.96	13.82	23.72	10.31	11.56	10.07	12.86	5.36	9.15				
HEMBB1000430	87.5	75.56	120.02	34.45	32.4	42.59	83.02	74.93	33	*		-	
HEMBB1000434	34.1	37.7	48.77	30.73	22.51	21.34	32.9	22.77	33.21	*		-	
HEMBB1000438	4.47	5.36	6.73	3.08	3.98	3.03	2.33	1.63	2.04	*	**	-	-
HEMBB1000441	14.04	26.42	32.37	16.04	15.64	13.8	26.09	16.54	18.05				
HEMBB1000447	26.11	49.46	42.13	39.56	42.28	10.3	26.83	15.38	20.58				
HEMBB1000449	4.61	5.17	16.11	3.66	5.27	3.1	5.36	1.18	6.41				
HEMBB1000453	36.46	39.41	48.95	17.29	27.48	11.55	15.42	4.83	8.75	*	**	-	-
HEMBB1000455	7.98	15.4	31.12	12.14	13.6	12.23	19.02	4.77	15.17				
HEMBB1000472	8.9	8.65	20.38	10.03	8.41	7.69	7.24	3.85	5.6				
HEMBB1000480	18.47	20.31	37.47	19.05	17.04	11.84	20.16	15.95	20.84				
HEMBB1000486	36.69	36.48	47.19	21.3	19.24	16.88	39.82	23.52	22.96	**		-	
HEMBB1000487	6.37	6.26	12.27	7.11	4.47	4.08	6.03	4.45	5.18				
HEMBB1000490	32.85	71.05	75.4	38.48	33.85	25.5	47.17	24.97	28.6				
HEMBB1000491	10.98	13.88	21.94	11.39	11.14	7.83	9.44	3.7	10.75				
HEMBB1000492	11.93	15.38	18.28	8.6	7.89	5.65	7.79	2.28	4.01	*	*	-	-
HEMBB1000493	3.37	12.88	19.63	10.93	27.47	71.09	13.51	1.84	8.84				
HEMBB1000510	11.39	18.53	31.92	20.35	17	14.3	15.03	12.6	21.32				
HEMBB1000516	5	6.48	9.48	3.37	2.52	5.44	4.17	3.02	4.74				
HEMBB1000518	5.79	7.56	16.99	3.63	4.25	4.51	8.74	3.95	5.88				
HEMBB1000523	16.51	22.61	33.14	14.54	14.09	13.74	17.51	11.52	13.77				
HEMBB1000530	6.45	6.62	14.38	4.57	5.23	3.03	6.95	3.14	3				
HEMBB1000542	11.01	10.05	25.81	5.58	5.42	6.88	5.64	1.26	2.47				
HEMBB1000550	7.5	9.67	18.88	5.5	6.7	4.85	3.66	1.58	2.78				
HEMBB1000554	23.66	38.54	60.71	31.87	34.21	23.57	36.99	19.84	22.96				
HEMBB1000556	5.71	9.66	13.39	4.65	5.23	10.47	3.94	4.86	6.74				
HEMBB1000564	7.31	9.82	18.45	11.61	10.28	10.62	15.74	5.76	7.4				
HEMBB1000567	20.61	20.17	47.53	8.75	7.89	6.38	13.88	8.67	4.74				
HEMBB1000569	5.63	6.5	12.71	2.7	3.07	4.45	4.1	3.02	2.02				
HEMBB1000573	32.51	36.2	72.29	43.4	30.21	37.17	37	20.09	25.58				
HEMBB1000575	14.84	26.39	42.18	17.14	17.78	15.29	22.14	11.44	16.53				
HEMBB1000579	12.25	14.06	28.61	6.45	6.01	11.92	12.64	5.71	5.94				
HEMBB1000585	4.75	6.58	10.45	5.85	6.89	6.63	6.35	0.91	4.03				
HEMBB1000586	9.22	12.19	32.5	16.92	12.87	17.45	7.51	6.24	9.01				
HEMBB1000589	11.66	16.54	23.61	18.44	15.28	16.1	11.67	7.91	7.82				
HEMBB1000591	12.71	17.74	34.25	24.96	19.88	19.6	12.6	9.24	10.66				
HEMBB1000592	4.57	3.51	5.52	1.66	2.6	2.47	2.07	3.49	1.32	*		-	
HEMBB1000593	91.28	145.08	255.41	284.78	269.98	262.29	122.51	62.28	150.94				
HEMBB1000595	28.02	34.64	53.56	11.28	18.32	41.15	22.88	29.26	17.38				
HEMBB1000598	22.01	31.15	65.04	24.88	33.54	29.35	68.32	20.78	23.46				
HEMBB1000611	2.41	5.2	8.28	7.8	5.78	3.85	5.15	1.83	3.38				
HEMBB1000617	53.65	47.37	106.59	110.75	55.04	84.65	42.52	37.92	47.84				
HEMBB1000623	31.42	31.62	79.25	50.87	28.93	40.28	29.97	27.06	51.77				
HEMBB1000630	5.75	17.04	13.07	8.82	8.82	8.76	7.96	4.83	11.56				

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Table 383

HEMBB1000631	17.85	20.22	28.17	18.29	17.71	18	15.1	13.03	22.53				
HEMBB1000632	9.09	8	17.51	9.07	9.79	9.7	5.89	4.13	8.31				
HEMBB1000636	2.41	3.55	6.37	2.23	5.22	2.73	5.28	1.01	4.17				
HEMBB1000637	10.09	17.58	15.59	10.48	18.82	18.4	10.07	3.67	7.99				
HEMBB1000638	2.99	4.17	4.52	3.32	2.17	3.48	2.49	1.75	2.68		*		-
HEMBB1000642	39.5	47.36	81.46	47.61	39.34	45.01	39.82	28.49	56.57				
HEMBB1000643	19.66	15.32	32.08	23.95	12.4	14.81	11.1	10.59	13.67				
HEMBB1000649	12.99	15.1	28.14	16	12.05	14.32	13.77	8.35	17				
HEMBB1000652	14.35	8.01	17.67	7.91	13.41	10.82	9.88	9.25	11.18				
HEMBB1000655	4.61	7.58	7.57	5.6	5.2	3.31	4.16	0.72	5.12				
HEMBB1000665	4.16	6.24	9.15	3.47	7.38	6.78	5.21	1.62	5.11				
HEMBB1000668	16.93	27.34	0.25	1.82	1.14	0.36	23.87	15.76	19.86				
HEMBB1000671	38.43	46.48	92.78	44.14	31.73	40.3	25.53	28.64	41.28				
HEMBB1000673	32.99	36.97	43.71	17.4	18	19.87	6.02	26.42	8.4	**	*	-	-
HEMBB1000679	47.01	69.39	88.27	46.41	43.74	44.85	52.81	42.78	53.45				
HEMBB1000684	6.8	10.16	24.24	9.32	9.77	12.54	6.96	8.48	13.11				
HEMBB1000692	16.03	14.55	25.59	15.28	15.92	17.55	16.09	8.5	14.57				
HEMBB1000693	1.76	2.64	8.52	1.53	4.27	2.95	4.06	0.19	6.13				
HEMBB1000705	14.59	17.08	31.29	17.89	15.24	18.52	13.25	7.08	17.6				
HEMBB1000706	11.29	12.22	20.56	12.35	17.3	12.09	6.4	4.7	7.15		*		-
HEMBB1000709	45.75	62.83	118.05	70.74	40.37	58.09	48.11	45.53	67.69				
HEMBB1000714	31.43	34.95	47.38	12.83	21.37	16.81	5.14	8.31	8.35	*	**	-	-
HEMBB1000725	5.12	8.87	10.38	4.23	3.1	4.36	4.23	1.66	4.96				
HEMBB1000726	0.86	1.95	5.91	0.06	0.38	0.65	0.77	3.05	1.2				
HEMBB1000729	6.42	9.45	14.46	7.38	5.18	5.16	5.32	4.5	6.56				
HEMBB1000738	18.18	14.39	28.4	16.66	7.78	8.45	31.84	5.87	7.73				
HEMBB1000749	19.05	25.87	36.38	23.07	19.8	20.09	17.18	15.06	19.35				
HEMBB1000763	2.4	3.95	6.27	1.43	7.01	5.93	4.26	0.57	3.97				
HEMBB1000770	32.56	40.83	87.59	46.89	28.6	43.89	33.53	25.96	52.34				
HEMBB1000774	35.04	53.35	80.31	43.91	38.96	45.26	39.09	37.25	56.98				
HEMBB1000777	45.62	74.38	70.43	17.25	25.76	25.38	18.75	21.39	27.43	*	*	-	-
HEMBB1000781	6.33	5.26	11.47	6.25	5.6	4	3.41	2.88	6.03				
HEMBB1000788	18.37	23.49	32.23	14.46	15.9	16.37	22.44	12.27	19.59				
HEMBB1000789	23.79	24.39	34.32	14.31	19.85	15.3	18.54	10.27	14.08	*	*	-	-
HEMBB1000790	5.59	8.56	17.48	2.6	6	2.29	4.26	1.79	6.06				
HEMBB1000794	18.79	29.68	40.8	14.17	25.07	14.74	20.31	17.36	24.13				
HEMBB1000807	12.94	8.25	2.03	1.02	2.13	2.36	2.69	4.28	6.87				
HEMBB1000809	78.77	111.21	120.34	77.13	62.86	41.38	80.78	69.07	111.98				
HEMBB1000810	10.52	9.56	13.14	4.85	2.89	5.55	9.37	2.32	10.71	**		-	
HEMBB1000821	11.49	9.52	21.32	7.91	10.41	6.87	11.4	5.99	7.83				
HEMBB1000822	14.47	17.81	31.19	12.64	15.48	12.05	15.29	6.81	15.5				
HEMBB1000826	7.31	8.22	12.01	4.01	6.22	5.16	2.28	1.16	3.63		*		-
HEMBB1000827	3.32	10.97	13.01	2.13	2.92	3.29	2.14	1.1	3.35				
HEMBB1000831	2664.2	3968.9	2993.4	2288.3	2955.9	3122.5	3699.5	1769.3	603.46				
HEMBB1000835	65.9	87.92	134.3	99.52	82.05	71.78	46.56	49.76	78.94				
HEMBB1000840	22.85	22.57	43.26	24.08	23.34	18.79	20.99	18.48	32.32				
HEMBB1000848	11.78	12.27	18.41	9.27	11.15	6.47	11.75	6.28	10.74				
HEMBB1000852	6.96	7.13	13.91	5.13	5.29	6.06	3.72	3.05	2				
HEMBB1000857	14.9	19.2	33.57	16.67	15.76	14.92	14.34	9.21	17.14				
HEMBB1000858	18.62	21.62	40.52	17.01	24.14	29.4	19.12	14.81	25.58				
HEMBB1000867	3.35	5.16	11.87	1.01	3.43	0.49	5.8	0.59	7.29				
HEMBB1000870	5.48	10.65	17.84	3.33	10.48	4.74	3.16	0.41	3.45				
HEMBB1000876	9.67	10.87	29.49	19.7	15.97	14.54	9.25	6.54	15.24				
HEMBB1000881	16.87	17.18	33.12	17.09	13.5	10.07	12.12	11.55	18.55				
HEMBB1000883	6.22	6.79	8.96	2.61	2.5	1.97	4.54	1.83	3.25	**	*	-	-
HEMBB1000887	5.96	5.57	6.2	3.69	2.17	1.88	2.97	1.27	2.62	**	**	-	-
HEMBB1000888	3.12	5.25	10.45	4.39	3.56	2.35	3.24	2.38	1.97				
HEMBB1000890	10.06	35.98	23.82	9.78	19.94	41.91	13.4	7.59	9.49				
HEMBB1000893	34.65	25.07	51.31	20.43	19.67	19.95	21.33	13.24	12.88				
HEMBB1000900	14.11	15.32	20.53	11.04	14.54	9.38	11.56	4.15	3.3		*		-
HEMBB1000905	8.7	11.8	4.84	3.81	3.66	3.74	10.34	4.58	8.59				
HEMBB1000908	10.34	11.07	11.16	10.97	10.92	24.1	19.82	7.35	8.29				
HEMBB1000910	14.49	13.52	29.52	12.54	13.67	12.24	17.07	12.01	16.77				
HEMBB1000913	52.28	41.72	87.34	40.16	51.04	32.05	56.11	40.33	43.91				

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Table 384

HEMBB1000915	26.06	60.99	57.47	25.29	36.05	22.49	27.81	17.27	27.94				
HEMBB1000917	5.69	5.32	12.64	3.03	4.44	3.24	2.96	0.58	2.57				
HEMBB1000927	17.9	20.69	49.41	20.99	18.29	12.76	18.76	15.57	19.4				
HEMBB1000932	14.04	31.9	58.79	23.84	30.24	22.56	24.51	13.79	19.35				
HEMBB1000933	73.2	82.97	106.78	17.69	17.17	51.59	30.19	46.68	77.12	*		-	
HEMBB1000936	28.64	37.39	39.34	11.49	17.42	18.08	9.46	19.76	21.12	**	*	-	-
HEMBB1000939	13.01	16.47	24.62	8.79	10.18	11.8	13.33	5.75	13.18				
HEMBB1000941	55.55	67.95	96.78	34.29	51.94	34.02	64.38	50.22	47.74				
HEMBB1000947	13.1	15.93	33.36	11.69	15.06	7.82	14.81	8.66	11.7				
HEMBB1000954	9.7	14.84	29.47	10.7	10.34	11.24	13.58	8.18	14.09				
HEMBB1000959	5.31	7.05	16.81	1.63	2.59	1.53	2.83	0	2.89				
HEMBB1000973	7.09	9.47	31.83	11.47	11.07	10.69	11.63	4.69	9.55				
HEMBB1000975	3.47	3.38	0.39	0.25	0.11	0.78	2.64	0.48	3.5				
HEMBB1000981	13.64	11.74	28.6	8.77	7.91	9.41	10.88	6.85	13.87				
HEMBB1000985	21.62	19.08	51.54	22.07	25.82	18.12	29.3	14.45	17.75				
HEMBB1000991	46.57	60.97	104.38	49.12	52.31	37.89	58.02	46.82	42.32				
HEMBB1000996	7.55	10.13	19.44	15.43	7.58	7.76	25.49	7.93	12.48				
HEMBB1001000	8.66	10.27	29.46	13.94	12.61	10.4	13.32	7.07	9.02				
HEMBB1001004	4.52	20.53	22.05	7.15	7.85	4.71	7.51	4.91	9.37				
HEMBB1001008	27.45	57.49	106.29	36.82	29.09	41.72	54.86	25.88	43.51				
HEMBB1001011	13.92	18.59	22.13	8.85	6.12	13.6	9.78	8.17	13.65				
HEMBB1001014	4.93	5.88	7.48	5.94	4.03	6.17	3.66	1.76	2.96		*		-
HEMBB1001020	38.49	45.64	94.13	52.12	43.15	44.7	42.48	28.95	25.72				
HEMBB1001024	14.35	17.88	33.12	21.84	15.86	15.33	12.31	9.54	11.76				
HEMBB1001026	36.33	37.82	64.87	35.84	31.03	31.81	34.99	27.91	28.23				
HEMBB1001037	29.37	38.91	99.73	42.44	38.61	41.96	49.51	23.14	48.42				
HEMBB1001042	40.43	19.68	79.17	12.87	30.43	38.57	43.54	27.06	24.73				
HEMBB1001046	1.02	3.17	4.37	2.13	2.63	1.33	3.19	0	2.81				
HEMBB1001047	3.32	3.99	7.05	6.87	5.14	9.57	4.92	2.39	5.02				
HEMBB1001048	14.93	18.87	36.47	38.03	15.11	21.97	9.91	8.51	13.37				
HEMBB1001051	16.67	10.51	26.31	24.66	18.42	23.37	16.85	8.02	15.72				
HEMBB1001056	5.76	6.07	15.19	9.62	10.04	7.15	7.61	2.99	9.72				
HEMBB1001058	13.02	13.37	20.82	14.04	12.97	13.5	13.64	8.33	17.02				
HEMBB1001060	6.48	6.79	11.56	3.09	7.6	8.52	5.42	2.73	5.08				
HEMBB1001063	7.02	9.34	7.27	6.14	6.79	5.01	6.52	5.39	11.16				
HEMBB1001068	12.88	13.51	18.25	11.13	9.67	11.92	6.97	9.12	12.67				
HEMBB1001082	19.71	21.28	25.07	26.2	26.41	15.74	14.59	12.53	27.85				
HEMBB1001095	9.14	8.65	18.5	8.62	9.69	8.93	5.69	6.23	9.72				
HEMBB1001096	44.08	45.29	88.46	46.23	37.21	42.49	31	20.55	25.13				
HEMBB1001101	14.24	13.37	19.97	9.53	14.04	14.7	13.73	9.26	15.99				
HEMBB1001102	5.29	6.01	11.42	4.54	5.69	5.17	5.82	3.61	6.55				
HEMBB1001104	38.08	39.86	49.87	41.44	36.7	31.13	23.82	16.12	29.93		*		-
HEMBB1001105	44.24	54.5	42.57	26.76	34.74	25.96	40.78	32.97	47.69	*		-	
HEMBB1001112	7.32	12.27	12.46	6.67	5.72	6.06	2.52	6.54	5.01		*		-
HEMBB1001113	12.36	16.73	27.57	10.87	11.17	11.23	11.03	6.35	13.81				
HEMBB1001114	10.5	25.04	16.53	8.31	9.62	7.81	7.26	6.53	13.76				
HEMBB1001115	5.38	5.54	12.69	5.57	5.33	6.84	5.79	8.01	10.93				
HEMBB1001117	24	32.48	48.34	30.8	26.94	25.33	34	33.8	46.28				
HEMBB1001119	6.59	8.79	10.75	5.08	5.94	5.54	5.24	3.59	5.78		*		-
HEMBB1001126	22.85	31.95	38.8	19.87	19.28	19.37	24.09	9.52	26.55				
HEMBB1001133	2.49	4.42	8.71	2.43	5.35	3.57	4.22	0.99	2.59				
HEMBB1001137	7.73	11.05	0	0.73	0.56	0.68	7.84	6.26	16.01				
HEMBB1001142	3.94	3.85	6.48	2.73	4.14	2.88	2.5	3.32	8.04				
HEMBB1001145	7.24	10.68	17.23	5.39	7.36	5.26	4.34	3.98	7.6				
HEMBB1001151	3.26	6.63	6.67	3.5	3.71	2.34	0.95	2.94	4.05				
HEMBB1001153	3.1	3.77	9.68	1.47	2.32	1.7	2.21	0	1.53				
HEMBB1001158	5.14	4.68	9.64	3.27	3.84	3.55	2.97	1.38	2.99				
HEMBB1001169	31.33	46.44	55.42	27.9	34.88	25.03	41.78	26.83	37.34				
HEMBB1001170	8.62	15.69	19.05	7.59	11.25	8.63	12.14	5.58	9.38				
HEMBB1001175	2.65	3.14	5.1	4.52	2.61	4.91	2.72	1.86	6.12				
HEMBB1001177	5.44	6.28	5.09	1.64	3.43	6.94	2.77	2.32	6.91				
HEMBB1001182	18.97	18.18	22.47	9.28	11.35	10.35	7.83	8.39	8.5	**	**	-	-
HEMBB1001192	9.02	9.64	12.65	5.82	4.73	5.18	6.79	2.78	10.91	*		-	
HEMBB1001199	4.71	4.4	13.79	2.26	2.76	5.59	3.91	3.02	2.96				

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Table 385

HEMBB1001200	13.2	15.34	26.9	9.43	12.58	11.64	13.65	8.01	17.32				
HEMBB1001208	18.63	26.31	21.34	16.48	23.59	8.33	19.57	7.02	6.33				
HEMBB1001209	6.61	9.43	16.76	4.47	13.17	7.28	9.02	4.73	7.13				
HEMBB1001210	2.22	5.57	9.4	5.43	2.97	2.71	2.73	1.63	4.83				
HEMBB1001215	9.7	12.03	15.37	9.6	10.02	9.52	8.36	4.91	10.29				
HEMBB1001217	10.51	10.25	17.62	6.77	6.49	7.62	10.25	4.74	16.86				
HEMBB1001218	6	5.57	10.2	5.12	3.8	3.11	4.86	3.23	6.96				
HEMBB1001221	26.87	26.88	47.38	27.34	25.86	18.24	28	17.58	20.46				
HEMBB1001224	16.71	16.42	17.84	3.84	6.91	9.28	7.94	2.93	4.93	**	**	-	-
HEMBB1001230	17.23	21.95	42.64	15.78	20.28	10.72	28.16	18.31	25.4				
HEMBB1001234	6.94	12.6	13.24	4.58	8.31	8.14	5.53	1.54	8.42				
HEMBB1001235	4.87	3.91	1.57	0	1.12	0.17	1.32	0.88	4.29	*		-	
HEMBB1001237	5.75	2.45	7.86	3.45	3.48	1.87	2.9	1.6	4.06				
HEMBB1001242	16.88	13.35	16.55	9.1	8.16	9.95	11.54	6.31	10.57	**	*	-	-
HEMBB1001244	35.65	49.79	60.5	32.41	25.43	27.28	45.76	28.88	37.22		-		
HEMBB1001249	22.08	31.03	56.18	21.17	26.84	20.21	27.38	14.91	24.06				
HEMBB1001253	28.9	34.49	70.42	28.32	28.95	21.57	41.19	24.41	34.07				
HEMBB1001254	7.43	6.21	17.96	4.5	6.62	3.53	4.22	0.83	3.95				
HEMBB1001266	69.19	45.43	92.09	93.11	71.97	69.72	54.64	34.46	57				
HEMBB1001267	104.19	98.07	152.36	13.92	33.06	57.1	34.39	45.85	70.55	*	*	-	-
HEMBB1001271	34.55	33.29	51.36	34.34	20.46	23.71	30.23	24.87	29.48				
HEMBB1001282	9.97	10.71	15.91	7.88	6.97	9.33	8.95	7.26	10.69				
HEMBB1001287	3.47	3.55	8.03	3.1	1.84	1.48	2.02	1.47	1.7				
HEMBB1001288	15.95	79.12	35.23	25.95	31.84	28.36	30.82	15.48	12.44				
HEMBB1001289	22.37	27.51	58.3	21.33	26.2	17.4	27.36	15.96	26				
HEMBB1001290	4.47	6.46	15.08	5.02	4.85	3	3.41	2.52	3.43				
HEMBB1001294	300.12	442.69	478.77	294.44	431.41	291.22	536.94	211.14	291.4				
HEMBB1001299	11.76	27.27	23.84	14.94	18.67	41.4	14.69	12.85	20.6				
HEMBB1001302	14.9	20.75	33.76	16.74	10.48	13.15	15.46	13.18	16.41				
HEMBB1001304	20.54	137.19	27.35	22.15	29.27	12.7	29.77	14.5	13.73				
HEMBB1001314	6.45	11.88	16.63	9.21	7.91	6.84	9.36	5.15	7.34				
HEMBB1001315	4.17	4.2	11.99	3.59	3.25	2.94	5.12	2.66	3.24				
HEMBB1001317	58.08	165.69	115.47	26.35	66.22	33.54	41.88	11.39	13.42		*		-
HEMBB1001326	7.12	11.9	25.13	9.45	10.76	5.58	7.57	2.63	8.72				
HEMBB1001331	60.43	105.03	131	66.61	74.76	59.35	124.09	50.05	41.99				
HEMBB1001335	0.53	0.14	1.28	1.92	0.74	0.41	1.38	0	1.24				
HEMBB1001337	19.31	21.8	38.53	21.67	17.28	16.88	20.3	14.12	26.23				
HEMBB1001339	6.1	5.5	14.98	6.52	5.57	3.43	4.24	2.59	4.91				
HEMBB1001344	11.08	7.69	21.58	3.98	10.13	4.45	6.01	7.37	4.42				
HEMBB1001346	14.51	8.09	19.68	7.72	9.53	5.04	11.31	3.15	5.25				
HEMBB1001348	2.18	3.12	12.35	0.43	2.84	1.52	3.82	0.54	2.87				
HEMBB1001350	52.05	108.41	129.66	78.51	93.58	81.19	64.58	43.45	65.59				
HEMBB1001356	7.52	9.31	26.43	13.44	18.12	16.4	11.29	5.29	11.49				
HEMBB1001364	8.27	9.27	21.55	13.04	8.88	12.02	9.82	4.71	9.74				
HEMBB1001366	11.82	16.33	29.77	17.62	9.11	9.15	17.69	10.49	12.45				
HEMBB1001367	34.9	33.46	79.86	33.05	29.6	26.79	45.62	23.04	29.37				
HEMBB1001369	13.59	34.47	15.16	9.61	17.82	9.58	10.33	11.36	4.3				
HEMBB1001380	5.78	6.69	14.57	4.06	3.91	3.5	3.91	2.87	4.28				
HEMBB1001381	7.8	18.4	21.36	7.96	16.58	12.19	13.62	2.72	8.14				
HEMBB1001384	64.99	90.97	10.61	0.27	3.72	0.15	67.41	60.83	3.42				
HEMBB1001387	12.67	18.5	30.56	17.22	19.87	15.36	19.61	9.85	12.99				
HEMBB1001394	1.26	2.69	4.65	6.43	2.24	3.63	0.47	1.11	0.58				
HEMBB1001407	7.9	11.42	30.12	19.8	14.97	11.43	10.87	6.27	10.35				
HEMBB1001410	2.04	3.94	3.61	2.8	2.74	2.85	1.42	0.21	2.14				
HEMBB1001413	4.48	4.13	8.85	5.53	3.83	5.6	1.34	2.67	1.9				
HEMBB1001419	11.47	23.84	24.98	19.26	14.85	15.61	11.95	7.31	16.96				
HEMBB1001421	5.76	4.41	16.42	7.89	11.28	6.94	5.16	2.14	5.02				
HEMBB1001424	2.91	4.4	4.11	0.76	0	0.56	5.88	1.84	0.07	**		-	
HEMBB1001426	14.06	23.97	51.32	27.45	25.66	29	18.89	8.5	8.91				
HEMBB1001429	6.88	11.32	20.01	14.76	14.71	20	10.35	6.2	12.32				
HEMBB1001436	18.71	17.94	33.05	24.24	11.69	16.55	21.47	12.89	21.69				
HEMBB1001443	19.58	21.95	43.4	20.44	16.81	19.91	22.72	13.56	24.01				
HEMBB1001449	35.58	35.95	71.7	35.81	35.7	39.37	42.62	30.92	51.15				
HEMBB1001454	4.44	10.09	10.48	10.32	5.73	8.72	4.72	2.95	5.93				

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Table 386

HEMBB1001458	9.69	12.19	21.36	34.84	17.29	10.08	13.2	9.97	12.41				
HEMBB1001461	19.67	23.1	39.56	20.5	28.42	24.75	17.54	14.4	25.15				
HEMBB1001463	19.56	21.33	35.61	31.93	33.77	43.28	30.72	20.68	36.42				
HEMBB1001464	28.01	27.99	31	14.62	14.82	15.04	16.45	13.58	23.87	**	*	-	-
HEMBB1001466	15.16	15.92	27.83	19.85	13.38	15.96	13.7	10.31	15.02				
HEMBB1001482	17.23	20.81	35.32	19.01	19	19.25	19.83	14.79	21.88				
HEMBB1001500	41.82	45.54	68.26	37.83	39.48	37.77	46.2	37.01	39.45				
HEMBB1001505	20.94	22.59	32.35	26.78	22.08	24.15	26.64	17.19	32.59				
HEMBB1001521	8.53	7.62	10.6	8.16	6.3	6.64	6.41	3.73	7.14				
HEMBB1001527	2.99	3.88	4.38	4.6	7.15	3.37	3	1.09	4.09				
HEMBB1001530	3.48	3.01	4.27	1.8	4.75	3.13	7.05	4.01	3.15				
HEMBB1001531	36.17	50.68	53.86	24.43	15.05	19.88	14.37	19.2	25.31	*	*	-	-
HEMBB1001532	17.53	24.2	32.45	18.39	15.75	13.6	15.22	13.76	17.31				
HEMBB1001535	12.38	16.91	23.89	12.47	13.36	10.82	9.04	12.27	13.78				
HEMBB1001536	66.38	84.8	143.72	91.2	78.03	69.03	101.64	71.92	118.47		-		
HEMBB1001537	11.79	11.39	16.93	9.29	11.02	10.91	6.73	5.87	10.85				
HEMBB1001542	14.96	22.23	29.71	13.95	16.64	16.35	12.71	5.92	15.48				
HEMBB1001543	23.66	28.65	30.69	20.28	24.21	31.58	17.34	19.58	58.07				
HEMBB1001547	23.94	50.04	39.45	14.74	15.27	12.72	12.08	2.84	4.52	*	*	-	-
HEMBB1001548	3.11	4.4	5.6	1.9	1.94	2.29	3.65	4.19	3.74	*		-	
HEMBB1001551	3.8	7.07	10.09	4.64	4.24	4.26	3.14	1.65	6.16				-
HEMBB1001555	8.19	9.59	15.51	4.72	6.09	5.64	3.45	5.22	5.59				
HEMBB1001562	17.05	18.48	38.18	19.29	13.39	17.57	16.22	12.15	22.52				
HEMBB1001564	38.37	50	64.37	49.41	38.27	48.76	40.56	25.46	46.57				
HEMBB1001565	18.11	21.08	35.2	23.9	18.29	10.69	18.09	9.6	15.5				
HEMBB1001569	18.83	22.86	28.98	20.6	18.61	17.83	18.18	11.82	14.18				
HEMBB1001573	3.68	5.99	8.15	7.26	5.87	2.52	10.81	4.11	5.2				
HEMBB1001585	31.55	42.11	57.35	32.5	28.22	32.05	31.45	26.22	33.57				
HEMBB1001586	19.62	27.08	60.2	25.12	17.34	21.21	21.42	13.56	26.31				
HEMBB1001588	3.6	1.4	8.8	2.53	0.56	1.81	2.28	0.36	3.78				
HEMBB1001595	10.36	11.37	25.05	8.69	10.88	9.92	9.72	7.65	13.65				
HEMBB1001596	50.23	70.48	94.67	85.43	78.99	83.08	60.67	47.9	57.78				
HEMBB1001599	12.08	19.55	22.95	3.76	11.11	7.77	4.14	3.06	5.8		*		-
HEMBB1001603	15.69	23.5	36.56	18.96	19.27	14.23	19.02	14.12	17.69				
HEMBB1001606	8.92	10.53	14.14	3.61	11.6	8.26	6.12	2.83	3.66		*		-
HEMBB1001612	12.97	18.3	27.94	17.56	18.03	14.45	13.69	13.84	21.14				
HEMBB1001618	47.24	51.05	53.93	31.05	43.7	40.99	38.7	45.72	63.89	*		-	
HEMBB1001619	21.53	28.8	35.45	21.69	15.6	18.53	19.99	9.27	17.16				
HEMBB1001623	32.27	35.63	43.91	23.19	18.98	32.29	44.61	25.32	56.22				
HEMBB1001625	8.57	7.58	12.04	5.34	5.5	6.91	4.26	3.63	6.59		*		-
HEMBB1001630	10.5	14.13	23.29	7.12	9.43	7.75	11.72	5.74	8.87				
HEMBB1001635	8.75	10.43	14.63	5.84	10.39	7.88	13.65	6.82	10.88				
HEMBB1001637	32.58	33.36	51.7	33.85	36.88	33.36	45.82	19.62	25.12				
HEMBB1001641	50.01	60.79	92.28	48.36	49.98	43.85	47.93	38.87	56.74				
HEMBB1001653	12.57	22.18	30.48	17.59	15.29	13.82	24.06	13.06	30.12				
HEMBB1001665	3.93	2.53	9.42	3.83	1.95	2.69	2.78	1.9	1				
HEMBB1001666	19.92	21.89	36.37	13.51	17.12	14.78	11.97	10.86	17.21				
HEMBB1001667	16.89	20.47	51.29	17.31	18.04	14.47	10.43	9.14	14.45				
HEMBB1001668	4.06	3.82	13.97	2.65	3.74	1.89	2.27	0.07	2.33				
HEMBB1001669	4.2	4.89	17.86	5.72	6.1	3.19	6.26	1.74	4.46				
HEMBB1001670	46.37	46.73	48.84	13.56	78.84	42.13	34.32	15.02	19.72		*		-
HEMBB1001673	67.96	61.75	141.78	71.26	44.3	44.21	62.82	56.55	66.02				
HEMBB1001675	17.04	14.33	30.97	18.1	10.45	10.58	21.47	8.1	12.88				
HEMBB1001679	6.24	17.91	21.96	5.19	4.96	3.87	10.86	6.26	8.43				
HEMBB1001684	10.61	21.58	17.28	4.97	9.8	7.91	15.07	5.39	2.51				
HEMBB1001685	5.57	8.99	14.97	3.84	6.75	3.87	5.52	1.85	2.86				
HEMBB1001695	5.09	9.94	17.45	5.82	8.3	5.19	6.66	2.16	2.97				
HEMBB1001703	4.68	6.84	16.43	5.87	6.69	4.05	8.72	2.46	4.64				
HEMBB1001704	5.61	7.88	21.01	10.94	17.96	9.05	14.4	6.3	9.45				
HEMBB1001706	7.42	2.91	5.37	4.07	5.66	4.18	6.33	3.36	3.19				
HEMBB1001707	3.87	5.86	5.44	3.17	4.08	5.01	5.27	1.48	7.88				
HEMBB1001717	14.88	12.76	30.35	13.57	11.78	8.58	13.5	11.39	12.48				
HEMBB1001731	39.25	68.03	95.93	39.11	36.32	32.38	46.55	35.06	44.86				
HEMBB1001734	5.17	6.48	12.05	1.52	7.19	2.49	5.94	1.69	6.44				

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Table 387

HEMBB1001735	41.8	74.33	131.1	48.7	40.13	60.42	53.81	28.45	83.52
HEMBB1001736	7.77	13.39	28.59	8.57	9.16	5.35	8.09	5.45	9.42
HEMBB1001747	2.69	8.82	13.53	4.41	6.88	3.98	4.96	1.05	3.48
HEMBB1001749	10.28	24.28	26.11	5.15	8.2	10.2	5.99	4.27	10.01
HEMBB1001753	10.3	11.05	20.9	9.25	9.8	9.74	6.82	5.36	10.12
HEMBB1001756	6.53	8.08	12.86	3.9	3.99	4.72	5	3.97	3.65
HEMBB1001757	7.8	24.09	26.61	6.4	12.83	5.96	11.18	14.36	9.41
HEMBB1001760	14.27	19.82	42.06	14.81	14.45	11.21	17.24	9.18	15.44
HEMBB1001762	0.8	3.04	8.27	0.57	4.82	0.71	2.56	0.81	3.52
HEMBB1001780	13.76	23.09	49.83	16.38	14.53	12.62	15.44	6.8	13.71
HEMBB1001785	6.49	12.36	24.07	15.82	12.17	15.29	9.31	2.84	7.32
HEMBB1001788	25.43	19.69	45.01	19	16.71	23.01	19.54	20.38	26.43
HEMBB1001793	5.14	15.25	7.48	1.07	13.29	8	16.96	8.27	6.44
HEMBB1001797	14.78	27.69	37.34	12.45	18.06	22.63	22.37	14.75	11.18
HEMBB1001802	13.95	6.42	12.11	6	9.1	3.62	4.89	7.62	4.73
HEMBB1001812	19.94	26.82	51.97	30.77	23.99	24.59	25.74	15.27	19.71
HEMBB1001815	11.81	15.53	37.64	17.99	17.45	14.83	20.39	13.54	19.43
HEMBB1001816	17.77	23.19	75.37	26.22	24.8	18.06	30.17	15.34	21.15
HEMBB1001831	8.13	8.07	23.31	9.34	10.75	10.45	10.25	3.73	10.62
HEMBB1001834	14.4	18	35.74	22.13	11.64	13.05	15.55	10.35	12.6
HEMBB1001836	30.28	39.5	43.48	42.55	36.92	34.82	31.2	18.99	16.41
HEMBB1001838	14.36	16.68	38.4	17.83	16.75	14.74	12.83	10.7	10.84
HEMBB1001841	25.77	32.45	51.17	33.9	26.13	25.07	27.91	22.04	19.78
HEMBB1001844	15.48	34.84	44.55	31	24.08	23.04	21.12	16.3	25.7
HEMBB1001847	17.89	27.89	60.83	26.2	23.47	23.52	21.19	9.97	20.24
HEMBB1001848	4.85	5.43	11.29	3.58	4.51	3.65	6.07	3.08	5.61
HEMBB1001850	38.14	52.12	78.88	56.18	68.55	53.58	61.43	34.94	43.46
HEMBB1001859	30.81	27.05	59.36	68.19	35.46	57.28	19.8	14.26	20.24
HEMBB1001863	3.46	3.98	8.32	5.64	4.36	4.8	7.82	2.45	4.74
HEMBB1001867	14.5	16.62	28.09	12.79	10.98	12.92	14.13	8.77	15.8
HEMBB1001868	5.84	8.18	12.72	7.12	6.24	5.61	8.09	8.94	8.48
HEMBB1001869	54.86	64.59	94.37	86.31	67.89	82.85	80.48	51.3	89.82
HEMBB1001872	6.07	11.98	13.6	18.68	9.46	7.21	18.78	6.55	10.02
HEMBB1001874	3	3.3	6.61	4.59	12.05	11.19	3.13	1.36	5.74
HEMBB1001875	12.99	18.2	23.61	26.52	29.44	24.9	34.89	17.55	28.83
HEMBB1001880	18.04	17.79	33.89	31.27	17.63	20.15	14.84	10.37	14.08
HEMBB1001899	34.29	45.59	63.32	39.63	32.89	31.82	35.58	26.2	35.72
HEMBB1001903	8.16	10.41	29.09	8.47	10.89	12.17	9.48	4.66	7.91
HEMBB1001905	28.16	29.19	50.5	33.46	32.78	32.37	33.69	21.9	33.71
HEMBB1001906	4.65	5.05	9.2	6.27	6.88	4.65	7.25	6.26	9.65
HEMBB1001908	2.42	5.7	6.4	5.21	4.63	6.7	4.19	0.96	5.33
HEMBB1001910	5.2	10.62	10.84	8.51	10.51	9.98	6.79	2.76	7.39
HEMBB1001911	29.98	51.31	56.74	43.98	49.18	34.13	49.74	26.26	62.6
HEMBB1001915	21.14	31.44	37.82	20.71	15.99	14.9	18.9	21.96	29.35
HEMBB1001921	7.15	10.68	16.34	7.38	7.15	5.66	5.97	5.19	7.01
HEMBB1001922	17.41	22.59	26.93	13.84	10.93	18.21	23.02	11.95	17.79
HEMBB1001925	13.97	12.3	26.77	11.6	11.78	10.4	15.51	12.85	15.94
HEMBB1001930	40.03	59.19	73.92	44.03	41.91	43.37	40.7	31.14	54.53
HEMBB1001944	1.94	5.58	8.4	6.66	4.5	5.16	2.67	2.16	4.4
HEMBB1001945	11.9	14.15	28.25	12.61	15.86	30.85	15.45	10.36	15.75
HEMBB1001947	12.74	2.15	16.64	14.03	14.01	12.25	15.71	4.99	12.24
HEMBB1001950	17.57	25.59	40.32	25.51	11.85	16.5	13.53	12.65	19.84
HEMBB1001952	26.14	33.12	47.22	23.32	21.94	24.22	34.78	37.99	49.1
HEMBB1001953	17.2	26.64	33.2	20.18	17.54	17.43	18.02	10.46	24.03
HEMBB1001957	5.93	5.66	12.29	2.67	5.82	5.6	4.01	5.73	6.62
HEMBB1001959	4.28	3.66	11.59	1.82	2.82	5.97	1.57	2.64	3.72
HEMBB1001962	11.92	43.87	27.13	12.9	32.94	14.36	12.1	15.99	21
HEMBB1001967	34.68	44.03	60.34	44.77	38.71	38.73	44.26	27.2	37.33
HEMBB1001973	28.25	35.18	38.62	28.67	29.33	21.67	37.28	18.87	23.03
HEMBB1001978	70.1	95.85	135.62	108.46	60.16	80.87	54.72	61.03	86.88
HEMBB1001983	4.69	4.06	8.04	3.84	5.22	5.54	5.15	3.31	5.57
HEMBB1001987	10.55	12.27	28.1	12.58	12.32	11.95	11.85	6.54	23.57
HEMBB1001988	9.33	7.22	23.4	8.24	11.34	8.88	13.31	6.58	9.69
HEMBB1001990	26.2	19.68	27.76	43.3	26.68	36.79	27.71	13.13	24.3

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Table 388

HEMBB1001996	27.04	42.61	48.67	17.55	24.82	18.56	28.17	23.4	25.36	*		-	
HEMBB1001997	14.71	23.01	29.3	15.9	17.15	12.6	18.98	11.27	17.5				
HEMBB1001999	15.2	22.46	20.51	13.68	17.9	14.36	19.76	8.32	11.63				
HEMBB1002002	6.41	8.68	14.02	3.86	4.69	7.48	2.32	2.31	9.35				
HEMBB1002005	13.93	14.9	24.54	14.07	12.64	13.23	24.2	15.6	24.4				
HEMBB1002009	13.81	20.37	28.5	12.9	13.24	9.2	14.63	11.53	16.62				
HEMBB1002013	35.52	43.43	61.55	22.34	25.62	25.39	38.97	23.31	36.2	*		-	
HEMBB1002015	17.64	16.37	26.67	10.62	13.94	14.86	13.44	9	13.73				
HEMBB1002024	5.8	10.6	13.79	2.3	5.04	3.13	2.77	1.85	3.6		*		-
HEMBB1002035	52.65	85.52	32.75	21.71	70.63	38.58	40.44	20.7	17.84				
HEMBB1002039	4.95	5.73	12.99	4.99	10.04	5.87	7.91	2.61	3.57				
HEMBB1002041	26.99	42.34	59.33	33.42	31.41	30.59	35.5	25.94	36.66				
HEMBB1002042	7.32	8.11	15.44	8.43	5.37	4.7	6.95	4.45	6.64				
HEMBB1002043	15.38	16.33	33.37	9.15	15.16	12.75	12.63	10.91	12.91				
HEMBB1002044	6.28	7.19	15.99	4.63	6.03	3.49	8.95	3.61	5.78				
HEMBB1002045	13.55	14.05	38.81	21.11	17.68	16.3	14.27	7.83	17.46				
HEMBB1002049	20.72	21.4	45.82	13.96	20.22	15.6	21.11	13.82	17				
HEMBB1002050	12.83	16.25	37.04	11.52	18.46	11.6	18.41	9.54	14.5				
HEMBB1002051	28.94	18.92	52.44	23.53	26.05	15.13	33.91	14.41	28.65				
HEMBB1002068	64.56	61.13	134.22	53.82	39.3	49.08	48.07	48.15	30.52				
HEMBB1002069	20.88	27.08	36.85	26.67	17.79	18.95	23.6	16.68	23.73				
HEMBB1002075	15.68	17.27	22.02	11.81	12.44	12.63	5.87	5.58	11.32	*	*	-	-
HEMBB1002079	27.46	41.14	33.47	23.15	21.35	9.24	13.25	11.63	12.65		**		-
HEMBB1002080	27.32	43.03	71.5	48.33	38.81	19.92	37.68	22.99	28.59				
HEMBB1002082	11.54	12.93	24.86	5.24	21.72	15.36	15.59	4.71	14.1				
HEMBB1002084	17.19	20.49	48.44	15.57	24.56	30.61	24.16	14.34	22.35				
HEMBB1002088	4.86	8.19	14.88	4.12	8	4.95	6.55	2.38	8.06				
HEMBB1002092	144.34	116.11	135.03	45.77	56.49	60.46	15.5	25.51	16.94	**	**	-	-
HEMBB1002094	15.12	19.26	35.12	17.76	15.07	8.88	14.96	9.23	22.31				
HEMBB1002103	5.46	7.53	11.18	8.4	4.51	4.6	8.52	3.47	4.97				
HEMBB1002109	59.58	83.46	107.06	62.19	50.92	51.12	65.01	50.9	42				
HEMBB1002115	5.46	60.72	14.77	39.13	16.84	5.85	5.92	6.74	5.3				
HEMBB1002120	6.4	5.75	12.8	2.74	5.51	2.64	3.13	1.57	3.49				
HEMBB1002121	19.45	25.43	55.52	28.56	24.08	19.83	25.58	15.89	20.17				
HEMBB1002134	10.91	24.24	43.39	24.03	23.79	24.09	19.26	8.44	14.1				
HEMBB1002136	18.33	18.78	45.57	23.81	13.25	20.44	11.9	15.85	24.31				
HEMBB1002138	50.09	51.59	110.11	35.51	42.15	39.79	27.69	28.58	25.22				
HEMBB1002139	8.36	15.47	10.43	4.01	4.89	4.74	7.89	6.83	4.81	*		-	
HEMBB1002141	9.19	16.96	13.1	1.9	10.98	7	5.65	7.53	4.35		*		-
HEMBB1002142	6.36	8.37	8.62	2.74	2.82	2.25	4.04	2.02	5.71	**	*	-	-
HEMBB1002145	10.49	16.24	32.26	9.14	12.19	10.34	12.54	5.18	7.82				
HEMBB1002152	24.88	22.9	59.51	8.84	21.58	20.2	34.39	10.44	7.92				
HEMBB1002162	46.61	80.75	107.44	66.24	81.5	44.12	82.89	47.69	70.76				
HEMBB1002173	3.56	25.4	7.84	5.45	25.86	14.76	4.91	5.53	5.99				
HEMBB1002189	5.91	5.36	11.91	4.49	4.74	3.73	7.69	4.5	2.15				
HEMBB1002190	8.05	5.19	7.81	3.82	3.51	3.24	3.4	1.73	2.03	*	*	-	-
HEMBB1002193	13.5	31.42	40.95	12.51	15.71	29.81	30.17	23.34	31.46				
HEMBB1002217	11.76	15.56	34.59	12.72	11.26	16.37	17.63	11.07	12.8				
HEMBB1002218	25.74	52.63	73.43	32.82	28.59	24.52	35.6	20.64	25.88				
HEMBB1002228	108.24	84.59	214.25	80.62	78.36	108.65	166.71	123.42	65.1				
HEMBB1002232	10.76	24.39	31.98	19.41	21.33	17.37	22.17	6.39	14.13				
HEMBB1002245	29.32	39.47	46.03	33.69	25.42	30.62	28.25	20.36	26.6				
HEMBB1002247	23.04	30.4	36.26	21.55	23.11	19.18	30.01	21.82	18.27				
HEMBB1002249	8.45	5.4	12.9	9.1	8.18	7.58	2.92	2.96	4.18				
HEMBB1002254	13.55	8.54	22.22	9.35	11.14	10.19	5.38	9.93	4.18				
HEMBB1002255	24	39.55	56.2	39.15	37.05	37.31	39.64	23.55	35.88				
HEMBB1002266	19.55	37.2	69.12	27.4	30.03	37.09	27.79	17.42	23.42				
HEMBB1002271	8.4	14.75	33.73	16.63	15.77	17.75	17.9	8.81	11.82				
HEMBB1002280	0	1.32	3.2	1.59	2.57	0.19	2.26	0	1.09				
HEMBB1002296	13.25	17.07	48.86	29.84	17.46	25.16	17	14.47	20.56				
HEMBB1002300	7.2	17.96	22.84	22.43	7.83	12.63	8.34	8.09	9.04				
HEMBB1002302	8.19	9.95	13.55	11.87	6.29	9.78	7.21	2.24	3.19		*		-
HEMBB1002306	4.46	4.94	10.04	8.42	4.47	9.84	5.18	3.92	6.24				
HEMBB1002316	9.41	18.69	11	13.6	12.17	15.43	7.32	2.42	6.96				

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Table 389

HEMBB1002326	6.79	10.97	11.32	21.02	12.83	6.76	6.12	3.86	6.53				
HEMBB1002327	29.86	39.37	46.64	28.75	34.27	35.49	23.76	23.05	28.43				
HEMBB1002329	12.21	17.09	28.97	18.73	8.27	19.71	9.42	11.59	11.1				
HEMBB1002340	3.57	5.21	5.98	7.77	3.22	9.25	5.09	2.16	1.79				
HEMBB1002342	6.21	7.8	10.28	6	3.29	3.42	3.33	3.85	5.15		*		-
HEMBB1002358	32.09	38.53	65.28	39.45	32.86	34.65	33.44	21.57	27.85				
HEMBB1002359	3.96	3.69	6.45	3.93	4.64	4.39	3.95	0.63	2.74				
HEMBB1002364	3.43	4.07	8.33	6.97	4.3	5.26	4.27	1.48	3.01				
HEMBB1002366	7.13	10.16	14.56	9.95	9.83	9.89	9.48	6.8	10.03				
HEMBB1002371	17.53	29.76	21.32	21.87	21.71	16.54	9.41	9.09	4.87		*		-
HEMBB1002381	7.92	12.33	16.15	8.95	3.96	8.62	4.76	5.05	4.4		*		-
HEMBB1002383	135.68	179.56	228.28	286.57	191.47	226.83	107.86	116.89	120.62				
HEMBB1002387	23.79	23.11	43.55	20.25	12.08	15.04	3.85	6.21	4.42		*		-
HEMBB1002409	13.31	12.51	22.34	8.77	11.21	10.89	4.44	4.37	4.87		*		-
HEMBB1002413	3.49	3.12	9.08	4.81	2.78	4	1.3	1.86	1.66				
HEMBB1002415	2.64	3.61	7.39	2.66	2.05	3.42	0.86	1.28	2.41				
HEMBB1002424	6.07	9.92	9.97	6.37	9	12.89	6.72	4.73	6.15				
HEMBB1002425	4.48	7.81	11.5	5.69	9.56	5.52	4.13	1.79	5.11				
HEMBB1002427	29.25	30.49	60.22	43.33	23.55	33.03	24.65	22.4	31.01				
HEMBB1002442	6.2	17.54	17.42	9.79	7.28	9.01	4.36	12.11	11.81				
HEMBB1002447	110.71	207.61	155.4	83.72	84.2	96.3	26.65	37.71	31.85		*		-
HEMBB1002453	5.36	5.98	9.95	2.72	2.55	3.56	2.41	1.81	3.86	*	*	-	-
HEMBB1002457	16.89	16.27	19.17	6.78	17.09	11.88	7.07	5.54	6.6		**		-
HEMBB1002458	23.11	31.15	52.26	31.43	27.93	29.52	25.75	14.57	26.97				
HEMBB1002463	24.77	42.25	57.37	32.51	37.48	24.85	28.18	20.41	30.3				
HEMBB1002465	3.27	5.17	9.01	3.69	4.27	4.31	3.51	0.9	2.26				
HEMBB1002477	4.25	7.51	5.14	7.06	3.76	4.24	1.98	3.33	2.58		*		-
HEMBB1002479	20.58	32.93	33.42	17.09	21.13	16.76	11.95	15.32	21.36				
HEMBB1002489	48.69	62.6	67.58	34.04	44.48	57.32	35.3	36.02	39.44		*		-
HEMBB1002492	11.53	17.66	26.19	13.16	10.94	12.55	11.2	5.85	15.28				
HEMBB1002495	5.18	3.21	9.5	2.92	4.34	3.1	3.82	2.25	3.88				
HEMBB1002502	34.71	31.95	38.03	46.31	31.48	35.99	26.54	23.82	25.15		**		-
HEMBB1002509	11.07	15.55	26.84	12.73	16.51	11.29	10.77	7	12.74				
HEMBB1002510	28.51	45.37	36.84	31.94	38.1	20.25	23.53	21.31	17.08		*		-
HEMBB1002520	14.34	15.62	18.28	10.3	7.17	4.37	1.27	2.73	3.96	*	**	-	-
HEMBB1002522	27.23	55.84	54.45	41.8	39.8	28.31	15.32	22.78	36.38				
HEMBB1002527	2.56	2.91	5.88	1.86	2.03	3.34	1.71	1.04	2.87				
HEMBB1002530	5.16	6.33	11.67	5.25	3.42	5.09	4.28	2.92	7.5				
HEMBB1002531	26.73	31.41	45.92	22.42	21.99	29.07	24.79	13.7	18.84				
HEMBB1002534	27.18	46.28	57.65	25.13	29.76	23.09	34.17	26.17	36.08				
HEMBB1002536	13.04	20.55	23.13	9.22	13.07	13	15.33	12.24	18.4				
HEMBB1002544	23	32.2	43.29	21.03	30.23	27.52	19.17	15.09	14.85				
HEMBB1002545	3.59	4.33	9.7	5.81	3	3.66	1.12	0.96	13.79				
HEMBB1002550	7.33	13.21	13.27	3.83	6.5	4.73	2.81	3.61	2.61	*	*	-	-
HEMBB1002556	19.36	24.38	22.91	7.86	11.05	11.87	7.3	3.24	5.41	**	**	-	-
HEMBB1002571	7.32	4.72	8.5	4.01	3.71	2.33	1.87	1.16	2.04	*	*	-	-
HEMBB1002579	3.21	4.8	10.5	2.3	2.84	2.3	2.51	1.04	2.73				
HEMBB1002582	9.95	12.82	19.84	6.39	8.66	6.74	3.36	2.01	3.49		*		-
HEMBB1002584	4.7	5.64	13.38	4.24	5.58	5.79	3.53	1.46	2.34				
HEMBB1002587	8.59	15.17	29.93	11.81	13.87	11.06	10.85	4.49	11.04				
HEMBB1002590	27.91	31.34	78.12	45.05	22.1	24.36	21.48	22.81	39.4				
HEMBB1002596	9.4	9.36	12.16	12.87	8.92	9.94	3.39	4.59	5.2		**		-
HEMBB1002600	7.35	8.89	8.63	4.2	3.37	4.13	3.83	2.53	0.85	**	**	-	-
HEMBB1002601	13.59	25.38	25.69	13.58	12.98	10.65	15.53	14.47	12.11				
HEMBB1002603	4.01	4.35	8.49	3.09	3.23	2.33	3.4	1.13	1.07				
HEMBB1002607	5.59	8.75	13.05	6.25	8.3	3.46	5.04	2.83	4.29				
HEMBB1002610	6.17	9.3	18.74	7.02	8.85	5.16	5.21	2.01	3.82				
HEMBB1002613	5.1	6.85	16.57	4.47	6.62	3.43	4.07	1.86	3.63				
HEMBB1002614	108.18	118.26	257.79	160.19	127.61	115.27	80.95	70.77	100.61				
HEMBB1002615	3.76	4.74	6.46	3.53	4.89	3.11	2.31	1.58	0.85		*		-
HEMBB1002617	15.34	16.43	20.69	14.06	10.46	7.36	16.03	9.38	12.23				
HEMBB1002623	43.46	62.43	70.11	89.32	59.95	64.13	46.57	40.8	51.16				
HEMBB1002624	20.45	39.7	56.1	29.45	24.85	24.11	26.5	22.1	22.65				
HEMBB1002631	12.8	24.72	22.26	5.67	13.71	7.87	12.49	14.8	9.64				

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Table 390

HEMBB1002635	3.81	5	11.37	1.21	3.62	1.08	2	1.05	2.82				
HEMBB1002644	6.38	7.38	19.6	6.87	6.62	5.91	7.04	3.57	7.83				
HEMBB1002654	44.15	47.27	98.13	55.06	50.78	51.15	27.74	20.25	41.98				
HEMBB1002661	16.29	22.35	33.51	18.43	18.3	14.62	15.42	10.61	19.12				
HEMBB1002663	12.29	20.14	24.54	5.77	16.48	12.72	3.66	7.87	3.2		*		-
HEMBB1002664	26.04	27.32	31.97	12.71	14.38	12.28	15.87	10.5	16	**	**	-	-
HEMBB1002677	2.85	4.67	7.35	1.19	3.8	1.22	2.58	0.54	2.04				
HEMBB1002683	408.12	530.85	581.04	161.92	536.41	322.12	493.61	190.86	318.34				
HEMBB1002684	5.89	14.15	21.74	5.64	5.67	5.5	2.78	0.53	2.33				
HEMBB1002686	2.08	2.21	13.73	0.94	2.87	1.96	2.53	0.03	2.4				
HEMBB1002692	6.27	8.28	18.48	7.56	4.81	4.6	4.23	1.22	6.95				
HEMBB1002693	37.13	59.89	50.13	8.18	9.08	32.77	12.89	24.23	25.51	*	*	-	-
HEMBB1002697	12.19	19.73	29.39	11.74	11.32	12.96	13.01	7.86	10.37				
HEMBB1002699	12.29	7.97	29.87	3.99	12.05	3.69	6.19	2.34	1.91				
HEMBB1002702	4.21	4.82	9.81	4.02	2.81	2.59	2.32	3.46	2.32				
HEMBB1002705	42.01	58.09	92.41	42.52	47.93	35.39	82.62	52.43	59.52				
HEMBB1002712	82.07	113.22	149.92	77.66	93.78	72.72	96.78	72.75	86.71				
IMR321000028	2.68	4.75	13.62	4.72	4.88	2.62	2.74	1.07	1.92				
IMR321000031	7.53	10.04	0	0.26	16.99	0.79	7.55	3.43	9.54				
IMR321000034	9.42	10.78	32.44	15.73	16.03	17.46	6.96	5.24	7.94				
IMR321000039	1.72	2	2.81	3.07	3.78	1.79	0.76	0	1.77				
IMR321000044	5.65	7.08	18.45	11.11	7.14	7.03	4.83	2.08	3.62				
IMR321000063	10.51	11.67	19.12	13.18	11.6	12.05	6.47	7.76	7.56				
IMR321000085	3.33	5.05	8.66	2.61	3.29	3.45	1.96	0.92	3.07				
IMR321000089	3.15	5.89	14.29	4.37	6.53	5.77	3.28	1.07	2.45				
IMR321000091	59.8	78.47	131.41	171.62	125.26	143.68	43.76	27.21	45.98				
LIVER1000004	4.13	4.93	5.75	3.08	2.76	4.02	2.18	1.07	1.36		**		-
LIVER1000008	10.35	13.6	22.11	11.7	10.53	14.7	11.26	5.83	10.54				
LIVER1000011	59.6	50.92	129.92	124.27	66.83	94.45	48.23	37.68	48.06				
LIVER1000022	2.42	3.87	7.13	5.18	2.89	5.96	3.99	0.85	2.2				
LIVER1000025	11.19	21.41	14.85	14.92	17.52	18.14	8.19	3.93	7.48		*		-
LIVER1000030	5.79	4.25	9.83	9.98	5.67	5.82	4.77	2.89	3.63				
LIVER1000045	4.77	5.86	5.47	6.22	7.71	6.61	4.81	3.96	4.97				
LIVER1000046	23.39	30.93	40.35	28.67	14.67	17.18	8.63	19.03	18.73				
LIVER1000072	9.51	20.72	24.34	17.51	14.57	15.78	8.13	9.06	13.17				
LIVER1000077	7.51	7.91	13.85	13.48	8.07	9.05	5.23	4.4	6.07				
LIVER1000080	5.07	5.78	10.96	6.47	4.34	6.39	3.86	2.15	4.56				
LIVER1000086	11.03	13.61	23.46	8.67	23.05	12.3	11.46	8.1	16.78				
LIVER1000092	10.59	15.75	23.53	19.18	22.61	13.71	8.85	6.69	7.35				
LIVER1000095	51.53	68.53	98.85	69.98	49.46	69.44	74.79	43.47	64.56				
LIVER1000097	8.95	15.6	14.45	10.75	13.82	9.14	5.8	2.85	3.46		*		-
LIVER1000098	41.49	40.97	103.47	50.66	24.2	43.26	26.16	32.27	27.07				
LIVER1000100	3.55	4.13	7.44	3.5	3.68	3.78	2.58	3.54	3.3				
LIVER1000101	44.76	62.72	56.32	36.92	31.17	34.9	40.25	36.83	38.75	*	*	-	-
LIVER1000106	3.93	4.77	8.45	2.61	3.61	4.62	2.14	3.23	3.22				
LIVER1000108	6.19	8.29	14.94	4.01	4	6.54	5.47	6.84	5.37				
LIVER1000115	1.31	3.43	5.31	1.07	1.91	1.17	0.78	1.21	1.27				
LIVER1000120	5.87	8	12.35	7.59	6.45	6.85	5.23	2.59	6.22				
LIVER1000138	5.5	7.3	19.82	7.01	10.38	6.37	5.23	4.12	9.23				
LIVER1000146	4.13	5.06	8.45	8.15	4.26	4.91	1.55	2.41	3.37				
LIVER1000148	10.81	16.45	14.93	9.88	11.05	13.74	6.11	8.29	5.5		*		-
LIVER1000157	4.51	3.83	6.67	3.38	5.06	4.69	1.48	2.24	4.29				
LIVER1000161	85.1	101.44	127.49	155.4	95.91	123.47	63.19	53.6	81.33				
LIVER1000167	9.34	7.8	16.08	6.28	7.39	6.18	4.07	3.11	4.06		*		-
LIVER1000174	14.38	23.84	29.19	10.08	10.54	10.6	4.27	1.62	4.26	*	*	-	-
LIVER1000185	15.55	11.69	24.81	3.86	12.76	7.24	6.4	3.76	4.58		*		-
LIVER1000187	40.28	72.32	62.92	52.19	53.14	45.8	30.48	15.14	10.77		*		-
LIVER1000190	13.01	13.24	16.57	5.85	5.19	5.07	2.85	4.77	5.27	**	**	-	-
LIVER1000192	3.52	6.68	4.51	4.92	4.75	3.34	0.75	1.7	3.55				
MAMMA1000008	5.18	9.12	9.31	4.2	4.16	3.51	1.94	1.4	2.13	*	*	-	-
MAMMA1000015	5.78	4.65	11.74	5.4	3.83	5.36	2.48	1.65	3.15				
MAMMA1000019	8.71	5.86	17.78	9.05	5.32	5.22	3.67	4.83	8.34				
MAMMA1000020	101.37	73.62	112.56	134.32	82.42	106.51	82.61	44.53	81.2				
MAMMA1000024	19.83	36.9	36.17	7.46	24.94	15.61	12.77	15.51	6.89		*		-

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Table 391

MAMMA1000025	3.49	6.73	9.73	4.76	8.15	5.09	3.99	1.9	3.02					
MAMMA1000043	8.59	8.02	15.22	6.68	3.56	4.76	2.11	1.9	6.1					
MAMMA1000045	9.03	8.98	17.21	11.43	6.71	9.34	5.16	4.47	6.29					
MAMMA1000046	41.47	53.57	56.97	30.34	27.99	31.56	37.45	30.61	48.64	*		-		
MAMMA1000055	10.6	18.89	12.32	4.6	6.26	5.89	3.62	4.44	2.53	*	*	-	-	
MAMMA1000057	3.76	2.41	12.19	2.23	1.8	1.43	1.21	1.53	2.81					
MAMMA1000060	10.21	8.2	18.54	5.99	7.11	5.88	5.98	4.17	6.29					
MAMMA1000069	143.75	270.15	259.45	49.26	67.48	38.63	33.36	39.16	49.31	*	*	-	-	
MAMMA1000084	3.34	5.16	10.93	3.47	4.79	2.05	3	0.67	2.88					
MAMMA1000085	3.86	4.9	7.86	4.65	4.18	4.46	2.36	1.98	8.94					
MAMMA1000092	1.88	4.62	8.98	3.96	2.75	3.09	2.27	0.07	1.18					
MAMMA1000096	3.52	3.48	7.14	2.58	2.53	2.5	0.67	1.83	1.35					
MAMMA1000097	4.98	3.73	8.88	2.04	2.02	1.49	1.93	0.71	1.64		*		-	
MAMMA1000102	16.31	20.65	29.78	15.97	14.1	11.62	28.48	21.84	17.26					
MAMMA1000103	24.25	30.87	39.49	18.45	29.7	17.72	21.24	13.56	7.51		*		-	
MAMMA1000106	8.95	10.76	22.4	12.82	11.13	10.63	6.32	4.47	6.45					
MAMMA1000117	2.83	6.06	12.12	2.65	4.11	2.11	5.97	1.27	1.18					
MAMMA1000118	8.06	8.77	19.58	14.56	12.82	9.23	5.17	8.7	14.06					
MAMMA1000129	4	2.76	5.79	3.46	3.6	1.79	1.7	2.01	2.69					
MAMMA1000133	5.05	7.04	6.39	3.71	2.31	3.3	8.78	9.22	3.38	*		-		
MAMMA1000134	7.25	6.71	12.23	3.97	5.46	2.89	5.9	4.64	5.77					
MAMMA1000139	8.81	13.92	27.94	9.57	7.21	7.44	10.8	7.32	10.69					-
MAMMA1000141	10.59	12.38	22.86	16.46	15.91	12.46	8.35	6.81	8.98					
MAMMA1000143	47.46	88.55	73.36	60.42	67.69	52.39	70.22	26.61	57.3					
MAMMA1000150	7.57	5.6	14.19	2.79	8.22	2.73	5.6	1.58	3.48					
MAMMA1000155	11.41	12.76	22.27	10.11	6.62	6.85	2.76	1.55	4.85		*		-	
MAMMA1000163	15.02	19.25	32.92	19.25	12.39	13.68	10.19	9.3	14.14					
MAMMA1000171	7.6	10.37	13.24	2.98	2.32	1.89	2.54	1.28	1.33	**	**	-	-	
MAMMA1000173	6.75	5.29	9.57	2.32	2.23	1.04	2.07	1.37	0.99	*	*	-	-	
MAMMA1000175	3.46	6.59	11.02	3.52	2.3	2.43	3.53	1.51	2.66					
MAMMA1000183	25.33	42.54	44.08	23.65	35.89	24.05	16.46	12.47	14.16		*		-	
MAMMA1000191	5.92	8.95	18.7	5.23	6.43	6.14	3.97	2.29	6.56					
MAMMA1000192	11.99	14.56	36.16	26.22	18.77	12.98	9.82	7.53	11.64					
MAMMA1000193	3.19	3.37	6.86	4.95	4.82	4.54	1.06	1.39	2.14					
MAMMA1000198	47.48	56.45	65.4	32.82	40.48	48.35	28.71	22.96	42.97		*		-	
MAMMA1000204	11.23	12.69	25.02	6.96	11.44	9.78	5.53	7.76	6.1					
MAMMA1000207	12.4	7.47	19.55	6.26	5.09	4.84	6.03	8.39	7.97					
MAMMA1000214	8.42	8.75	15.08	9.58	9.32	7.56	7.33	4.95	7.33					
MAMMA1000220	22.52	15.12	36.99	5.02	6.29	6.82	6.38	3.87	3.09	*	*	-	-	
MAMMA1000221	10.4	16.64	24.93	5.03	11.07	6.49	6.69	3.21	1.94		*		-	
MAMMA1000226	13.64	11.97	28.4	5.25	12.91	9.41	26	12.92	3.5					
MAMMA1000227	14.38	17.15	40.21	23.86	16.67	19.14	13.63	7.29	12.46					
MAMMA1000230	3.53	5.09	7.34	3.64	2.92	4.31	1.76	1.24	2.65		*		-	
MAMMA1000241	2.76	3.88	6.29	2.63	1.66	1.65	1.27	0.15	1.78		*		-	
MAMMA1000245	6.45	7.89	22.51	9.95	8.51	9.68	6.76	3.1	4.13					
MAMMA1000248	21.38	25.61	55.84	30.22	20.66	19.73	24.19	11.24	13.89					
MAMMA1000251	5.31	4.84	10.73	2.94	4.44	3.42	3.67	1.53	2.11					
MAMMA1000254	2.32	3.23	8.55	2.43	2.71	1.01	0.9	0.97	0.54					
MAMMA1000257	2.97	3.77	9.11	1.37	3.58	0.82	2.27	0.96	1.23					
MAMMA1000262	45.74	36.4	0	0.39	0	0	34.58	23.42	46.99					
MAMMA1000264	9.34	12.72	36.1	26.8	15.94	23	7.31	7.08	9.25					
MAMMA1000266	0.66	1	3.04	2.63	2.61	0.59	0.15	0	1					
MAMMA1000270	13.12	14.9	18.21	14.67	11.46	11.77	8.4	9.61	6.99		*		-	
MAMMA1000271	3.88	3.72	7.35	4.08	3.89	3.79	1.47	2.83	1.69					
MAMMA1000277	41.4	51.52	103.66	30.74	33.8	53.69	17.12	13.52	16.27					
MAMMA1000278	11.35	16.91	37.8	22.57	16.53	16.11	10.35	6.71	12.84					
MAMMA1000279	3.26	3.91	6.49	3.15	3.6	2.86	2.52	0.56	1.77					
MAMMA1000283	29.38	33.95	49.97	69.77	34.21	54.3	27.86	21.79	21.83					
MAMMA1000284	5.55	5.62	6.77	4.76	4.06	5.69	4.18	2.05	4.21		*		-	
MAMMA1000287	18.44	27.31	36.41	15.51	4.83	9.89	4.34	3.99	2.59	*	*	-	-	
MAMMA1000294	14.59	17.3	29.88	19.53	15.7	20.07	17.98	12.1	15.45					
MAMMA1000298	4.06	4.13	7.44	4.06	5.42	8.4	4.25	2.39	4.19					
MAMMA1000302	3.99	3.48	11.09	6.9	6.86	5.91	4.93	2.1	3.71					
MAMMA1000303	1.77	4.16	5.21	2.14	3.15	3.07	3.83	0.5	1.85					

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Table 392

MAMMA1000305	32.01	34.24	58.88	37.52	42.02	39.78	30.9	18.25	28.49					
MAMMA1000307	7.32	11.17	15.9	9.52	5.29	9	4.83	4.75	5.32					
MAMMA1000309	13.21	12.45	16.61	13.37	8.5	8.68	5.45	4.69	8.26		**		-	
MAMMA1000312	3.8	4.66	7.38	5.51	4.44	4.58	3.65	2.16	2.53					
MAMMA1000313	5.23	3.78	8.22	6.32	8.18	4.37	4.06	1.99	2.36					
MAMMA1000331	3.57	2.97	7.78	3.29	3.56	6.01	3.84	1.96	2.66					
MAMMA1000335	1.93	3.97	7.5	5.14	3.16	3.87	4.24	1.18	2.51					
MAMMA1000339	4.85	7.71	8.76	4.7	9.96	8.63	2.97	1.94	3.31		*		-	
MAMMA1000340	13.8	21.06	20.08	19.65	20.75	20	20.39	11.88	8.29					
MAMMA1000348	6.6	5.86	10.24	5.86	4.39	5.28	1.91	2.51	3.44		*		-	
MAMMA1000356	48.67	74.66	87.35	53.83	37.37	46.85	35.71	39.77	39.98					
MAMMA1000358	9.54	13.7	18.74	8.76	9.05	7.26	6.27	7.75	6.04					
MAMMA1000360	4.42	6.35	14.28	5.25	6.74	5.72	3.05	4.95	4.76					
MAMMA1000361	62.5	108.93	116.66	101.62	117.16	105.86	87.17	73.39	114.81					
MAMMA1000363	4.98	6.13	8.18	4.8	3.56	6.25	3.82	2.21	3.44		*		-	
MAMMA1000370	5.17	12.45	10.14	5.35	7.18	7.58	3.49	1.29	2.83		*		-	
MAMMA1000371	2.39	4.39	9.15	3.68	6.58	4.68	2.76	1.36	2.71					
MAMMA1000372	17.51	21.43	34.07	12.37	14.77	13.39	11.25	17.12	32.9					
MAMMA1000385	2.59	3.13	9.36	4.39	3.21	2.85	3.43	3.75	2.78					
MAMMA1000388	15.23	16.36	27.37	8.49	18.09	20.18	11.94	20.32	17.28					
MAMMA1000395	2.71	2.65	9.67	2.23	1.16	2.27	1.54	2.51	1.57					
MAMMA1000402	17.65	14.83	40.38	21.39	34.95	27.07	11.67	5.88	6.61					
MAMMA1000403	4.76	5.81	8.95	2.66	5.93	4.73	3.53	2.03	3.28					
MAMMA1000410	8.38	10.39	14.35	8.64	10.52	7.1	6.79	5.15	5.87		*		-	
MAMMA1000413	13.08	31.41	34.59	25.16	26.53	19.73	20.54	9.59	10.58					
MAMMA1000414	26.2	35.15	53.64	41.13	33.28	34.97	22.92	16.5	31.45					
MAMMA1000416	93.85	138.41	125.21	46.14	53.85	91.17	35.64	64.76	53.2	*	*	-	-	
MAMMA1000421	12.39	14.43	18.48	7.65	12.15	12.39	5.74	4.49	4.48		**		-	
MAMMA1000422	142.54	131.07	148.31	147.75	137.43	173.26	122.42	112.28	99.77		*		-	
MAMMA1000423	5.22	2.76	10.5	5.24	3.96	3.14	2.65	0.29	3.52					
MAMMA1000424	16.73	20.92	35.59	20.88	21.28	23.97	15.73	11.76	16.32					
MAMMA1000429	9.36	15.84	18.54	7.22	10.71	6.57	4.21	3.75	2.1		*		-	
MAMMA1000431	1.71	4.16	6.38	1.45	4.13	3.04	2.28	2.32	2.5					
MAMMA1000432	63.4	133.96	122.67	9.74	51.75	20.93	35.92	64.94	54.93	*		-		
MAMMA1000437	7.75	15.03	14.39	12.33	7.79	9.82	5.47	8.03	11.07					
MAMMA1000444	7.3	9.64	12.3	7.17	6.74	4.04	4.84	3.63	6.39		*		-	
MAMMA1000446	72.49	65.48	72.84	97.18	57.65	80.67	67.4	46.57	58.28					
MAMMA1000449	18.1	22.35	31.63	13.49	17.76	14	17.72	12.22	18.97					
MAMMA1000457	18.4	25.87	17.2	2.76	17.71	11.5	15.1	3.75	16.53					
MAMMA1000458	7.78	16.72	16.75	9.69	10.94	4.65	4.37	2.84	7.72					
MAMMA1000468	16.03	28.35	43.07	20.2	27.28	30.25	21.32	9.68	14.64					
MAMMA1000472	6.66	14.63	17.94	8.59	8.34	7.38	4.92	4.41	8.54					
MAMMA1000473	18.92	28.23	28.07	15.83	15.65	17.15	17.93	13.07	20.76	*		-		
MAMMA1000477	3.29	5.76	7.67	2.77	2.69	3.84	2.99	1.75	1.93					
MAMMA1000478	3.8	4.66	7.21	2.84	2.45	2.89	2.43	1.21	0.87		*		-	
MAMMA1000483	141.82	256.33	267.79	98.09	257.9	180.98	169.43	158.7	175.76					
MAMMA1000490	11.74	16.92	30.01	11.37	13.37	11.4	15.98	7.97	17.05					
MAMMA1000496	29.48	25.33	53.38	30.03	31.05	22.35	19.18	13.04	15.93					
MAMMA1000500	4.21	8.78	19.16	2.1	8.22	5.73	7.01	0.97	6.78					
MAMMA1000501	3.3	3.92	7.8	5.4	3.37	3.89	2.1	0.03	4.12					
MAMMA1000503	8.55	8.62	11.61	8.76	3.91	6.21	3.65	2.45	1.88		**		-	
MAMMA1000506	19.56	37.71	40.79	41.28	34.62	14.86	17.29	25.75	7.33					
MAMMA1000510	6.43	9.68	12.68	8.8	8.42	5.47	7.38	4.77	5.1					
MAMMA1000515	16.44	20.18	30.29	25.14	20.54	20.81	15.29	9.87	15.02					
MAMMA1000516	5.05	38.96	14.92	3.26	5.69	7.88	10.33	1.91	1.96					
MAMMA1000522	27.99	43.17	68.38	38.83	18.51	22.66	24.89	20.61	23					
MAMMA1000524	5.97	11.73	10.41	4.38	10.1	5.92	5.73	2.46	2.76		*		-	
MAMMA1000528	3.99	4.53	7.16	4.83	4.31	6.82	4.96	1.75	1.88					
MAMMA1000534	20.75	20.93	19.83	14.18	15.4	10.89	14.95	12.85	11.39	**	**	-	-	
MAMMA1000541	7.6	8.83	11.36	1.44	4.17	2.11	2.2	1.84	1.98	**	**	-	-	
MAMMA1000550	2.63	1.99	8.54	2.03	3.94	1.32	3.32	0.71	2.83					
MAMMA1000556	761.19	1381.9	1153	543.64	1435.2	1032.9	1229.3	435.34	855.29					
MAMMA1000559	6.09	5.3	11.69	2.67	3.19	2.37	2.27	0.81	3.09					
MAMMA1000565	3.15	5.75	13.35	1.46	4.28	0.82	2.18	0.1	1.13					

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Table 393

MAMMA1000567	2.83	9.61	12.53	4.59	4.66	3.08	3.91	1.78	2.49				
MAMMA1000576	14.4	23.94	41.43	6.77	7.53	16.66	14.73	20.93	24.41				
MAMMA1000582	342.62	404.06	589.09	206.24	397.1	307.2	195.5	234.99	295.12				
MAMMA1000583	3.44	4.94	9.73	2.95	5.37	2.97	1.64	1.64	2.31				
MAMMA1000585	10.36	9.76	14.3	7.6	6.3	4.54	9.1	4.55	7.57	*		-	
MAMMA1000587	9.1	16.85	23.22	12.86	13.24	10.32	9.64	5.62	11				
MAMMA1000591	24.67	34.19	52.67	17.16	22.85	23.65	15.05	11.26	16.03				
MAMMA1000594	25.66	32.59	51.71	40.6	49.12	36.4	18.51	9.64	20.88				
MAMMA1000597	10.6	17.98	38.06	21.57	17.46	15.09	12.1	5.53	10.65				
MAMMA1000605	8.03	8.9	14.02	3.22	4.68	8.25	3.07	3.06	5.3		*		-
MAMMA1000612	3.76	3.67	7.3	1.87	2.17	1.53	2.62	0.72	2.53				
MAMMA1000614	8.91	9.36	17.48	7.74	5.34	6.31	7.11	2.55	5.61				
MAMMA1000616	10.09	7	22.98	5.69	13.58	6.11	4.8	4.98	3.1				
MAMMA1000621	18.37	26.27	42.33	24.96	17.41	18.13	16.86	13.76	19.28				
MAMMA1000623	5.51	4.72	11.4	2.5	4.83	2.59	2.52	1.82	1.65		-		
MAMMA1000625	3.19	6.18	12.95	3.95	4.29	3.37	3.1	1.01	2.69		-		
MAMMA1000635	3.08	4.28	9.79	5.68	3.5	2.91	2.33	0.32	2.12				
MAMMA1000643	3.16	4.8	8.96	4.43	4.19	14.5	3.27	1.73	4.43				
MAMMA1000646	53.05	63.8	128.68	68.06	63.84	76.26	48.7	34.2	32.4				
MAMMA1000652	7.49	6.59	12.24	7.34	7.8	10.34	5.92	2.92	1.26				
MAMMA1000657	4.53	4.12	7.44	5.71	2.66	4.08	1.96	2.59	1.6		*		-
MAMMA1000664	18.71	22.51	38.34	17.17	14.96	16	10.64	12.09	11.81				
MAMMA1000667	8.69	17.36	17.2	3.58	6.25	8.92	3.77	5.36	2.7		*		-
MAMMA1000668	23.14	46.99	61.08	27.38	33.9	32.87	41.85	23.92	33.78				
MAMMA1000669	3.03	3.5	9.1	2.2	6.51	1.81	2.38	2.13	1.46				
MAMMA1000670	4.89	6.68	9.53	5.24	3.91	6.43	9.4	3.5	1.93				
MAMMA1000672	127	118.39	232.08	362.26	175.38	245.8	112.44	89.34	106.16				
MAMMA1000681	42.17	56.4	66.57	28.1	10.46	18.45	7.15	8.3	5.57	*	**	-	-
MAMMA1000684	6.35	5.06	11.76	8.34	4.22	4.13	4.18	2.86	3.12				
MAMMA1000696	7.53	9.04	16.29	12.54	11.44	15.76	4.16	3.21	5.89				
MAMMA1000702	2.37	2.75	7.2	4.27	3.94	4.85	2.38	1.14	1.76				
MAMMA1000706	7.11	13.17	13.46	6.85	13.62	11.39	5.11	2.82	4.43		*		-
MAMMA1000707	5.79	9.88	8.46	5.04	7.37	7.72	4.37	2.73	5.56				
MAMMA1000713	13.18	25.83	23.83	10.07	8.95	6.62	3.02	4.1	4.74	*	*	-	-
MAMMA1000714	21.05	29.79	38.76	24.92	18.64	21.26	20.38	21.53	20.97				
MAMMA1000718	7.11	5.26	13.51	4.07	3.72	3	2.71	1.31	2.37				
MAMMA1000720	56.24	56.67	100.19	108.88	65.38	82.83	53.41	37.73	50.75				
MAMMA1000723	83.95	62.78	122.37	158.83	112.68	140.59	85.25	48.89	63.98				
MAMMA1000731	13.21	20.89	24.92	19.74	19.6	18.49	13.07	8.64	14.74				
MAMMA1000732	4.13	6	9.07	5.99	9.97	7.96	4.16	1.33	3.64				
MAMMA1000733	12.22	18.56	20.77	15.57	15.03	11.37	17.6	9.79	15.79				
MAMMA1000734	4.23	6.43	10.91	7.98	3.73	6.91	3.13	3.72	3.43				
MAMMA1000736	4.58	4.07	5.19	5.1	2.18	3.84	1.49	1.8	2.72		**		-
MAMMA1000738	27.47	31.39	43.2	35.52	27.09	30.72	11.08	15.85	19.91		*		-
MAMMA1000744	11.43	16.18	20.32	9.63	9.84	10.4	16.64	15.89	17.27				
MAMMA1000746	5.14	6.4	11.37	3.9	6.11	4.85	2.11	2.43	3.5				
MAMMA1000748	2.95	3.98	9.11	2.66	4.26	3.02	2.63	1.16	2.48				
MAMMA1000751	3.53	4.94	7.73	2.22	4.21	3.15	2.53	1.56	2.63				
MAMMA1000752	9.18	9.76	16.46	16.7	13	12.37	10.17	5.29	10.03				
MAMMA1000757	17.77	21.89	38.71	25.58	19.94	21.44	12.48	15.54	20.02				
MAMMA1000760	6.79	10.56	9.64	3.73	4.03	3.96	1.97	4.15	4.68	*	*	-	-
MAMMA1000761	4.06	4.2	7.68	1.53	2.88	3.67	1.98	1.33	1.45		*		-
MAMMA1000775	4.12	5.64	14.4	7.07	2.94	5.07	2.8	2.71	4.1				
MAMMA1000776	26.15	27.77	36.92	48.47	26.15	33.74	22.66	12.7	18.46		*		-
MAMMA1000778	38.93	73.17	60.3	15.58	59.91	40.66	15.6	19.11	12.75		*		-
MAMMA1000781	10.71	16.72	21.46	6.1	15.65	13.14	10.25	9.83	6.19				
MAMMA1000782	5.28	6.95	8.31	4.59	9.33	5.12	3.95	1.7	2.78		*		-
MAMMA1000784	12.93	21.78	27.25	9.87	8.6	8.24	5.41	7.95	18.83	*		-	
MAMMA1000788	14.83	19.2	21.42	14.77	17.9	16.09	9.03	8.51	18.38				
MAMMA1000798	10.63	12.91	13.99	6.66	4.6	7.92	6.32	3.01	7.59	*	*	-	-
MAMMA1000802	10.59	10.38	19.17	11.33	9.98	8.79	5.57	3.43	5.21		*		-
MAMMA1000810	6.03	6.16	13.72	6.5	6.85	7.38	2.82	2.22	3.59				
MAMMA1000813	22.11	37.42	37.78	16.99	20.99	20.43	27.71	18.27	23.96				
MAMMA1000814	1.64	5.26	13.69	2.27	7.88	1.6	3.8	1.06	1.8				

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Table 394

MAMMA1000824	52.75	82.46	54.98	22.75	86.37	46.11	53.27	21.38	20.22				
MAMMA1000827	3.29	5.2	12.5	6.91	5.04	2.83	2.54	1.96	3.02				
MAMMA1000831	31.08	35.42	39.96	20.36	22.38	25.87	17.52	21.92	26.79	*	*	-	-
MAMMA1000838	4.58	6.92	8.85	2.9	2.71	3.02	3.13	2.4	1.8	*	*	-	-
MAMMA1000839	4.7	5.1	9.24	1.82	2.67	4.2	2.02	1.34	1.48		*		-
MAMMA1000841	4.43	2.78	9.96	2.71	2.83	2.07	3.01	0.81	2.24				
MAMMA1000842	6.22	8.19	14.72	3.28	5.48	4.22	5.77	2.92	7.82				
MAMMA1000843	10.02	23.1	28.88	14.54	17.26	10.11	4.63	3.65	6.21		*		-
MAMMA1000845	2.57	2.89	10.34	0.88	3.81	2.04	1.66	1.53	3.4				
MAMMA1000851	40.29	50.53	100.08	64.55	45.92	39.66	42.2	36.12	64.01				
MAMMA1000854	3.86	5.86	8.12	2.91	1.76	3.56	1.11	0.53	1.24		*		-
MAMMA1000855	91.57	117.96	159.35	213.71	138.54	171.88	95.66	65.57	93.06				
MAMMA1000856	3.13	2.69	5.73	1.9	1.05	2.66	1.82	0.46	1.81				
MAMMA1000859	3.59	5.65	10.37	1.76	1.83	1.2	3.38	1.09	1.24				
MAMMA1000862	8.58	10.61	23.09	5.34	11.79	7.43	5.15	1.27	2.11				
MAMMA1000863	17.14	20.47	45.55	14.36	24.31	16.09	24.81	12.68	16.34				
MAMMA1000865	3.2	5.96	11.12	4.18	4.78	11.8	2.48	0	2.86				
MAMMA1000867	12.55	18	37.97	18.03	16.36	15.97	9.25	8.53	14.8				
MAMMA1000875	197.47	247.19	307.15	151.05	163.7	159.54	127.81	148.8	137.51	*	*	-	-
MAMMA1000876	4.29	6.54	6.75	2.84	2.75	3.43	2.51	1.58	2.61	*	*	-	-
MAMMA1000877	2.84	3.61	4.96	2.05	1.13	1.68	2.93	0.77	2.2	*		-	
MAMMA1000878	5.22	9.31	15.62	6.72	6.36	5.06	10.1	4.12	5.11				
MAMMA1000880	13.15	18.7	32.08	12.61	12.85	8.92	10.54	7.92	11.52				
MAMMA1000881	6.97	11.85	26.23	10.06	11.84	7.67	8.29	6.16	7.32				
MAMMA1000883	11.76	21.56	31.01	16.67	19.82	18.1	18.77	10.78	19.11				
MAMMA1000897	18.89	25.07	44.99	26.44	17.53	21.31	17.58	14.36	19.92				
MAMMA1000898	4.54	4.74	8.26	5.15	4.11	4	3.9	1.83	1.2				
MAMMA1000905	19.81	46.58	24.87	13.58	12.04	12.03	17.95	11.63	11.81				
MAMMA1000906	13.7	9.74	18.2	5.83	6.94	4.39	4.39	2.34	1.82	*	*	-	-
MAMMA1000908	8.3	13.83	18.11	10.1	14.32	5.63	5.09	3.21	3.69		*		-
MAMMA1000911	13.12	16.04	26.46	13.81	12.11	7.57	12.29	5.96	12.25				
MAMMA1000914	2.41	3.47	11.09	1.11	2.25	1.29	1.59	0	0.87				
MAMMA1000920	68.92	152.1	139.06	77.3	106.8	94.98	122.37	27.22	25.46				
MAMMA1000921	3.68	5.93	12.67	7.11	6.12	6.97	3.45	2.44	2.92				
MAMMA1000931	35.49	29.12	32.19	9.74	14.81	15.82	7.85	20.92	4.78	**	*	-	-
MAMMA1000940	16.07	19.99	34.79	11.62	14.07	12.51	10.88	8.84	14.41				
MAMMA1000941	36.94	28.9	55.32	14.85	46.69	25.1	44.15	31.17	20.09				
MAMMA1000942	19.99	18.82	58.05	28.3	25.6	20.38	16.91	16.31	24.51				
MAMMA1000943	14.05	10.94	26.95	6.92	4.75	8.24	3.89	2.4	1.4		*		-
MAMMA1000952	3.98	5.7	16.6	3.37	4.97	3.51	7.54	1.89	3				
MAMMA1000956	5.62	5.18	14.83	6.99	6.03	6.18	4.85	2.51	6.15				
MAMMA1000957	0.61	0.47	2.13	0.38	0.27	1.52	0.16	0	0				
MAMMA1000962	26.82	25.6	21.85	10.69	8.37	7.64	7.43	8.92	3.07	**	**	-	-
MAMMA1000966	13.96	15.32	18.62	3.18	4.77	5.42	5.48	5.55	2.07	**	**	-	-
MAMMA1000968	3.82	3.17	8.04	2.19	4.04	1.69	2.56	0.98	1.54				
MAMMA1000972	109.05	38.4	166	38.59	38.3	60.84	51.28	65.81	23.12				
MAMMA1000973	4.24	3.6	8.43	1.16	3.43	2.39	3.18	1.23	1.88				
MAMMA1000975	4.83	5.04	16.94	6.44	6.12	4.99	5.27	1.93	5.12				
MAMMA1000976	10.4	12.69	31.13	7.88	10.7	11.37	8.68	4.42	4.88				
MAMMA1000979	15.33	18.37	49.49	29.29	22.41	26.44	15.03	8.9	16				
MAMMA1000986	11.83	20.17	19.1	14.27	9.07	14.47	9.64	5.8	3.91		*		-
MAMMA1000987	35.85	39.55	84.06	67.43	62.8	61.8	45.73	25.89	38.89				
MAMMA1000988	12.53	13.76	42.26	22.92	17.53	17.38	12.36	7.34	12.64				
MAMMA1000994	6.93	10.09	26.01	16.14	13.54	12.99	6.56	3.79	6.83				
MAMMA1000998	3.85	8.09	10.95	3.78	4.4	5.85	1.97	0.73	2.47		*		-
MAMMA1001003	11.87	14.9	34.42	24.16	21.08	20.65	13.23	10.02	16.87				
MAMMA1001007	4	4.13	6.2	3.14	6.73	3.28	4.14	1.49	4.79				
MAMMA1001008	20.12	23.76	44.26	26.75	20.79	27.13	18.57	19.08	24.22				
MAMMA1001013	9.3	12.99	14.08	13.97	3.4	7.56	6.85	5.46	5.5		*		-
MAMMA1001014	3.74	2.89	7.41	3.98	5.49	5.98	4.67	4.19	1.31				
MAMMA1001021	58.82	76.19	93.74	67.98	54.85	51.75	72.35	45.95	58.5				
MAMMA1001024	88.7	92.15	131.2	139.16	94.51	99.4	87.98	68.05	106.24				
MAMMA1001025	69.9	102.4	41.66	70.13	59.68	30.76	22.6	25.23	39.06				
MAMMA1001028	80.18	111.56	110	73.96	84.44	72.45	97.15	91.69	100.75				

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Table 395

MAMMA1001030	7.4	11.72	12.89	11.66	7.79	10.11	7.28	6.15	7.3					
MAMMA1001035	39.22	53.03	74.6	50.1	27.34	38.76	23.51	31.74	38.44					
MAMMA1001036	3.31	5.83	5.4	5.92	5.35	4.3	4.37	2.81	3.74					
MAMMA1001037	24.23	31.03	53.22	27.23	25.26	31.34	28.91	17.23	25.45					
MAMMA1001038	12.98	20.58	21.05	13.13	14.71	11.55	14.52	10.1	18.77					
MAMMA1001041	1.54	2.15	5.75	4.24	4.69	7.8	3.02	1.22	2.08					
MAMMA1001043	1.39	2.46	4.67	3.06	4.27	3.32	4.35	1.52	2.3					
MAMMA1001050	1.33	4.39	4.83	3.8	5.59	5.14	4.27	1.05	2.57					
MAMMA1001054	19.75	24.03	50.38	32.02	21.79	27.11	13.83	16.21	20.46					
MAMMA1001059	3.19	4.55	5.53	3.65	3.25	5.05	2.54	10.99	3.33					
MAMMA1001066	5.02	4.16	8.84	5.66	2.95	3.72	1.82	2.25	3.08					
MAMMA1001067	17.58	21.79	31.08	14.83	16.92	18.84	15.29	17.34	18.26					
MAMMA1001072	2.53	1.88	3.3	1.93	1.68	2.41	2.3	1.25	2					
MAMMA1001073	0.84	2.27	6.85	1.01	1.41	5.24	0.75	4.07	1.61					
MAMMA1001074	24.28	39.17	47.61	31.96	28.12	24.54	31.91	23.64	32.81		-			
MAMMA1001075	1.48	5.48	8.44	3.99	4.91	2.99	2.44	2.09	3.72					
MAMMA1001078	21.72	26.12	44.96	33.39	16.5	21.38	18.07	17.35	25.34					
MAMMA1001080	12.04	17.72	15.6	14.26	12.06	16.7	6.39	6.97	11.08		*		-	
MAMMA1001082	4.59	9.29	12.12	6.84	2.79	4.23	4.41	1.12	3.78					
MAMMA1001091	16.73	23.95	30.14	19.81	16.46	17.71	21.25	12.1	23.6					
MAMMA1001092	7.81	11.13	15.6	7.44	8.17	6.28	7.18	4.54	7.68					
MAMMA1001094	11.74	16.72	20.33	14.77	10.66	23.71	14.53	12.3	17.29					
MAMMA1001105	45.26	57.55	66.73	41.25	47.01	32.75	30.09	24.22	28.58		*		-	
MAMMA1001110	7.59	14.4	12.56	8.44	9.45	9.37	9.82	4.24	0.9					
MAMMA1001126	37.56	44.85	64.49	49.13	34.88	37.49	24.63	36.31	49.73					
MAMMA1001133	5.76	9.31	8.87	3.28	3.01	4.08	2.64	5.37	6.55	*		-		
MAMMA1001139	7.27	14.13	10.95	4.54	4.49	4.1	6.16	2.44	5.84	*		-		
MAMMA1001141	6.69	8.3	15.1	2.9	4.24	4.06	2.47	2.3	5.32					
MAMMA1001143	3.83	3.21	9.91	1.84	2.97	1.81	3.49	1.28	2.11					
MAMMA1001145	2.22	12.54	14.95	2.6	3.58	6.73	2.4	2.76	3.58					
MAMMA1001150	10.97	15.54	29.9	12.2	13.68	9.93	10.31	8.5	12.03					
MAMMA1001154	5.02	9.06	11.37	4.94	8.36	4.03	3.8	2.43	3.42					
MAMMA1001159	6.91	7.68	15.13	5.63	3.35	4.72	2.34	2.78	4.72					
MAMMA1001161	109.99	168.02	168.22	189.81	141.37	144.88	81.63	94.69	118.15					
MAMMA1001162	7.19	5.58	7.65	7.64	5.6	5.96	4.02	2.29	5.78					
MAMMA1001181	2.37	3.1	6.4	4.16	1.93	2.21	2.1	2.11	4.15					
MAMMA1001186	3.02	2.01	9.14	2.7	2.02	2.05	2.34	0.77	3.58					
MAMMA1001189	17.92	24.89	44.3	19.97	22.86	16.26	24.9	14.32	18.92					
MAMMA1001191	10.11	15.9	19.2	7.11	13.06	8.79	15.3	10.81	16.52					
MAMMA1001198	4.68	8.28	11.96	3.49	7.28	5.15	6.52	2.84	2.49					
MAMMA1001202	30.38	37.04	84.46	54.02	29.63	36.02	18.16	17.9	40.13					
MAMMA1001203	8.99	12.77	20.34	10.56	11.45	9.96	10.07	8.3	11.49					
MAMMA1001206	14.27	17.3	21.28	14.44	9.47	13.95	15.09	7.44	16.29					
MAMMA1001208	3.37	1.85	7.28	0.99	1.62	0.23	1.58	0.63	2.48					
MAMMA1001215	12.57	20.58	26.01	4.39	17.55	6.44	10.98	8.12	6.27					
MAMMA1001220	12.2	14.97	20.97	18.99	11.55	15.4	10.87	5.54	12.65					
MAMMA1001222	13.14	15.27	54.43	12	15.72	10.61	17.61	13.51	15.3					
MAMMA1001223	5.47	11.04	23.87	8.51	8.76	8.32	9.09	3.98	9.79					
MAMMA1001232	5.9	6.27	10.44	10.05	4.68	7.4	3.45	2.12	5.89					
MAMMA1001234	78.47	62.1	106.68	104.09	22.14	88.22	44.43	81.83	25.73					
MAMMA1001237	4.23	3.61	4.51	2.39	3.8	1.85	3.83	2.61	1.63					
MAMMA1001243	26.51	33.45	37.19	22.72	19.97	20.13	13.4	8.73	6.36	*	**	-	-	
MAMMA1001244	3.29	3.23	5.47	2.05	2.81	0.99	2.32	0.99	1.85					
MAMMA1001249	32.97	38.57	66.31	31.72	40.81	37.57	44.31	25.2	27.49					
MAMMA1001256	13.8	15.37	22.1	10.86	16.44	20.14	15.27	12.69	11.49					
MAMMA1001259	3.58	4.73	9.83	2.71	2.66	1.74	5.81	0.4	3.31					
MAMMA1001260	16.61	19.65	19.14	11.02	7.29	22.35	9.03	6.24	10.39		**		-	
MAMMA1001262	8.3	48.53	16.27	15.78	7.11	6.47	9.48	5.41	7.71					
MAMMA1001268	7.26	6.65	12.6	5.74	6.05	4.12	3.69	3.37	4.04					
MAMMA1001271	4.99	4.56	6.83	2.12	3.55	3.26	4.68	2.4	2.94	*		-		
MAMMA1001274	197.38	283.08	348.26	54.68	91.98	70.74	33.35	19.31	25.39	*	**	-	-	
MAMMA1001280	10.76	14.33	28.14	10.36	11.35	10.7	14.52	8.71	14.89					
MAMMA1001283	4.11	3.31	10.89	0.34	3.46	2.07	2.94	1.3	1.97					
MAMMA1001284	6.24	6.15	16.76	7	6.77	4.3	3.05	1.61	4.29					

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MAMMA1001286	29.08	30.31	35.52	8.75	7.01	14.48	10.18	16.99	22.31	**	*	-	-
MAMMA1001289	8.87	7.96	10.4	9.73	7.53	9	7.31	3.62	7.73				
MAMMA1001292	24.97	44.07	66.64	9.34	36.59	35.11	13.77	28.43	10.4				
MAMMA1001296	4	4.17	8.01	2.8	3.49	2.38	2.75	2.82	4.19				
MAMMA1001298	7.53	9.89	10.46	2.88	6.46	2.62	5.34	3.84	1.86	*	*	-	-
MAMMA1001305	3.74	4.35	13.81	2.61	4.06	3.12	3.76	5.53	2.5				
MAMMA1001309	10.42	15.14	31.52	12.87	13.99	9.19	10.23	3.68	9.96				
MAMMA1001310	2.92	5.46	13.25	3.59	3.89	1.96	3.03	0.43	1.21				
MAMMA1001322	2.17	2.64	6.93	3.3	2.91	2.5	1.12	1.37	2.03				
MAMMA1001324	4.53	3.59	5.55	3.63	2.78	3	2.65	1.6	1.68		*		-
MAMMA1001330	4.9	5.1	12.68	7.84	4.19	4.82	3.36	2.64	3.18				
MAMMA1001333	4.95	3.16	7.58	2.56	3.62	3.33	2.38	2.25	1.89				
MAMMA1001334	31.92	25.66	43.45	18.83	15.13	18.08	17.92	22.66	13.99	*		-	
MAMMA1001337	4.26	3.84	13.74	3.62	4.64	5.34	4	3.29	3.16				
MAMMA1001341	4.05	4.96	11.41	4.38	5.21	4.83	5.24	4.52	3.64				
MAMMA1001343	2.73	5.65	10.8	3.22	4.68	4.2	3.94	1.64	3.95				
MAMMA1001344	2.25	2.47	7.73	4.27	4.36	3.62	2.73	1.3	3.12				
MAMMA1001346	5.84	6.71	17.37	10.65	9.35	8.33	6.74	3.26	6.06				
MAMMA1001383	6.99	8.47	18.39	14.27	8.27	9.89	7.45	4.12	6.12				
MAMMA1001388	25.28	28.84	63.23	32.5	23.98	25.52	24.7	25.15	17.69				
MAMMA1001396	15.94	20.37	30.49	14.54	24.62	26.46	14.45	46.08	11.25				
MAMMA1001397	14.75	18.37	41.81	21.11	18.82	16.79	17.96	11.5	21.37				-
MAMMA1001401	2.94	3.12	6.56	1.21	2.62	3.02	2.46	0.76	2.89				
MAMMA1001408	1.5	3.57	7.4	2.81	1.88	3.96	5.62	0.76	2.46				
MAMMA1001411	6.08	3.93	9.81	9.46	6.06	8.29	3.36	4.18	4.81				
MAMMA1001414	6.51	7.32	14.7	23.79	6.86	10.67	5.51	4.82	6.45				
MAMMA1001415	3.95	8.97	8.68	5.52	5.96	8.18	6.06	2.79	4.69				
MAMMA1001418	8.77	9.1	12.47	12.83	10.06	11.32	13.03	7.4	7.63				
MAMMA1001419	7.73	7.93	11.48	9.88	6.73	10.35	9.18	5.19	6.18				
MAMMA1001420	5.14	4.76	6.97	10.23	6.22	6.56	5.34	3.95	4.64				
MAMMA1001426	5.19	7.71	9.63	5.55	8.11	6.73	7.6	4.91	8.87				
MAMMA1001428	3.64	3.18	7.92	6.62	3.95	5.99	3.35	1.43	3.18				
MAMMA1001432	12.35	13.88	21.83	18.83	11.53	18.33	8.1	11.28	14.53				
MAMMA1001435	20.05	30.02	44.24	21.04	23.96	21.39	14.97	14.52	16.51				
MAMMA1001442	6.94	7.75	11.08	5.53	5.57	7.7	6.68	4.54	7.44				
MAMMA1001446	26.48	31.11	44.32	20.63	23.27	24.39	8.85	5.14	8.85		**		-
MAMMA1001450	11.55	15.7	15.65	12.27	11.07	10.5	14.48	8.46	14.95				
MAMMA1001452	4.86	7.91	8.36	9.2	4.08	6.24	7.72	3.93	6.05				
MAMMA1001465	8.92	12.52	15.39	11.83	13.04	10.87	16.92	7.42	13.06				
MAMMA1001476	132.51	144.85	285.99	418.67	194.96	350.68	82.5	94.08	100.24				
MAMMA1001478	18.64	21.54	45.82	21.72	20.69	19.34	14.71	16.9	28				
MAMMA1001479	11.41	20.27	19.2	13.74	10.72	9.96	13.4	11.81	15.33				
MAMMA1001487	48.7	29.91	37.89	41.22	44.32	54.61	29.8	35.15	13.96				
MAMMA1001498	4.35	2.96	3.82	3.07	3.33	1.99	1.92	4.02	3.09				
MAMMA1001501	4	5.27	10.62	3.92	4.81	5.08	4.06	2.78	3.9				
MAMMA1001502	3.5	3.68	8.07	3.61	4.35	4.14	3.43	1.95	7.01				
MAMMA1001510	11.46	20.55	16.62	13.12	12.05	13.04	13.33	7.95	10.37				
MAMMA1001522	4.88	10.87	13.99	8.11	4.33	5	2.46	3.76	5.04				
MAMMA1001529	69.97	69.9	94.57	30.63	46.88	57.69	31.84	37.9	51.83		*		-
MAMMA1001532	28.38	37.51	51.46	23.78	26.52	23.49	26.6	24.11	41.98				
MAMMA1001533	19.86	8.23	26.5	6.01	12.03	8.61	7.93	4.83	6.28				
MAMMA1001534	11.45	13.72	20.66	6.58	8.79	8.61	9.6	5.71	8.05				
MAMMA1001535	10.07	15.11	17.7	7.42	8.38	7	2.75	2.21	3.48	*	**	-	-
MAMMA1001547	5.79	10.79	16.77	6.18	7.64	6.73	7.59	4.04	7.84				
MAMMA1001551	1.79	3.35	10.09	2.36	3.75	2.54	3.47	0.46	2.39				
MAMMA1001569	5.44	7.64	12.53	5.97	3.18	5.89	2.71	3.74	6.78				
MAMMA1001575	19.87	31.06	32.95	20.06	20.37	18.83	18.83	16.95	22.11				
MAMMA1001576	4.97	13.68	9.34	4.55	6.26	3.49	1.76	5.49	4.16				
MAMMA1001584	17.12	20.22	32.05	43.71	22.66	30.09	21.3	15.63	24.89				
MAMMA1001586	3.44	2.63	9.42	2.75	2.52	1.44	2.63	0.98	2.02				
MAMMA1001590	4.74	3.32	9.43	0.65	2.72	2.98	5.93	1.26	2.67				
MAMMA1001599	6.91	10.35	19.33	5.33	6.4	5.4	7.64	5.96	7.44				
MAMMA1001600	12.56	24.27	25.25	10.57	15.9	13.61	21.16	12.02	17.72				
MAMMA1001604	20.93	20.87	41.04	17.28	15.57	5.46	4.43	10.16	15.17				

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MAMMA1001606	37.25	38.33	44.14	13.41	26.09	29.22	7.5	16	15.16	*	**	-	-
MAMMA1001609	2.18	4.53	5.97	1.87	1.39	1.8	4.17	2.27	1.51				
MAMMA1001614	10.91	17.85	21.09	12.42	12.51	13.02	16.85	9.92	19.29				
MAMMA1001615	1.95	3.17	11.55	2.77	2.24	1.36	2.33	1.46	2.06				
MAMMA1001619	11.51	16.15	15.55	6.34	13.88	8.59	8.19	7.08	5.14		*		-
MAMMA1001620	4.59	6.42	11.46	1.77	3.88	3.43	3.11	1.71	4				
MAMMA1001623	46.36	31	53.81	63.16	42.72	47.15	31.15	25.06	25.66				
MAMMA1001626	23.59	24.5	38.75	33.26	30.12	18.9	7.93	11.89	22.41				
MAMMA1001627	23.89	43.37	29.47	17.73	21.82	12.9	6.43	10	7.98		*		-
MAMMA1001630	9.27	13.78	11.56	7.25	5.63	6.82	2.81	4.06	2.66	*	**	-	-
MAMMA1001633	3.1	2.16	7.03	2.23	2.28	2.16	0.8	0.79	2.49				
MAMMA1001634	3.53	6.28	9.01	3.76	4.19	2.88	3.9	2.94	2.79				
MAMMA1001635	3.28	4.64	15.97	2.28	2.56	1.53	6.22	1.65	2.6				
MAMMA1001649	3.05	5.72	15.55	3.26	4.9	2.56	4.26	1.39	3.94				
MAMMA1001654	4.23	5.9	13.55	3.26	5.84	3.8	3.63	1.4	2.71				
MAMMA1001660	39.09	42.24	88.43	56.56	52.47	44.31	41.47	39	60.86				
MAMMA1001663	8.52	11.06	11.71	10.2	6.57	5.19	7.96	6.94	8.33				
MAMMA1001670	5.91	7.75	6.72	4.07	2.57	5.22	5.32	3.26	4.27	*	*	-	-
MAMMA1001671	56.61	62.54	66.07	56.8	37.97	53.72	50.14	43.96	58.96				
MAMMA1001679	6.69	13.86	10.25	4.05	5.47	3.58	4.46	7.43	6.03				
MAMMA1001683	15.6	21.19	31.72	12.85	17.62	10.3	18.14	10.49	14.57				
MAMMA1001686	4.11	3.45	11.77	4.66	4.36	4.4	4.89	1.58	2.59				
MAMMA1001688	4.96	5.41	15.23	3.79	4.7	4.42	2.65	1.46	3.58				
MAMMA1001689	28.44	25.89	32.18	7.85	17.39	15.22	8.44	8.89	20.79	*	*	-	-
MAMMA1001692	5.97	3.79	10.24	3.42	9.67	3.1	3.28	4.26	5.93				
MAMMA1001711	4.75	4.66	8.45	3.21	3.28	2.22	2.67	8.04	0.88				
MAMMA1001715	4.22	4.73	9.43	3.9	2.04	3.47	3.76	4.11	2.61				
MAMMA1001730	3.39	2.22	8.02	1.72	1.43	1.79	1.71	1.46	1.86				
MAMMA1001735	8.81	9.96	22.03	12.16	11.12	10.37	6.84	5.43	7.1				
MAMMA1001740	2.28	4.25	11.56	2.64	4.24	1.86	2.43	1.41	3.14				
MAMMA1001743	10.52	18.5	19.92	5.55	7.23	6.37	6.45	1.87	3.83	*	*	-	-
MAMMA1001744	4.59	3.07	5.75	3.86	4	4.16	2.05	2.19	3.63				
MAMMA1001745	12.62	11.29	21.77	12.13	11.56	10.5	13.92	9.55	13.74				
MAMMA1001751	11.11	8.28	15.68	3.47	4.56	3.38	2.93	2.2	1.66	*	*	-	-
MAMMA1001752	5.63	3.02	9.77	2.83	5.25	2.56	2.97	2.42	0.97				
MAMMA1001754	23.39	32.69	51.88	31.96	35.9	26.06	34.24	24.41	25.71				
MAMMA1001757	5.44	8.41	15.4	4.99	7.7	6.28	7.54	3.86	5.12				
MAMMA1001760	2.58	5.03	10.84	4.07	3.09	11.35	3.87	1.47	1.67				
MAMMA1001764	1.11	5.18	12.27	3.88	5.02	2.55	4.09	0.44	2.15				
MAMMA1001767	3.1	2.25	5.04	3.83	2.36	7.31	2.64	1.02	1.81				
MAMMA1001768	11.92	10.35	26.44	10.9	12.51	10.66	12.91	3.89	9.69				
MAMMA1001769	14.67	15.11	32.18	14.99	14.79	13.17	17.74	10.66	13.05				
MAMMA1001771	5.81	5.01	9.7	5.52	6.04	4.42	3.1	4.15	2.2				
MAMMA1001773	40.73	46.88	88.4	41.31	38.76	36.3	25.57	21.1	22.63				
MAMMA1001778	15.44	10.48	54.31	14.07	14.31	18.11	19.19	12.85	7.66				
MAMMA1001783	12.5	12.45	33.56	11.62	10.75	17.89	7.63	5.83	3.14				
MAMMA1001785	4.08	3.99	8.35	2.35	3.38	3.07	3.75	1.41	2.66				
MAMMA1001788	6.1	6.55	20.74	18.01	10.68	15.67	7.37	4.2	7.06				
MAMMA1001790	1.31	0.72	1.87	1.36	1.35	1.32	1.67	0.59	1.36				
MAMMA1001800	2.19	1.86	2.06	3.44	3.43	3.44	1.48	0.44	1.31	**	*	+	-
MAMMA1001804	9.74	13.74	26.09	23.09	17.83	16.06	15.63	9.04	8.32				
MAMMA1001806	15.42	15.2	24.16	21.08	16.33	17.7	13.08	11.61	12.4				
MAMMA1001812	2.66	2.87	5.53	5.25	2.56	2.24	1.76	1.16	2				
MAMMA1001815	0.82	1.33	4.14	2.35	1.64	0.9	2.33	0	1.04				
MAMMA1001817	7.15	8.39	26.7	8.94	11.15	9.35	10.6	5.97	8.95				
MAMMA1001818	11.74	18.24	23.68	11.92	10.04	13.23	8.57	10.06	9.02				
MAMMA1001819	15.72	24.34	43.46	17.35	11.3	16.16	12.64	12.63	16.41				
MAMMA1001820	22.82	19.64	37.64	42.37	24.16	31.98	15.13	16.66	19.01				
MAMMA1001824	8.99	12.77	18.28	12.69	14.09	15.06	12.72	9.76	11.95				
MAMMA1001832	7.22	10.73	12.96	9.65	7.55	9.34	6.24	4.93	7.88				
MAMMA1001836	9.42	23.13	19.47	21.69	15.29	10.85	11.8	5.71	11.11				
MAMMA1001837	3.6	4.29	8.23	5.89	6.7	8.36	4.62	1.11	4.3				
MAMMA1001848	16.38	27.46	23.83	25.7	38.67	49.58	24.68	13.45	27.7				
MAMMA1001850	4.58	4.63	5.84	6.14	2.91	3.96	4.34	2.05	2				

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Table 398

MAMMA1001851	3.04	3.08	4.42	3.11	3.54	2.54	2.52	0.56	2.38				
MAMMA1001852	4.14	3.26	11.19	3.61	3.33	5.4	1.88	2.12	2.02				
MAMMA1001854	1.51	2.81	6.9	2.97	1.88	2.16	2.29	1.4	2.53				
MAMMA1001858	19.51	21.77	35.8	19.05	16.81	16.88	15.59	11.41	20.06				
MAMMA1001864	13.26	17.9	34.07	19.43	19.24	16.98	19.91	10.97	23.39				
MAMMA1001868	36.41	51.95	37.39	27.02	32.06	24.02	38.47	28.02	40.25				
MAMMA1001874	10.43	12.98	12.56	15.09	16.33	15.06	13.47	8	7.34	*		+	
MAMMA1001878	8.74	13.09	17.2	10.72	7.64	9.1	6.72	5.47	7.12				
MAMMA1001880	4.07	4.26	5.15	5.16	2.51	4.87	2.76	4.1	3.13				
MAMMA1001885	11.53	16.59	20.89	11.02	9.99	7.12	10.84	10.3	12.47				
MAMMA1001890	18	26.55	27.35	18.41	24.49	18.88	18.85	18.1	22.42				
MAMMA1001893	9.74	13.29	21.33	8.06	11.26	12.34	13.42	8.15	13.42				
MAMMA1001901	5.91	10.54	9.81	6.07	8.49	8.27	5.4	3.05	2.51		*		-
MAMMA1001907	2.61	3.62	7.04	35.62	7.01	7.16	2.77	1.6	2.87				
MAMMA1001908	8.52	7.37	12.33	6.04	6.79	5.83	5.18	1.69	2.73		*		-
MAMMA1001919	28.87	31.67	48.08	80.53	41.26	66.58	17.81	21.06	28				
MAMMA1001931	5.05	3.95	9.8	4.52	3.24	2.79	3.04	5.51	2.52				
MAMMA1001937	14.26	19.97	17.05	11.88	9.67	16.46	11.3	11.49	14.97				
MAMMA1001951	10.03	11.71	22.7	11.88	9.84	10.7	11.47	12.01	12.62				
MAMMA1001956	993.12	926.97	1643.3	1427.1	1487.9	1519.7	1062.9	902.24	975.35				
MAMMA1001957	5.28	8.16	19.85	8.48	7.2	6.6	6.19	4.02	7.97				
MAMMA1001960	4.45	5.22	11.99	3.94	5.66	4.15	4.01	2.89	2.74				
MAMMA1001963	9.87	14.96	20.98	14.68	14.73	14.4	8.07	6	3.43				
MAMMA1001969	11.23	14.81	19.75	14.09	10.96	16.21	10.31	8.8	19.07				
MAMMA1001970	4.02	5.46	5.52	3.48	4.15	15.31	4.95	4.07	2.18				
MAMMA1001978	13.78	19.86	26.28	16.09	13.28	16.86	13.67	12.24	23.16				
MAMMA1001992	6	4.83	12.16	2.11	5.12	11.04	3.79	2.55	5.99				
MAMMA1001994	4.27	7.76	10.55	16.33	8.69	5.41	3.19	4.78	5.52				
MAMMA1002008	2.62	3.39	13.27	3.37	3.96	2.92	2.97	2.86	1.68				
MAMMA1002009	3.5	5.4	13.89	4.02	6.32	3.6	2.53	1.71	1.09				
MAMMA1002011	3.21	3.57	5.26	2.05	5.5	3.92	2.9	2.56	2.89				
MAMMA1002022	23.41	32.84	43.13	18.55	24.01	20.69	18.94	17.16	21.03				
MAMMA1002024	4.69	8.48	7.51	4.82	3.7	4.18	3.88	2.33	4.09				
MAMMA1002032	22.72	24.3	34.55	17.1	16.95	18.46	20.89	15.73	25.86				
MAMMA1002033	5.27	4.69	9.29	4.37	4.11	4.75	8.94	7.94	5.81				
MAMMA1002041	6.92	11.13	16.18	4.7	5.73	4.73	2.24	3.33	5.35				
MAMMA1002042	4.21	5.9	12.97	1.93	6.7	3.65	5.79	7.29	5.48				
MAMMA1002045	3.58	4.86	12.3	4.27	5.48	4.41	3.9	4.78	2.67				
MAMMA1002047	6.8	7.34	9.55	7.31	12.68	11.46	8.75	3.44	4.92				
MAMMA1002056	2.57	2.86	6.49	3.74	3.21	3.7	1.38	1.89	2.78				
MAMMA1002058	12.8	12.32	19.01	10.51	10.24	9.8	10.2	7.07	10.6				
MAMMA1002060	3.44	2.98	10.21	3.91	3.36	3.73	4.39	1.38	3.75				
MAMMA1002065	5.77	6.94	12.55	3.81	3.34	3.54	3.78	2.53	2.66				
MAMMA1002068	5.43	5.26	11.94	2.41	4.51	4.09	4.21	2.57	4.68				
MAMMA1002070	3.38	5.43	10.65	2.42	2.8	1.57	1.88	0.34	3.17				
MAMMA1002078	3.03	3.94	12.3	1.63	3.98	2.25	2.32	1.3	2.65				
MAMMA1002080	11.92	16.79	18.92	3	9.03	5.76	7.02	2.85	4.16	*	**	-	-
MAMMA1002082	8.32	5.53	12.97	8.62	3.65	5.55	2.81	1.42	4.34				
MAMMA1002084	5.95	5.89	9.82	6.01	4.3	5.5	3.1	3.76	3.18		*		-
MAMMA1002087	4.18	2.51	5.36	3.1	3.55	1.79	2.57	2.24	1.51				
MAMMA1002091	4.77	6.45	9.77	6.57	5.69	2.84	2.82	2.99	2.11		*		-
MAMMA1002093	7.77	50.44	12.78	4.52	8.15	3.8	10.66	4.49	6.61				
MAMMA1002095	2.07	3	10.99	1.29	1.85	0.7	1.89	0.49	1.88				
MAMMA1002108	11.08	15.62	32.13	20.98	14.75	19.73	14.58	13.23	20.21				
MAMMA1002112	11.23	16.95	26.2	16.44	15.29	9.14	16.6	9.46	11.52				
MAMMA1002118	15.81	20.81	31.7	25.23	19.06	12.25	11.43	15.5	24.54				
MAMMA1002119	10	9.39	20.1	14.99	8.54	8.01	7.06	7.05	10.3				
MAMMA1002125	8.81	6.62	15.53	7.95	7.53	5	5.63	5.81	8.41				
MAMMA1002126	38.45	22.62	47.44	8.75	23.38	14.29	26.49	8	13.65				
MAMMA1002128	9.97	18.56	26.22	10.58	12.77	9.47	19.63	7.42	11.63				
MAMMA1002132	6.21	7.25	34.7	5.61	8.67	4.88	6.36	3.29	9.25				
MAMMA1002140	16.11	29.14	22.82	11.98	12.1	5.91	9.18	3.59	4.66	*	*	-	-
MAMMA1002142	3.45	5.23	11.28	4.42	6.67	3.75	4.53	0.93	3.45				
MAMMA1002143	16.35	16.97	31.08	20.92	14.17	21.18	9.45	9.06	16.49				

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MAMMA1002145	59.23	60.84	77.53	26.62	46.01	14.01	21.49	27.44	27.68	*	**	-	-
MAMMA1002147	5.58	4.1	8.16	3.48	3.17	3.48	3.61	1.58	1.54				
MAMMA1002153	2.82	4.71	7.06	3.26	5.54	4.01	3.33	4.14	1.01				
MAMMA1002155	2.48	3.25	10.86	2.89	3.23	2.81	4.53	1.33	2.05				
MAMMA1002156	1.89	5.51	11.57	0.4	3.84	3.05	2.17	1.45	3.44				
MAMMA1002158	31.98	68.42	55.01	8.28	17.41	13.99	16.74	7.42	4.4	*	*	-	-
MAMMA1002164	1.74	3.48	10.17	3.33	5.39	3.9	5.07	0.22	3.21				
MAMMA1002165	14.96	21.57	31.25	20.06	14.73	17.78	14.07	10.69	17.29				
MAMMA1002170	22.65	29.54	35.22	10.64	9.2	7.67	9.57	17.6	7.86	**	*	-	-
MAMMA1002174	5.6	8.95	10.45	5.64	4.66	7.45	4.49	3.82	4.25		*		-
MAMMA1002175	51.5	30.74	138.92	91.4	93.51	53.96	49.64	44.62	29.88				
MAMMA1002180	26.41	35.57	64.21	33.73	28.48	23.51	38.7	27.33	38.33				
MAMMA1002198	37.99	80.63	138.79	18.29	47.55	46.05	13.24	10.75	8.83				
MAMMA1002205	15.14	20.56	52.79	21.27	16.14	13.46	24.47	10.14	16.64				
MAMMA1002206	2.93	3.59	10.31	2.52	3.96	2.18	3.53	0.98	3.24				
MAMMA1002209	183.5	268.42	348.13	282.08	352.1	269.26	189.69	127.24	124.82				
MAMMA1002215	24.38	31.33	40.05	29.39	28.67	24.47	25.62	23.02	20.25				
MAMMA1002219	2.71	0.94	3.73	1.84	2.07	2.08	0.86	0.6	1.35				
MAMMA1002224	15.23	8.24	19.36	12.34	12.12	11.67	6.61	10.38	6.31				
MAMMA1002229	16.46	14.44	27.79	9.51	10.83	11.84	7.32	11.92	8.59				
MAMMA1002230	22	37.1	57.12	14.15	20.28	20.13	22.25	15.46	15.8				
MAMMA1002233	70.38	89.47	122.68	8.19	33.96	39.69	218.52	154.84	147.67	*	*	-	+
MAMMA1002234	7.92	8.85	12.79	4.92	10.39	5.68	11.44	4.89	8.58				
MAMMA1002236	136.07	148.16	220.88	36.8	57.62	87.11	34.48	55.67	55.33	*	*	-	-
MAMMA1002243	20.02	20.33	38.87	38.33	25.12	25.3	21.56	17.63	24.13				
MAMMA1002250	2.68	3.81	6.67	5.79	2.6	4.11	4.54	2.26	2.04				
MAMMA1002253	0.57	1.7	6.1	2.21	1.65	3.98	2.62	1.41	1.86				
MAMMA1002267	9.29	9.06	17.68	10.28	11.75	12.03	8.49	4.34	11.22				
MAMMA1002268	0.57	3.72	6.93	16.18	7.45	4.5	3.59	1.73	3.92				
MAMMA1002269	1.7	2.24	4.35	2.97	8.98	8.51	2.83	1.4	3.35				
MAMMA1002282	2.85	3.76	4.32	2.98	7.03	4.77	3.56	5.53	5.39				
MAMMA1002292	15.43	25.26	45.69	33.39	19.64	22.84	15.48	15.23	21.7				
MAMMA1002293	3.2	3.94	4.4	4.2	3.49	3.24	3.79	4.35	3.43				
MAMMA1002294	8.41	6.68	12.5	3.33	7.99	10.5	5.31	8.44	4.21				
MAMMA1002297	5.35	6.59	11.35	7.95	7.71	8	2.76	2.6	3.09				
MAMMA1002298	3.44	2.01	8.19	4.11	4.61	4.39	2.48	2.96	3.08				
MAMMA1002299	2.99	4.55	14.53	7.08	6.73	6.49	4.69	0.99	4.04				
MAMMA1002308	5.47	9.33	18.02	10.01	8.02	7.61	7.23	3.03	7.9				
MAMMA1002310	9.13	10.94	18.01	13.86	17.88	11.7	14.2	7.14	10.5				
MAMMA1002311	10.67	15.07	18.09	4.83	5.07	6.09	1.95	3.51	2.65	*	**	-	-
MAMMA1002312	30.9	42.06	49.45	34.33	28.66	29.57	22.98	30.71	35.68				
MAMMA1002317	5.72	5.28	10.29	3.9	3.7	4.94	4.31	4.41	4.7				
MAMMA1002319	11.12	14.39	20.39	9.58	9.59	6.6	12.89	13.6	13.85				
MAMMA1002322	2.09	3.24	7.26	1.71	2.86	1.28	1.75	1.09	1.05				
MAMMA1002329	17.33	19.74	32.38	18.64	18.47	17.53	19	10.56	17.8				
MAMMA1002332	2.58	4.23	6.84	4.89	4.12	2.94	2.37	0.43	2.61				
MAMMA1002333	1.45	2.08	7.07	4.55	5.97	6.64	2.39	0.64	2.14				
MAMMA1002335	12.65	18.48	23.72	7.59	6.81	10.8	3.17	6.12	8.64	*	*	-	-
MAMMA1002338	7.58	15	19.05	10.2	7.54	10.35	7.33	10.1	11.23				
MAMMA1002347	10.15	21.39	24.74	8.5	9.44	11.14	10.35	10.5	16.39				
MAMMA1002351	7.61	10.35	21.39	9.12	8.67	7.13	7.44	4.46	10.65				
MAMMA1002352	3.96	6.91	9.29	4.01	3.84	4.53	2.75	1.39	5.61				
MAMMA1002353	8.39	10.78	23.6	6.39	12.46	12.35	7.8	9.12	7.88				
MAMMA1002355	25.93	29.71	53.72	28.58	30.76	23.64	29.82	21.55	27.08				
MAMMA1002356	28.68	42.92	56.16	40.53	46.92	35.69	34.66	27.13	37.63				
MAMMA1002359	9.7	13.9	19.55	15.93	13.24	12.52	6.92	6.02	14.49				
MAMMA1002360	85.31	125.75	125.12	50.2	80.78	78.44	18.48	22.03	30.83		**		-
MAMMA1002361	4.68	5.33	13.4	6.92	5.11	6.08	3.35	2.61	7.85				
MAMMA1002362	4.53	5.8	12.93	6.01	7	5.37	5.23	3.68	7.06				
MAMMA1002367	13.67	17.12	24.55	7.42	11.11	9.42	8.07	3.62	6.96		*		-
MAMMA1002371	2.82	3.35	9.8	0.89	2.2	2.61	2.45	2.44	1.99				
MAMMA1002380	7.87	13.26	17.64	9.95	9.26	6.58	10	7.71	10.46				
MAMMA1002384	91.44	168.34	87.56	61.83	126.23	76.47	56.65	15.61	10.22		*		-
MAMMA1002385	2.04	1.77	7.54	5.82	2.53	3.4	1.44	1.54	1.62				

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Table 400

MAMMA1002390	16.21	20.25	27.48	13.4	13.61	14.48	13.02	8.71	18.23				
MAMMA1002392	4.77	2.83	6.02	7.9	2.39	4.12	3.41	2.08	4.6				
MAMMA1002396	2.99	1.82	9.4	2.48	1.34	2.01	2.08	1.84	0.91				
MAMMA1002399	9.87	15.29	24.4	2.74	8.91	5.25	5.52	3.6	3.73		*		-
MAMMA1002400	72.48	90.25	98.09	48.92	68.69	49.07	35.95	25.31	45.88	*	**	-	-
MAMMA1002409	6.49	9.18	17.47	3.97	6.62	4.36	5.84	1.59	5.43				
MAMMA1002411	9.51	7.57	20.49	9.69	12.54	10.88	11.51	6.91	7.16				
MAMMA1002413	34.97	38.81	65.44	49.38	40.42	34.55	32.31	27.95	41.66				
MAMMA1002417	36.82	49.91	68.59	44.18	31.29	40.31	29.78	24.72	27.25				
MAMMA1002427	6.8	10.05	17.81	10.58	7.31	11.82	13	6.65	9.6				
MAMMA1002428	5.09	6.45	11.72	5.54	5.32	4.74	5.8	2.19	4.39				
MAMMA1002433	14.18	24.47	33.83	12.49	14.56	9.41	13.05	9.04	12.93				
MAMMA1002434	4.26	3.86	13.18	2.12	3.76	2.95	4.67	2.76	3.7				
MAMMA1002446	8.39	8.67	27.55	10.82	15.66	10.5	11.46	8.07	9.95				
MAMMA1002447	4.71	6.42	13.3	4.25	7.94	6.39	4.34	1.12	6.19				
MAMMA1002454	3.91	4.62	7.05	7.12	5.04	6.67	4.66	2.3	3.21				
MAMMA1002461	27.3	34.86	56	30.05	20.73	23.5	29.37	22.7	32.72				
MAMMA1002463	9.24	10.49	15.67	10.5	6.07	6.24	8.27	4.83	7.57				
MAMMA1002464	3.98	2.85	5.66	1.75	3.24	1.37	1.77	2.41	1.96				
MAMMA1002466	4.86	7.93	15.75	8.06	8.89	6.34	6.75	3.95	4.7				
MAMMA1002470	4.68	6.3	14.57	5.95	13.1	4.89	3.64	2.83	3.84				
MAMMA1002475	17.39	22.9	40.72	24.51	29.14	16.55	20.39	12.61	16				
MAMMA1002480	51.48	94.76	100.05	63.97	58.87	37.35	60.56	13.3	33.46				
MAMMA1002485	19.11	15.89	43.85	26.44	20.15	19.25	16.32	13.38	18.32				
MAMMA1002494	22.86	28.77	50.5	24.3	23.02	18.38	23.12	24.83	27.28				
MAMMA1002498	5.27	2.99	4.95	1.99	2.08	1.95	2.18	0.89	1.64	*	*	-	-
MAMMA1002524	11.96	11.09	24.02	7.72	7.78	5.46	10.41	6.02	6.07				
MAMMA1002530	277.32	388.85	679.97	473.31	550.87	394.12	467.12	251.99	328.81				
MAMMA1002538	1.65	4.73	10.72	1.52	2.62	2.66	2.05	0.61	2.49				
MAMMA1002545	2.59	2.37	13.88	1.77	4.03	1.39	1.68	0.09	1.93				
MAMMA1002554	115.83	185.59	273.08	258.19	207.86	207.1	180.88	93.96	83.88				
MAMMA1002556	4.03	6.04	7.54	5.06	3.68	5.28	2.7	3.76	3.11				
MAMMA1002561	15.67	18.37	24.06	5.72	9.69	8.96	6.7	7.18	2.52	*	**	-	-
MAMMA1002565	20.13	19.37	64.78	24.22	20.52	19.19	20.48	14.5	21.19				
MAMMA1002566	5.49	3.26	6.28	2.19	3.2	3.17	4.16	1.97	2.42				
MAMMA1002571	12.97	18.44	36.1	16.95	12.11	12.28	16.66	10	13.05				
MAMMA1002573	4.02	5.04	11.33	1.38	3.48	2.19	3.22	1.15	2.21				
MAMMA1002576	13.78	23.79	37.39	16.06	19.72	15.26	13.9	8.77	10.92				
MAMMA1002584	9.21	12.39	27.02	16.71	13.29	9.15	13.96	6.48	12.24				
MAMMA1002585	6.36	5.36	13.56	11.07	9.12	8.7	7.18	4.4	6.71				
MAMMA1002586	21.75	21.37	47.64	26.29	19.9	20.88	19.88	14.32	18.17				
MAMMA1002589	31.16	39.3	81.02	35.29	36.93	32.17	47.24	33.3	29.17				
MAMMA1002590	8.65	6.16	15.55	9.32	8.84	9.26	5.05	3.24	4.01				
MAMMA1002593	8.47	7.53	30	8.1	8.37	7.45	8.63	8.66	8.47				
MAMMA1002597	11.34	16.94	30.07	13.1	12.76	11.04	12.91	7.38	12.5				
MAMMA1002598	9.23	11.39	26.12	15.11	13.9	10.6	14.04	4.47	10.54				
MAMMA1002603	7.01	8.63	19.81	9.42	12.79	9.69	13.58	3.61	8.05				
MAMMA1002612	0.64	0.54	1.4	4.76	2.04	2.86	2.1	0	0.92				
MAMMA1002617	1.99	2.39	4.19	2.19	2.2	2.69	2.8	1.84	1.34				
MAMMA1002618	16.06	18.63	46.52	25.87	25.59	22.23	19.52	10.7	17.56				
MAMMA1002619	7.62	6.62	18.84	13.61	11.83	9.5	6.72	6.93	5.26				
MAMMA1002622	3.06	2.72	4.49	4.32	2.96	14.63	2.48	0.95	1.91				
MAMMA1002623	2.38	2.14	3.99	2.64	2.39	1.68	1.62	0	1.12				
MAMMA1002625	158.57	183.87	332.03	71.22	106.04	287.72	518.89	291.59	178.62				
MAMMA1002627	6.48	11.48	14.86	11.21	19	9.56	12.93	6.03	9.03				
MAMMA1002629	20.19	19.33	33.94	25.61	18.48	21.46	13.72	14.18	19.09				
MAMMA1002631	4.6	4.73	9.76	3.98	2.11	3.82	1.12	0.35	1.47		*		-
MAMMA1002633	64.25	69.26	104.49	122.15	95.76	107.58	86.41	60.3	67.07				
MAMMA1002636	30.48	34.84	49.63	34.43	30.9	28.96	42.01	28.77	46.58				
MAMMA1002637	2.95	5.14	7.06	4.15	3.68	2.57	4.18	1.82	4.8				
MAMMA1002646	3.86	4.18	6.8	3.4	4.56	2.51	2.73	1.37	2.49				
MAMMA1002648	136.47	120.19	147.15	150.69	135.33	106.16	124.23	86.88	146.01				
MAMMA1002650	1.26	1.85	1.15	1.57	0.72	1.64	0.26	0.46	0.54		*		-
MAMMA1002652	32.12	44.28	46.88	48.41	32.58	36.9	24.05	25.91	28.22		*		-

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Table 401

MAMMA1002655	11.4	14.99	17.9	15.12	13.04	14.83	12.19	8.95	8.53					
MAMMA1002662	6.09	7.03	11.38	9.76	5.9	8.37	9.45	4.05	7.02					
MAMMA1002665	45.5	69.25	80.49	54.25	62.78	56.03	66.39	47.78	71.4					
MAMMA1002671	18.2	21.13	33.24	18.58	22.22	20.8	25.58	15.85	14.12					
MAMMA1002673	11.32	15.65	15.97	11.87	13.24	9.54	13.67	9.79	13.55					
MAMMA1002684	12.93	20.62	16.77	15.69	20.34	11.67	14.21	4.61	5.68					
MAMMA1002685	5.98	5.53	9.57	4.13	4.23	3.62	3.38	2.66	3.46		*		-	
MAMMA1002692	8.9	8.42	9.87	7.25	7.35	7.75	2.28	5.77	1.68	*	*	-	-	
MAMMA1002693	9.54	10.93	23.31	11.25	9.77	9.02	7.69	7.85	6.66					
MAMMA1002698	6.28	7.75	12.56	8.05	7.51	8.6	5.96	6.56	6.22					
MAMMA1002699	5.33	9.37	9.52	5.1	10.31	6.85	7.2	5.75	6.86					
MAMMA1002701	26.1	32.61	44.74	24.49	33.98	29.72	36.76	18.9	37.16					
MAMMA1002708	10.78	13.98	19.02	10.41	15.42	12.16	15.37	13.13	12.91					
MAMMA1002711	14.75	23.34	34.41	24.21	29.1	25.59	25.28	14.17	20.72					
MAMMA1002712	11.97	12.21	14.44	7.62	10.08	13.25	6.69	8.26	7.29		**		-	
MAMMA1002716	4.68	7.56	7.57	4.77	4.14	4.42	3.66	3.97	3.59		*		-	
MAMMA1002721	14.39	14.75	20.55	11.28	10.99	13.97	10.36	11.19	14.35					
MAMMA1002723	7.42	10.89	16.39	7.15	8.24	4.7	4.46	4.93	6.1					
MAMMA1002727	5.86	7.13	17.65	5.65	6.92	6.82	4.72	3.49	6.01					
MAMMA1002728	203.39	279.55	292.72	297.21	297.38	218.05	240.28	159.35	257.9					
MAMMA1002742	14.02	17.19	15.98	10.59	10.28	10.18	5.71	6.31	6.17	**	**	-	-	
MAMMA1002743	13.89	22.29	19.83	22.11	23.47	15.54	12.39	9.78	3.07					-
MAMMA1002744	41.83	52.92	97.53	82.43	49.67	62.65	35.95	33.09	52.81					
MAMMA1002746	1.97	3.26	4.93	1.96	3.41	2.27	2.78	1.33	2.98					
MAMMA1002748	7.49	8.51	12.58	5.49	4.9	6.1	6.53	3.04	7					
MAMMA1002754	14.85	17.76	22.12	11.35	12.08	11.06	11.12	5.72	16.48	*		-		
MAMMA1002758	3.59	1.64	11.4	2.56	2.22	2.31	1.99	1.02	1.03					
MAMMA1002762	132.2	159.47	185.48	173.16	185.47	170.91	152.23	100.87	138.71					
MAMMA1002764	11.39	16.4	28.38	10.76	16.28	13.47	14.81	9.65	13.58					
MAMMA1002765	7.34	7.13	16.56	5.42	10.33	6.06	7.41	3.51	6.05					
MAMMA1002769	10.29	13.85	24.43	5.77	11.7	10.08	4.64	4.85	10.59					
MAMMA1002771	3.01	3.94	5.73	4.17	3.21	3.23	5.9	1.8	2.75					
MAMMA1002775	37.45	33.73	58.09	84.46	48.03	62.49	34.89	23.26	53.34					
MAMMA1002780	5.07	6.15	6.67	4.47	3.43	3.09	4.23	2.8	2.68	*	*	-	-	
MAMMA1002782	5.1	4.96	13.58	4.26	5.86	4.79	6.17	2.83	4.75					
MAMMA1002795	4.5	6.79	10.64	2.77	4.7	2.89	3.8	0.29	3.67					
MAMMA1002796	5.94	10.22	11.38	3.51	7	2.99	1.75	1.74	3.7		*		-	
MAMMA1002805	7.95	9.3	18.26	5.36	11.22	10.66	9.08	3.61	6.4					
MAMMA1002806	3.62	2.38	6.98	3.71	4.26	2.36	4.15	0.61	2.13					
MAMMA1002807	18.13	22.17	39.72	27.6	21.23	23.03	24.44	17.51	32.38					
MAMMA1002814	44.71	48.76	77.02	44.68	36.22	39.5	45.03	34.09	60.73					
MAMMA1002817	3.99	4.65	7.4	2.69	1.42	2.37	1.9	1.38	3.31	*		-		
MAMMA1002820	8.85	7.77	12.62	4.45	5.02	3.82	4.58	3.34	5.96	*	*	-	-	
MAMMA1002830	214.03	277.57	281.23	229.96	268.12	260.12	256.75	84.59	195.17					
MAMMA1002833	35.45	43.35	56.35	30.19	48.83	31.33	56.07	31.41	58.94					
MAMMA1002835	2.83	4.62	14.15	2.49	4.86	1.91	2.5	0.14	2.49					
MAMMA1002838	11.11	14.42	31.43	18.22	13.58	15.03	12.7	4.89	21.91					
MAMMA1002842	18.2	19.62	33.31	21.65	17.53	15.65	18.5	8.81	13.46					
MAMMA1002843	8.38	8.96	10.43	6.56	6.63	6.17	6.89	4.51	5.73	*	*	-	-	
MAMMA1002844	7.03	7.49	9.64	4.13	4.73	3.32	3.78	1.87	4.09	*	*	-	-	
MAMMA1002845	2.68	3.31	8.62	2.22	3.45	1.79	1.92	0.92	2.1					
MAMMA1002857	706.2	952.23	1146	1100.2	1170.5	914.39	1224.8	597.31	410.7					
MAMMA1002858	2294.5	2940.8	1870.4	2372.6	1763.7	1167.7	3253.7	1423.1	844.59					
MAMMA1002863	7.34	6.7	14.07	6.73	7.47	6.7	10.22	2.68	6.73					
MAMMA1002868	37.22	42.58	112.8	66.03	44.4	46.77	34.24	23.46	47.24					
MAMMA1002869	27.07	27.29	44.22	74.9	47.13	42.55	24.18	21.4	25.44					
MAMMA1002871	14.38	15.38	24.35	3.88	5.79	4.67	3.41	1.65	2.57	*	**	-	-	
MAMMA1002875	10.61	9.93	8.16	4.59	5.33	3.55	2.05	0.93	2.17	**	**	-	-	
MAMMA1002879	85.9	153.46	165.38	90.95	121.6	91.59	134.87	73.22	108.93					
MAMMA1002880	3.99	4.47	13.13	3.43	2.59	1.91	2.37	0	2.3					
MAMMA1002881	8.75	7.92	17.49	5.86	8.28	6.29	10.75	4.45	6.2					
MAMMA1002885	3.52	4.77	10.68	3.3	3.4	4.24	2.69	0.63	2.73					
MAMMA1002886	26.73	26.24	71.16	37.73	28.68	31.72	26.26	17.17	36.38					
MAMMA1002887	4.31	6.26	14.8	6.26	3.45	6.36	3.77	1.7	3.28					

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MAMMA1002890	11.31	9.48	18.16	8.56	8.49	19.82	9.15	5.95	8.48				
MAMMA1002892	13.36	11.62	14.89	12.15	11.02	9.05	7.92	7.62	11.8				
MAMMA1002893	8.64	14.35	13.28	7.89	13.97	5.96	10.13	7.23	1.86				
MAMMA1002895	3.34	5.32	14.4	3.46	5.81	1.87	4.28	2.34	3.5				
MAMMA1002898	4.08	5.01	17.31	2.16	5.01	1.78	3.17	0.38	2.02				
MAMMA1002905	4	11.4	20	7.75	8.82	9.71	6.71	1.7	4.46				
MAMMA1002906	2.68	1.92	5.05	4.09	2.8	3.58	1.97	0.54	1.64				
MAMMA1002908	14.98	16.18	26.75	12.12	15.62	14.31	16.05	8.69	18.72				
MAMMA1002909	30.34	34.63	68.19	28.69	18.89	22.65	34.89	20.01	32.36				
MAMMA1002918	13	10.64	27.29	16.01	18.07	12.45	12.7	8.75	10.42				
MAMMA1002925	49.1	23.96	62.42	27.59	36.92	32.28	67.91	43.67	13.09				
MAMMA1002926	25.41	28.93	57.26	38.61	37.53	35.54	28.57	14.19	28.89				
MAMMA1002930	27	34.75	73.56	25.58	25.59	23.42	47.23	26.24	37.21				
MAMMA1002937	65.34	59.27	78.68	106.43	76.67	71.14	57.91	26.1	50.41				
MAMMA1002938	1.94	2.84	7.68	5.03	4.18	4.4	2.05	0.91	2.65				
MAMMA1002941	7.09	6.07	17.41	12.34	8.56	8.04	6.56	3.92	5.66				
MAMMA1002947	16.06	20.72	33.43	32.88	25.81	27	19.39	13.57	20.15				
MAMMA1002964	14.52	21.96	48.58	29.27	22.13	24.66	18.71	13.88	18.49				
MAMMA1002967	6.96	4.19	15.96	5.47	7.15	5.12	3.82	5.07	4.36				
MAMMA1002970	16.09	29.77	65.22	27.91	25.08	19.79	28.99	12.64	23.95				
MAMMA1002971	4.02	4.7	8.35	3.51	4.7	2.27	5.82	2.89	2.46				
MAMMA1002972	3.94	3.63	9.75	6.43	4.91	5.11	4.27	0.9	3.28				
MAMMA1002973	20.96	22.17	31	24.13	16.86	22.18	16.66	11.21	13.94		*		-
MAMMA1002979	129.92	194.32	219.31	151.08	71.59	113.43	55.53	74.31	23.22		*		-
MAMMA1002982	2.18	1.25	7.22	2.29	3.22	3.34	5.33	0.9	3.23				
MAMMA1002987	10.35	12.2	15.88	9.6	9.29	9.6	13.48	8.42	11.93				
MAMMA1003003	10.92	12.48	21.55	9.72	10.82	10.86	12.69	9.52	10.22				
MAMMA1003004	9.35	12	11.41	6.36	11.7	10.34	5.34	4.84	8.09		*		-
MAMMA1003007	5.35	7.51	8.39	5.22	6.88	6.35	8.36	3.78	6.7				
MAMMA1003011	3.33	3.62	5.57	4.14	2.91	4.01	2.44	1.93	2.62				
MAMMA1003013	52.58	50.01	73.47	127.57	69.44	113.36	42.21	37.2	47.45				
MAMMA1003015	4.4	9.22	10.22	6.68	9.17	6.66	6.79	4.74	5.08				
MAMMA1003019	6	3.52	10.72	6.3	3.92	5.12	4.27	1.82	2.44				
MAMMA1003020	9.29	17.63	21.88	11.76	13.24	12.14	9.04	4.99	7.31				
MAMMA1003026	2.19	2.41	7.93	1.47	3.27	2.09	1.98	0.75	2.98				
MAMMA1003031	12.83	17.1	23.06	9.93	17.27	14.35	13.73	7.28	15.8				
MAMMA1003033	7.59	11.58	13.68	6.87	12.75	8.45	8.32	3.56	9.08				
MAMMA1003035	14.44	18.88	35.58	17.37	11.86	13.06	6.41	9.44	10.62				
MAMMA1003039	5.57	9.4	15.11	7.17	7.63	9.67	4.3	4.16	6.95				
MAMMA1003040	22.42	25.75	39.61	22.72	19.76	23.47	30.8	25.19	32.64				
MAMMA1003044	23.58	26.13	43.98	21.92	19.68	21.85	23.01	22.17	23.66				
MAMMA1003047	25.89	30.87	33.12	18.34	23.66	19.64	30.18	18.74	28.8	*		-	
MAMMA1003049	2.33	2.17	8.04	1.08	1.14	1.06	1.63	0.08	1.3				
MAMMA1003055	17.22	25.14	35.08	23.45	17.28	15.29	23.26	16.76	22.03				
MAMMA1003056	1.24	3.89	8.92	1.85	1.6	1.77	4.37	0	1.6				
MAMMA1003057	7.01	11.35	14.1	7.31	6.88	7.83	3.86	5.43	8.7				
MAMMA1003066	16.42	21.28	30.29	14.08	16.97	16.54	12.01	11.17	25.5				
MAMMA1003075	6.07	7.85	12.07	6.85	6.1	6.14	7.15	5.26	7.72				
MAMMA1003089	37.69	44.94	70.13	31.56	35.51	31.8	38.3	22.85	38.78				
MAMMA1003092	2.7	6.77	9.29	2.59	2.39	2.86	1.65	0.84	2.49				
MAMMA1003095	11.71	16.36	22.28	5.96	7.13	4.55	3.24	2.25	2.45	*	*	-	-
MAMMA1003099	12.83	14.7	25.29	10.89	15.86	9.22	14.89	11.45	12.15				
MAMMA1003102	3.77	5.08	9.09	1.68	4.54	2.6	2.97	0.85	1.92				
MAMMA1003104	2.23	3.23	4.66	5.3	4.9	4.18	1.01	1.61	4.75				
MAMMA1003113	12.38	25.98	27.12	11.65	17.89	10.18	7.19	8.58	13.27				
MAMMA1003126	20.48	25.06	25.6	15.4	13.83	15.96	10.44	8.97	17.98	**	*	-	-
MAMMA1003127	11.67	12.89	22.02	11.38	12.69	10.66	9.71	8.8	11.4				
MAMMA1003131	8.9	14.73	17.42	6.88	7.18	8.51	7.06	3.18	4.59		*		-
MAMMA1003135	3.06	2.9	10.48	1.24	2.69	1.3	3	1.87	1.55				
MAMMA1003140	5.46	6.32	15.55	2.89	4.63	3.63	3.24	3.7	5.1				
MAMMA1003148	4.31	6.5	9.12	2.65	6.5	3.58	4.41	3.82	3.28				
MAMMA1003150	4.32	7.47	10.56	5.78	4.99	3.76	3.2	3.41	5.87				
MAMMA1003154	2.93	3.77	5.99	2.37	2.94	2.85	2.68	0.86	2.1				
MAMMA1003155	35.26	33.7	28.41	18.29	14.13	13.99	27.83	12.47	20.55	**		-	

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MAMMA1003157	9.8	11.92	16.49	8.35	7.14	7	5.32	5.07	5.53		*		-
MAMMA1003163	6.69	5.07	11.11	7.07	6.08	5.54	2.67	4.3	4.05				
MAMMA1003164	9.65	8.42	12.05	4.3	5.95	3.77	2.65	1.16	3.38	*	**	-	-
MAMMA1003166	13.16	17.5	21.96	14.35	15.87	10.73	8.74	5.62	7.88		*		-
NB9N31000010	22.17	30.34	35	8.06	26.76	14.32	17.42	5.42	10.61		*		-
NB9N31000016	6.11	10.91	22.1	11.04	8.39	6.1	4.87	1.93	11.92				
NB9N31000043	10.01	15.51	20.02	13.55	11.04	7.12	6.17	3.99	7.07		*		-
NB9N31000045	170.84	205.1	142.2	172.26	138.41	173.74	84.94	88.64	18.56		*		-
NB9N31000054	36.72	46.14	51.85	45.82	42.67	36.97	50.28	31.68	29.41				
NB9N31000076	7.95	11.11	16	8.53	7.69	7.72	11.59	4.88	6.85				
NB9N31000086	4.15	2.68	11.91	2.36	4	2.05	3.15	0.81	2.03				
NT2RM1000001	7.05	9.84	23.41	7.46	11.26	6.73	9.81	4.19	5.49				
NT2RM1000018	6.2	11.24	12.18	4.32	8.37	5.02	4.96	1.12	2.49		*		-
NT2RM1000032	6.17	20.65	14.02	3.2	3.21	6.55	7.1	3.44	6.93				
NT2RM1000035	5.32	12.32	11.65	5.42	4.73	4.54	3.82	4.31	2.73				
NT2RM1000037	6.94	9.49	8.81	3.59	2.53	4.32	3.57	2.25	1.49	**	**	-	-
NT2RM1000039	17.35	20.78	18.95	11.31	10.08	7.38	8.83	5.7	8.35	**	**	-	-
NT2RM1000042	285.1	504.24	359.39	438.78	386.15	125.88	306.06	229.38	295.8				
NT2RM1000055	3.2	5.45	10.27	2.35	2.5	0.71	3.16	1.31	1.79				
NT2RM1000059	6.89	5.26	12.3	2.6	4.12	1.14	3.74	1.4	3.81				
NT2RM1000062	3.25	17.72	14.57	2.77	4.02	2.38	6.97	0.66	3.27				
NT2RM1000065	129.93	146.35	187.39	51.11	120.84	109.9	91.66	120.6	204.01				
NT2RM1000066	8.15	10.03	11.93	3.29	5.25	5.44	3.51	4.17	3.47	*	**	-	-
NT2RM1000071	663.12	662.77	828.24	110.41	580.78	259.28	351.73	417.5	139.33		*		-
NT2RM1000080	24.34	23.12	24.37	3.56	11.29	8.21	9.27	5.24	4.03	**	**	-	-
NT2RM1000086	10.86	12.97	11.53	2.83	5.32	3.9	5.64	4.4	2.88	**	**	-	-
NT2RM1000092	20.13	29.95	35.15	36.08	29.43	24.61	19.3	14.65	20.49				
NT2RM1000118	1.37	1.52	9.04	0	0.67	0	0.36	0	0.79				
NT2RM1000119	1.84	9.53	13.52	3.77	3.18	2.59	3.62	0	1.09				
NT2RM1000121	4.53	3.89	4.67	2.15	3.4	5.49	1.08	0.78	1.77		**		-
NT2RM1000122	12.06	9.02	14.76	4.72	5.56	4.77	3.17	7.39	6.45	*	*	-	-
NT2RM1000127	4.86	3.09	8.85	2.65	2.99	2.48	1.52	1.46	1.57				
NT2RM1000131	2.61	0.69	3.44	0.91	1.56	0.43	1.25	0.9	1.02				
NT2RM1000132	14.01	8.86	18.39	14.15	9.4	7.78	17.49	15	6.09				
NT2RM1000153	5.01	3.78	14.31	1.42	4.08	2.81	5.68	1.59	2.53				
NT2RM1000184	281.4	361.08	212.97	228.94	161.22	121.63	212.54	317.63	41.9				
NT2RM1000186	2.47	4.7	12.56	1.93	2.64	2.03	5.08	0.92	2.79				
NT2RM1000187	13.51	16.82	27.58	4.35	7.1	11.13	3.58	3.22	6.78		*		-
NT2RM1000199	2.37	2.51	5.33	3.1	3.18	3.27	2.76	0.66	1.97				
NT2RM1000213	14.38	13.17	27	9.3	8.17	9.61	8.4	3.99	3.63				
NT2RM1000215	127.65	93.55	105.56	47	125.55	90	93.27	92.32	37.71				
NT2RM1000218	17.5	12.81	37.21	8.7	7.66	13.12	12.93	9.58	4.51				
NT2RM1000224	38.8	21.38	99.03	21.96	23.06	30.11	56.22	41.03	10.49				
NT2RM1000236	128.23	106.27	224.67	36.44	158.46	117.76	233.25	180.75	49.09				
NT2RM1000242	0.21	0.74	2.56	0	1.12	0	0.56	0	0.76				
NT2RM1000244	7.07	7.69	14.14	11.09	6.96	9.63	3.01	2.46	3.87		*		-
NT2RM1000252	3.63	3.86	6.34	5.75	3.24	4.11	5.02	2.57	2.44				
NT2RM1000256	13.89	13.11	17.86	12.49	12.19	15.55	9.96	9.49	3.8		*		-
NT2RM1000257	7.26	4.79	22.28	12.27	7.82	12.93	3.88	4.6	1.41				
NT2RM1000260	44.37	50.35	69.11	33.91	47.16	50.17	26.8	25.27	25.69		*		-
NT2RM1000269	4.48	3.66	6.5	3.35	3.23	4.63	2.09	1.54	1.92		*		-
NT2RM1000271	2.07	1.72	5.77	1.75	2.06	0.52	0.83	0.09	0.38				
NT2RM1000272	93.8	125.17	184.07	85.39	186.36	110.41	166.71	67.77	97.63				
NT2RM1000273	44.49	55.95	63.71	32.07	31.24	23.66	15.32	26.55	33.94	*	*	-	-
NT2RM1000274	455.63	719.55	944.44	916.81	390.33	402.82	570.68	746.39	848.53				
NT2RM1000280	6.37	12.22	16.78	15.15	6.91	15.12	10.36	3.5	4.59				
NT2RM1000295	0.98	1.35	3.23	1.46	0.9	2.46	0.9	0.93	3.62				
NT2RM1000300	6.74	6.95	12.1	10.61	8.44	10.7	5.89	3.63	7.13				
NT2RM1000304	737.06	1023.4	718.47	1038.7	1097.8	469.75	946.67	780.24	888.74				
NT2RM1000314	4.67	4.01	6.01	3.26	3.98	4.08	4.92	1.32	3.56				
NT2RM1000318	421.37	294.99	289.4	315.7	574.37	386.7	448.45	209.13	302.89				
NT2RM1000335	11.96	11.64	18.91	9.64	8.09	12	6.06	5.29	8.48		*		-
NT2RM1000341	1.94	1.67	2.31	1.53	0.88	0.82	1.64	0.39	2.21	*		-	
NT2RM1000350	8.91	10.88	13.15	11.12	8.93	9.83	7.57	4.14	7.11		*		-

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Table 404

NT2RM1000354	0.4	1.68	2.48	0.51	1.02	0.95	0.87	0.21	0.21				
NT2RM1000355	18.03	21.12	26.82	24.57	24.38	11.58	16.5	8.01	13.65				
NT2RM1000361	2.57	1.81	2.89	1.57	3.04	3.2	2.49	0.23	2.67				
NT2RM1000365	0.53	2.31	3.79	0	3.39	1.9	2.3	0	1				
NT2RM1000372	55.88	63.08	56.77	80.59	90.54	75.31	135.63	66.87	19.91	**		+	
NT2RM1000377	29.22	32.95	43.33	46.89	24.42	30.81	18.03	18.61	14.45		*		-
NT2RM1000388	3.72	3.27	4.82	4.15	1.73	3.91	2.28	2.59	2.31		*		-
NT2RM1000394	1.56	1.31	3.56	1.15	0.93	0.79	1.9	2.42	1.43				
NT2RM1000399	5.42	3.53	8.67	4.2	3.61	3.12	6.84	2.24	2.92				
NT2RM1000407	1.68	1.87	7.64	2.01	1.44	1.69	2.05	1.13	3.04				
NT2RM1000421	0.74	0.94	3.14	1.35	1.14	2	1.61	0	0.06				
NT2RM1000422	134.24	176.38	156.33	143.97	232.16	154.32	116.71	110.46	75.99		*		-
NT2RM1000430	4.06	4.21	6.87	5.11	7.78	3.82	6.49	1.64	1.64				
NT2RM1000462	17.49	21.49	23.94	21.57	15.84	20.24	13.6	12.18	18.48				
NT2RM1000499	11.77	14.5	12.66	4.08	5.8	6.16	2.2	2.63	4.58	**	**	-	-
NT2RM1000512	50.79	65.54	89.54	15.65	74.29	59.09	19.69	52.23	56.59				
NT2RM1000519	108.54	108.15	106.36	60.23	134.25	94.69	58.45	58.56	60.96		**		-
NT2RM1000527	51.37	48.34	68.1	100.86	64	65.36	54.81	19.74	44.25				
NT2RM1000539	19.83	27.84	33.74	35.02	28.56	31.96	16.52	8.8	16.69				
NT2RM1000542	2.91	2.41	11.46	0.76	1.72	0.95	1.66	0.17	0.24				
NT2RM1000553	49.27	35.57	63.05	73.97	60.28	58.45	40.5	24.9	19.69				
NT2RM1000555	85.13	121.39	124.03	87.28	76.76	74.83	41.33	57.49	77.7		*		-
NT2RM1000558	26.75	25.54	23.49	36.55	31.73	36.63	21.2	19.34	35.09	**		+	
NT2RM1000563	9.05	10.86	14.09	10.89	9.42	9.24	7.48	6.52	10.32				
NT2RM1000566	6.73	8.38	15.32	6.55	8.24	9.4	8.98	6.08	9.24				
NT2RM1000570	125.7	201.18	105.25	41.82	195.51	106.3	185	132.56	153.14				
NT2RM1000571	50.08	74.69	65.76	14.46	84.43	39.98	43.45	24.14	6.89		*		-
NT2RM1000574	2.53	1.65	9.83	1.89	3.52	1.98	1.99	0.19	1.58				
NT2RM1000580	7.86	7.46	8.12	4.52	12.24	4.74	8.38	3.22	4.57				
NT2RM1000620	22.3	25.58	42.74	35.73	32.55	28.94	25.27	21.57	27.34				
NT2RM1000623	1.13	1.82	2.51	0.54	0.62	1.17	0.35	0.18	1.57				
NT2RM1000630	3.11	2.76	5.89	2.21	1.76	2.12	2.49	0.75	1.9				
NT2RM1000633	91.32	89.94	117.97	56.97	108.85	75.65	98.98	107.05	51.97				
NT2RM1000634	11.16	13.34	24.68	9.79	14.73	9.21	12.08	6.93	12.7				
NT2RM1000642	12.72	15.83	20.12	6.07	8.95	6.42	3.63	2.38	4.98	*	**	-	-
NT2RM1000647	58.32	165.39	134.62	67.85	112.06	61.29	71.96	52.24	87.23				
NT2RM1000648	7.26	13.24	8.89	5.57	12.68	6.6	14.52	3.49	7.15				
NT2RM1000650	6.62	9.44	9.46	2.83	6.47	6.87	3.69	5.63	4.1		*		-
NT2RM1000661	15.88	18.26	26.1	21.53	19.01	24.34	8.08	7.55	8.54		*		-
NT2RM1000666	1.96	1.18	6.92	1.86	1.52	1.45	0.88	0.27	0.92				
NT2RM1000669	17.26	18.78	20.02	4.09	4.91	3.69	2.13	1.18	2.17	**	**	-	-
NT2RM1000672	13.67	18.24	42.69	19.37	17.89	17.56	7.45	2.82	5.99				
NT2RM1000681	9.08	16.58	18.31	9.41	17.68	12.92	13.31	5.99	9.03				
NT2RM1000691	4.68	7.55	17.93	4	7.1	7.03	5.99	3.47	5.58				
NT2RM1000698	12.42	13.98	20.53	4.92	32.5	5.23	15.99	3.16	6.38				
NT2RM1000699	5.67	7.09	9.09	7.34	5.78	7.37	2.45	1.86	3.56		*		-
NT2RM1000702	25.96	30.69	39.69	30.16	23.23	32.77	24.6	18.35	22.21				
NT2RM1000703	32.53	88.64	53.23	36.64	56.43	43.04	42.73	50.17	17.73				
NT2RM1000704	43.17	84	45.95	47.88	42.53	19.03	39.69	25.24	10.87				
NT2RM1000726	5.67	6.22	17.4	3.29	4.23	3.21	4.45	0.93	1.78				
NT2RM1000731	21.17	21.67	40.88	23.29	32.82	14.51	24.97	11.69	10.31				
NT2RM1000741	3.88	5.18	10.63	4.4	7.39	2.14	6.17	0	1.39				
NT2RM1000742	28.88	28.51	36.7	38.75	29.44	32.74	34.48	36.03	27.02				
NT2RM1000744	18.57	21.62	27.17	23.44	20.36	17.29	20.61	18.9	23.17				
NT2RM1000746	7.85	8.11	11.72	4.17	4.62	5.27	5.53	3.03	1.14	*	*	-	-
NT2RM1000747	30.16	38.37	65.95	28.71	33.95	34.03	30.94	18.08	23.76				
NT2RM1000752	6.43	11.58	14.15	3.61	7.68	5.76	4.96	2.69	4.73				
NT2RM1000767	82.05	87.93	86.38	98.35	104.39	73.49	112.1	59.62	78.42				
NT2RM1000770	9.08	11.59	19.18	5.23	6.92	2.95	3.61	2.19	4.43		*		-
NT2RM1000772	0.81	1.85	7.5	1.21	3.6	1.86	2.53	0	2.7				
NT2RM1000779	107.98	131.01	176.51	63.61	94.24	109.72	76.84	69.35	114.65				
NT2RM1000780	6.52	7.85	9.21	2.66	6.05	5.1	2.74	1.38	1.99		**		-
NT2RM1000781	6.79	4.22	9.28	1.5	2.8	0.61	2.07	1.26	0.75	*	*	-	-
NT2RM1000789	63.83	77.27	95.07	93.46	102.47	101.3	60.5	47.17	81.09				

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Table 405

NT2RM1000800	8.8	11.31	17.21	5.12	7.9	6.45	6.62	2.19	3.3		*		-
NT2RM1000802	37.09	50.36	74.58	36.6	34.84	28.86	14.15	4.56	9.84		*		-
NT2RM1000811	12.36	9.86	24.52	8.71	10.02	9.58	14.12	5.95	8.7				
NT2RM1000826	30.88	47.18	81.3	44.32	50.77	35.09	43.27	14.54	16.43				
NT2RM1000829	19.85	28.15	42.49	15.46	18.32	22.11	18.5	10.73	22.04				
NT2RM1000831	641.62	637.04	913.82	275.83	388.75	407.08	509.83	541.98	267.92	*		-	
NT2RM1000833	131.01	121.94	243.56	117.55	172.46	143.86	179.55	110.44	138.22				
NT2RM1000834	26.33	24.31	2.89	0	0.65	2.02	26.66	20.39	19.97				
NT2RM1000841	24.25	46.24	73.12	11.51	14.12	14.5	18.59	16.34	8.01				
NT2RM1000848	14.13	26.98	37.82	13	21.43	18.99	20.71	11.34	13.28				
NT2RM1000850	24.68	26.73	36.64	21.15	32.91	25.01	46.02	20.2	29.9				
NT2RM1000852	13.97	15.95	23.78	18.75	27.94	15.23	31.21	18.1	21.46				
NT2RM1000853	4.2	3.72	6.66	7.37	4.53	5.05	3.89	2.23	2.94				
NT2RM1000855	68.98	71.69	82.2	36.85	37.1	51.79	74.89	42.55	21.65	**		-	
NT2RM1000857	18.68	28.42	44.59	21.2	21.59	23.12	20.54	14.01	19.44		-		
NT2RM1000858	19.44	18.6	24.07	17.38	13.26	16.79	12.93	7.9	10.41		*		-
NT2RM1000867	47.06	39.97	81.53	51.39	22.67	30.69	24.25	41.66	28.02				
NT2RM1000874	15.53	21.9	42.18	11.95	15.55	12.17	9.14	4.05	6.39				
NT2RM1000882	8.95	14.01	25.71	7.66	9.72	9.63	17.06	6.72	11.92				
NT2RM1000883	14.26	11.55	31.41	10.17	21.02	6.37	28.25	10.83	25.46				
NT2RM1000885	24.96	25.3	31.55	8.98	10.57	16.46	9.36	11.69	11.59	**	**	-	-
NT2RM1000893	28.28	40.4	46.33	35.83	16.57	27.75	26.99	25.66	21.62				-
NT2RM1000894	11.16	14.78	12.12	9.67	5.22	9.03	7.62	4.24	5.7		**		-
NT2RM1000898	16.49	18.47	21.09	20.98	15.98	15.23	9.37	6.69	9.26		**		-
NT2RM1000899	5.15	4.63	7.57	5.14	7.26	5.6	4.73	2.38	2.79				
NT2RM1000905	294.53	321.81	294.85	264.7	213.45	208.71	204.71	142.52	169.18	*	**	-	-
NT2RM1000910	73.69	67.82	69.43	87.95	125.51	72.31	61.51	49.51	44.37		*		-
NT2RM1000914	51.65	67.13	49.73	46.16	55.8	39.43	58.15	36.24	73.81				
NT2RM1000919	31.63	34.55	49.42	11.97	21.16	18.78	16.17	26.42	28.42	*		-	
NT2RM1000921	6.87	9.33	11.95	7.94	8.86	8.21	8.17	4.59	6.66				
NT2RM1000922	13.29	8.81	21.03	4.57	14.42	11.98	8.29	7.63	6.27				
NT2RM1000924	4.71	2.79	7.57	4.61	10.85	2.89	2.79	1.75	0.64				
NT2RM1000927	6.24	8.21	11.68	5.06	6.28	6.3	9.48	5.11	7.76				
NT2RM1000951	43.38	31.87	51.83	47.29	42.21	49.1	23.28	12.15	25.07		*		-
NT2RM1000956	14.05	17.39	13.26	12.15	19.17	13.5	7.97	3.02	6.22		**		-
NT2RM1000960	27.19	36.09	41.59	49.18	53.65	39.11	40.71	16.46	20.8				
NT2RM1000961	31.7	37.01	55	10.53	21.75	21.52	13.1	26.97	26.19	*		-	
NT2RM1000962	27.85	38.63	33.9	11.13	12.72	11.99	4.23	8.24	8.72	**	**	-	-
NT2RM1000973	43.5	24.74	82.26	40.71	70.49	56.15	24.22	34.19	11.88				
NT2RM1000978	0.68	0.64	4.81	0	0.42	0.84	0.61	2.06	0.63				
NT2RM1000982	16.77	17.99	20.27	10.66	18.58	11.05	7.48	6.36	6.54		**		-
NT2RM1000991	7.55	12.77	12.19	10.81	11.04	11.17	5.79	6.02	8.13				
NT2RM1000994	39.31	47	23.95	9.37	52.07	40.12	12.98	9.18	11.27		*		-
NT2RM1001002	32.74	42.78	50.1	43.61	48.24	33.17	37.45	15.22	13.9				
NT2RM1001003	22.14	23.85	35.08	16.55	19.31	27.31	8.71	13.75	14.54		*		-
NT2RM1001008	2.98	2.17	4.26	1.07	1.49	2.65	1.82	2.32	1.41				
NT2RM1001011	24.49	19.42	39.5	9.16	16.59	21.83	7.1	5.35	13.23		*		-
NT2RM1001013	7.58	6.4	15.54	3.26	7.12	6.38	8.21	10.22	6.35				
NT2RM1001017	2.99	2.36	7.63	0.68	1.65	2.36	1.32	0	2.89				
NT2RM1001018	389.38	678.69	541.36	131	345.59	266.19	206.53	225.12	141.21		*		-
NT2RM1001026	7.53	12.1	18.29	9.07	8.15	5.48	3.88	1.52	2.01		*		-
NT2RM1001028	4.9	7.17	9.41	6.47	12.06	5.7	11.7	4.86	5.5				
NT2RM1001043	26.98	28.41	30.47	32.28	26.93	18.1	7.33	9.19	17.19		**		-
NT2RM1001044	13.61	15.79	12.73	5.11	11.55	9.29	6.83	6	8.45		**		-
NT2RM1001059	17.62	17.16	21.39	29.41	18.53	17.53	21.59	10.53	22.05				
NT2RM1001063	4.42	2.79	10.14	1.51	2.68	1.95	3.55	2.61	2.37				
NT2RM1001066	5.44	6.05	11.22	3.97	4.37	2.62	5.3	2.25	4.68				
NT2RM1001072	2.1	2.09	9.94	0.59	2.67	1.88	2.14	0.14	1.84				
NT2RM1001074	4.98	10.47	11.14	5.42	6.47	3.23	4.47	1.73	1.4		*		-
NT2RM1001076	7.28	10.41	10.61	10.91	16.92	6.26	16.73	6.71	6.46				
NT2RM1001082	15.79	21.18	26.04	16.26	13.72	10.05	11.58	9.75	14.56				
NT2RM1001085	1.82	1.24	5.39	0.21	0.47	1.19	1.3	0.55	1.17				
NT2RM1001092	38.97	56.81	56.39	54.52	49.61	49.24	59.76	48.35	50.33				
NT2RM1001102	10.81	9.79	17.74	9.01	8	8.42	8.99	8.26	5.92				

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Table 406

NT2RM1001103	12.11	14.64	19.71	7.84	12.92	9.54	14.04	7.04	13.96				
NT2RM1001105	4.22	7.99	12.4	1.52	4.66	3.36	1.61	1.94	3.34				
NT2RM1001112	5.26	6.44	10.76	4.28	9.37	3.52	5.38	1.59	3.46				
NT2RM1001115	7.42	6.2	16.09	7.99	9.99	7.63	6.92	3.96	3.94				
NT2RM1001122	13.95	16.42	25.8	14.65	15.41	13.67	7.73	7.37	13.09				
NT2RM1001136	4.38	9.14	8.72	2.16	2.27	3.09	2.35	0.89	0.34	*	*	-	-
NT2RM1001139	10.44	16.1	18.58	8.95	9.3	8.97	8.52	6.5	7.34		*		-
NT2RM2000003	3.68	3.81	8.36	4.11	1.99	1.48	3.39	1.06	1.76				
NT2RM2000006	19.96	26.87	32.42	17.36	19.88	13.64	34.18	15.67	16.17				
NT2RM2000010	13.11	32.27	43.36	20.14	26.86	16.98	10.37	4.84	2.67				
NT2RM2000013	111.85	65.82	177.02	150.21	118.48	155.88	73.81	57	69.05				
NT2RM2000030	47.5	43.12	78.78	78.26	63.56	52.76	55.62	28.2	43.38				
NT2RM2000032	27.93	34.32	46.51	34.09	25.35	35.27	22.38	22.42	18.15				
NT2RM2000039	15.44	18.82	11.91	10.78	6.19	11.58	11	10.28	4.44				
NT2RM2000042	22.91	29.95	35.12	39.39	23.39	35.58	21.42	15.87	21.82				
NT2RM2000092	3.58	4.4	7.65	2.5	2.61	1.79	2.27	5.17	2.19				
NT2RM2000093	9.7	29.83	14.41	14.47	18.41	7.29	12.45	10.38	11.19				
NT2RM2000101	92.12	99.66	118.62	114.91	128.83	118.95	69.62	52.13	78.59		*		-
NT2RM2000104	62.95	69.41	129.33	110.95	90.54	74.09	72.52	52.94	63.78				
NT2RM2000124	8.36	13.36	22.64	10.6	20.3	10.85	19.19	7.38	15.25				
NT2RM2000155	8.61	19.1	14.45	7.85	7.12	5.48	4.06	1.65	4.16		*		-
NT2RM2000191	45.98	51.15	77.89	79.82	71.61	59.62	35.22	25.83	44.53				
NT2RM2000192	4.72	2.97	6.83	2.91	2.72	2.95	2.76	1.61	1.47				
NT2RM2000239	13.1	14.91	17.36	3.56	5.21	3.86	9.92	3.36	2.39	**	*	-	-
NT2RM2000241	10.79	19.6	19.09	8.89	13.98	6.49	11.45	3.01	8.51				
NT2RM2000250	5.15	5.11	16.92	5.37	6.41	3.58	6.45	1.4	5.59				
NT2RM2000259	7.84	17.03	22.56	4.92	6.83	6.63	8.62	2.03	2.42				
NT2RM2000260	9.47	10.65	9.59	4.97	5.31	6.44	6.43	4.5	4.7	**	**	-	-
NT2RM2000265	1.13	1.27	5.15	0.34	1.13	1.33	1.14	0	0.82				
NT2RM2000287	47.66	55.1	96.28	31.39	36.17	31.93	36.1	33.17	17.11				
NT2RM2000306	66.48	31.19	72.95	23.2	54.18	20.2	25.43	22.47	8.61				
NT2RM2000312	32.44	17.61	49.51	8.46	13.33	15.12	25.48	21.27	10.02				
NT2RM2000322	7.99	6.33	16.54	4.19	5.04	3.2	3.47	0.77	1.48				
NT2RM2000343	85.23	93.06	177.62	122.74	138.14	108.3	83.09	46.31	57.15				
NT2RM2000359	6.22	10.59	23.8	9.56	9.52	5.13	12.03	2.74	6.22				
NT2RM2000362	121.28	140.62	246.7	173.62	223.63	249.97	108	78.11	121.29				
NT2RM2000363	3.84	6.52	9.96	6.57	3.72	4.83	5.89	2.02	2.82				
NT2RM2000368	26.44	19.81	43.02	11.49	11.34	10.46	8.57	3.39	3.24		*		-
NT2RM2000371	547.25	508.14	752.99	148.13	425.69	273.34	355.28	228.93	135.68	*	*	-	-
NT2RM2000374	12.96	13.63	33.5	14.47	12.05	8.49	18.75	11.86	10.92				
NT2RM2000387	30.78	60.24	91.33	10.11	11.64	24.36	10.29	9.16	3.11		*		-
NT2RM2000393	10.16	9.5	18.93	3.77	7.23	5.64	6.78	3.44	2.74				
NT2RM2000395	3.42	4.7	7.68	4.26	7.48	3.65	6.98	2.09	2.77				
NT2RM2000402	19.66	22.97	34.41	26.49	10.93	25.33	8.72	3.41	2.72		*		-
NT2RM2000405	3.7	3.95	7.31	4.5	3.17	3.25	3.78	1.94	0.68				
NT2RM2000407	6.18	7.05	11.03	8.23	7.83	7.22	4.36	3.58	3.42		*		-
NT2RM2000410	6.69	5.24	14.77	10.81	8.59	8.57	4.92	7	5.39				
NT2RM2000420	12.46	12.68	20.53	7.85	6.53	12.66	7.69	6.33	9.37				
NT2RM2000422	13.42	17.5	14.12	8.88	9.58	15.24	10	8.21	5.9		*		-
NT2RM2000423	15.54	22.01	50.31	29.73	23.33	19.31	31.02	12.98	24.15				
NT2RM2000452	3.39	4.23	12.53	5.47	7.75	4.42	5.91	1.75	4.57				
NT2RM2000469	3.15	2.51	7.63	7.05	2.6	1.83	2.99	3.89	3.38				
NT2RM2000490	12.63	13.33	17.91	18.49	9.81	12.7	9.63	10.71	10.64				
NT2RM2000497	6.31	3.98	9.54	8.32	2.31	5.44	4.36	6.15	6.13				
NT2RM2000502	7.65	10.01	17.15	15.2	7.83	12.64	18.37	19.29	16.37				
NT2RM2000504	8.62	13.61	12.8	14.35	8.61	11.65	11.39	5.05	12.11				
NT2RM2000514	3.24	4.13	6.05	5.11	2.16	2.21	3.1	2.79	1.66				
NT2RM2000522	0.79	1.87	2.28	5.66	1.51	1.86	2.44	0.56	1.28				
NT2RM2000540	36.37	16.56	24.89	25.09	10.1	17.62	15.11	17.92	16.53				
NT2RM2000565	10.96	7.91	19.23	7.94	6.73	6.21	4.49	7.85	6.72				
NT2RM2000566	35.88	29.95	48.96	40.83	31.02	33.77	42.8	32.01	34.75				
NT2RM2000567	5.01	5.28	9.14	7.2	2.55	2.31	2.41	4.02	2.26				
NT2RM2000569	11.75	12.7	16.59	10.42	10.16	8.54	12.04	11.54	10.63				
NT2RM2000577	23.09	36.16	46.55	20.42	16.61	17.63	9.65	9.61	18.29		*		-

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Table 407

NT2RM2000581	16.64	23.76	26.4	16.81	10.83	8.04	10.45	10.74	12.79		*		-
NT2RM2000582	34.62	16.91	29.03	32.54	12.57	23.96	20.07	22	22.14				
NT2RM2000588	206.96	155.13	213.15	202.22	154.41	234.16	169.86	193.16	204.6				
NT2RM2000589	21.73	20.45	25.51	21.73	16.89	13.34	11.8	15.99	14.79		*		-
NT2RM2000594	3.88	3.97	9.16	5.31	1.87	1.58	2.08	3.22	2.03				
NT2RM2000599	23.3	37.43	42.86	41.55	34.51	20.59	19.28	20.01	29.72				
NT2RM2000609	11.28	11.34	20.18	17.86	7.32	5.53	10.38	8.31	8.85				
NT2RM2000612	12.76	13.34	15.09	12.28	9.14	7.94	10.91	11.84	11.22		*		-
NT2RM2000622	141.09	153.93	193.67	159.94	144.1	158.9	186.97	168.17	180.75				
NT2RM2000623	10.1	4.92	12.51	17.89	6.76	12.96	6.19	8.79	10.66				
NT2RM2000624	40.95	32.48	53.61	29.49	39.42	24.44	20.09	35.85	21.95				
NT2RM2000632	4.22	16.93	13.59	10.55	4.72	5.77	3.71	9.75	42.27				
NT2RM2000635	17.3	14.29	24.16	11.9	11.44	7.82	6.12	9.2	22.13				
NT2RM2000636	8.64	6.1	10.92	8.1	4.79	4.03	4.23	7.12	5.02				
NT2RM2000639	12.38	11.39	15.28	10.66	6.59	7.7	5.72	6.03	7.49	*	**	-	-
NT2RM2000649	21.7	22.5	30.17	18.52	14.23	12.19	12.61	12.94	13.29	*	*	-	-
NT2RM2000658	32.82	43.08	46.86	26.73	41.37	32	30.61	19.44	22.2		*		-
NT2RM2000660	14.51	13.27	29.92	14.04	12.55	16.72	10.13	15.37	13.11				
NT2RM2000669	10.87	10.69	21.85	10.05	8.58	6.66	4.07	7.21	13.35				
NT2RM2000689	95.32	133.69	72.27	57.73	75.12	39.22	34.72	103.73	96.38				
NT2RM2000691	8.29	7.99	12.66	7.17	5.02	1.98	1.67	3.91	3.3		*		-
NT2RM2000714	22.27	18.36	27.51	17.39	20.26	19.54	14.42	10.68	9.4		*		-
NT2RM2000718	7.47	11.22	8.73	7.49	4.21	3.74	6.42	4.3	4.39		*		-
NT2RM2000732	30.31	39.24	31.84	16.98	20.8	19.07	19.55	19.14	20.81	**	**	-	-
NT2RM2000735	9.9	11.53	13.44	9.07	5.38	4.22	4.93	3.86	5.02	*	**	-	-
NT2RM2000740	6.93	5.88	14.03	10.18	2.3	7.44	6.84	7.79	7.93				
NT2RM2000743	6.68	6.8	14.3	6.91	4.28	3.65	5.06	3.56	3.44				
NT2RM2000772	27.24	33.91	37.64	22.25	28.4	15.62	5.89	15.75	8.53		**		-
NT2RM2000773	52.46	53.2	70.82	31.56	39.87	27.02	30.18	38.39	37.45	*	*	-	-
NT2RM2000776	68.74	76.62	73.41	45.06	64.43	20.51	36.77	44.34	50.74		**		-
NT2RM2000784	15.31	17.83	22.47	11.93	15.96	6.63	6.13	10.15	9.45		*		-
NT2RM2000795	27.14	19.23	31.28	19.3	19.19	9.44	22.75	21.68	23.6				
NT2RM2000796	7.18	4.13	6.34	5.73	2.37	1.38	4.64	1.74	1.29				
NT2RM2000798	220.92	157.62	241.6	287.45	173.39	313.04	164.61	215.06	234.9				
NT2RM2000801	206.47	181.87	250.93	201.4	210	276.53	117.76	135.99	178.08				
NT2RM2000821	19.71	21.75	22.88	13.91	8.23	8.65	3.33	5.35	4.94	**	**	-	-
NT2RM2000829	32.72	37.9	42.47	37.61	27.12	23.67	12.82	16.2	13.46		**		-
NT2RM2000837	12.85	10.7	21.49	8.33	5.59	2.89	4.75	4.19	3.96		*		-
NT2RM2000924	66.24	48.22	89.49	72.54	62.16	39.92	33.79	29.08	40.4				
NT2RM2000930	48.55	63.69	52.84	46.58	51.6	35.79	27	25.97	35.7		**		-
NT2RM2000937	31.8	58.4	47.42	22.54	35.77	15.38	12.6	7.67	4.38		**		-
NT2RM2000939	6.62	8.62	14.57	7.32	3.05	3.47	2.42	2.17	3.83		*		-
NT2RM2000942	734.65	670.2	631.32	344.25	467.07	301.87	150.27	478.62	381.55	**	*	-	-
NT2RM2000951	4.26	4.86	13.05	5.55	2.39	1.46	1.13	1.84	1.19				
NT2RM2000952	9.67	43.75	19.11	12.99	13.49	9.68	6.64	9	6.45				
NT2RM2000966	187.94	165.71	228.75	214.51	217.85	161.14	133.25	108.26	108.39		*		-
NT2RM2000973	104.1	257.68	179.14	123.46	180.6	103.68	80.15	78.39	82.31				
NT2RM2000983	44.05	48.21	49.47	28.35	25.15	19.95	21.95	14.49	14.64	**	**	-	-
NT2RM2000984	14.04	16.71	14.65	9.74	5.64	4.75	5.34	3.15	3.97	**	**	-	-
NT2RM2000994	36.03	29.02	31.03	22.45	13.36	11.64	9.34	22.92	20.85	*	*	-	-
NT2RM2001004	87.18	99.34	120.85	105.48	104.79	118.66	75.52	78.54	88.2				
NT2RM2001022	465.07	829.81	488.65	279.37	461.13	292.23	411.29	508	337.91				
NT2RM2001035	119.48	128.64	135.94	69.22	98.88	76.14	85.64	92.65	116	*	*	-	-
NT2RM2001038	30.1	53.09	55.15	35.29	31.06	27.29	33.8	26.97	56.89				
NT2RM2001043	17.78	17.9	22.19	14.07	14.29	12.96	14.08	13.2	13.27	*	*	-	-
NT2RM2001050	16.36	10.75	11.34	9.74	5.11	3.09	5.76	4.31	3.75		*		-
NT2RM2001055	7.49	7.2	8.19	5.79	2.69	1.59	3.42	2.92	3.04	*	**	-	-
NT2RM2001065	18.94	19.43	21.19	16.28	10.87	7.49	3.44	9.8	10.97	*	**	-	-
NT2RM2001075	352.66	309.42	355.51	314.53	188.83	298.2	178.61	439.36	452.62				
NT2RM2001083	7.08	9.84	12.58	9.39	11.2	5.35	6.46	10.07	4.34				
NT2RM2001100	132.53	127.49	140.57	168.49	157.74	186.39	108.36	105.08	125.06	*	*	+	-
NT2RM2001105	19.7	23.88	18.02	9.87	6.9	7.5	7.31	7.33	7.99	**	**	-	-
NT2RM2001109	20.13	43.33	44.99	10.64	14.91	10.34	19.4	14.81	19.72	*		-	
NT2RM2001110	32.89	28.37	36.47	39.19	23.1	32.21	27.03	23.61	20.38		*		-

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Table 408

NT2RM2001126	10.89	14.19	16.02	9.38	4.33	6.54	7.81	4.58	5.85	*	*	-	-
NT2RM2001131	35.31	23.37	27.48	39.22	24.25	32.19	17.26	18.93	15.18		*		-
NT2RM2001141	23.07	16.72	24.48	15.15	8.42	15.3	16.57	25.01	24.73				
NT2RM2001152	7.28	6.36	6.81	7.22	2.67	4.03	3.72	4.85	2.92		**		-
NT2RM2001177	16.43	13.33	22.76	9.09	9.55	10.29	11.03	12.82	14.78	*		-	
NT2RM2001194	18.95	35.2	33.45	15.63	10.75	13.96	9.18	10.24	10.12	*	*	-	-
NT2RM2001195	22.22	32.77	41.71	19.89	14.02	10.87	14.76	17.07	21.12	*		-	
NT2RM2001196	12.18	14.33	14.56	8.23	2.8	2.96	2.65	3.74	5.12	**	**	-	-
NT2RM2001201	112.26	151.54	152.39	113.21	71.67	129.08	182.51	124.84	110.23				
NT2RM2001221	15.16	10.19	12.98	12.97	6.39	8.39	4.13	7.92	7.64		*		-
NT2RM2001238	7.02	4.76	7.61	7.38	2.47	4.7	2.6	3.8	3.66		*		-
NT2RM2001243	28.44	25.47	29.19	20	12.3	9.83	7.01	16.89	8.25	*	**	-	-
NT2RM2001244	14.84	14.77	26.94	13.43	7.79	12.02	6.46	7.21	5.59		*		-
NT2RM2001247	149.17	156.12	167.83	262.88	153.51	292.21	159.18	102.66	137.39				
NT2RM2001256	12.96	15.03	17.12	8.24	5.02	5.55	4.85	4.32	6.34	**	**	-	-
NT2RM2001269	10.95	13.1	12.53	11.07	7.62	4.32	9.04	9.38	5.97		*		-
NT2RM2001278	10.38	10.85	11.45	12.61	4.01	9.04	14.51	13.94	16.53		**		+
NT2RM2001291	8.24	5.62	12.69	7.3	4.57	5.55	4.22	4.08	3.96				
NT2RM2001294	64.54	65.77	111.27	63.88	47.1	58.52	73.02	74.33	85.75				
NT2RM2001295	8.24	9.79	14.29	5.61	3.8	3.62	3.42	2.36	2.25	*	*	-	-
NT2RM2001302	3.39	6.85	11.75	6.43	3.29	2.51	3.71	3.87	1.57				
NT2RM2001306	11.41	14.23	14.66	11.73	5.3	7.08	5.43	5.34	3.99		**		-
NT2RM2001312	3.55	4.56	12.72	6.28	2.54	2.63	4.61	2.59	2.39				
NT2RM2001319	5.86	9.67	14.24	9.42	5.49	4.3	4.35	3.58	2.75				
NT2RM2001324	18.95	7.8	13.76	18.03	4.46	12.42	10.21	14.53	14.86				
NT2RM2001345	28.65	21.37	24.71	26.89	8	18.65	5.12	14.99	21.21				
NT2RM2001360	17.92	12.3	24.16	13.81	8.68	10.67	6.5	8.95	13.99				
NT2RM2001370	10.29	7.05	19.66	11.56	5.81	4.36	5.18	4.87	5.67				
NT2RM2001391	7.29	4.99	11.62	6.8	2.82	5.45	4.23	6.86	5.98				
NT2RM2001393	12.33	6.71	15.2	11.88	7.78	6.57	5.84	9.03	6.99				
NT2RM2001420	8.12	9.09	13.52	7.85	4.31	5.05	3.66	4.14	3.54		*		-
NT2RM2001423	17.63	16.34	28	15.84	12.17	12	10.06	5.58	6.91		*		-
NT2RM2001424	27.85	17.9	24.35	16.51	10.81	12.46	10.74	18.59	16.89	*		-	
NT2RM2001482	8.67	6.53	15.28	13.75	6.43	10.52	8.21	10.88	32.33				
NT2RM2001499	6.83	5.56	14.66	6.11	6.28	4.16	4.43	4.99	9.08				
NT2RM2001504	10.92	6.52	14.65	8.66	7.17	4.96	4.36	8.69	6.66				
NT2RM2001524	14.94	10.41	10.01	10.19	8.66	6.87	5.54	6.7	4.33		*		-
NT2RM2001530	3.04	4.86	7.01	5.84	1.95	3.09	2.61	3.78	1.3				
NT2RM2001533	31.06	33.52	48.05	22.65	24.5	20.86	46.4	35.86	44.09				
NT2RM2001540	13.31	12.86	17.79	14.39	9.31	10.73	9.68	7.65	7.91		*		-
NT2RM2001544	6.59	3.7	12.06	6.73	1.95	5.1	3.34	3.2	4.05				
NT2RM2001547	17.98	17.35	32.25	17.06	12.78	13.61	10.07	14.99	28.06				
NT2RM2001558	3.53	3.66	12.29	5.32	1.92	2.05	1.78	3.67	4.24				
NT2RM2001575	12.53	9.85	20.98	9.37	6.51	6.57	9.69	11.4	8.27				
NT2RM2001582	18.86	18.39	26.78	16.91	11.16	8.85	13.11	10.99	13.56		*		-
NT2RM2001588	33.5	33.04	38.62	26.73	19.6	15.21	19.42	19.94	22.31	*	**	-	-
NT2RM2001592	8.06	9.31	10.24	8.08	7.97	5.3	6.26	2.96	5.52		*		-
NT2RM2001603	18.68	34.48	37.52	19.83	12.18	16.75	16.12	15.01	10.86				
NT2RM2001605	2.46	1.84	10.05	3.68	0.89	3.29	1.27	2.06	1.52				
NT2RM2001611	8.26	11.08	21.04	8.21	4.42	4.61	5.24	5.95	7.18				
NT2RM2001613	31.23	41.23	53.28	26.42	31.28	14.27	16.42	46.76	35.82				
NT2RM2001626	7.76	5	11.59	5.79	3.19	1.08	2.56	3.93	1.62				
NT2RM2001632	12.51	10.55	19.26	10.94	8.41	4.21	3.48	2.87	3.67		*		-
NT2RM2001633	9.38	12.28	13.2	7.51	9.17	4.14	3.74	4.79	3.89		**		-
NT2RM2001635	8.99	10.05	10.56	5.7	4.03	2.66	6.33	4.93	5.79	**	**	-	-
NT2RM2001636	13.44	12.39	18.22	10.09	11.69	6.86	5.49	5.27	4.75		**		-
NT2RM2001637	5.38	4.7	11.19	6.81	1.81	3.12	2.09	2.96	1.51				
NT2RM2001639	12.13	12.21	20.77	10.63	8.64	7	4.1	7.5	7.85				
NT2RM2001641	8.65	5.25	15	6.44	4.6	3.79	6.08	10.65	9.66				
NT2RM2001643	13.92	14.16	22.25	10.74	7	2.7	2.29	4.88	4.18		*		-
NT2RM2001648	39.15	45.91	36.48	26.92	23.84	12.46	22.53	23.65	32.08	*	*	-	-
NT2RM2001652	12.26	10.35	14.74	6.98	5.99	3.53	3.25	2.26	3.06	*	**	-	-
NT2RM2001659	16.4	10.95	13.51	8.64	9.21	1.42	3.18	2.99	3.04		**		-
NT2RM2001660	10.08	9.77	12.95	6.57	5.46	2.86	2.55	2.98	2.6	*	**	-	-

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Table 409

NT2RM2001664	5.02	5.48	16.95	8.08	4.37	8.84	2.47	6.43	6.78				
NT2RM2001668	15.06	19.03	25.63	5.79	6.13	6.44	2.42	3.93	2.92	*	**	-	-
NT2RM2001670	5.32	7.34	15.89	6.82	2.18	2.28	5.04	5.37	3.96				
NT2RM2001671	8.87	8.86	12.78	9.4	4.31	5.72	3.03	4.34	3.98		**		-
NT2RM2001675	5.39	3.86	9.7	4.63	1.07	1.86	1.29	1.4	0.96		*		-
NT2RM2001681	10.15	3.72	7.87	6.68	2.43	1.75	3.17	2.29	1.77				
NT2RM2001685	5.99	4.42	4.61	4.4	0.95	1.7	1.76	0.44	1.52		**		-
NT2RM2001688	7.35	10.19	21.96	10.5	8.43	4.5	8.27	2.69	4.73				
NT2RM2001695	21.84	15.61	27.76	16.05	12.1	18.2	12.98	24.27	27.96				
NT2RM2001696	11.41	12.78	17.34	10.47	4.47	6.07	3.84	8.22	8.43		*		-
NT2RM2001698	4.46	5.04	9.55	6.62	3.5	2.86	2.2	3.3	2.08				
NT2RM2001699	9.41	7.54	15.28	7.73	5.45	4.44	4.63	5.76	3.45				
NT2RM2001700	6.01	3.92	15.92	7.19	8.76	1.93	1.65	2.78	1.4				
NT2RM2001704	15.56	11	13.6	7.65	5.94	5.33	7.22	3.63	5.28	**	**	-	-
NT2RM2001706	17.58	13	15.93	12.4	7.58	8.26	9.21	8.02	9.01	*	**	-	-
NT2RM2001714	6.57	6.52	7.48	5.63	2.25	2.43	2.36	2.21	2	*	**	-	-
NT2RM2001716	8.11	6.76	8.16	6.9	3	2.28	1.75	4.87	3.64		*		-
NT2RM2001718	5.27	4.14	10.17	6.69	1.77	2.4	3.07	2.63	3.19				
NT2RM2001723	7.52	14.9	19.44	7.99	8.79	1.56	2.66	6.02	4.35				
NT2RM2001727	13.96	15.14	20.23	10.17	9.39	6.64	16.21	10.41	9.88	*		-	
NT2RM2001730	19.9	22.32	24.32	11.37	7.04	10.08	9.63	10.59	8.89	**	**	-	-
NT2RM2001738	24.21	32	34.82	11.52	20.69	8.94	10.25	6.51	7.37	*	**	-	-
NT2RM2001743	11.04	12.3	13.73	7.4	4.32	2.84	7.29	5	5.26	**	**	-	-
NT2RM2001753	33.97	33.52	45.06	27.22	20.28	23.67	19.89	16.73	21.61	*	*	-	-
NT2RM2001755	5.43	4.23	7.05	6	2.04	4.11	2.32	3.16	2.92		*		-
NT2RM2001760	42.97	46.84	32.99	27.92	15.82	19.33	23.92	44.69	49.12	*		-	
NT2RM2001765	3.06	3.62	6.89	4.79	2.41	2.93	4.69	3.78	2.64				
NT2RM2001767	156.3	123.32	123.27	161.08	199.81	185.95	99.49	113.99	123.4	*		+	
NT2RM2001768	10.21	7.85	24.02	6.47	5.49	3.96	2.75	3.87	3.14				
NT2RM2001771	8.46	12.44	14.25	6.18	3.66	4.08	3.36	4	3.1	*	**	-	-
NT2RM2001778	7.68	9.54	13.49	7.21	3	4.06	5.69	4.22	4.13		*		-
NT2RM2001782	8.45	16.26	12.43	10.97	4.91	8.55	7.19	5.67	4.31				
NT2RM2001784	2.33	3.38	2.94	5.28	0.42	1.26	1.88	3.54	2.58				
NT2RM2001785	26.54	25.99	26.3	14.79	12.05	14.71	11.42	23.99	14.87	**		-	
NT2RM2001792	9.85	6.48	8.81	6.44	5.86	3.8	3.68	3.95	3.88		*		-
NT2RM2001795	6.29	3.46	12.45	6.74	1.68	4.68	1.95	2.66	2.03				
NT2RM2001797	5.8	5.87	12.89	5.74	3.15	4.35	4.29	3.75	2.07				
NT2RM2001800	8.98	9.98	12.02	6.5	3.87	3.21	3.89	2.41	4.66	*	**	-	-
NT2RM2001803	9.13	11.59	12.8	14.78	5.7	4.76	5	4.89	6.43		**		-
NT2RM2001805	5.23	4.93	4.93	5.77	2.81	1.86	2.38	1.02	1.76		**		-
NT2RM2001806	9.59	8.37	10.47	8.03	2.61	4.16	1.45	2.5	1.61		**		-
NT2RM2001813	4.64	2.78	4.37	7.6	3.08	5.69	2.05	4.02	2.1				
NT2RM2001814	4.12	2.59	2.69	6.32	1.65	3.13	2.04	1.23	1.1		*		-
NT2RM2001818	2.04	2.24	0.99	4.82	0.99	0.95	0.43	0.73	1.2				
NT2RM2001823	3.33	1.51	3.32	5	0.06	3.46	1.75	2.14	2.76				
NT2RM2001825	18.28	14.86	18.88	21.81	10.23	18.33	13.27	20.99	16.7				
NT2RM2001832	8.66	8.97	9.59	7.39	2.65	5.19	2.03	4.44	3.08	*	**	-	-
NT2RM2001839	39.76	56.2	55.7	17.75	23.24	41.75	69.27	61.03	74.92				
NT2RM2001840	16.73	9.83	12.67	16.44	10.4	10.16	11.51	19.3	18.18				
NT2RM2001851	13.19	13.13	16.5	15.12	5.82	6.1	7.33	10.63	8.57		*		-
NT2RM2001855	24.09	22.55	30.11	14.9	11.35	11.17	11.7	10.3	11.91	**	**	-	-
NT2RM2001867	4.7	5.27	10.74	7.68	2.21	3.72	3.8	4.17	5.58				
NT2RM2001869	150.4	263.47	450.85	333.27	292.69	360.02	366.03	265.55	360.35				
NT2RM2001879	4.5	3.92	9.65	7	2.4	3.74	3.05	3.17	3.3				
NT2RM2001883	0.5	1.23	3.35	4.6	1.17	2.06	2.26	1.81	2.31				
NT2RM2001886	5.2	8.33	7.95	8.22	4.29	6.46	4.42	3.66	6				
NT2RM2001887	10.27	7.46	19.23	10.21	4.91	6.33	4.19	5.06	5.45				
NT2RM2001896	1909.2	1304.9	1706.8	669.09	517.88	706.49	508.04	455.61	977.52	**	*	-	-
NT2RM2001902	4.57	4.04	12.43	5.26	2.22	2.22	1.58	3.18	2.3				
NT2RM2001903	63.33	63.93	80.39	57.98	54.4	31.36	56.94	50.98	47.6		*		-
NT2RM2001930	4.16	7.96	10.97	7.26	3.74	5.15	3.87	4.57	4.22				
NT2RM2001935	6.31	7.33	13.94	7.14	3.83	4.76	3.89	3.34	2.47				
NT2RM2001936	4.31	7.8	13.64	6.57	5.23	5.41	6.76	3.21	3.62				
NT2RM2001939	1.41	2.6	6.02	7.8	3.89	3.31	3.06	4.67	3.29				

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Table 410

NT2RM2001941	6.04	4.24	11.07	8.57	3.76	4	3.69	5.77	3.42				
NT2RM2001950	10.88	9.24	13.32	9.74	3.68	5.38	5.27	9.54	12.08				
NT2RM2001952	5.22	5.96	18.37	6.97	3.67	2.12	3.56	5.93	8.5				
NT2RM2001976	43.9	27.85	44.8	42.85	38.56	26.62	16.38	23.06	20.86		*		-
NT2RM2001982	3.43	5.03	6.82	6.99	3.67	2.56	3.51	3.09	3.63				
NT2RM2001983	12.18	15.12	21.04	15.68	19.01	6.03	9.47	6.45	4.73		*		-
NT2RM2001984	20.37	33.54	33.12	16.47	10.56	10.16	8.25	7.86	3.8	*	**	-	-
NT2RM2001989	3.86	5.39	6.78	8.98	3.51	2.63	4.78	3.3	2.04				
NT2RM2001996	16.29	18.4	29.01	16.49	15.54	12.47	7.55	13.49	15.15				
NT2RM2001997	11.71	10.41	18.16	7.7	4.63	5.51	3.14	5.18	8.39	*		-	
NT2RM2001998	9.82	8.18	17.59	8.92	5.29	6.42	2.82	8.96	6.36				
NT2RM2001999	18.02	20.28	27.06	10.57	9.9	5.15	3.81	3.98	3.66	*	**	-	-
NT2RM2002003	50.92	53.27	55.93	27	36.02	21.81	18.72	19.18	19.35	**	**	-	-
NT2RM2002004	4.18	6.17	7.32	5.72	2.78	2.44	2.58	3.1	3.84				
NT2RM2002009	12.24	20.57	21.82	12.13	12.36	8.91	7.8	3.92	5.72		*		-
NT2RM2002014	2.73	6.1	5.88	8.11	3.54	6	6.1	6.78	3.31				
NT2RM2002019	125.13	124.6	184.05	89.22	90.25	54.05	33.48	56.11	68.43	*	*	-	-
NT2RM2002029	13.94	31.19	27.2	28.59	19.23	17.84	11.48	35.39	33.05				
NT2RM2002030	16.61	18.25	22.39	8.8	11.56	5.36	5.58	12.47	9.07	*	*	-	-
NT2RM2002034	58.72	73.27	50.5	59.63	56.44	27.9	21	20.77	37.34		*		-
NT2RM2002049	21.26	22	23.61	14.68	15.64	11.74	6.05	9.95	7.32	**	**	-	-
NT2RM2002055	3.27	6.4	6.36	5.47	2.96	2.6	3.63	3.29	2.55				
NT2RM2002072	40.82	52.88	39.93	24.05	29.78	18.81	18.47	15.25	18	*	**	-	-
NT2RM2002088	82.31	80.35	97	73.51	51.16	68.26	90.62	55.31	84.87				
NT2RM2002091	22.22	21.11	34.44	9.76	9.27	5.82	2.71	4.2	5.17	*	**	-	-
NT2RM2002100	12.27	9.78	20.49	8.79	6.55	5.99	3.91	6.96	6.5				
NT2RM2002109	4.21	5.64	16.28	7.68	3.73	3.18	3.74	2.46	4.42				
NT2RM2002126	27.51	39.25	34.46	33.04	40.35	13.28	17.62	8.06	21.42		*		-
NT2RM2002128	4.47	5.67	11.09	4.57	2.71	1.5	2.22	2.89	1.62				
NT2RM2002129	22.51	19.86	17.11	13.35	16.48	7.76	5.96	8.88	6.92		**		-
NT2RM2002142	23.72	27.99	22.69	11.44	14.47	7.07	5.7	5.27	5.78	**	**	-	-
NT2RM2002144	5.53	4.42	5.98	7	2.78	3.75	3.22	1.93	3.5		*		-
NT2RM2002145	12.68	17.57	21.16	8.81	4.88	6.47	2.77	6.22	7.99	*	*	-	-
NT2RM2002153	10.64	8.88	12.47	8.77	5.52	6.62	3.59	3.26	3.47		**		-
NT2RM2002163	3.34	3.58	10.5	5.65	2.59	1.58	0.8	1.56	1.92				
NT2RM2002170	9.23	12.24	23.46	10.21	7.83	3.14	3.4	4.81	4.17				
NT2RM2002178	9.54	6.98	11.63	5.56	4.58	2.92	3.63	2.57	1.48	*	**	-	-
NT2RM2002179	8.2	10.06	9.02	7.04	6.34	2.72	2.79	2.76	2.85		**		-
NT2RM2002270	5.65	6.66	8.96	6.13	3.31	1.8	2.35	2.99	1.98		*		-
NT2RM2002326	8.26	5.94	6.26	7.55	3.63	3.3	2.53	3.14	5.2		*		-
NT2RM2002337	9.91	15.68	18.49	12.85	7.23	4.54	5.02	6.94	5.77		*		-
NT2RM2002339	6.62	10.73	17.92	7.67	6.02	5.59	3.93	4.03	4.49				
NT2RM2002345	12.28	11.64	16.5	11.35	8.87	6.37	4.6	5.99	5.18		**		-
NT2RM2002368	11.9	12.43	21.01	8.78	6.6	5.66	4.97	7.35	7.34		*		-
NT2RM2002381	5.04	4.54	7.61	5.17	3.68	1.33	2.23	2.48	3.79				
NT2RM2002424	6.19	9.87	12.12	6.06	3.81	1.42	2.55	2.13	2.39		*		-
NT2RM2002450	5.83	4.84	6.17	9.5	2.45	2.17	3.24	2.41	1.89		**		-
NT2RM2002482	6.57	3.99	6.22	7.86	2.37	2.81	5.1	2.33	2.52				
NT2RM2002492	115.88	159.06	153.05	67.65	86	93.3	108.8	133.63	153.04	*		-	
NT2RM2002575	8.81	10.86	19.91	10.34	8.51	6.85	6.71	8.36	8.38				
NT2RM2002580	12.81	11.63	17.51	7.68	4.03	7.15	4.84	5.41	5.92	*	**	-	-
NT2RM2002592	30.1	60.89	57.77	16.85	24.42	15.38	23.91	11.59	15.71	*	*	-	-
NT2RM2002608	107.02	108.16	125.35	69.13	83.62	75.26	86.4	51.95	98.01	**		-	
NT2RM2002615	21.13	24.19	16.26	10.72	11.75	7.36	11.09	7.92	5.92	*	*	-	-
NT2RM2002622	37.43	55.62	40.03	34.45	40.44	21.34	16.57	11.49	8.97		**		-
NT2RM2002630	17.23	13.55	15.45	18.01	9.28	15.57	19.85	13.91	16.46				
NT2RM2002634	10.84	11.13	17.05	9.62	2.19	5.41	7.89	7.53	7.31				
NT2RM2002645	19.66	20.09	27.47	17.63	14.57	10.2	9.86	18.1	25.3				
NT2RM2002646	40.87	51.15	69.9	15.35	22.28	15.25	17.48	14.11	15.62	*	*	-	-
NT2RM2002647	50.8	59.26	54.64	17.81	19.82	20.32	24.11	18.36	23.98	**	**	-	-
NT2RM2002652	15.86	23.36	17.16	10.87	6.59	8.39	7.1	6.49	11.22	*	*	-	-
NT2RM2002692	6.96	5.59	6.84	5.88	3.32	1.36	2.92	2.3	3.51		**		-
NT2RM2002721	65.28	100.72	114.83	36.62	27.49	27.32	87.26	32.69	72.44	*		-	
NT2RM2002748	96.93	107.15	111.07	119.35	46.49	100.69	117.84	48.85	124.45				

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Table 411

NT2RM2002764	5.49	12.15	7.39	6.52	3.1	7.78	2.89	4.03	5.76				
NT2RM2002772	29.76	33.25	38.82	20.56	12.45	9.21	4.96	16.05	9.09	**	**	-	-
NT2RM2002811	16.39	25	25.21	9.15	15.71	3.55	6.58	8.61	10.62	*	*	-	-
NT2RM2002818	20.34	18.56	21.22	13.83	9.54	15.73	17.66	20.72	25.61	*		-	
NT2RM2002879	25.35	30.35	32.28	9.31	5.54	8.46	5.48	6.4	6.89	**	**	-	-
NT2RM2002979	45.6	67	65.04	29.24	39.73	11.12	45.71	18.88	50.67	*		-	
NT2RM2002981	6.39	5.25	5.04	5.13	2.8	1.9	2.21	1.27	2.8		**		-
NT2RM2002995	4.58	2.61	3.97	7.89	1.25	3.74	3.35	2.92	4.03				
NT2RM2003031	4.98	5.14	6.7	6.97	3.27	6.19	2.14	4.35	4.33				
NT2RM2003042	32.29	28.58	51.11	28.69	7.79	11.66	9.6	10.82	7.31		*		-
NT2RM2003044	5.51	2.76	2.92	6.07	1.88	3.64	2.44	2.91	3.92				
NT2RM2003090	15.51	15.57	25.03	16.18	8.25	19.49	18.74	20.12	15.75				
NT2RM2003095	23.07	26.27	29.36	22.31	14.66	13.94	29.67	24.13	25.38	*		-	
NT2RM2003116	19.38	32.85	27.63	12.52	9.52	10.31	6.49	8.73	7.15	*	**	-	-
NT2RM2003222	4.03	3.37	4.48	6.23	1.12	2.42	2.91	3.67	3.87				
NT2RM2003224	23.91	19.9	24.52	18.14	9.42	15.36	24.57	16.25	13.82	*		-	
NT2RM2003250	119.92	69.2	166.74	153.09	107.43	107.61	63.52	77.81	74.98				
NT2RM2003258	14.27	11.09	23.88	11.45	8.67	5.92	4.04	5.75	7.4				
NT2RM2003262	13.63	6.96	21.6	7.07	3.47	2.7	6.15	5.4	5.15				
NT2RM4000023	16.25	15.39	24.54	14.62	6.88	9.36	9.34	7.69	6.58		*		-
NT2RM4000024	5.57	7.1	11.59	9.02	4.21	3.87	3.82	4.08	2.65				
NT2RM4000027	4.73	3.54	9.85	6.85	4.18	2.53	4.65	2.99	2.04				
NT2RM4000030	5.72	8.1	11.8	8.56	5.42	3.94	5.02	4.04	3.02				
NT2RM4000033	5.95	4.77	7.64	13.08	3.98	7.38	10.23	6.96	6.85				
NT2RM4000034	14.03	8.95	17.36	14.71	7.52	11.06	7.66	12.11	11.07				
NT2RM4000046	5.52	5.71	10.27	5.43	2.75	2.16	4.42	4.99	3.5				
NT2RM4000052	3.65	3.61	9.75	4.88	2.31	3.26	1.99	3.02	2.4				
NT2RM4000054	24.72	16.37	22.59	16.92	16.99	12.56	13.57	15.39	11.37		*		-
NT2RM4000061	2.45	2.46	7.19	5.03	3.91	3.49	2.41	2.69	0.75				
NT2RM4000074	109.94	111.99	162.79	132.85	134.31	127.91	155.38	114.81	153.05				
NT2RM4000085	16.76	26.39	27.87	18.47	15.63	12.58	12.15	6.78	9.96		*		-
NT2RM4000086	5.66	6.66	7.88	8.93	4.39	5.02	8.75	6.18	6.29				
NT2RM4000100	33.67	23.83	35.82	31.94	18.51	25.58	27.68	38.43	48.27				
NT2RM4000101	24.08	19.83	27.89	18.1	9.03	12.06	10.92	15.22	16.58	*	*	-	-
NT2RM4000102	31.73	28.52	43	29.96	36.82	28.28	11.54	34.43	29.82				
NT2RM4000104	12.56	10.41	15.15	10.13	9.81	7.37	8.35	10.19	9.76				
NT2RM4000115	5.71	9.33	11.32	11.36	6.79	5.37	7.68	7.13	8.99				
NT2RM4000129	2.55	5.58	5.12	5.02	4.24	3.57	3.26	2.78	3.18				
NT2RM4000139	5.53	8.52	11.67	6.45	6.29	5.11	4.73	4.33	5.31				
NT2RM4000149	3.74	4.09	4.62	8.9	2.03	3.09	4.1	3.49	3.35				
NT2RM4000155	17.15	10.36	17.5	14.41	8.06	9.43	4.52	7.7	6.79		*		-
NT2RM4000156	43.23	34.65	52.17	33.06	31.74	35.59	32.83	34.2	32.88				
NT2RM4000167	5.13	4.59	12.54	4.2	2.19	0.82	1.69	2.03	1.71				
NT2RM4000169	116.9	136.33	190.06	211.72	166.35	130.17	146.08	152.04	180.53				
NT2RM4000191	10.04	6.72	12.84	9.1	7.11	6.9	7.89	7.38	7.91				
NT2RM4000197	3.31	6.64	7.83	5.96	3.1	2.95	2.4	2.51	3.17				
NT2RM4000198	13.19	12.13	17.78	14.45	8.75	9.44	12.48	10.4	9.17				
NT2RM4000199	3.72	4.46	6.47	8.34	4.51	5.35	6.27	5.09	6.45				
NT2RM4000200	3.27	5.32	11.6	5.66	2.52	4.69	3.52	3.66	3.02				
NT2RM4000202	7.07	4.86	13.64	7.53	1.78	3.26	4.51	5.82	5.86				
NT2RM4000210	5.45	5.44	15.45	6.67	3.23	1.92	1.86	2.7	2.32				
NT2RM4000215	8.8	9.1	12.69	7.49	4.69	2.59	3.73	4.19	3.48	*	**	-	-
NT2RM4000220	21.3	15.96	19.47	12.48	9.78	7.44	10.31	10.33	6.87	*	**	-	-
NT2RM4000229	4.29	6.1	7.3	4.96	2.64	1.79	2.82	2.26	3.55		*		-
NT2RM4000231	12.18	22.17	22.16	12.3	13.79	7.12	11.29	7.48	7.64		*		-
NT2RM4000233	21.08	19.41	23.05	29.48	16.53	15.89	23.49	16.8	20.56				
NT2RM4000244	7.04	6.33	12.22	6.72	4.83	3.85	2.65	5.84	4.45				
NT2RM4000251	8.01	7.64	14.53	7	8.84	3.91	3.55	5.44	5.4				
NT2RM4000255	8.99	6.74	14.46	7.34	5.4	4.93	3.56	3.66	2.79		*		-
NT2RM4000265	13.77	11.08	20.66	10.54	8.41	4.23	9.98	13.42	10.55				
NT2RM4000283	213.58	220.77	174.14	136.23	205.5	145.83	158.43	132.77	224.43				
NT2RM4000284	85.27	81.74	108.73	78.21	81.89	45.3	89.45	84.2	83.7				
NT2RM4000290	13.22	11	18	10.81	6.15	3.95	7.71	6.59	6.44		*		-
NT2RM4000295	9.32	6.67	7.61	11.47	5.8	4.29	6.42	5.34	6.78				

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Table 412

NT2RM4000306	39.39	31.22	45.45	18.05	17.89	26.02	12.1	14.22	20.93	*	**	-	-
NT2RM4000307	10.91	9.3	17.74	9.83	6.51	5.04	4.55	5.59	9.36				
NT2RM4000309	6.25	6.98	13.33	6.03	3.16	3.04	0.89	2.68	1.25		*		-
NT2RM4000313	8.25	9.27	15.88	8.4	4.79	4.48	3.48	4.24	4.11		*		-
NT2RM4000318	7.74	12.3	19.97	11.61	7.91	4.9	8.74	11.58	10.87				
NT2RM4000324	7.02	4.79	7.97	5.66	2.78	1.11	2.3	1.61	0.69		**		-
NT2RM4000326	9.61	6.92	8.36	6.7	2.41	2.62	3.8	2.41	1.32		**		-
NT2RM4000327	10.62	7.04	10.88	10.24	4.86	9.97	11.64	7.37	9.72				
NT2RM4000344	28.12	43.85	37.76	23.98	18.35	22.38	19.35	25.83	27.75	*		-	
NT2RM4000349	54.86	44.05	74.07	45.06	38.46	49	53.73	62.48	76.26				
NT2RM4000354	3.83	4.95	10.6	6.31	1.75	1.8	2.77	2.77	2.79				
NT2RM4000356	5.03	3.65	9.35	5.42	1.79	2.58	1.32	3.38	0.81				
NT2RM4000366	170.18	124.74	186.28	108.07	122.86	98.86	143.05	122.68	104.4				
NT2RM4000368	16.94	13.21	17.9	9.95	5.92	5.45	9.44	7.79	10.81	*	*	-	-
NT2RM4000373	32.64	29.04	37.96	31.16	21.65	24.87	33.11	24.62	25.87				
NT2RM4000386	6.62	6.28	8.3	8.65	4.71	4.93	6.02	2.91	5.23				
NT2RM4000395	10.95	13.82	15.83	10.78	7.59	9.02	5.57	7.71	10.22		*		-
NT2RM4000414	4.69	4.37	11.16	5.76	0.91	3.43	2.88	1.6	3.45				
NT2RM4000417	11.27	10.89	8.84	6.8	4.15	6.41	8.68	3.94	4.92	*		-	
NT2RM4000421	10.28	10.99	14.3	8.17	4.31	2.7	2.33	2.02	4.78	*	**	-	-
NT2RM4000425	91.24	92.57	106.69	64.91	58.82	58.32	76.16	70.13	74.53	**	*	-	-
NT2RM4000433	6.13	6.12	8.53	7.28	5.88	4.18	2.6	4.18	3.51		*		-
NT2RM4000436	18.9	19.36	27.32	20	14.51	11.77	15.16	14.79	15.69				
NT2RM4000444	18.5	21.83	23.5	27.88	22.92	21.75	22.28	13.95	20.52				
NT2RM4000457	13.16	19.12	21.52	10.27	6.05	7.18	7.2	10.64	8.19	*	*	-	-
NT2RM4000471	11.07	11.03	12.38	8.14	9.49	4.57	3.84	6.85	3.58		**		-
NT2RM4000472	19.66	22.31	17.4	12.44	15.19	12.8	11.64	22.04	27.4	*		-	
NT2RM4000486	10.68	18.04	19.73	11.41	9.93	10.39	10.79	12.22	9.89				
NT2RM4000490	14.19	17.43	15	9.61	4.76	5.97	7.87	5.19	5.16	**	**	-	-
NT2RM4000496	4.23	6.24	5.23	3.18	0.15	0.92	1.52	0.44	1.12	*	**	-	-
NT2RM4000505	107.79	139.53	149.56	114.44	75.32	107.4	136.82	107.52	141.57				
NT2RM4000511	73.01	84.21	82.3	77.22	39.83	88.6	83	54.31	48.26				
NT2RM4000514	15.58	17.06	20.66	15.1	9.63	16.07	11.41	15.96	14.62				
NT2RM4000515	15.97	18.43	19.43	7.56	4.12	3.43	3.77	6.97	4.37	**	**	-	-
NT2RM4000517	351.24	469.1	440.94	138.38	381.29	140.48	205.12	297.92	317.1		*		-
NT2RM4000520	3.56	5.44	6.75	6.2	2.43	4.29	3.06	2.99	1.91				
NT2RM4000531	7.21	6.94	9.49	7.75	2.88	4.52	5.61	3.99	4.45		*		-
NT2RM4000532	6.55	5.58	4.11	7.27	2.1	1.72	3.22	3.22	3.25		*		-
NT2RM4000533	5.69	4.73	4.92	6.83	1.35	2.87	3.57	2.18	3.55		*		-
NT2RM4000534	4.83	3.29	2.48	5.97	1.61	1.76	3.52	3.71	3.07				
NT2RM4000563	23.61	15.27	21.44	28.24	15.01	45.63	27.71	31.71	29.82		*		+
NT2RM4000566	9.4	6.65	10.24	13	4.81	13.26	8.88	9.31	9.58				
NT2RM4000568	24.52	13.96	20.25	24.28	11.25	22.83	7.78	15.36	11.01				
NT2RM4000585	3.91	1.91	3.09	7.76	1.73	4.77	2.79	4.1	3.39				
NT2RM4000587	7.59	6.74	8.76	10.89	3.52	5.69	7.38	7.94	10.18				
NT2RM4000590	2.8	2.23	4.43	6.82	1.35	3.31	2.85	3.67	2.59				
NT2RM4000593	8.21	5	10.19	8.56	3.29	5.21	6.43	4.7	4.53				
NT2RM4000595	4.79	4.42	3.36	7.11	6.02	3.43	4.16	2.82	3.87				
NT2RM4000603	5.4	2.57	9.66	6.3	2.52	2.39	2.28	2.67	2.18				
NT2RM4000611	28.57	18.91	36.37	25.67	15.39	24.58	19.91	19.95	26.79				
NT2RM4000616	9.69	7.13	13.2	7.2	3.11	4.07	2.46	3.02	2.66		*		-
NT2RM4000621	3.69	1.04	7.35	6.04	1.52	1.99	3.47	3.26	2.31				
NT2RM4000648	7.93	5.22	9.62	8.39	3.12	4.35	6.48	5.01	6.06				
NT2RM4000649	4.41	3.44	7.74	6.28	2.95	1.85	3.85	1.71	2.41				
NT2RM4000658	5.46	6.14	9.39	8.84	2.67	4.42	4.63	4.69	4.24				
NT2RM4000661	15.52	9.28	15.4	13.03	7.61	7.72	5.33	7.59	7.97		*		-
NT2RM4000673	13.87	8.93	21.18	9.61	6.09	5.58	4.94	6.04	10.95				
NT2RM4000674	33.39	14.79	28.45	15.54	18.31	16.46	9.71	12.48	12.12				
NT2RM4000689	13.32	8.68	20.09	9.6	6.2	5.32	9.33	7.16	5.74				
NT2RM4000698	3.25	4.45	8.82	7.51	4.65	2.16	4.55	4.72	3.77				
NT2RM4000700	9.2	12.82	18.94	9.98	10.71	10.66	5.56	6.11	5.56		*		-
NT2RM4000701	37.49	38.63	57.82	37.22	35.87	38.99	50.37	52.92	48.89				
NT2RM4000712	26.37	34.47	28.93	18.91	14.79	13.59	9.02	8.85	10.91	**	**	-	-
NT2RM4000717	24.65	10.07	20.07	21.94	7.33	18.21	17.18	23.49	18.21				

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Table 413

NT2RM4000733	9.25	6.15	14.75	8.98	6.63	6.77	4.25	7.21	11				
NT2RM4000734	6.83	6.23	12.29	7.58	4.56	3.67	3.75	5.75	9.29				
NT2RM4000741	13.34	10.33	15.73	9.84	9.36	7.54	6.59	7.87	3.9		*		-
NT2RM4000744	885.53	451.3	1241	1383.2	1506.5	707.31	777.95	717.55	894.48				
NT2RM4000749	51.3	49.81	57.77	49.46	44.79	42.49	59.41	56.25	54.64				
NT2RM4000751	10.01	10.59	16.02	7.97	7.75	5.05	5.19	5.27	4.04		*		-
NT2RM4000752	14.18	16.62	13.54	10.44	6.55	5.76	8.04	11.07	5.33	*	*	-	-
NT2RM4000760	66.66	27.61	44.38	43.74	22.69	40.29	50.15	65.89	60.41				
NT2RM4000761	19.9	12.95	27.34	11.59	8.66	7.67	5.75	12.58	17.06				
NT2RM4000764	28.14	13.4	30.32	14.61	9.8	20.16	18.5	24.69	24.19				
NT2RM4000768	91.29	73.54	83.67	77.4	70.39	93.31	63.42	64.16	68.6		*		-
NT2RM4000778	8.24	6.22	8.88	7.38	4.94	5.13	2.54	2.81	2.48		**		-
NT2RM4000779	13.14	10.85	20.24	8.82	8.68	7.51	2.45	7.69	5.22		*		-
NT2RM4000787	15.66	16.22	17.04	13.21	10.45	11.66	11.77	12.92	11.34	**	**	-	-
NT2RM4000790	2620.9	2248.3	2489	2090	3251.6	2752.2	3676.2	1775.7	1256.3				
NT2RM4000795	7.92	4.23	13.52	7.6	3.13	5.92	6.03	8.23	6.4				
NT2RM4000796	26.78	15.24	27.73	18.41	12.57	18.03	14.45	19.92	38.07				
NT2RM4000798	7.01	8.1	18.9	8.2	4	6.33	3.86	7.47	8.07				
NT2RM4000800	5.35	6.72	10.01	6.15	1.63	3.53	2.61	2.89	3.11		*		-
NT2RM4000813	11.25	10	13.48	6.95	4.25	5.74	3.76	4.39	3.13	**	**	-	-
NT2RM4000820	26.13	26.55	28.07	22.17	20.99	17.91	22.8	23.35	20.32	**	*	-	-
NT2RM4000827	10.03	14.9	13.91	7.34	7.52	5.34	7.29	6.84	3.6	*	*	-	-
NT2RM4000830	12.07	12.08	13.71	8.9	8.35	9.39	11.27	7.81	7.47	**	*	-	-
NT2RM4000833	11.24	7.17	16.3	8.57	3.24	6.92	2.5	5.31	5.24				
NT2RM4000841	12.98	15.96	14.24	9.21	12.52	7.68	4.07	5.69	5.39		**		-
NT2RM4000846	9.5	7.99	19.32	10.93	5.53	8.29	6.17	10.68	8.48				
NT2RM4000848	7.99	8	13.35	6.98	3.66	2.79	2.7	4.77	2.57		*		-
NT2RM4000852	14.87	14.63	15.93	7.89	7	3.89	3.95	4.67	2.59	**	**	-	-
NT2RM4000855	6.4	5.44	7.14	5.82	2.45	2.19	1.77	2.66	1.11		**		-
NT2RM4000859	16.62	15.67	16.78	13.33	8.27	6.7	12.27	10.96	12.51	*	**	-	-
NT2RM4000868	19.91	23.16	23.62	14.39	12.92	10.23	4.82	6.2	3.98	**	**	-	-
NT2RM4000870	13	13.65	19.75	13.98	14.72	8.66	5.75	8.62	12.86				
NT2RM4000879	41.44	32.18	43.25	14.78	13.02	16.56	3.72	8.51	8.81	**	**	-	-
NT2RM4000882	15	11.7	22.42	13.18	7.01	7.9	5.18	5.53	4.92		*		-
NT2RM4000887	41.97	33.25	51.62	36.36	23.39	28.87	18.02	26.87	25.16		*		-
NT2RM4000895	26.8	20.11	33.05	17.45	16.12	7.46	11.88	6.83	10.98		*		-
NT2RM4000897	9.87	8.53	11.07	8.99	4.54	3.34	4.8	3.39	4.04		**		-
NT2RM4000901	10.96	12.11	11.53	7.56	7.1	4.42	5.41	4.23	6.77	**	**	-	-
NT2RM4000950	9.78	8.98	10.35	8.13	5.43	3.19	2.51	2.31	1.79	*	**	-	-
NT2RM4000965	28.19	32.79	35.21	15.2	12.26	17.85	6.17	10.47	12.16	**	**	-	-
NT2RM4000971	97.81	77.57	101.74	132.86	95.27	155.13	87.73	92.85	108.16				
NT2RM4000979	6.96	6.06	14.84	8.87	6.06	5.77	4.88	5.81	4.09				
NT2RM4000987	998.76	831.62	1103.5	625.74	1156.8	778.33	1010.1	1262.3	668.26				
NT2RM4000989	20.87	13	27.71	19.07	13.82	14.2	14.36	15.32	14.94				
NT2RM4000991	41.92	23.13	35.75	37.46	31.48	28.64	21.97	22.75	24.51				
NT2RM4000992	10.32	6.68	8.53	6.07	2.23	2.13	3.02	2.16	2.78	*	**	-	-
NT2RM4000996	22.09	29.46	18.01	12.6	11.82	10.41	9.81	3.95	3.92	*	*	-	-
NT2RM4000997	28.21	30.93	25.95	19.16	13.92	19.47	16.5	21.62	24.11	**	*	-	-
NT2RM4001001	7.63	6.6	15.15	9.35	5.11	5.88	3.96	7.75	5.13				
NT2RM4001002	459.98	441	503.26	494.01	440.37	522.33	521.26	628.75	590.54		*		+
NT2RM4001016	19.09	20.3	24.95	12.05	10.46	13.91	10.42	12.83	14.8	*	*	-	-
NT2RM4001025	6.64	7.24	14.2	7.08	5.08	3.26	5.04	3.42	2.59				
NT2RM4001027	4.69	5.86	4.64	4.07	1	1.53	1.18	1	1.23	*	**	-	-
NT2RM4001032	13.63	13.78	6.47	6.13	6.41	2.73	4.98	2.77	2.21		*		-
NT2RM4001047	17.2	23.07	17.27	11.83	13.43	8.74	14.05	4.88	2.78	*	*	-	-
NT2RM4001049	14.8	12.01	16.43	12.47	5.42	11.65	9.35	13.4	14.12				
NT2RM4001051	23.07	23.96	19.46	18.43	11.09	9.95	3.77	14.4	12.67	*	*	-	-
NT2RM4001052	9.72	6.17	11.79	8.32	6.45	2.86	8.57	9.7	6.4				
NT2RM4001053	8.35	8.46	10.92	7.64	6.3	5.31	6.88	7.16	3.68				
NT2RM4001054	15.68	17.03	15.78	11.07	4.7	7.63	9.63	9.71	11.5	*	**	-	-
NT2RM4001059	5.24	11.23	8.09	5.5	2.85	2.53	2.48	2.39	3		*		-
NT2RM4001071	23.88	28.79	33.58	18.66	9.28	10.59	17.49	15.69	16.83	*	*	-	-
NT2RM4001084	12.62	12.59	13.06	12.4	5.97	9.54	14.16	9.85	15.23				
NT2RM4001092	7.67	7.08	7.41	8.26	5.02	4.62	2.05	6.72	4.2				

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Table 414

NT2RM4001100	10.34	6.97	14.94	8.81	5.31	8.81	7.75	11.53	7.75				
NT2RM4001116	6.46	5.43	9.66	8.08	5.44	5.9	5.27	4.35	5.99				
NT2RM4001119	4.41	2.95	6.53	4.88	4.54	2.33	3.03	2.56	2.24				
NT2RM4001140	6.58	8.81	10.22	5.74	2.39	2.78	3.27	2.64	2.47	*	**	-	-
NT2RM4001148	77.43	82.01	87.89	109.01	92.69	80.91	71.63	54.14	60.54		*		-
NT2RM4001151	25.3	23.87	22.4	14.14	12.5	10.51	24	19.61	17.03	**		-	
NT2RM4001155	7.7	10.96	9.45	14.26	6.55	9.63	8.68	7.88	7.8				
NT2RM4001157	4.69	2.46	3.77	5.35	1.74	4.67	1.85	2.85	2.34				
NT2RM4001160	10.13	5.87	8.44	9.04	3.06	4.73	3.63	6.09	4.88				
NT2RM4001163	8.69	6.99	8.41	6.85	4.09	5.89	3.57	3.78	3.99		**		-
NT2RM4001187	15.55	10.66	18.41	9.39	4.2	6.99	4.74	5.75	3.81	*	*	-	-
NT2RM4001191	6.6	5.61	4.99	6.79	10.14	6.02	8.39	4.7	8.34				
NT2RM4001200	2.58	2.46	3.46	4.38	3.72	1.51	1.91	2.35	0.33				
NT2RM4001203	6.43	5.54	5.53	5.95	1.89	1.97	3.96	4.4	1.73		*		-
NT2RM4001204	9.94	10.43	11.48	7.05	1.89	2.44	3.49	2.67	2.11	*	**	-	-
NT2RM4001217	24.69	17.41	30.8	23.78	12.47	18.57	27.41	26.41	29.34				
NT2RM4001245	156.95	84.48	149.16	130.37	116.53	157.67	151.03	141.35	178.46				
NT2RM4001247	4.65	4.91	11.8	4.49	3.5	3.11	6.79	3.17	2.29				
NT2RM4001256	9.61	7.67	12.78	9.59	5.91	6.14	7.73	8.06	8.51				
NT2RM4001258	70.47	64.71	70.52	44.98	46.66	50.08	53.38	45.51	40.98	**	**	-	-
NT2RM4001267	5.89	4.4	10.4	6.42	2.33	2.85	4.9	3.94	4.52				
NT2RM4001273	1.34	2.22	3.89	5.02	1.41	1.99	4	2.5	2.16				
NT2RM4001281	8.06	5.61	14.03	10.91	4.33	7.34	4.05	7.62	5.35				
NT2RM4001286	51.19	32.28	36.36	29.23	18.59	18.64	13.09	20.76	31.46				
NT2RM4001290	8.38	5.81	13.36	7.76	4.34	4.65	5.33	4.36	7.29				
NT2RM4001309	98.2	68.64	139.85	90.19	105.33	108.01	85.7	73.37	76.26				
NT2RM4001313	6.16	7.7	10.44	8.55	3.72	5.52	2.76	5.94	3.03				
NT2RM4001316	10.67	13.16	19.79	13.68	8.94	6.99	6.58	5.71	5.93		*		-
NT2RM4001320	20.75	22.22	27.83	18.9	15.02	17.67	25.16	19.45	25.01				
NT2RM4001321	3.2	9.27	5.51	7.64	4.65	3.21	6.77	5.74	7.05				
NT2RM4001325	6.99	10.29	13.71	11.04	4.07	7.04	5.14	7.06	21.4				
NT2RM4001333	11.2	7.57	11.93	8.81	7.22	5.3	2.36	6.09	14.33				
NT2RM4001340	59.12	52.84	78.91	69.02	66.75	67.91	59.71	47.75	38.99				
NT2RM4001344	6.4	4.63	10.13	7.69	4.29	5.37	3.9	5.77	3.72				
NT2RM4001347	414.8	327.64	302.6	368.33	392.69	323.06	333.75	373.98	353.9				
NT2RM4001357	6.26	7.97	8.82	6.78	6.02	4.63	3.22	2.89	2.9		**		-
NT2RM4001360	8.63	8.04	10.78	8.59	6.1	3.5	4.75	7.61	3.39				
NT2RM4001371	15.56	11.85	10	11.21	16.5	13.92	36.9	13.45	6.6				
NT2RM4001377	21.16	11.62	19.22	16.27	7.45	12.65	8.88	10.18	9.45				
NT2RM4001382	16.22	9.22	22.97	11.49	7.37	7.19	3.28	8.65	16.08				
NT2RM4001384	4.53	5.9	14.13	5.13	2.13	2.71	2.62	2.27	2.98				
NT2RM4001400	10.43	9.23	12.46	8.14	5.92	4.37	4.37	6.39	3.72	*	**	-	-
NT2RM4001409	4.67	5.55	8.19	6.09	3.26	2.83	3.17	3.27	3.39				
NT2RM4001410	6.89	14.26	12.51	8.64	5.38	3.51	3.98	6.53	3.24				
NT2RM4001411	25.9	30.99	34.06	31.33	32.6	28.51	31.72	28.52	32.83				
NT2RM4001412	825.39	1226.8	1011.2	1004.1	804.98	983.25	1210.2	810.05	943.27				
NT2RM4001414	12.79	6.6	16.28	6.35	2.72	5.16	2.14	4.73	3.09		*		-
NT2RM4001436	63.2	35.96	69.06	56.83	54.08	67.38	42.65	35.42	49.83				
NT2RM4001437	26.18	27.89	39.17	20.31	15.52	18.05	16.35	28.68	22.74	*		-	
NT2RM4001444	3.41	3.61	9.9	6.98	3.02	1.89	2.57	2.59	2.26				
NT2RM4001454	19.23	20.25	21.89	16.73	15.4	12.09	15.71	18.45	13.57	*	*	-	-
NT2RM4001455	5.88	19	6.35	4.26	2.07	3.65	1.94	1.57	2.98				
NT2RM4001483	8.69	16.03	11.64	7.61	4.41	5.78	3.96	3.81	3.42		*		-
NT2RM4001489	12.59	12.07	8.74	5.56	6.34	2.86	4.94	5.52	3.23	*	**	-	-
NT2RM4001495	36.43	24.24	20.4	12.41	16.18	17.63	5.62	16.36	11.58				
NT2RM4001499	22.29	18.15	30.48	16.01	14.05	14.71	4.23	11.08	11.85		*		-
NT2RM4001515	6.81	5.91	14.18	6.91	2.64	4.03	2.9	4.57	2.36				
NT2RM4001519	8.21	4.24	9.85	5.65	1.45	0.78	1.08	3.15	1.34		*		-
NT2RM4001522	8.19	6.53	12.02	6.15	2.52	1.81	2.28	3.64	1.62		*		-
NT2RM4001523	73.84	75.98	71.57	35.61	37.16	20.7	26.91	23.43	33.3	**	**	-	-
NT2RM4001550	10.75	6.21	9.98	6.43	6.16	2.2	5.6	2.68	8.03				
NT2RM4001553	11.94	9.8	11.96	9.12	5.14	4.64	3.81	2.93	3.19	*	**	-	-
NT2RM4001554	151.86	72	141.69	164.83	103.78	171.98	80.79	76.13	147.24				
NT2RM4001557	51.14	42.32	58.99	56.35	49.65	76.92	34.69	30.81	38.74		*		-

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Table 415

NT2RM4001565	12.7	17.39	26.89	14.14	12.4	12.69	7.45	6.92	4.69		*		-
NT2RM4001566	17.21	11.12	20.03	22.75	14.87	13.43	10.31	12.88	15.08				
NT2RM4001569	3.45	2.79	9.43	4.65	1.24	1.1	2.19	2.38	1.74				
NT2RM4001579	7.75	7.8	9.32	7.49	3.8	1.35	2.94	2.54	2.36		**		-
NT2RM4001582	6.95	5.09	5.63	5.76	1.73	2.34	1.66	1.19	2.1		**		-
NT2RM4001589	113.7	167.05	103.64	41.43	57.6	46.23	27.72	15.73	11.4	*	**	-	-
NT2RM4001592	6.17	5.42	14.24	6.52	2.18	4.41	4.13	6.42	4.93				
NT2RM4001594	386.49	313.56	285.69	287	185.32	238.47	160.25	299.69	275.08				
NT2RM4001597	6.23	6.27	13.54	6.73	3.64	4.25	2.96	4.23	3.88				
NT2RM4001605	16.38	18.33	22.25	14.56	11.19	8.87	10.5	12.13	9.23	*	*	-	-
NT2RM4001609	23.54	15.9	22.4	13.71	9.55	9.27	6.4	7.54	6.99	*	**	-	-
NT2RM4001610	10.55	8.52	11.74	9.35	5.13	4.46	6.11	6	5.63		*		-
NT2RM4001611	14.22	14.7	15.89	10.73	7.27	6.47	6.73	5.19	3.38	**	**	-	-
NT2RM4001618	13.74	16.13	14.23	8.24	4.82	5.02	4.84	2.49	3.4	**	**	-	-
NT2RM4001622	5.3	5.16	10.27	7.37	3.16	3.66	2.49	3.88	1.85				
NT2RM4001624	7.85	5.37	11.44	5.27	1.81	3.96	3.07	2.98	3.67		*		-
NT2RM4001625	8.28	12.41	10.38	15.36	14.48	2.63	7.15	9.31	10.39				
NT2RM4001629	14.67	21.52	22.9	19.11	13.87	22.31	12.28	12.44	12.55		*		-
NT2RM4001632	325.71	457.93	338.97	242.41	290.06	370.51	594.61	333.67	482.68				
NT2RM4001642	5.97	4.92	5.47	4.64	2.19	2.19	0.94	2.25	0.91	*	**	-	-
NT2RM4001647	18.42	12.21	17.82	18.58	14.27	17.66	13.87	14.03	11.49				
NT2RM4001650	27.91	31.97	47.33	36.24	30.14	33.6	22.2	16.78	26.83				
NT2RM4001662	12.58	10.55	10.99	18.39	7.75	15.61	11.98	12.75	8.09				
NT2RM4001666	7.92	11.39	9.77	4.29	5.85	7.46	4.49	4.14	4.36	*	**	-	-
NT2RM4001670	25.82	19.71	20.86	17.87	11.22	17.38	19.89	23.01	24.94				
NT2RM4001682	8.89	10.21	10.73	7.71	7.31	3.19	3.94	4.22	3.18		**		-
NT2RM4001710	8	9.89	13.67	6.48	2.86	3.01	1.39	4.38	1.64	*	*	-	-
NT2RM4001712	6.13	6.94	9.77	4.06	2.96	2.15	2.17	4.16	1.89	*	*	-	-
NT2RM4001714	18.44	20.46	18.31	8.4	3.92	5.06	6.84	3.44	4.9	**	**	-	-
NT2RM4001715	22.24	32.3	32.67	17.97	6.58	16.35	15.07	7.8	8.58	*	*	-	-
NT2RM4001727	17.83	12.1	16.99	14.9	8.57	19.16	13.54	13.69	14.31				
NT2RM4001731	9.18	5.56	7.2	4.83	1.9	3.44	2.33	4	3.02	*	*	-	-
NT2RM4001735	15.03	8.65	13.3	10.72	9.69	6.1	6.95	9.42	9.18				
NT2RM4001739	3.31	4.05	7.1	6.51	1.7	2.71	2.2	2.1	1.76				
NT2RM4001741	5.03	6.39	6.03	4.45	2.85	1.9	3.44	3.9	2.72	*	**	-	-
NT2RM4001746	27.18	35.45	35.48	20.34	15.62	12.62	17.33	16.68	21.57	**	*	-	-
NT2RM4001754	47.9	62.7	56.46	79.4	39.53	40.99	48.7	37.13	39.56				
NT2RM4001757	4.77	10.74	3.2	6.77	1.73	2.53	2.83	4.79	2.31				
NT2RM4001758	8.89	8.75	6.1	8.32	3.51	5.38	5.98	8.51	9.88				
NT2RM4001768	3.37	0.36	1.12	5.36	1.88	2.21	0.35	1.5	0.9				
NT2RM4001775	6.53	3.93	5.59	8.91	3.97	5.25	4	3.54	3.16				
NT2RM4001776	28.42	28.92	28.25	33.08	15.74	17.3	19.26	20.43	19.52		**		-
NT2RM4001783	4.96	4.55	4.74	5.37	2.6	3.32	2.42	2.8	2.84		**		-
NT2RM4001793	14.95	13.94	19.52	14.23	7.85	12.31	14.46	13.31	17.08				
NT2RM4001810	23.52	24.77	30.47	26.07	19.33	20.51	34.17	38.53	24.96				
NT2RM4001813	9.51	6.59	9.34	11.22	3.7	8.5	12.3	12.03	14.87		*		+
NT2RM4001818	4.65	1.67	8.39	7.01	2.88	5.12	5.55	5.88	5.41				
NT2RM4001819	80.16	35.79	68.43	71.44	40.61	80.22	41.62	48.42	47.06				
NT2RM4001823	10.42	6.03	12.1	10.8	5.46	5.65	5.68	8.09	6.63				
NT2RM4001828	3.57	2.82	6.95	5.66	1.65	1.21	2.42	1.92	2.31				
NT2RM4001835	4.94	4.42	12.73	8.71	1.8	3.96	4.63	4.11	5.11				
NT2RM4001836	5.12	3.81	8.12	5.95	1.63	1.85	2.61	3.45	2.12				
NT2RM4001841	6.73	6.82	10.79	10.33	4.39	6.34	6.7	6.45	7.77				
NT2RM4001842	2.89	4.82	4.7	7.5	2.83	2.4	3.82	3.29	2.69				
NT2RM4001843	48.57	28.12	59.83	46.07	40.73	45.97	28.16	28.11	29.49				
NT2RM4001856	14.1	14.11	19.35	11.87	5.04	7.86	7.47	6.5	8.37	*	*	-	-
NT2RM4001858	20.02	12.7	24.11	14.43	7.61	10.18	17.09	15.78	20.13				
NT2RM4001861	14.08	10.48	18.84	13.72	9.53	5.84	12.28	18.05	13.36				
NT2RM4001863	27.15	15.67	30.03	15.24	18.38	17.87	16.63	16.94	11.79				
NT2RM4001865	8.03	9.87	15.29	7.44	8.43	5.34	6.68	5.7	6.95				
NT2RM4001869	12.34	16.35	21.36	13.19	9.35	9.55	19.86	14.54	12.88				
NT2RM4001873	6.51	9.79	10.96	7.15	2.28	3.17	4.21	4.29	2.39		*		-
NT2RM4001876	13.28	10.02	39.33	14.58	13.74	11.65	8.08	13.34	13.31				
NT2RM4001880	22.41	18.46	28.54	18.91	14.09	15.45	13.74	18.99	19.02				

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Table 416

NT2RM4001885	71.31	49.62	81.98	53.98	43.04	45.93	68.83	64.57	48.87				
NT2RM4001889	10.85	7.93	15.01	8.59	4.29	4.67	4.77	6.73	3.99				
NT2RM4001894	30.62	32.08	44.07	33.7	34.28	35.89	33.56	30.42	25.18				
NT2RM4001897	8.76	10.37	11.73	7.79	4.55	4.65	3.35	3.47	2.33	*	**	-	-
NT2RM4001899	4.19	5.18	10.36	7.76	5.5	4.54	4.99	5.17	3.45				
NT2RM4001905	8.04	9.67	9.34	12.13	4.62	8.49	17.26	7.42	9.7				
NT2RM4001922	10.52	7.5	13.46	10.13	4.31	4.77	4.26	7.33	9.75				
NT2RM4001930	42.04	27.93	35.21	26.34	18.3	24.57	35.05	37.8	24.49				
NT2RM4001938	11.86	11.93	17.44	9.19	6.81	6.54	7.09	10.88	7.99	*		-	
NT2RM4001940	40.15	39.79	42.12	29.48	25.03	26.5	19.62	21.25	18.41	**	**	-	-
NT2RM4001942	7.8	8.46	12.88	6.27	3.74	4.54	3.46	2.56	2.64		*		-
NT2RM4001953	2.56	5.71	6.3	5.41	2.95	2.84	2.21	3.3	2.4				
NT2RM4001965	9	9.88	11.74	9.82	12.01	7.33	7.4	10.04	8.64				
NT2RM4001966	51.68	52.74	61.28	70.45	40.89	59.05	88.01	53.06	72.22				
NT2RM4001969	9.53	10.35	15.87	9.41	5.57	8.09	5.17	7.89	12.14				
NT2RM4001974	12.36	21.98	16.69	16.74	8.35	12.5	5.35	17.32	22.51				
NT2RM4001979	23.89	19.24	22.43	14.04	16.93	18.71	17.76	22.69	22.51				
NT2RM4001980	94.16	97.18	94	64.27	69.09	81.77	75.44	72.18	71.63	*	**	-	-
NT2RM4001984	9.67	8.39	11.58	7.27	4.78	4.84	2.35	4.35	2.8	*	**	-	-
NT2RM4001987	7.05	10.61	11.42	5.92	3.18	5.3	2.56	4.02	2.33	*	**	-	-
NT2RM4002013	15.54	16.72	17.68	12.71	8.41	7.52	18.32	10.81	11.68	*		-	
NT2RM4002018	18.51	18.01	18.38	23.63	14.06	15.67	18.72	13.95	13.04				
NT2RM4002033	6.2	4.97	12.78	7.92	4.07	6.05	2.33	3.53	3.27				
NT2RM4002034	9.06	7.36	15.25	10.05	4.49	7.82	4.17	10.89	9.93				
NT2RM4002044	29.35	20.58	32.58	18.82	16.22	17.19	21.2	22.06	24.1				
NT2RM4002047	20.66	17	25.07	17.46	15.74	9.49	16.1	15.14	16.08				
NT2RM4002054	31.19	30.54	36.08	20.52	17.55	11.13	16.47	15.97	19.8	**	**	-	-
NT2RM4002055	21.78	18.7	21.85	12.08	11.37	8.76	14.04	16.74	17.09	**	*	-	-
NT2RM4002059	10.36	12.77	15.52	6.8	7.53	3.99	4.33	4.04	2.53	*	**	-	-
NT2RM4002061	9	11	9.24	10.93	6.62	5.33	6.65	4.88	4.34		**		-
NT2RM4002062	97.19	68.62	99.9	109.04	77.98	163.08	52.62	59.12	71.01				
NT2RM4002063	8.61	5.55	11.75	8.31	3.06	3.95	4.25	4.81	4.94				
NT2RM4002066	7.96	8.56	22.27	12.72	22.89	4.97	2.38	10.48	2.89				
NT2RM4002067	10.87	18.12	21.45	11.17	10.75	7.5	4.23	11.4	5.44				
NT2RM4002073	34.87	29.49	32.35	16.42	15.53	13.85	5.51	8.53	5.15	**	**	-	-
NT2RM4002074	13.13	16	13.48	9.5	9.68	8.27	2.81	4.16	5.74	**	**	-	-
NT2RM4002075	12.66	9.69	13.41	10.12	6.41	6.32	4.7	4.84	4.77		**		-
NT2RM4002076	5.05	4.42	4.84	7.24	1.99	2.02	1.56	2.18	1.6		**		-
NT2RM4002078	61.79	41.41	62.13	44.43	23.08	49.45	46.13	69.55	79.59				
NT2RM4002081	12.47	11.63	21.52	11.3	5.46	8.36	4.38	5.75	7.06		*		-
NT2RM4002082	28.78	23.31	28.71	31.25	27.4	16.48	17.58	15.02	15.49		**		-
NT2RM4002093	9.61	9.51	12.26	11.79	5.58	6.25	5.84	7.44	5.28		*		-
NT2RM4002109	5.91	6.93	10.41	8.11	5.84	4.18	3.3	3.14	2.63		*		-
NT2RM4002115	9.41	7.3	7.03	6.27	4.66	1.89	3.74	1.98	2.7		**		-
NT2RM4002118	37.45	58.41	50.21	20.19	26.02	17.58	13.66	5.39	8.55	*	**	-	-
NT2RM4002128	8.86	5.7	4.74	7.73	3.31	3.74	6.06	4.03	5.02				
NT2RM4002137	10.72	7.46	13.29	9.5	3.57	7.97	5.86	8.61	6.51				
NT2RM4002139	4.03	2.83	9.32	5.97	2.53	3.54	2.11	4.86	1.91				
NT2RM4002140	13.52	11.7	18.78	14.09	10.76	8.24	10.97	13.55	10.92				
NT2RM4002145	9.85	17.52	15.66	7.49	7.31	6.12	9.29	8.25	6.8	*		-	
NT2RM4002146	53.03	50.09	60.28	48.49	40.37	39.91	51.33	53.96	59.3	*		-	
NT2RM4002161	42.85	50.59	52.56	30.41	24.15	28.58	27.02	24.86	21.9	**	**	-	-
NT2RM4002174	10.01	10.09	12.11	7.53	4.92	3.2	3.7	2.29	3.16	*	**	-	-
NT2RM4002178	12.55	13.35	13.21	15.19	8.36	11.5	9.67	9.09	6.99		**		-
NT2RM4002180	29.73	19.51	29	18.7	7.96	18.84	13.92	22.12	26.06				
NT2RM4002185	43.79	41.64	55.35	22.67	17.47	26.66	26.11	42.39	45.09	**		-	
NT2RM4002189	7.67	6.99	10.29	5.96	5.23	2.74	5.92	2.8	1.53		*		-
NT2RM4002194	41.77	35.89	39.22	19.41	14.19	21.77	29.88	28.52	30.53	**	**	-	-
NT2RM4002198	65.16	103.48	83.23	24.68	28.75	36.65	24.56	34.17	38.68	**	*	-	-
NT2RM4002205	10.02	12.63	11.47	6.5	3.78	3.22	4.61	2.19	6.22	**	**	-	-
NT2RM4002213	21.88	23.22	24.09	13.45	7.91	12.62	20.89	17.99	21.66	**		-	
NT2RM4002216	7.77	7.03	5.96	10.01	6.36	6.33	6.06	4.45	6.36				
NT2RM4002226	41.57	37.46	37.46	67.73	42.88	64.61	42.92	35.21	34.67				
NT2RM4002237	7.28	7.73	10.06	4.52	3.54	3.6	2.94	7.15	4.84	**		-	

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Table 417

NT2RM4002240	41.31	33.08	34.96	23.86	21.39	33.98	42.08	38.96	43.61				
NT2RM4002251	3.39	3.69	6.47	4.89	3.61	2.4	2.93	2.15	17.6				
NT2RM4002256	4.28	3.3	5.05	4.37	2.61	2.38	2.35	2.33	1.46		*		-
NT2RM4002262	25.4	21.79	26.58	14.04	9.23	12.13	20.41	14.34	24.05	**		-	
NT2RM4002266	32	29.71	28.68	24.62	15.02	21.58	34.67	32.96	37.69	*	*	-	+
NT2RM4002276	14.45	13.71	15.67	14.53	13.36	16.53	16.37	10.08	9				
NT2RM4002278	18.11	14.14	14.01	7.25	7.14	10.52	3.65	6.03	7.88	*	**	-	-
NT2RM4002281	9.29	5.59	12.79	12.53	4.74	10.06	6.18	9.79	8.22				
NT2RM4002287	17.77	15.59	14.41	11.94	5.05	12.57	14.23	12.4	14.92				
NT2RM4002294	5.99	6.14	6.14	5.51	2.38	5.99	3.64	2.35	2.91		**		-
NT2RM4002298	64.75	62.55	58.47	42.58	28.72	43.54	69.57	64.59	61.46	**		-	
NT2RM4002301	3.57	3.23	3.63	6.49	2.3	3.07	3.59	2.99	3.21				
NT2RM4002306	25.86	19.13	24.79	14.02	9.84	17.37	30.57	32.67	35.82	*	*	-	+
NT2RM4002323	7.61	6.27	5.98	7.59	3.26	7.4	8.04	6.9	4.8				
NT2RM4002334	14.45	6.6	16.75	21.2	9.98	15.23	10.19	12.3	13.22				
NT2RM4002339	36.85	25.91	51.52	34.79	27.9	40.82	21.13	20.38	29.16				
NT2RM4002344	17.19	8.04	22.21	10.94	8.27	8.93	15.04	14.72	15.42				
NT2RM4002345	7.58	5.39	12.54	5.63	3.79	3.52	2.31	4.45	2.41				
NT2RM4002352	44.06	33.96	54.03	33.98	35.28	37.69	25.21	30.31	27.97				
NT2RM4002362	39.95	26.35	45.23	28.03	24.7	27.77	28.92	25.64	24.85				
NT2RM4002373	9.44	6.99	7.1	8.69	3.38	4.42	5.88	3.57	3.37		*		-
NT2RM4002374	0.94	1.53	2.98	5.8	0.19	1.91	2.19	2.71	2.57				
NT2RM4002376	14.29	7.3	14.66	12.48	5.38	11.68	12.33	14.05	16.09				
NT2RM4002383	5.57	4.67	12.54	5.61	3.39	2.94	3.24	5.28	5.45				
NT2RM4002390	8.2	7.31	15.14	6.97	3.2	6.3	4.57	6.71	7.54				
NT2RM4002398	16.51	8.98	16.5	15.05	12.49	8.92	7.11	8.76	5.38				
NT2RM4002409	3.91	1.86	5.55	4.87	1.55	2.44	2.22	2.93	0.87				
NT2RM4002414	18.86	15.16	32.88	21.65	23.59	21.32	20.36	19.06	17.22				
NT2RM4002438	3.96	4.99	8.08	7.18	3.61	4.94	4.85	4.1	2.07				
NT2RM4002440	32.39	17.01	28.92	38.22	20.77	30.03	30.94	26.11	25.22				
NT2RM4002446	10.16	7.87	12.29	14.29	6.56	8.04	5.21	8.63	33.19				
NT2RM4002450	5.69	5.77	10.55	7.51	2.92	4.53	1.81	3.53	7.42				
NT2RM4002452	15.3	12.15	20.1	12.34	7.95	8.52	9.04	11.33	9.95				
NT2RM4002457	5.93	4.98	9.2	5.51	3.34	2.74	3.42	3.45	3.16				
NT2RM4002458	5.3	7.18	9	7.94	5.54	4.54	4.93	4.05	3.12				
NT2RM4002460	5.82	9.3	10.61	8.18	6.55	6.42	6.02	6.26	3.91				
NT2RM4002464	5.03	6.81	7.71	5.37	2.82	2.94	2.52	3.29	2.23		*		-
NT2RM4002479	40.28	37.05	46.08	41.61	24.81	36.24	37.84	34.54	34.16				
NT2RM4002482	13.66	18.31	28.36	15.72	10.35	15.81	9.15	8.99	19.35				
NT2RM4002489	15.44	12.03	20.84	12.49	8.35	8.73	7.84	10.26	14.04				
NT2RM4002493	8.53	4.66	11.35	5.77	2.46	3.69	1.55	3.88	3.31				
NT2RM4002499	16.96	15.44	26.91	11.24	8.53	18.09	18.09	16.97	14.06				
NT2RM4002504	24.74	20.57	17.4	17.01	12.22	12.67	5.73	8.11	7.63		**		-
NT2RM4002506	9.92	11.26	12.04	6.45	4.68	4.22	2.88	4.99	2.98	**	**	-	-
NT2RM4002510	17.14	20.34	27.62	13.7	8.64	11	8.3	5.68	5.29	*	**	-	-
NT2RM4002527	5.27	5.32	5.24	9.73	2.73	4.8	7.63	6.1	4.65				
NT2RM4002532	2.04	3.38	12.81	3.92	2.01	0.75	2.59	1.83	2.16				
NT2RM4002534	6.24	4.2	12.1	6.74	2.8	3.26	1.86	3.47	2.45				
NT2RM4002535	9.02	8.87	16.41	7.91	3.99	2.92	0.97	4.02	2.94		*		-
NT2RM4002554	6.47	7.38	8.92	4.87	2.87	2.29	2.04	1.83	1.15	*	**	-	-
NT2RM4002558	10.72	10.21	14.55	8.7	6.67	5.1	5.89	7.82	7.9	*	*	-	-
NT2RM4002565	7.12	9.02	9.26	6.37	4.46	3.35	5.55	4.05	5.46	*	*	-	-
NT2RM4002567	8.35	6.05	12.48	6.62	4.6	3.2	2.87	5.5	6.18				
NT2RM4002571	3.38	3.03	4.65	5.3	2.26	1.53	2.86	1.83	1.84				
NT2RM4002572	3.42	1.92	7.29	5.02	1.66	0.9	0.78	0.74	1.09				
NT2RM4002577	17.78	12.61	20.74	8.52	7.02	10.13	3.18	8.47	5.97	*	*	-	-
NT2RM4002583	26.66	37.71	48	24.28	17.87	13.18	6.06	13.66	11.34		*		-
NT2RM4002584	24.55	35.28	41	25.45	15.38	14.04	7.11	11.26	5.72		**		-
NT2RM4002593	13.18	11.32	14.62	7.42	4.65	4.9	3.83	4.05	2.43	**	**	-	-
NT2RM4002594	17.08	15.66	20.52	11.9	10.96	5.12	3.63	4.19	2.45	*	**	-	-
NT2RM4002604	8.24	6.88	8.88	5.84	3.74	2.95	2.65	0.99	1.52	*	**	-	-
NT2RM4002614	14.57	8.99	9.81	12.06	5.4	4.41	5.49	5.87	6.71		*		-
NT2RM4002616	31.41	23.47	38.09	26.19	21.94	0.64	13.84	17.54	27				
NT2RM4002623	6.22	6.78	13.92	7.63	3.69	4.81	3.87	5.8	5.63				

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Table 418

NT2RM4002634	8.22	4.99	13.16	9.11	4.37	3.31	1.21	3.45	2.39				
NT2RM4002636	6.59	6.68	10.88	5.63	3.08	3.09	2.42	3.32	2.29		*		-
NT2RP1000002	38.84	33.13	45.9	29.04	32.42	26.61	13.28	16.85	17.96		**		-
NT2RP1000006	16.16	12.37	15.85	10.42	5.99	5.72	9.46	7.81	8.28	*	**	-	-
NT2RP1000015	7.32	9.13	12.92	6.24	3.84	1.22	4.29	2.29	4.19		*		-
NT2RP1000018	7.99	5.66	4.74	10.16	3.74	4.75	7.93	7.02	6.47				
NT2RP1000034	93.68	89.94	88.11	64.65	53.66	86	72.54	94.51	102.97				
NT2RP1000035	18.17	13.62	22.35	15.17	8.64	11.35	7.31	9.51	10.39		*		-
NT2RP1000040	16.4	12.21	23.34	12.38	8.64	8.09	5.04	9.39	4.11		*		-
NT2RP1000042	3.77	4.47	8.66	6.24	2.47	2.4	1.5	1.51	0.43		*		-
NT2RP1000048	11.21	13.33	14.61	8.93	8.14	5.51	8.58	7.29	5.06	*	*	-	-
NT2RP1000050	5.73	12.28	7.67	5.34	2.29	5.33	2.26	2.09	1.81		*		-
NT2RP1000056	13.77	17.86	17.27	9.41	8.14	4.91	6.92	3.33	2.85	**	**	-	-
NT2RP1000058	2.7	2.41	1.36	4.8	0.95	2.39	2.76	1.39	2.38				
NT2RP1000063	17.16	17.65	11.27	8.7	3.73	4.52	5.36	8.5	8.3	*	*	-	-
NT2RP1000068	29.14	23.7	36.49	16.13	16.83	12.51	21.73	27.58	32.86	*		-	
NT2RP1000072	39.99	32.45	48.63	26.8	23.08	25.9	35.59	35.1	31.66	*		-	
NT2RP1000073	30.81	35.89	43.46	17.05	9.38	10.22	9.08	9.67	9.54	**	**	-	-
NT2RP1000078	9.27	9.25	12.57	6.24	5.48	5.5	2.69	7.89	4.73	*	*	-	-
NT2RP1000079	5.69	6.1	5.36	5.53	2.36	2.02	2.99	2.23	1.19		**		-
NT2RP1000080	8.49	8.44	8.35	6.53	2.81	2.65	4.1	3.05	2.07	*	**	-	-
NT2RP1000086	8.5	9.4	9.89	12.4	14.28	6.92	7.93	6.49	7.97		*		-
NT2RP1000087	90.2	68.37	62.22	84.59	56.96	88.52	51.31	53.27	70.97				
NT2RP1000089	42.88	33.03	33.53	24.16	25.57	29.27	22.12	38.13	29.4	*		-	
NT2RP1000090	36.01	34.5	36.9	42.34	38.64	45.67	26.7	26.11	29.29	*	**	+	-
NT2RP1000100	842.61	1542.2	1396.7	306.69	827.1	384.76	1509.9	896.88	763.21	*		-	
NT2RP1000101	35.43	98.15	94.63	31.12	33.53	50.26	29.26	23.54	17.24				
NT2RP1000111	7.76	7.95	10.33	5.26	2.18	1.26	2.31	1.62	2.57	*	**	-	-
NT2RP1000112	23.37	50.82	42.64	24.98	11.61	20.15	18.5	13.38	13.37		*		-
NT2RP1000124	25.62	22.22	19.79	7.84	2.34	7.4	4.52	4.07	4.19	**	**	-	-
NT2RP1000125	10.72	8.67	12.07	7.14	2.95	7.79	4.48	7.44	4.25		*		-
NT2RP1000129	53.88	53.28	57.25	42.69	30.82	50.19	47.48	64.98	53.17				
NT2RP1000130	19.47	14.75	28.76	11.14	15.19	12.69	8.3	10.06	14.98				
NT2RP1000154	3.93	3.52	5.78	5.04	1.58	2.69	2	2.85	2.74				
NT2RP1000163	9.61	17.58	16	11.58	5.58	5.03	6.39	4.65	5.07		*		-
NT2RP1000170	4.53	4.62	7.7	6.31	2.3	2.01	2.67	3.54	2.2				
NT2RP1000174	9.99	10.63	9.3	6.41	2.75	3.81	5.44	4.09	3.96	**	**	-	-
NT2RP1000181	14.26	14.61	16.73	10.84	15.44	12.79	10.24	5.66	5.53		**		-
NT2RP1000191	12.96	10.86	7.92	16.4	11.07	15.31	6.1	13.72	9.91				
NT2RP1000202	24.16	14.94	24.74	18.17	11.59	9.79	7.42	9.13	15.3				
NT2RP1000239	9.53	5.6	7.62	9.29	2.89	11.94	8.48	12.01	11.59				
NT2RP1000243	6.22	4.43	4.68	7.85	5.29	6.41	2.34	3.31	5.03				
NT2RP1000255	12.37	12.15	15.41	16.34	7.48	13.06	9.35	10.82	12.98				
NT2RP1000259	10.81	8.35	10.69	9.6	2.44	9.12	13.53	11.26	13.39				
NT2RP1000261	8.39	2.66	5.85	15.75	5.57	6.12	7.38	4.73	4.58				
NT2RP1000269	2.25	3.12	1.21	5.48	2.06	2.18	4.74	1.71	2.26				
NT2RP1000271	20.23	11.57	26.77	18.9	8.83	20.16	9.94	14.85	10.84				
NT2RP1000272	2.12	2.3	9.68	5.22	1.59	2.18	2.89	2.48	2.25				
NT2RP1000279	10.54	8.91	14.66	10.51	4.61	8.63	10.77	11.05	13.98				
NT2RP1000290	6.06	4.1	11.1	13.63	4.43	7.63	6.81	6.19	8.17				
NT2RP1000293	3.83	4.19	7.55	5.54	1.62	3.86	2.95	1.13	3.16				
NT2RP1000331	4.37	2.83	13.34	5.34	2.19	3.45	2.73	6.07	2.66				
NT2RP1000333	10.16	8.8	16.01	10.64	5.56	6.94	8.71	5.87	8.68				
NT2RP1000336	18.67	16.33	24.52	12.77	10.82	14.23	17.03	16.82	19.7				
NT2RP1000347	3.46	4.07	7.92	6.45	3	4.58	4.14	3.03	3.73				
NT2RP1000348	34.17	39.38	47.03	19.99	17.54	15.37	14.54	7.37	12.73	**	**	-	-
NT2RP1000349	3.22	4.33	6.7	6.49	4.16	3.15	4.9	4.23	3.34				
NT2RP1000353	180.66	121.66	192.83	151.27	98.19	147.88	118.94	165.86	159.59				
NT2RP1000356	8.01	8.29	12.26	8.92	4.2	7.42	6.21	5.29	12.39				
NT2RP1000357	38.01	31.52	38.61	32.16	21.31	27.89	24.36	33.21	30.56				
NT2RP1000358	9.65	6.55	14.28	10.15	5.03	7.68	4.14	4.11	2.37		*		-
NT2RP1000360	11.08	7.25	16.85	18.78	9.48	8.41	8.09	9.21	9.08				
NT2RP1000363	37.26	30.39	52.28	41.73	39.62	39.87	33.79	24.41	33.64				
NT2RP1000376	6.26	6.27	9.53	5.76	4.97	3.76	4.87	4.58	3.63				

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Table 419

NT2RP1000386	37.77	48.73	51.62	24.07	21.15	29.99	24.61	14.84	15.66	*	**	-	-
NT2RP1000407	20.7	11.19	17.51	22.94	11.29	15.13	8.7	15.9	29.09				
NT2RP1000409	24.93	20.8	32.63	23.46	10.36	22.79	11.36	15.76	11.35		*		-
NT2RP1000413	24.89	20.12	32.27	23.23	14.81	20.34	6.71	17.88	15.72				
NT2RP1000416	9.92	9.55	19.32	9.98	6.1	6.11	5.35	8.54	6.35				
NT2RP1000418	5.47	5.48	8.66	6.04	3.54	3.99	4.07	4.75	2.23				
NT2RP1000420	22.79	21.95	33.37	16.39	16.84	13.03	9.29	9.88	11.08		*		-
NT2RP1000434	13.91	15.33	17.37	9.5	9.94	9.87	16.13	15.05	16.89	**		-	
NT2RP1000439	25.29	35.1	29.04	26.55	26.88	19.87	29.22	23.74	23.38				
NT2RP1000443	20.2	15.54	27.59	12.04	8.66	7.66	5.79	6.64	10.23	*	*	-	-
NT2RP1000447	8.08	15.72	18.03	9.49	4.04	7.9	4.98	7.69	18.07				
NT2RP1000448	3.96	4.08	14.01	5.34	1.34	3.27	1.83	3.09	2.48				
NT2RP1000451	4.39	7.13	7.39	6.28	2.08	2.05	2.16	2.95	1.76		*		-
NT2RP1000458	7.7	7.09	11.38	7.06	4.06	2.49	4.41	2.72	2.94		*		-
NT2RP1000465	3.88	6.63	8.77	6.04	2.34	3	3.32	3.69	3.78				
NT2RP1000468	10.59	11.91	14.42	9.41	9.31	7.51	8.52	6	7.58	*	*	-	-
NT2RP1000470	5.79	2.68	10.41	5.27	1.59	4.02	1.42	2.51	2.5				
NT2RP1000477	92.32	107.32	97.76	75.25	82.97	57.94	30.6	83.57	85.18	*		-	
NT2RP1000478	15.37	19.72	31.56	11.53	8.67	8.82	5.74	7.51	6.16		*		-
NT2RP1000481	26.31	30.78	29.03	24.24	26.58	11.39	8.04	10.78	12.11		**		-
NT2RP1000493	20.43	14.94	23.34	16.46	8.49	8.21	13.43	15.08	18.68				
NT2RP1000513	46.32	35.58	52.07	60.82	43.2	48.5	36.73	37.16	31.64				
NT2RP1000522	31.35	42.08	42.76	21.13	28.37	20.27	18.09	8.09	12.01	*	**	-	-
NT2RP1000533	3.26	4.01	2.16	4.33	1.36	1.15	1.34	1	0.91		*		-
NT2RP1000544	15.77	9.6	19.95	8.16	5.29	4.62	4.57	9.59	8.27	*		-	
NT2RP1000547	6.82	3.97	11.11	7.34	2.91	3.12	1.8	4.52	2.98				
NT2RP1000551	7.57	6.25	20.26	6.79	4.51	3.96	3.69	5.06	3.29				
NT2RP1000567	7.5	7.79	12.24	11.47	5.44	5.98	2.72	3.24	2.13		*		-
NT2RP1000574	10.39	7.63	14.91	6.66	4.35	2.94	2.41	2.6	3.1		*		-
NT2RP1000577	6.72	6.64	7.37	6.99	2.31	2.08	2	3.14	1.89		**		-
NT2RP1000579	6.59	4.72	10.08	5.29	2.62	2.74	2.3	1.65	2.85		*		-
NT2RP1000581	11.66	12.4	16.41	11.21	8.47	7.93	11.76	7.04	4.88				
NT2RP1000593	11.3	18.39	27.51	6.2	5.55	5.03	1.75	7.5	4.02	*	*	-	-
NT2RP1000604	24.51	26.11	37.01	27.05	13.43	25.97	13.69	26.68	23.37				
NT2RP1000609	11.66	13.43	21.36	13.95	9.13	6.99	3.92	12.37	8.18				
NT2RP1000613	17.95	20.62	29.59	15.28	14.93	12.95	12.7	12.66	9.93		*		-
NT2RP1000622	5.38	3.34	9.13	5.39	2.07	1.13	2.51	2.21	0.46				
NT2RP1000627	4.69	3.23	5.07	4.57	2.03	1.44	1.45	1.18	1.66		**		-
NT2RP1000629	8.08	7.69	11.36	7.12	3.71	2.97	5.95	2.89	3.59		*		-
NT2RP1000630	7.73	9.3	8.35	7.9	4.49	4.92	4.54	3.4	2.81		**		-
NT2RP1000639	15.2	13.58	16.62	7.62	5.84	8.02	4.83	7.17	5.87	**	**	-	-
NT2RP1000640	7.36	9.59	17.46	9.53	6.74	8.49	5.28	6.04	7.68				
NT2RP1000646	4.24	5.51	12.04	6.49	2.96	3.77	4.79	5.79	2.35				
NT2RP1000659	23.32	18.8	20.24	8.66	11.69	4.88	4.8	5.33	5.99	**	**	-	-
NT2RP1000674	5.93	7.17	11.83	6.23	3.45	3.46	1.76	2.58	3.57		*		-
NT2RP1000677	14.6	24.32	25.71	10.51	12.87	7.3	5.18	10.1	7.28	*	*	-	-
NT2RP1000679	49.27	69.62	36.95	29.7	31.01	14.48	34.6	17.18	10.04				
NT2RP1000688	8.01	6.65	7.8	7.2	2.8	2.42	6.02	2.46	2.38		*		-
NT2RP1000689	32.73	30.66	30.93	19.81	8.55	17.9	17.63	24.88	21.39	*	**	-	-
NT2RP1000695	17.35	14.65	15.87	10.45	3.47	5.36	2.82	6.77	7.19	*	**	-	-
NT2RP1000701	7.19	4.67	10.84	7.55	5.43	2.64	2.6	6.76	2.45				
NT2RP1000702	7.2	10.25	10.38	5.65	2.25	1.64	3.18	3.24	2.79	*	**	-	-
NT2RP1000713	7.21	6.46	7.91	6.66	2.57	3.12	4.23	3.89	1.7		*		-
NT2RP1000721	15.01	8.63	33.56	6.6	3.3	4.77	2.95	3.62	2.32				
NT2RP1000730	34.22	37.43	42.87	27.42	15.22	17.38	23.72	15.85	27.4	*	*	-	-
NT2RP1000733	9.85	10.41	8.91	8.92	3.88	5.5	7.94	2.92	5.71		*		-
NT2RP1000738	1.62	1.49	4.67	5.56	1.13	3.01	1.45	2.92	1.28				
NT2RP1000739	19.87	17.5	27.32	13.76	6.59	15.22	15.07	28.31	27.46				
NT2RP1000740	10.94	13.28	13.49	8.2	7.61	6.64	6.43	11.92	8.57	**		-	
NT2RP1000746	3.82	5.92	7.73	5.64	4.22	2.64	2.76	3.96	2.29				
NT2RP1000750	12.79	9.22	13.66	7.67	4.28	4.14	7.19	4.29	4.16	*	*	-	-
NT2RP1000751	10.42	10.46	12.4	8.57	5.65	4.98	4.2	5.02	5.07	*	**	-	-
NT2RP1000767	10.46	7.93	10.97	6.93	2.33	2.54	1.45	2.21	3.81	*	**	-	-
NT2RP1000769	4.03	4.96	3.53	5.29	3.09	2.58	3.04	5.45	2.56				

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Table 420

NT2RP1000780	19.06	11.29	17.88	11.55	12.19	16.36	7.6	12.92	8.96				
NT2RP1000782	3.8	1.98	4.82	5.26	2.11	4.2	3.73	3.14	3.38				
NT2RP1000796	23.21	12.88	16.72	13.54	7.34	8.03	3.16	8.05	3.72		*		-
NT2RP1000797	8.11	7.21	12.88	6.28	1.88	5.78	3.95	3.02	3.35		*		-
NT2RP1000800	6.36	7.42	8.45	6.35	6.28	4.56	5.14	4.53	6.09		*		-
NT2RP1000825	6.14	10.58	8.77	8.58	2.44	5.18	5.33	5.66	4.12				
NT2RP1000833	6.32	4.62	5.45	7.5	3.18	3.17	4.57	14.3	3				
NT2RP1000834	12.66	13.91	14.59	8.48	3.38	6.31	7.69	5.15	4.86	**	**	-	-
NT2RP1000836	6.87	3.86	10.29	7.94	2.62	4.87	5.98	4.8	8.86				
NT2RP1000837	4.76	2.83	13.29	5.43	1.86	3.86	3.47	3.54	3.43				
NT2RP1000846	14.34	10.47	22.36	10.56	7.41	9.61	13.44	9.9	11.55				
NT2RP1000847	17.63	21.93	45.89	20.33	17.15	15.75	21.4	13.87	15.38				
NT2RP1000851	3.61	3.71	7.21	5	2.22	2.83	3.04	2.47	2.36				
NT2RP1000856	15.4	23.9	24.75	12.89	7.5	8.85	6.97	4.98	5.2	*	**	-	-
NT2RP1000860	5.61	4.82	11.39	9.47	4.26	7.06	6.83	5.9	5.93				
NT2RP1000902	10.67	7.93	13.65	15.09	8.49	17.09	4.79	9.4	9.51				
NT2RP1000903	14.49	11.64	18.42	14.24	5.67	14.38	12.23	14.45	21.38				
NT2RP1000905	11.82	8.69	16.54	6.96	4.86	6.4	5.28	5.14	5.21		*		-
NT2RP1000915	63.69	60.39	85.78	55.83	55.49	63.74	77.2	80.56	84.89				
NT2RP1000916	81.28	82.59	69.7	73.31	86.67	61.79	53.76	46.45	55.88		**		-
NT2RP1000921	71.86	52.08	72.49	27.75	31.76	38.72	21.98	23.9	25.92	*	**	-	-
NT2RP1000943	6.66	5.16	12.72	6.58	6.6	3.97	5.26	4.45	3.75				
NT2RP1000944	36.56	43.79	53.16	29.61	24.97	30.98	38.1	30.4	32.9	*		-	
NT2RP1000947	229.13	162.3	242.56	211.36	169.75	208.5	187.13	230.69	193.69				
NT2RP1000954	8.73	6.8	11.31	9.14	2.72	5.18	2.45	4.94	9.97				
NT2RP1000958	12.83	9.08	19.99	13.3	9.58	12.08	6.34	10.95	18.7				
NT2RP1000959	51.88	27.73	29.26	17.4	13.14	15.25	9.23	12.74	9.9		*		-
NT2RP1000966	30.03	20.71	21.11	23.97	20.83	19.34	9.71	14.32	8.82		*		-
NT2RP1000974	16.61	13.83	23.36	13.15	11.64	14.93	7.2	7.22	7.83		*		-
NT2RP1000980	85.21	82.27	107.69	76.1	98.09	99.97	80	57.54	67.02				
NT2RP1000981	14.84	15.8	18.22	12.59	10.09	13.46	23.72	16.48	19.72	*		-	
NT2RP1000988	21.09	10.38	16.08	11.96	7.25	9.77	8.85	10.68	7.42				
NT2RP1001002	23.42	12.11	26.95	15.71	9.49	11.37	4.76	9.9	15.94				
NT2RP1001004	3.32	4.31	12.34	5.67	1.55	2.59	2.12	2.77	2.28				
NT2RP1001007	5.36	4.39	9.57	6.91	2.92	2.64	2.01	3.93	1.56				
NT2RP1001011	5.98	6.54	6.16	6.28	2.04	2.66	2.36	4.56	2.02		*		-
NT2RP1001013	158.04	170.77	232.56	168.44	147.11	154.85	176.26	171.79	185.19				
NT2RP1001014	13.02	16.54	16.26	8.7	8	7.08	6.95	5.62	4.04	**	**	-	-
NT2RP1001020	12.63	15.72	12.22	15.74	11.78	16.3	13.8	9.3	14.27				
NT2RP1001023	16.05	14.39	18.27	13.53	16.55	17.02	5.93	11.56	12.91				
NT2RP1001027	5.55	8.55	17.95	9.25	6.73	6.98	2.42	5.11	5.43				
NT2RP1001031	5.67	4.8	13.77	5.12	2.4	2.34	1.77	3.34	2.2				
NT2RP1001033	7.93	6.3	11.72	6.43	4.31	2.18	2.83	5.21	2.62		*		-
NT2RP1001042	63.59	58.82	65.69	59.83	59.66	45.94	71.71	83.48	74.44		*		+
NT2RP1001045	9.83	10.21	13.29	8.26	4.99	5.95	3.06	4.58	3.85	*	**	-	-
NT2RP1001073	12.41	18.41	17.37	9.19	7.47	7.07	4.73	4.66	5.19	*	**	-	-
NT2RP1001079	38.47	46.51	52.14	22.17	29.03	25.48	25.23	15.77	15.85	*	**	-	-
NT2RP1001080	21.61	6.66	17.31	12.32	7.25	12.68	6.59	12.92	8.31				
NT2RP1001113	57.87	45.81	82.08	49.33	42.8	51.52	16.27	50.38	44.76				
NT2RP1001159	7.51	4.75	14.77	8.2	4.64	7.14	4.3	5.24	3.99				
NT2RP1001173	4.39	5.23	11.13	7.48	3.15	1.42	1.19	2.31	1.17				
NT2RP1001176	52.66	45.96	57.66	32.33	25.13	21.71	19.56	17.05	21.12	**	**	-	-
NT2RP1001177	10.79	9.96	12.22	5.4	2.87	3.22	4.03	4.39	5.3	**	**	-	-
NT2RP1001185	14.18	11.86	11.53	9.31	7.59	5.91	7.44	8.55	7.87	*	**	-	-
NT2RP1001199	13.52	13.24	12.28	9.53	6.55	5.34	4.8	3.41	3.43	*	**	-	-
NT2RP1001205	93.58	72.48	94.49	51.42	53.78	86.93	52.32	75.19	84.87				
NT2RP1001215	17.01	15.57	25.94	10.31	11.47	12.47	9.75	16.75	14.31				
NT2RP1001225	11.8	18.2	17.52	11.07	6.07	5.97	4.13	11.34	3.6	*	*	-	-
NT2RP1001245	6.59	5.31	9.93	6.03	2.96	4.57	2.73	3.24	2.91		*		-
NT2RP1001247	6.32	3.32	10.27	4.35	3.87	3.01	3.42	3.7	1.09				
NT2RP1001248	15.25	12.77	20.45	15.52	14.1	11.98	13.33	13.26	15.08				
NT2RP1001253	84.68	116.5	77.6	46.18	37.13	24.55	27.4	9.2	25.65	*	**	-	-
NT2RP1001286	5.14	8.32	6.96	7.42	3.69	3.62	3.74	2.33	2.9		*		-
NT2RP1001294	57.97	32.23	60.31	62.38	43.54	78.24	53.21	40.65	43.49				

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Table 421

NT2RP1001302	13.32	15.35	23.89	11.51	7.14	10.86	5.3	9.24	8.54		*		-
NT2RP1001310	78.58	77.83	107.95	40.93	36.67	35.03	13.95	16.52	15.88	**	**	-	-
NT2RP1001311	12.5	10.19	20.17	13.97	8.87	11.71	8.61	11.48	9.2				
NT2RP1001313	47.33	35.38	51.8	18.55	17.75	13.75	4.5	6.14	3.62	**	**	-	-
NT2RP1001324	13.11	11.52	14.26	8.91	7.65	4.65	7	7.07	7.14	*	**	-	-
NT2RP1001349	8.69	8.34	8.01	6.09	3.96	4.38	3.75	1.87	3.49	**	**	-	-
NT2RP1001361	9.54	13.7	11.81	11.62	6.33	6.68	6.92	4.67	4.5		*		-
NT2RP1001379	13.14	11.82	15.33	13.1	6.47	9.99	7.99	14.61	8.34				
NT2RP1001385	24.66	22.66	28.03	8.27	7.17	9.45	13.37	13.91	22.49	**		-	
NT2RP1001395	5.65	15.28	10.96	10.51	4.01	1.7	3.74	3.38	2.71				
NT2RP1001410	13.37	15.22	15.93	8.65	10.09	5.26	5.57	5.86	7.15	*	**	-	-
NT2RP1001424	28.73	25.67	34.05	32.06	24.11	29.55	22.85	15.99	24.49				
NT2RP1001432	9.64	7.96	12.22	8.86	4.28	6.46	5.04	7.62	6.96				
NT2RP1001449	19.34	21.85	20.51	10.44	6.36	4.06	9.88	5.66	6.23	**	**	-	-
NT2RP1001457	23.3	38.81	37.3	24.2	13.72	10.77	10.68	7.09	13.11		*		-
NT2RP1001459	13.65	11.76	16.02	12.39	4.68	8.62	6.06	9.05	6.34		*		-
NT2RP1001466	8.39	4.23	8.84	7.44	4.36	4.01	3.12	6.63	4.14				
NT2RP1001475	11.89	17.85	12.86	11.05	10.38	6.52	5.05	12.24	6.54				
NT2RP1001482	15.19	20.93	20.15	19.85	11.71	18.03	11.8	14.09	12.75		*		-
NT2RP1001494	3.95	5.63	10.18	5.63	2.65	3.16	2.73	3.52	2.73				
NT2RP1001500	9.08	4.79	11.52	5.37	1.85	1.77	2.31	4.4	3.24				
NT2RP1001517	18.13	18.45	18.1	8.4	4.89	3.69	7.15	5.46	6.44	**	**	-	-
NT2RP1001540	28.09	31.99	28.56	25.07	15.6	22.78	25.04	22.39	21.45		*		-
NT2RP1001543	20.19	16.33	24.14	16.6	10.69	13.4	7.07	16.07	9.64				
NT2RP1001546	12.99	15.98	15.41	9.88	3.03	7.01	6.04	9.72	7.53	*	**	-	-
NT2RP1001550	8.32	14.7	14.31	7.95	15.82	5.57	6.4	9.76	9.43				
NT2RP1001553	5.3	7.23	13.14	7.37	4.11	4.11	3.68	3.77	3.88				
NT2RP1001555	54.76	52.6	55.46	31.87	21.44	34.31	43.17	41.32	32.44	**	*	-	-
NT2RP1001563	39.08	33.85	48.64	38.88	21.62	23.18	31.1	28.26	33.8				
NT2RP1001569	3.96	1.69	1.05	5.34	1.73	1.64	1.66	1.23	2				
NT2RP1001584	172.68	220.01	198.04	20.64	11.47	19.54	81.72	38.4	33.43	**	**	-	-
NT2RP1001599	4.12	3.82	5.18	7.25	3.83	4.97	3.61	3.84	3.39				
NT2RP1001616	4.03	1.77	2.09	6.09	1.64	4	2.04	2.76	1.59				
NT2RP1001654	14.62	9.64	12.33	11.97	7.7	10.52	5.54	7.93	4.12		*		-
NT2RP1001665	5.76	6.54	8.08	8.07	4.13	4.72	3.98	9.32	5.29				
NT2RP1001679	8.69	7.12	7.86	9.21	3.08	4.08	4.04	6.22	5.1		*		-
NT2RP1001681	18.99	18.82	24.49	14.39	5.58	9.22	11.12	13.68	12.99	*	*	-	-
NT2RP1001694	6.52	3.33	5.96	7.17	2.61	3.23	4.87	4.47	3.87				
NT2RP2000001	6.24	4.74	8.49	6.13	5.97	4.89	6.42	5.79	3.58				
NT2RP2000006	9.03	5.67	13.4	11.28	7.14	5.76	7.62	8.34	6.39				
NT2RP2000007	10.8	6.31	17.13	11.11	4.89	9.86	6.74	8.3	8.67				
NT2RP2000008	5.65	3.68	9.46	7.12	2.84	3.88	3.74	5.6	5.37				
NT2RP2000010	6.84	5.53	11.05	6.98	2.63	4.35	3.2	3.54	2.21		*		-
NT2RP2000011	9.36	13.46	17.26	10.79	6.33	9.28	5.31	3.23	5.5		*		-
NT2RP2000027	3.47	3.05	7.32	6.1	1.45	4.19	3.16	3	5.68				
NT2RP2000028	4.74	6.32	6.74	8.06	2.13	4.67	3.21	1.66	4.03		*		-
NT2RP2000032	3.24	7.28	8.03	10.28	5.5	7.28	3.26	3.13	4.05				
NT2RP2000040	15.29	8.48	28.46	11.5	6.66	9.38	4.88	6.35	7.25				
NT2RP2000042	21.14	15.46	35.04	11.42	8.01	11.22	12.48	11.99	17.82				
NT2RP2000045	5.83	3.94	13.32	7.43	3.18	3.46	3.62	5.2	3.95				
NT2RP2000051	13.61	9.89	23.1	13.04	8.32	9.72	10.33	13.1	11.12				
NT2RP2000054	16.51	12.89	19.57	11.63	9.66	11.02	9.64	7.65	7.91		*		-
NT2RP2000056	6.15	6.7	14.22	6.37	4.1	4.09	7.75	7.98	8.74				
NT2RP2000057	7.7	5.49	9.31	7.63	5.41	5.64	12.9	3.34	4				
NT2RP2000067	7.64	15.12	15.54	18.12	16.74	10.35	9.45	6.54	9.35				
NT2RP2000070	522.83	440.99	557.3	464.06	449.31	610.82	418.05	662.99	650.93				
NT2RP2000076	6.99	4.98	10.04	7.01	1.06	1.43	1.54	3.61	5.67				
NT2RP2000077	14.55	10.4	23.49	9.32	7.18	6.26	8.55	8.84	8.57				
NT2RP2000079	9.19	8.49	12.44	8.77	5.26	7.56	6.72	6.46	6.39		*		-
NT2RP2000088	17.05	20.32	26.56	22.32	20.65	23.39	19.38	14.35	14.55				
NT2RP2000091	33.24	19.21	39.37	24.16	20.9	17.89	11.58	9.95	7.77		*		-
NT2RP2000092	0.22	2.2	2.32	4.37	1.08	1	2.25	1.85	1.49				
NT2RP2000097	10.19	11.77	12.54	11.39	5.79	8.17	7.35	3.3	4.01		**		-
NT2RP2000098	14.34	13.24	18.96	13.26	6.07	9.3	5.48	9.38	18.69				

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Table 422

NT2RP2000108	10.87	8.33	17.31	10.58	6.71	6.74	4.11	5.62	13.35				
NT2RP2000114	14.61	10.83	24.65	15.49	7.8	10.66	10.74	13.91	10.18				
NT2RP2000116	12.92	13.17	18.63	12.07	8.1	10.87	4.57	5.57	3.24		**		-
NT2RP2000119	50.32	47.2	56.58	31.02	20.71	31.82	30.15	29.31	28.57	**	**	-	-
NT2RP2000120	7.9	9.18	10.99	6.62	6.21	6.5	4.81	5.84	4.99	*	*	-	-
NT2RP2000126	27.18	24.32	32.55	18.42	11.34	17.52	24.37	18.13	19.51	*		-	
NT2RP2000133	6.31	5.61	8.16	7.63	3.91	7.78	7.66	10.7	6.35				
NT2RP2000147	12.98	10.72	23.8	11.64	4.41	11.41	3.62	6.37	10.62				
NT2RP2000153	4.49	6.28	13.18	7.15	3.26	3.2	2.66	3.8	4.92				
NT2RP2000156	7.61	6.37	12.56	6.43	4.23	4.03	2.05	6.21	1.59				
NT2RP2000167	64.87	55.86	69.1	57.96	47.99	49.02	51.12	61.28	54.87				
NT2RP2000161	8.86	7.44	9.1	8.5	4.93	4.27	4.28	4.21	2.7		**		-
NT2RP2000168	8.64	8.81	11.56	8.06	4.98	11.13	4.05	3.85	9.74				
NT2RP2000173	5.87	12.11	13.07	7.31	10.56	7.74	13.29	16.36	4.1				
NT2RP2000175	6.28	5.9	5.57	9.33	4.37	3.63	5.8	5.65	4.1				
NT2RP2000178	7.4	9.25	18.07	7.99	4.34	5.36	2.6	5.71	4.5				
NT2RP2000183	5.74	7.89	15.69	7.74	4.42	5.84	3.67	6.86	4.04				
NT2RP2000195	16.12	12.54	17.86	16.63	13.32	13.8	5.12	8.05	4.54		**		-
NT2RP2000204	22.18	23.46	35.46	16.84	14.7	7.3	7.36	8.83	4.75		*		-
NT2RP2000205	306.16	263.17	279.79	153.75	186.84	122.03	44.13	69.43	57.15	**	**	-	-
NT2RP2000208	5.24	2.8	6.75	5.38	2.18	0.7	2.69	2.06	2.36				
NT2RP2000224	24.97	24.03	27.21	17.41	19.54	13.73	10.21	10.44	6.58	*	**	-	-
NT2RP2000230	26.52	31.48	20.02	29.78	28.26	14.04	27.93	14.94	32.18				
NT2RP2000231	102.91	95.51	132.32	51.89	45.81	56.22	28.1	59.69	105.21	**		-	
NT2RP2000232	18.39	14.23	28.59	15.4	9.71	12.46	6.13	9.73	7.72		*		-
NT2RP2000233	7.64	7.96	15.89	7.58	4.07	3.39	2.14	3	2.26		*		-
NT2RP2000239	66.01	139	172.9	85.94	84.53	44.49	55.89	55.75	25.78				
NT2RP2000240	5.47	3.94	10.61	4.6	1.25	2.17	1.78	2.32	0.43				
NT2RP2000248	6.07	5.52	8.36	6.23	4.28	2.64	2.65	2.47	2.64		**		-
NT2RP2000256	16.57	14.62	18.18	13.37	8.16	8.91	7.89	5.94	4.14	*	**	-	-
NT2RP2000257	39.73	47.22	36.2	40.72	25.44	29.27	36.28	29.33	25.56				
NT2RP2000258	13.09	11.66	21.23	12.78	8.27	8.08	5.57	13.01	9.17				
NT2RP2000261	8.27	7.35	17.74	7.68	2.93	4.17	3.42	5.31	3.64				
NT2RP2000270	3.96	6.69	13.81	17.92	6.26	3.85	3.35	9.95	4.71				
NT2RP2000274	91.36	80.94	71.7	59.79	55.47	43.9	66.54	63.63	61.61	*	*	-	-
NT2RP2000277	4.35	3.88	5.68	6.38	1.67	1.79	1.78	1.55	2.23		**		-
NT2RP2000279	7.44	6.18	9.49	6.39	2.22	2.73	3.81	2.76	3.21		*		-
NT2RP2000283	5.12	8.14	7.43	6.14	1.91	2.31	3.36	2.12	4.13		*		-
NT2RP2000288	10.29	7.99	9.75	9.32	5.86	5.55	9.02	7.12	9.38				
NT2RP2000289	21.4	17.79	32.55	15.37	7.32	16.77	22.06	23.42	27.43				
NT2RP2000297	4.51	6.32	10.63	6.94	2.23	3.64	3.53	4.19	2.55				
NT2RP2000298	8.05	8.79	13.64	5.87	3.8	2.92	2.96	3.04	1.11	*	*	-	-
NT2RP2000310	80.52	91.37	37.72	32.16	27.21	29.67	20.91	14.48	20.59	**	**	-	-
NT2RP2000327	9.08	9.43	13.33	5.88	3.81	4.9	2.31	2.04	2.13	*	**	-	-
NT2RP2000328	21.82	17.34	15.94	8.37	8.84	6.89	5.86	4.83	2.63	**	**	-	-
NT2RP2000329	17.76	16.87	20.08	10.58	7.07	6.38	10.73	6.62	8.14	**	**	-	-
NT2RP2000333	8.83	7.98	9.31	8.74	1.76	4.67	8.04	7.67	6.48				
NT2RP2000337	26.86	26.84	31.77	17.74	6.47	12.94	6.6	13.35	15.87	*	**	-	-
NT2RP2000346	6.79	9.29	9.75	14.24	7.42	4.48	6.69	17.82	10.4				
NT2RP2000357	14.11	13.18	22.49	5.83	2.27	3.95	3.56	4.39	2.66	*	*	-	-
NT2RP2000358	9.23	5.13	8.16	5.34	2.02	3.61	4.07	3.18	2.94		*		-
NT2RP2000366	5.06	4.61	6.09	5.12	1.19	2.67	2.27	2.31	1.55		**		-
NT2RP2000369	29.84	26.23	39.9	17.03	12.11	15.49	15.78	7.98	15.06	*	*	-	-
NT2RP2000376	26.15	35.86	51.75	24.31	15.42	18.34	35.37	27.75	35.03				
NT2RP2000394	11.62	6.66	9.45	10.5	5.28	8.79	9.06	9.09	12.53				
NT2RP2000396	2.03	7.18	10.2	4.43	3.16	1.53	2.05	5.24	2.77				
NT2RP2000412	13.13	15.96	18.35	14.6	6.73	8.07	6.73	16.17	12.59				
NT2RP2000414	19.9	19.23	18.62	8.95	6.33	5.66	6.29	8.15	6.52	**	**	-	-
NT2RP2000420	5.15	7.34	11.45	10.83	6.03	5.33	5.71	4.93	7.76				
NT2RP2000422	10.72	8.26	11.6	8.9	4.28	5.31	4.96	4.79	6.17		*		-
NT2RP2000426	7.55	6.99	6.8	4.75	1.02	1.72	2.91	2.26	1.94	*	**	-	-
NT2RP2000428	8.74	4.22	5.73	4.39	1.17	2.36	8.21	2.73	3.16				
NT2RP2000438	12.17	11.38	11.77	10.69	3.56	5.65	4.51	2.36	2.93		**		-
NT2RP2000447	12.75	6.94	10.08	6.36	4.33	7.41	3.21	7.55	5.61				

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Table 423

NT2RP2000448	25.71	13.78	32.06	17.1	19.22	17.26	5.88	10.24	7.42		*		-
NT2RP2000459	9.24	9.95	9.52	9.52	4.14	4.36	2.59	6.53	3.6		*		-
NT2RP2000479	6.63	5.55	7.74	7.89	3.36	5.52	5.8	5.59	6.42				
NT2RP2000498	11.27	6.84	9.95	5.98	2.48	3.08	4.73	2.88	2.16	*	*	-	-
NT2RP2000503	14.72	13.18	15.3	32.52	21.1	19.93	18.56	11.89	14.4				
NT2RP2000510	7.33	5.8	8.13	5.52	2.28	3.46	4.2	5.04	2.87	*	*	-	-
NT2RP2000514	4.57	2.69	2.25	7.44	1.96	3.28	5.71	4	3.87				
NT2RP2000516	6.54	4.62	8.39	7.51	4.34	6.37	3.47	4.35	4.95				
NT2RP2000523	4.11	2.38	11.01	7.29	1.39	3.22	3.15	2.27	3.38				
NT2RP2000533	2.68	1.37	7.63	4.63	1.22	2.09	0.79	2.38	0.48				
NT2RP2000540	6.16	5.88	8.08	5.48	4.38	3.8	3.01	4.98	1.52		*		-
NT2RP2000547	7.42	7.44	10.91	6.02	3.13	4.89	2.98	4.52	3.39		*		-
NT2RP2000557	49.31	60.55	82.94	43.46	53.17	74.9	83.43	53.58	63.67				
NT2RP2000558	18.68	19.95	27.42	20.69	14.13	19.17	24.64	17.82	18.81				
NT2RP2000564	0.43	0.11	2.04	5.89	0.93	1.24	2.05	1.59	0.53		-		
NT2RP2000565	13.78	7.23	14.74	12.39	9.94	11.42	3.9	7.3	8.83				
NT2RP2000583	10.87	6.32	13.24	7.55	3.8	5.68	4.41	5.83	9.68				
NT2RP2000591	7.05	5.42	12.75	6.46	3.08	3.75	3.89	6.69	2.85				
NT2RP2000599	45.38	33.04	53.33	45.68	38.74	39.04	49.46	50.96	42.92				
NT2RP2000601	5.8	2.35	8.26	6.01	2.72	4.74	3.53	6.5	4.71				
NT2RP2000603	10.6	10.97	14.76	12.57	11.91	10.27	11.35	11.32	10.57				
NT2RP2000610	16.79	27.41	21.69	12.86	12.08	9.62	7.92	6.77	7.19	*	**	-	-
NT2RP2000614	22.5	27.77	21.5	15.84	12.38	13.2	11.46	7.34	10.15	*	**	-	-
NT2RP2000616	15.9	10.73	17.88	14.04	10.65	8.26	8.53	13.65	30.31				
NT2RP2000617	7	4.89	10.44	5.79	2.49	3.27	2.33	3.91	6.08				
NT2RP2000623	30.93	27.18	42.39	23.25	19.11	22.34	22.03	24.06	17.67				
NT2RP2000634	5.41	5.13	8.98	7.02	5.17	5.22	4.91	6.31	5.96				
NT2RP2000636	6.22	7.05	7.96	5.06	2.33	3.65	3.42	4.64	2.62	*	*	-	-
NT2RP2000638	5.4	5.87	8.77	7.49	5.36	5.46	5.01	4.21	4.57				
NT2RP2000644	6.06	11.57	13.6	11.21	5.35	7.7	5.1	5.24	4.14				
NT2RP2000649	69.57	64.76	72	79.36	45.65	56.22	93.91	57.37	68.85				
NT2RP2000652	14.9	10.94	49.84	10.88	5.91	11.87	6.2	5.26	32.14				
NT2RP2000656	12.57	7.15	13.54	6.29	4.4	6.3	1.69	9.03	14.78				
NT2RP2000658	5.45	4.52	10.98	5.11	2.13	3.91	1.81	2.12	1.71				
NT2RP2000663	4.6	4.28	7.43	5.58	2.25	5.97	4.47	2.44	1.11				
NT2RP2000664	10.9	7.61	12.36	9.42	3.88	8.64	13.44	10.25	9.81				
NT2RP2000668	33.38	33.11	48.17	36.56	39	37.32	34.56	25.63	30.2				
NT2RP2000678	6.12	9.03	9.25	9.6	7.57	6.65	6.86	6.02	5.34				
NT2RP2000694	16.87	11.51	13.29	13.35	8.47	12.93	22.9	14.8	18.71				
NT2RP2000704	2.84	3.9	14.85	6.19	2.87	7.29	2.98	6.45	4.78				
NT2RP2000710	8.84	8.7	19.22	7.25	3.74	6.4	5.24	6.81	6.9				
NT2RP2000712	5.84	5.25	16.26	7.12	3.27	5.34	2.82	4.15	2.23				
NT2RP2000715	23.49	31.67	27.44	16.78	13.7	10.05	7.2	11.02	9.66	*	**	-	-
NT2RP2000720	14.6	11.95	17.99	9.67	7.04	6.8	9.67	8.11	6.87	*	*	-	-
NT2RP2000731	130.46	114.16	171.06	139.58	136.44	144.08	91.22	91.1	91.43		*		-
NT2RP2000739	10.56	11	13.93	9.61	7.28	5.99	9.06	6.03	5.15	*	*	-	-
NT2RP2000748	12.42	9.17	9.8	13.86	6.05	5.01	6.86	4.28	5.36		*		-
NT2RP2000749	11.23	7.84	14.76	7.12	4.44	6.62	1.43	4.83	4.58		*		-
NT2RP2000758	18.71	12.4	22.27	12.06	7.43	9.25	3.34	5.27	4.96		*		-
NT2RP2000764	8.83	9.65	16.17	9.68	4.51	6.36	4.78	3.89	4.68		*		-
NT2RP2000765	39.21	45.57	54.49	39.05	26.43	20.35	16.67	26.46	19.71		**		-
NT2RP2000777	37.43	31.1	43.71	20.28	16.78	21.16	3.56	8.61	6.24	**	**	-	-
NT2RP2000786	10.79	9.6	16.45	9.08	5.82	3.61	8.49	11.1	8.19				
NT2RP2000793	8.96	7.43	14.72	5.59	4.46	3.27	3.41	3.35	2.39		*		-
NT2RP2000796	13.41	11.17	11.19	12.52	8.7	5.88	4.89	4.55	5.82		**		-
NT2RP2000809	9.51	8.66	16.69	9.15	5.7	10.07	8.67	9.07	9.06				
NT2RP2000812	10.78	5.64	19.76	9.49	6.33	7.02	9.58	10.65	9.48				
NT2RP2000814	2.73	2.98	11.46	6.79	1.46	2.03	1.53	1.11	1.73				
NT2RP2000816	5.26	5.27	12.58	5.83	4.32	3.54	2.61	2.6	1.81				
NT2RP2000818	64.67	52.94	68.69	38.83	38.29	31.92	36.98	34.96	36.14	**	**	-	-
NT2RP2000819	10.64	9.84	11.3	8.11	4.61	3.58	6.06	2.23	3.74	*	**	-	-
NT2RP2000841	19.27	13.42	17.68	15.7	9.96	11	12.88	9.6	13.79				
NT2RP2000842	7.9	5.25	9.24	8.2	4.88	2.43	6.17	3.9	4.72				
NT2RP2000845	1.64	3.58	10.06	6.26	3.24	5.16	2.58	3.32	3.23				

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Table 424

NT2RP2000863	9.23	2.37	9.61	12.6	5.57	10.29	2.95	6.5	2.03				
NT2RP2000880	6.89	4.15	10.09	8.75	3.65	3.61	3.32	7.64	2.92				
NT2RP2000892	6.48	7.22	10.47	6.68	3.59	2.44	2.63	2.13	2.32		**		-
NT2RP2000894	6.84	8.43	12.75	7.7	5.61	3.86	6.32	3.41	5.03				
NT2RP2000903	14.72	12.47	10.22	6.37	7.06	6.25	6.3	4.12	3.45	*	**	-	-
NT2RP2000906	7.83	5.78	8.49	5.67	3.5	4.08	5.51	1.9	1.89	*	*	-	-
NT2RP2000910	7.08	7.41	7.6	9.95	3.31	4.88	6.74	6.36	7.22				
NT2RP2000931	17.23	16.66	19.14	9.83	11.03	7.29	5.66	13.37	8.87	**	*	-	-
NT2RP2000932	4.85	5.4	12.51	5.58	2.98	2.75	2.51	3.48	1.84				
NT2RP2000938	32.12	38.62	41.75	20.34	22.26	19.86	28.05	24.64	29.99	**	*	-	-
NT2RP2000943	6.65	4.28	8.98	6.63	2.06	1.49	2.39	2.3	2.44		*		-
NT2RP2000957	8.82	7.9	11.5	5.58	3.81	3.6	2.18	2.83	1.56	*	**	-	-
NT2RP2000958	5.64	6.03	15.9	6.17	2.43	2.74	1.92	2.26	3.56				
NT2RP2000959	11.75	9.04	10.68	6.59	3.84	2.64	4.69	3.69	5.66	*	**	-	-
NT2RP2000965	4.05	2.66	2.8	5.91	0.94	1.41	2.34	1.56	2.95		-		
NT2RP2000970	58.85	65.2	74.74	64.15	40.74	92.64	72.54	97.39	89.84				
NT2RP2000973	5.19	3.92	9.39	8.06	5.68	3.54	3.01	9.76	7.5				
NT2RP2000985	3.85	2.51	4.33	4.79	3.19	4.55	1.82	2.45	2.12				
NT2RP2000987	39.38	36.27	32.68	33.06	40.49	26.38	33.61	26.04	27.01				
NT2RP2000997	9.33	8.58	9.52	9.72	3.47	7.24	9.63	9.44	11.63				
NT2RP2001024	12.74	7.92	18.67	6.22	2.48	2.6	4.96	3.99	3.75	*	*	-	-
NT2RP2001028	38.71	37.69	41.88	33.98	15.8	30.64	34.47	25.69	33.62				
NT2RP2001036	10.56	11.08	9.13	9.7	2.35	6.59	6.06	3.75	3.17		**		-
NT2RP2001039	29.77	24.74	30.19	17.85	11.75	29.98	20.42	28.95	23.24				
NT2RP2001044	111.16	103.9	116.83	65.77	42.98	31.59	30.2	74.24	42.92	**	*	-	-
NT2RP2001056	16.47	11.38	12.03	9.34	5.04	8.68	12.51	8.41	8.95				
NT2RP2001065	12.87	18.54	21.09	9.6	6.83	8.58	6.23	6.54	8.28	*	*	-	-
NT2RP2001067	18.27	13.06	19.79	9.25	5.26	3.58	5.5	6.23	8.66	*	*	-	-
NT2RP2001070	4.55	6.03	7.25	6.14	2.9	2.2	3.37	2.83	1.95		*		-
NT2RP2001081	11.96	15.94	13.97	8.19	3.81	5.26	5.58	4.15	6.83	**	**	-	-
NT2RP2001087	65.9	61.9	76.08	39.7	16.73	50.09	38.08	21.24	22.36	*	**	-	-
NT2RP2001094	12.2	8.99	11.02	14.61	10.72	9.52	11.02	11.03	11.05				
NT2RP2001119	4.16	4.58	7.07	10.85	1.99	7.07	4.12	3.63	2.63				
NT2RP2001127	11.36	13.12	3.9	16.08	4.34	7.73	5.38	7.85	3.42				
NT2RP2001133	5.67	4.14	5.86	10.97	6.13	8.56	8.68	4.41	3.17				
NT2RP2001137	49.8	41.1	45.81	39.26	21.06	24.92	25.21	45.63	17.6	*		-	
NT2RP2001142	5.27	5.53	5.06	5.3	2.26	3.98	2.41	3.56	3.78		*		-
NT2RP2001149	6.92	5.61	5.45	13.36	3.82	6.27	6.19	4.78	4.91				
NT2RP2001168	6.12	7.49	5.66	8.34	5.85	5.09	5.44	4.63	5.1				
NT2RP2001173	4.74	3.23	8.28	7.11	2.4	3.67	4.61	6.54	6.37				
NT2RP2001174	44.63	21.39	37.72	44.99	18.88	46.31	52.67	53.94	56.67		*		+
NT2RP2001184	7.2	4.99	10.33	8.93	4.09	3.96	4.88	4.86	5.6				
NT2RP2001196	188.27	171.63	278.21	277.29	156.05	217.9	310.45	339.15	334.54		*		+
NT2RP2001200	5.84	6.42	11.03	6.08	6.9	5.52	4.06	2.49	4.45				
NT2RP2001218	12.41	10.49	14.66	10.34	6.96	7.23	9.11	8.8	8.23		*		-
NT2RP2001223	10.09	12.26	12.04	13.71	9	9.77	10.94	7.86	9.72				
NT2RP2001226	295.34	151.71	253.15	264.52	155.79	205.35	225.76	302.58	279.91				
NT2RP2001227	9.29	9.83	15.24	10.83	5.91	8.02	6.71	6.54	8.43				
NT2RP2001232	6.25	9.05	13.72	6.11	9.52	4.37	3.08	5.35	5.73				
NT2RP2001233	17.2	11.64	26.2	12.06	8.02	7.48	8.66	8.69	6.62				
NT2RP2001245	42.01	30.76	56.72	22.72	58.34	32.96	29.15	30.96	32.88				
NT2RP2001246	5.12	5.92	8.66	6.91	4.33	3.68	3.64	7.01	3.2				
NT2RP2001268	76.86	63.92	101.42	88.4	109.5	90.32	72.85	73.19	77.59				
NT2RP2001270	10.64	12.74	14.24	12.74	10.24	11.95	10.68	9.82	10.94				
NT2RP2001276	23.31	16.76	30.97	21.15	16.68	10.08	14.57	16.7	14.66				
NT2RP2001277	24.91	10.73	18.18	16.47	6.03	6.24	22.15	25.09	49.12				
NT2RP2001290	8.95	7.82	10.48	8.48	7.41	5.73	5.82	9.63	10.81				
NT2RP2001295	14.82	7.48	15.13	8.28	5.62	4.48	5.33	6.4	4.82				
NT2RP2001297	8.15	6.67	10.81	9.36	7.32	4.92	4.17	4.98	6				
NT2RP2001301	47.34	44.45	63.71	42.51	38.25	33.89	33.81	29.8	26.52		*		-
NT2RP2001312	8.43	10.98	14.02	7.43	5.35	5.08	6.81	4.46	4.32	*	*	-	-
NT2RP2001327	20.88	28.57	34.54	16.53	15.03	15.84	11.1	20.64	9.65	*		-	
NT2RP2001328	10.32	3.77	9.25	9.2	3.81	6.74	4.44	5.56	7.15				
NT2RP2001341	3499.3	2809.3	4099.1	1364.9	1644.2	898.17	1201.7	2570.4	2392	**		-	

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Table 425

NT2RP2001347	539.84	514.01	628.74	565.74	422.96	416.2	495.32	585.14	429.89				
NT2RP2001366	38.71	33.77	43.04	29.42	28.24	19.52	18.19	26.65	21.17	*	*	-	-
NT2RP2001378	8.65	6.18	12.14	10.82	6.77	5.51	3.49	4.36	4.96				
NT2RP2001381	20.33	22.01	25.11	15	9.62	10.21	6.87	12.31	12.9	**	**	-	-
NT2RP2001388	23.09	21.55	19.16	14.87	11.09	13.2	20	18.4	14.87	**		-	
NT2RP2001391	19.47	21.48	20.82	19.07	15.36	11.27	15.83	12.93	10.03		*		-
NT2RP2001392	6.22	2.39	9.23	6.23	2.48	4.35	2.68	3.41	3.72				
NT2RP2001394	9	9.52	18.06	7.33	4.64	3.55	4.34	5.54	7.88				
NT2RP2001397	5.52	4.95	15.76	7.71	3.52	1.79	2.61	4.45	3.74				
NT2RP2001400	33.05	35.87	41.2	15.06	15.67	8.49	5.11	9.86	5.55	**	**	-	-
NT2RP2001408	22.02	23.86	22.82	11.45	12.19	9.24	10.98	11.38	13.8	**	**	-	-
NT2RP2001420	13.99	18.37	19.98	12.59	10.04	8.9	9.18	10.79	13.16	*	*	-	-
NT2RP2001423	138.22	161.12	169.36	120.84	140.16	121.74	142.58	124.54	152.09				
NT2RP2001427	11.99	17.22	16.25	9.35	7.9	6.74	7.44	6.11	3.28	*	**	-	-
NT2RP2001428	11.05	7.81	14.33	11.13	3.4	8	3.33	6.84	8.32				
NT2RP2001436	28.98	21.86	34.92	22.78	25.35	19.1	15.23	27.9	27.44				
NT2RP2001440	21.88	12.74	27.62	14.71	9.47	17.13	15.85	24.15	14.86				
NT2RP2001445	9	10.8	19.43	10.91	10.54	6.62	8.66	8.73	7.21				
NT2RP2001449	28.07	34.09	40.82	25.02	19.29	16.65	14.58	19.57	13.99	*	*	-	-
NT2RP2001450	20.8	28.19	27.38	18.17	18.42	8.85	15.67	22.32	18.66				
NT2RP2001467	77.4	117.05	74.08	41.14	94.21	47.44	46.82	38.8	29.18		*		-
NT2RP2001469	12.38	11.13	18.21	9.61	8.91	7.86	5.16	5.66	4.91		*		-
NT2RP2001480	16.58	12.17	23.4	14.68	6.35	9.1	6.53	11.37	10.31				
NT2RP2001495	5.39	5.05	10.71	5.62	3.39	3.05	2.02	2.99	3.13				
NT2RP2001499	31.27	46.77	45.33	29.35	33.83	17.6	16.09	21.38	15.2		*		-
NT2RP2001506	7.58	7.79	10.57	9.25	7.24	4.11	3.34	2.96	2.75		**		-
NT2RP2001508	10.21	8.66	19.01	9.32	5.78	3.48	10.19	10.43	10.1				
NT2RP2001511	18.18	10.36	14.04	8.06	6.96	5.65	4.43	6.31	7.52	*	*	-	-
NT2RP2001514	8.2	7.15	8.01	6.7	3.51	2.31	2.13	3.46	3.84		**		-
NT2RP2001520	8.17	6.6	9.18	8.28	6.18	3.08	5.09	4.32	4.95		*		-
NT2RP2001526	15.63	17.52	16.82	11.75	3.98	10.59	5.68	10.57	11.64	*	*	-	-
NT2RP2001529	18.98	9.11	22.28	13.03	8.09	10.02	6.2	8.22	8.57				
NT2RP2001536	14.16	10.36	18.6	12.98	11.79	8.28	7.74	11.37	11.72				
NT2RP2001538	8.11	6.47	12.78	7.67	5.34	3.77	4	4.36	2.56		*		-
NT2RP2001547	9.99	10.57	12.92	9.74	7.58	3.49	4.05	3.74	4.33		**		-
NT2RP2001560	11.5	10.74	9.02	6.82	5.56	7.18	6.87	5.66	4.21	*	*	-	-
NT2RP2001562	17.39	15.7	17.62	10.84	8.02	7.21	8.92	9.2	10.24	**	**	-	-
NT2RP2001566	14.26	13.81	10.49	11.53	7.07	4.68	7.24	4.21	4.54		**		-
NT2RP2001569	25.02	15.42	32.18	22.03	11.09	26.81	24.28	25.39	21.94				
NT2RP2001576	129.89	178.91	114.02	47.3	49.96	55.77	33.67	55.78	72.18	*	*	-	-
NT2RP2001581	20.4	22.7	22.23	13.8	17.88	10.54	10.57	16.71	15	*	*	-	-
NT2RP2001597	17.49	9.3	13	11.25	8.35	11.5	4.54	4.57	3.83		*		-
NT2RP2001601	376.46	416.73	382.11	192.76	196.04	131.77	252.12	219.45	367.42	**		-	
NT2RP2001613	6.29	5.75	7.26	4.54	4.25	3.06	3.72	3.99	3.96	*	**	-	-
NT2RP2001628	20.46	20.27	25.19	14.18	13.5	11.94	11.98	13.91	12.32	**	**	-	-
NT2RP2001634	4.72	7.04	6	7.61	3.83	2.93	4.15	1.66	3.09		*		-
NT2RP2001635	20.18	16.77	22.18	15.58	7.6	10.65	10.91	15.44	14.53	*	*	-	-
NT2RP2001660	27.92	47.45	35.98	27.8	15.26	22.85	16.57	20.69	20.06		*		-
NT2RP2001662	141.98	137.52	151.45	151.4	116.43	136.78	154.6	188.28	148.8				
NT2RP2001663	102.28	119.36	140.87	48.03	51.07	39.15	80.45	80.81	83.65	**	*	-	-
NT2RP2001672	6.83	9.61	11.14	6.86	4.73	5.02	7.16	6.7	5.29				
NT2RP2001675	7.51	11.75	9.95	6.41	3.17	2.8	4.39	4.7	4.26	*	*	-	-
NT2RP2001677	18.83	22.14	19.19	10.64	6.34	6.91	9.72	6.83	7.68	**	**	-	-
NT2RP2001678	10.06	8.87	8.92	7.97	6.41	4.67	9.59	5.34	9.32	*		-	
NT2RP2001683	98.93	103.45	119.49	195.62	102.44	134.62	102.34	95.16	65.68				
NT2RP2001699	36.15	36.2	44.96	18.8	7.95	13.41	6.7	9.44	13.11	**	**	-	-
NT2RP2001707	6.77	3.9	7.75	5.48	4.72	5.02	3.35	4.21	3.45				
NT2RP2001720	8.16	6.41	9.93	7.22	8.68	5.49	4.59	6.11	5.89				
NT2RP2001721	33.41	34.55	34.5	25.33	18.3	17.93	32.85	38.18	33.9	**		-	
NT2RP2001740	64.22	76.89	65.2	34.74	42.49	31.73	26.06	24.24	41.05	**	**	-	-
NT2RP2001748	6.3	15.07	7.65	6.61	1.99	2.37	4.7	3.94	2.45				
NT2RP2001755	8.56	8.68	5.59	6.1	3.13	5.08	4.74	3.64	4.01		*		-
NT2RP2001762	4.42	4.43	4.61	6.06	1.37	4.5	3.19	3.5	2.83		**		-
NT2RP2001768	7.43	5.23	6.6	7.86	2.49	4.84	3.03	5.68	3.45				

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Table 426

NT2RP2001769	74.25	64.35	76.05	49.19	51.48	48.88	16.14	29.26	21.95	**	**	-	-
NT2RP2001784	6.1	6.64	9.79	6.92	5.74	5.64	4.78	4.07	4.19				
NT2RP2001805	18.64	23.08	28.59	18.75	15.28	15.88	12.77	15.01	19.71				
NT2RP2001813	12.2	15.41	15.49	8.88	4.21	6.14	9.29	6.92	9.66	*	*	-	-
NT2RP2001817	50.4	58.09	53.81	41.79	32.65	39.63	54.02	42.75	56.58	*		-	
NT2RP2001818	7.27	4.11	3.7	5.91	1.54	5.16	5.71	4.24	6.18				
NT2RP2001837	24.91	17.75	31.06	23.35	23.21	19.49	21.43	23.69	22.4				
NT2RP2001839	16.58	14.52	27.11	17.12	15.87	19.03	13.8	13.73	15.93				
NT2RP2001861	19.37	18.6	26.95	11.83	7.45	7.51	9.29	9.04	10.22	*	*	-	-
NT2RP2001869	8.35	8.88	14.85	9.01	6.82	4.27	3.19	6.52	4.2				
NT2RP2001876	52.07	48.1	60.43	41.56	38.63	33.22	53.55	54.23	52.55	*		-	
NT2RP2001878	10.64	8.11	16.99	8.71	6.81	6.18	8.15	6.26	6.36				
NT2RP2001881	11.51	12.01	17.12	11.39	8.77	9.36	10.8	14.93	9.65				
NT2RP2001883	15.67	6.93	15.2	18.32	7.55	11.74	13.41	14.76	12.05				
NT2RP2001884	1443.8	767.12	607.01	701.8	366.77	733.69	199.74	492.38	1929.8		-		
NT2RP2001885	86.63	81.18	119.19	86.34	68.67	72.27	80.49	93.38	87.15				
NT2RP2001898	13.46	6.9	14.73	6.96	6.72	3.84	5.67	4.43	5				
NT2RP2001900	20.73	14.58	24.69	18.79	8.43	10.74	17.28	16.1	17.71				
NT2RP2001903	11.05	14.47	16.38	12.77	7.63	7.86	11	14.28	12.43				
NT2RP2001907	9.79	12.89	12.82	8.11	6.3	4.57	8.52	7.33	7.63	*	*	-	-
NT2RP2001915	17.49	19.44	20.82	11.45	7.41	6.04	7.94	7.59	6.62	**	**	-	-
NT2RP2001921	13.67	9.05	20.66	11.35	6.61	9.21	6.21	10.48	17.99				
NT2RP2001926	34.47	22.9	35.27	22.68	13.7	11.83	10.15	26.13	26.9	*		-	
NT2RP2001933	36.39	16.3	35.12	23.35	20.81	17.87	10.85	17.5	22.37				
NT2RP2001936	11.42	9.59	15.71	9.32	7.07	4.58	8.12	12.42	62.46				
NT2RP2001943	14.71	11.45	18.53	11.8	23.77	7.53	6.86	10.79	7.88				
NT2RP2001946	20.64	20.42	25.84	8.64	12.56	9.33	5.24	6.37	7.54	**	**	-	-
NT2RP2001947	6.28	10.5	8.57	7.88	5.98	1.91	4.36	3.2	4.16		*		-
NT2RP2001956	21.67	10.17	24.79	16.61	12.12	14.12	16.82	19.29	13.33				
NT2RP2001969	201.65	149.79	301.42	176.35	143.62	157.42	143.79	183.78	182.57				
NT2RP2001976	4.33	7.95	17.7	7.78	4.49	4.49	2.81	5.46	10.35				
NT2RP2001978	14.35	12.6	20.91	12.02	5.57	5.03	3.1	3.56	4.91		**		-
NT2RP2001985	13.77	15.22	14.24	9.55	5.93	6.64	4.89	6.51	5.47	**	**	-	-
NT2RP2001991	37.12	36.77	50.48	37.16	44.84	28.4	28.39	20.28	24.2		*		-
NT2RP2001997	13.99	12.07	14.92	11.27	12.08	8.47	13.49	12.5	12.19				
NT2RP2002015	3.95	7.2	5.18	7.51	4.61	2.96	3.72	6.25	2.61				
NT2RP2002017	14.92	13.42	18.23	7.3	5.04	8.42	3.4	6.85	8.43	**	*	-	-
NT2RP2002025	39.84	48.8	68.43	33.02	35.2	30.44	23.31	31.13	31.97				
NT2RP2002030	28.92	28.65	40.93	26.27	23.9	23.74	29.55	36.7	30.22				
NT2RP2002032	41.77	39.39	41.34	31.44	32.7	25.79	15.28	25.82	17.93	**	**	-	-
NT2RP2002033	7.84	6.18	11.1	7.44	5.25	3.93	2.63	4.43	2.72		*		-
NT2RP2002041	63.15	38.11	58.94	48.43	54.38	37.99	33.68	26.24	30.79		*		-
NT2RP2002046	19.79	18.39	22.62	13.61	15.41	9.7	20.12	17.67	17.54	*		-	
NT2RP2002047	15.96	12.18	14.55	9.42	12.66	9.04	9.26	8.52	3.77		*		-
NT2RP2002050	6.47	7.96	8.94	7.07	2.69	4.33	1.22	3.6	2.62		**		-
NT2RP2002052	16.16	10.25	17.67	10.56	6.94	8.28	6.44	8.83	9.43				
NT2RP2002058	10.7	8.12	13.82	9.12	8.72	4.7	3.71	8.14	3.23				
NT2RP2002060	7.22	6.32	13.21	7.18	3.78	3.46	2.87	4.32	2.16				
NT2RP2002063	27.7	19.33	28	16.06	12.42	6.01	14.89	17.06	15.58	*	*	-	-
NT2RP2002066	14.12	10.25	16.69	11.69	8.3	5.49	7.86	7.37	6.79		*		-
NT2RP2002070	47.82	69.53	26.7	25.88	50.9	22.08	11.62	12.95	13.2		*		-
NT2RP2002076	50.79	54.44	56.91	34.7	35.7	26.78	21.75	13.06	12.15	**	**	-	-
NT2RP2002078	3.82	6.23	12.24	6.03	3.97	4.06	0.81	5.31	3.09				
NT2RP2002079	13.68	8.15	17.98	9.69	6.98	8.2	5.55	8.29	6.41				
NT2RP2002099	11.59	12.19	18.2	8.81	6.98	5.14	5.57	8.29	5.75	*	*	-	-
NT2RP2002105	15.09	12.54	15.38	10.34	7.26	6.01	5.5	9.12	6.68	*	**	-	-
NT2RP2002115	15.39	14.23	22.91	11.04	12.24	9.95	11	13.28	11.06				
NT2RP2002124	59.86	56.27	77.47	56.59	47.35	36.88	55.21	47.08	46.87				
NT2RP2002137	8.42	8.75	8.28	6.56	6.55	3.48	2.47	3.09	3.68	*	**	-	-
NT2RP2002139	93.62	131.25	91.96	52.77	52.45	52.95	81.88	52.45	48.22	*		-	
NT2RP2002154	6.04	5.02	12.4	5.24	1.47	5.98	2.02	3.26	3.03				
NT2RP2002155	16.04	17.28	22.84	17	10.94	11.7	12.12	14.76	13.07				
NT2RP2002172	26.05	32.14	34.35	17.74	14.37	15.16	12.78	22.56	16.28	**	*	-	-
NT2RP2002185	13.73	14.4	21.2	14.18	14.86	10.72	12.32	12.52	11.2				

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Table 427

NT2RP2002188	222.52	243.75	126.54	151.89	124.73	74.73	64.57	82.95	98.67		*		-
NT2RP2002192	66.59	140.59	123.86	61.74	74.83	59.86	111.82	74.79	70.77				
NT2RP2002193	9.92	9.38	5.54	5.64	8.2	3.35	4.38	2.62	2.3		*		-
NT2RP2002208	24.07	21.97	26.87	14.79	10.85	11.7	14.39	13.9	16.1	**	**	-	-
NT2RP2002219	67.68	67.68	54.54	42.26	45.01	39.83	12.23	52.49	39.63	*		-	
NT2RP2002231	7.62	8.91	9.95	5.33	3.41	3.41	3.43	5.73	5.85	**	*	-	-
NT2RP2002232	82.24	77.63	81.5	78.38	94.62	65.26	53.25	57.27	56.31		**		-
NT2RP2002235	28.16	33.42	30.04	28.68	25.16	22.07	20.58	21.22	23.01		**		-
NT2RP2002239	46.02	63.63	67.29	21.58	16.63	25.15	34.54	22.68	19.45	**	*	-	-
NT2RP2002252	7.05	9.07	9.23	8.29	3.79	3.9	4.57	3.45	2.91		**		-
NT2RP2002256	27.97	26.81	27.09	15.84	11.06	11.47	26.86	22.34	28.47	**		-	
NT2RP2002257	7.18	9.4	7.52	6.89	3.78	4.59	5.56	4.76	6.16		*		-
NT2RP2002259	18.53	13.43	11.26	24.93	14.6	14.24	10.77	18.34	15.94				
NT2RP2002264	26.23	33.28	22.8	12.91	13.58	12.04	9.7	17.76	13.48	**	*	-	-
NT2RP2002267	32.17	30.65	32.28	23.04	23.01	26.57	18.83	21.9	22.12	**	**	-	-
NT2RP2002270	24.56	42.02	39.93	12.58	23.51	8.23	20.01	17.31	11.5	*	*	-	-
NT2RP2002281	77.89	96.13	97.81	150.54	78.9	96.99	77.36	60.86	55.61		*		-
NT2RP2002288	21.39	25.5	23.86	18.7	13.7	14.18	19.97	22.13	17.3	*		-	
NT2RP2002292	54.6	51.47	64.64	33.71	24.08	25.61	33.57	27.11	23.57	**	**	-	-
NT2RP2002299	38.27	50.42	61.77	19.48	10.3	12.83	10.02	9.38	6.36	**	**	-	-
NT2RP2002304	11.94	6.17	8.22	10.44	3.85	9.51	5.62	11.16	9.83				
NT2RP2002312	27.46	21.25	33.99	24.99	23.29	27.25	22.52	32.61	25.31				
NT2RP2002316	51.29	40.93	55.81	26.92	27.74	16.77	8.08	18.25	13.09	*	**	-	-
NT2RP2002325	14.79	13.26	29.38	13.29	7.49	7.83	6.29	6.54	6.53				
NT2RP2002333	37.71	73.03	60.93	25.88	22.98	32.97	22.31	24.03	28.79	*	*	-	-
NT2RP2002371	18.55	14.9	20.81	15.66	7.83	11.84	19.13	18.46	18.7				
NT2RP2002373	7.7	6.37	4.6	6.91	3.79	4.83	4.84	5.13	5.14				
NT2RP2002381	9.55	13.3	13.26	6.59	3.77	3.7	6.54	4.52	6.36	**	*	-	-
NT2RP2002385	0.45	2.78	2.19	4.9	1.81	3.5	0.24	0.66	1.05				
NT2RP2002394	32.72	28.71	26.62	28.1	25	26.16	15.67	15.8	20.33		**		-
NT2RP2002408	6.97	5.52	5.11	6.31	2.85	4.31	2.1	5.36	5.24				
NT2RP2002409	7.43	7.51	7.75	10.28	4.99	7.17	4.61	5.21	4.74		**		-
NT2RP2002424	13.74	18.21	4.21	14.47	4.22	10.67	7.29	17.72	5.01				
NT2RP2002426	31.08	22.01	26.45	29.33	10.8	28.89	38.27	34.35	51.45				
NT2RP2002429	5.25	5.45	6.58	6.82	3.95	4.26	5.54	2.96	5.77				
NT2RP2002437	5.68	8.15	5.2	8.99	3.78	4.37	5.91	5.66	5.8				
NT2RP2002439	23.83	11.85	28.63	30	21.32	18.74	18.69	27.87	21.85				
NT2RP2002442	4.21	2.48	10.06	7.13	2.17	3.83	3.89	4.18	3.7				
NT2RP2002457	5.91	3.86	9.43	6.08	1.82	4.35	4.32	3.38	4.15				
NT2RP2002464	14.04	9.04	19.39	8.26	2.91	3.02	6.2	7.3	8.31				
NT2RP2002475	18.47	16.05	30.87	26.73	13.63	23.54	27.01	26.72	27.62				
NT2RP2002479	4.38	4.25	7.68	9.08	3.28	4.87	3.36	7.1	3.51				
NT2RP2002487	8.46	11.73	16.26	11.78	4.98	7.15	5.71	5.33	8.37				
NT2RP2002498	12.42	14.56	14.54	14.3	15.74	13.48	11.49	11.5	14.04				
NT2RP2002503	38.54	26.71	38.28	36.97	26.13	31.51	31.04	37.76	40.27				
NT2RP2002504	10.58	11.45	20.66	9.47	10.7	9.29	7	7.64	9.65				
NT2RP2002510	35.82	27.78	43.7	25.78	25.92	21.7	29.92	29.43	28.5				
NT2RP2002520	21.45	19.39	27.79	16.61	13.24	8.38	14.06	12.04	8.59	*	*	-	-
NT2RP2002527	36.1	23.32	35.4	20.76	25.32	20.27	27.42	26.23	15.63				
NT2RP2002533	13.17	14.75	23.11	11.93	9.58	7.87	8.62	7.96	9				
NT2RP2002537	13.08	12.39	14.79	10.65	13.69	8	8.5	6.59	7.09		**		-
NT2RP2002542	68.44	80.08	72.33	74.6	46.95	45.75	49.02	39.47	37.92		**		-
NT2RP2002546	14.88	18.96	17.6	15.64	9.66	8.83	6.06	11.83	13.87				
NT2RP2002549	14.96	11.64	16.89	10.43	8.76	6.03	5.02	9.52	9.5	*	*	-	-
NT2RP2002564	39.56	26.21	34.95	20.11	17.81	17.77	18.21	24.98	19.23	*	*	-	-
NT2RP2002591	42.59	28.9	37.43	32.97	30.53	25.24	25	30.71	25.2				
NT2RP2002595	5.68	8	12.85	9.34	7.39	5.51	5.35	4.75	4.31				
NT2RP2002602	54.53	55.87	75.68	59.64	57.23	46.71	59.72	54.59	54.85				
NT2RP2002606	12.52	13.19	14.5	13.95	17.61	9.8	13.98	12.61	14.58				
NT2RP2002609	11.6	17.33	13.31	20.12	19.43	14.55	10.05	12.64	13.06				
NT2RP2002618	14	10.22	19.04	13.28	7.51	9.59	7.56	12.06	11.33				
NT2RP2002621	11.85	9.77	15.54	8.04	5.31	5.01	3.35	5.97	7.64	*	*	-	-
NT2RP2002643	11.04	8.19	16.62	9.29	6.05	6.59	3.63	6.53	4.9				
NT2RP2002672	6.88	6.19	9.33	7.99	5.59	4.36	3.64	6.54	3.29				

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Table 428

NT2RP2002673	103.76	111.24	114.16	70.07	45.09	85.59	92.44	85.88	91.14	*	**	-	-
NT2RP2002674	28.24	27.69	34.14	21.06	20.78	16.49	24.37	22.8	22.81	*	*	-	-
NT2RP2002686	20.76	27.04	31.72	23.26	22.04	15.33	8.73	8.68	8.13		**		-
NT2RP2002688	13.92	12.24	10	14.56	10.69	8.28	14.43	8.67	10.91				
NT2RP2002695	19.25	14.55	23.17	14.75	11.8	15.12	11.5	15.77	21.62				
NT2RP2002701	4.75	5.4	12.91	6.52	3.02	5.45	3.43	3.42	5.6				
NT2RP2002706	14.53	15.48	22.22	9.32	11.09	8.76	5.34	11.12	9.16	*	*	-	-
NT2RP2002710	30.61	29.84	37.75	21.5	19.35	13.67	11.45	15.23	13.68	*	**	-	-
NT2RP2002721	7.29	6.84	7.35	5.81	4.84	2.96	3.61	3.96	1.62	*	**	-	-
NT2RP2002727	6.54	9.38	10.59	7.9	7.44	4.24	4.08	5.05	3.6		*		-
NT2RP2002734	48.13	41.34	40.09	29.15	43.09	31.56	39.87	34.2	33.11				
NT2RP2002736	9.71	9.47	8.91	9.58	7.4	9.48	7.64	7.21	5.83		*		-
NT2RP2002740	19.4	13.22	23.87	11.87	7.31	11.43	6.19	11.24	13.39				
NT2RP2002741	23.72	17.52	33.51	16.7	12.26	14.24	12.67	22.55	22.7				
NT2RP2002750	63.6	50.03	64.42	39.1	24.44	35.13	36.13	36.29	30.98	*	**	-	-
NT2RP2002752	10.52	9.47	15.12	8.58	15.15	3.88	2.8	5.03	3.54		*		-
NT2RP2002753	12.15	11.11	17.25	9.74	6.82	4.55	5.04	8.44	4.88		*		-
NT2RP2002760	73.48	81.4	101.38	101.02	88.73	62.2	63.54	64.02	59.41				
NT2RP2002769	92.25	85.07	85.98	43.44	97.23	54.77	13.8	14.78	19.89		**		-
NT2RP2002778	10.58	7.74	8.45	8.8	4.88	4.14	4.05	4.2	5.19		**		-
NT2RP2002791	21.96	17.69	24.67	15.97	10.79	19.44	8.98	15.96	17.2				
NT2RP2002800	57.56	44.66	67.26	27.41	29.24	35	38.77	66.85	61.35	*		-	
NT2RP2002805	10.55	19.25	27.64	13.98	23.59	9.88	7.4	10.07	7.75				
NT2RP2002811	13.01	13.43	18.61	12.19	7.67	8.64	7.15	10.12	7.7		*		-
NT2RP2002824	16.63	12.33	20.93	15.22	10.57	11.14	9.08	9.37	7.94		*		-
NT2RP2002839	7.61	6.4	5.94	5.9	4.06	3.3	9.77	3.03	3.13				
NT2RP2002845	12.27	9.25	11.68	10.47	8.06	5	6.84	6.96	4.06		*		-
NT2RP2002857	13.78	16.15	14.57	14.65	30.41	11.09	9.34	6.45	5.36		**		-
NT2RP2002862	39.8	48.81	41.43	30.51	20.27	24.76	25.07	37.41	27.22	*	*	-	-
NT2RP2002880	68.2	65.99	77.82	51.13	34.35	43.94	48.02	65.53	66.61	*		-	
NT2RP2002885	6.6	7.46	15.43	8.27	7.08	4.47	4.01	3.85	3.27				
NT2RP2002891	7.27	7.43	13.2	9.04	9.22	4.71	4.88	7.24	5.8				
NT2RP2002907	27.84	27.28	39.25	27.93	20.22	19.34	24.71	20.15	30.92				
NT2RP2002925	8.14	12.06	8.92	6.22	5.24	3.39	2.57	2.53	2.32	*	**	-	-
NT2RP2002927	11.04	11.53	9.75	8.5	11.71	5	4.88	3.47	4.87		**		-
NT2RP2002928	14.93	19.65	15.07	19.82	17.04	17.08	11.05	6.88	7.13		*		-
NT2RP2002929	34.38	37.86	32.48	20.14	17.6	22.45	18.17	27.25	31.67	**		-	
NT2RP2002934	25.44	20.87	30.69	18.19	13.85	16.46	17.37	22.76	21.39	*		-	
NT2RP2002939	16.49	24.31	21.25	14.42	15.1	11.79	7.22	8.55	7.99	*	**	-	-
NT2RP2002942	60.99	80.16	86.43	63.29	72.69	51.11	69.34	65.39	67.68				
NT2RP2002954	14.37	21.3	26.97	15.75	10.45	11.22	8.24	9.15	9.35		*		-
NT2RP2002959	11.9	10.85	14.73	7.3	8.01	4.57	5.17	3.69	3.58	*	**	-	-
NT2RP2002974	27.97	23.95	30.02	18.63	11.35	13.46	21.06	14.1	16.2	*	*	-	-
NT2RP2002976	33.37	27.08	30.74	41.03	19.52	40.87	48.18	35.03	46.65		*		+
NT2RP2002979	34.44	28.83	35.03	24.79	13.64	25.53	28.21	33.42	38.67				
NT2RP2002980	56.79	52.53	62.74	67.66	61.62	49.88	36.91	45.4	40.52		*		-
NT2RP2002986	8.8	8.37	8.86	6.06	9.31	3.85	4.83	5.06	6.03		**		-
NT2RP2002987	103.6	100.12	86.59	73.66	56.64	94.83	99.25	107.73	109.15				
NT2RP2002988	13.55	24.45	23.43	8.39	5.16	5.67	6.67	7.13	6.64	*	*	-	-
NT2RP2002993	30.07	31.12	32.86	20.82	20.33	19.14	25.73	28.68	29.96	**		-	
NT2RP2003000	23.19	27.52	36.47	14.21	13.97	11.57	16.09	13.68	17.86	*	*	-	-
NT2RP2003008	20.38	21.66	17.68	30.65	18.58	30.92	20.83	11.54	23.71				
NT2RP2003020	8.4	9.59	8.76	9.59	3.53	4.92	4.04	6.43	6.19		*		-
NT2RP2003032	16.62	21.12	22.97	11.47	10.11	7.97	7.7	9.72	7.64	**	**	-	-
NT2RP2003034	9.72	12.06	10.53	7.37	15.19	4.72	7.75	4.61	8.9				
NT2RP2003042	7.27	6.68	12.91	7.34	5.07	3.54	6.69	5.74	4.38				
NT2RP2003050	41.14	39.77	34.47	22.7	14.89	22.18	30.79	33.73	32.33	**	*	-	-
NT2RP2003060	13.62	10.73	6.38	6.73	19.61	3.28	5.01	3.28	4.49				
NT2RP2003073	11.88	8.02	5.9	7.53	3.76	4.73	2.61	3.98	5.14				
NT2RP2003099	15.8	18.78	12.88	19.36	10.86	16.96	13.15	11.19	10.41				
NT2RP2003108	16.99	10.19	16.94	12.41	6.81	13.81	6.41	10.09	7.95				
NT2RP2003115	140.52	119.44	125.07	149.82	106.25	154.27	145.7	152.43	149.71		*		+
NT2RP2003117	8.58	4.12	8.6	7.48	2.66	5.97	6.92	5.37	6.56				
NT2RP2003121	15.37	11.96	21.6	10.75	8.2	9.97	7.29	7.74	8.68		*		-

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Table 429

NT2RP2003125	148.62	154.21	165.76	136.93	87.76	119.3	202.39	170.18	181.03				
NT2RP2003127	8.19	13.35	12.24	9.29	4.08	4.24	7.52	6.27	6.75				
NT2RP2003129	5.37	4.98	2.74	4.8	1.83	1.5	2.73	2.54	2.23				
NT2RP2003137	9.57	8.81	8.47	10.46	3.57	7.13	10.02	8.73	11.39				
NT2RP2003138	289.53	193.02	256.72	147.84	144.9	131.2	108.58	156.98	150.94	*	*	-	-
NT2RP2003146	1.24	1.09	7.94	3.13	0.31	1.29	1.85	1.99	1.77				
NT2RP2003148	8.05	4.25	16.47	5.03	5.56	4.21	3.03	3.24	3.73				
NT2RP2003150	10.24	5.66	13.18	8.31	3.11	3.88	5.08	3.43	3.42				
NT2RP2003157	3.48	4.11	8.05	5.53	2.9	2.53	3.08	2.08	2.29				
NT2RP2003158	154.65	121	143.84	65.15	86.73	95.34	71.82	47.48	71.44	*	**	-	-
NT2RP2003161	7.49	10.19	13.16	11.02	5.25	6.57	6.09	5.72	4.72		*		-
NT2RP2003164	3.55	3.69	5.64	7.04	3.38	4.04	7.46	5.26	5.34				
NT2RP2003165	12.93	8.52	16.52	10.68	5.85	8.09	3.19	7.18	6.13				
NT2RP2003177	20.41	17.38	32.83	19.51	10.51	7.06	22.73	21.74	21.1				
NT2RP2003179	13.75	8.83	17.7	6.83	5.73	5.2	6.82	13.09	8.84	*		-	
NT2RP2003194	60.36	55.91	80.01	51.34	60.6	65.85	42.59	38.48	56.22				
NT2RP2003206	4.24	5.6	7.88	6.81	4.57	3.96	3.75	3.9	1.77				
NT2RP2003210	9.9	9.36	13.05	7.55	5.04	4.08	4.47	4.65	4.08	*	**	-	-
NT2RP2003227	13.08	17.16	19.16	9.3	7.87	5.3	8.38	6.37	6.65	*	**	-	-
NT2RP2003228	16.97	20.02	17.73	19.68	23.22	23.38	16.96	9.41	24.11				
NT2RP2003230	8.37	4.38	11.24	9.26	4.24	4.38	5.34	6.55	20.33				
NT2RP2003231	19.49	17.75	28.22	19.04	13.83	13.5	4.32	15.06	15.52				
NT2RP2003237	7.53	6.29	14.94	7.53	4.21	4.44	2.72	5.12	9.5				
NT2RP2003239	14.69	12.62	13.82	13.64	7.63	7.59	6.01	11.3	7.74		*		-
NT2RP2003243	18.5	16.09	21.39	14.68	13.35	11.44	13.72	14.6	10.6	*	*	-	-
NT2RP2003265	4.16	3.24	4.88	3.11	1.7	1.76	2.29	2.88	1.56	*	*	-	-
NT2RP2003267	60.51	57	71.61	43.05	41.52	45.26	62.57	46.27	55.1	*		-	
NT2RP2003272	18.93	12.31	21.16	15.62	7.25	9.68	9.71	5.82	7.07		*		-
NT2RP2003277	51.75	42.05	60.1	30.74	24.84	22.69	27.09	34.52	27.77	*	*	-	-
NT2RP2003280	28.6	31.79	33.98	27.16	26.4	22.37	7.26	22.23	17.9	*	*	-	-
NT2RP2003286	5.27	5.54	11.77	5.48	3.75	3.02	2.08	4.89	2.65				
NT2RP2003293	449.62	544.88	531.61	480.84	613.42	591.27	492.68	295.17	642.99				
NT2RP2003295	31.05	28.41	29.77	21.7	14.01	19.1	19.18	18.46	19.51	**	**	-	-
NT2RP2003297	16.92	17.67	19.83	9.38	11.73	7.84	3.24	6.26	6.08	**	**	-	-
NT2RP2003300	2.42	4.36	4.19	5.32	2.8	1.56	2.33	1.69	1.31				
NT2RP2003302	4.27	4.34	3.48	7.02	4.29	2.92	3.56	4.67	4.2				
NT2RP2003307	17.52	15.84	29.67	14.93	9.5	10.4	16.58	17.1	22.41				
NT2RP2003308	7.26	8.66	14.15	6.9	4.51	4.44	3.22	4.76	6.65				
NT2RP2003311	29.64	20.85	41.04	22.79	16.59	15.7	26.2	28.58	26.19				
NT2RP2003329	11.36	11.27	19.3	9.84	10.72	8.3	6.72	6.84	5.55		*		-
NT2RP2003339	44.06	51.39	68.66	63.28	61.45	41.92	35.03	31.79	30.76		*		-
NT2RP2003345	25.41	28.87	30.12	15.65	24.89	17.7	13.62	14.02	13.58	*	**	-	-
NT2RP2003347	8.25	20.81	11.17	7.75	7.09	4.08	5.16	5.37	4.53				
NT2RP2003367	15.71	9.07	15.92	25.01	12.88	13.97	19.6	13.55	17.34				
NT2RP2003369	28.62	21.24	26	8.89	11.95	10.09	4.71	10.13	9.11	**	**	-	-
NT2RP2003383	14.02	11.63	23.31	10.33	7.37	5.29	4.94	12.01	8.63				
NT2RP2003390	5.02	4.43	9.92	6.51	4.16	1.23	2.19	2.28	1.48				
NT2RP2003391	7.9	10.18	14.85	7.86	4.63	3.15	3.6	3.53	4.66		*		-
NT2RP2003393	17.88	10.78	13.47	5.99	12.67	3.97	3.38	3.45	4.48		**		-
NT2RP2003394	86	76.58	96.35	85.96	75.14	69.1	44.7	55.38	51.85		**		-
NT2RP2003401	6.44	4.6	7.19	7.26	3.17	2.2	2.64	2.79	2.35		*		-
NT2RP2003403	18.73	19.58	18.59	16.65	31.07	15.94	9.34	7.98	7.02		**		-
NT2RP2003433	8.13	7.64	13.92	4.56	2.36	2.9	0.77	3.05	2.35	*	*	-	-
NT2RP2003445	11.02	10.94	17.56	8.16	5.02	3.19	3.72	5.83	4.71	*	*	-	-
NT2RP2003446	7.38	5.87	15.32	8.9	3.31	1.64	2.84	3.34	2.61				
NT2RP2003456	14.58	16.09	17.24	7.76	9.78	4.68	6.41	6.61	4.94	**	**	-	-
NT2RP2003466	163.89	136.64	191.26	110.44	140.48	151.43	83.63	87.04	121.39		*		-
NT2RP2003469	5.44	3.7	5.03	4.74	2.31	1.35	2.28	1.42	1.62		**		-
NT2RP2003470	4.83	5.55	5.49	5.65	3.19	3.4	4.42	1.43	3				
NT2RP2003471	12.29	11.22	13.81	11.17	23.08	8.88	5.31	3.9	2.98		**		-
NT2RP2003480	133.45	297.88	151.87	131.22	166.23	117.7	104.84	202.75	202.47				
NT2RP2003495	2.81	3.4	10.31	5.19	1.55	2.41	0.68	1.49	0.7				
NT2RP2003499	5.25	3.3	9.47	3.94	2.15	2.35	2.44	6.25	5.89				
NT2RP2003505	1.66	1.94	6.72	4.41	2.46	0.11	0.21	3	0				

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Table 430

NT2RP2003506	18.91	15.11	21.41	10.64	13.4	7.04	4.15	4.83	3.94	*	**	-	-
NT2RP2003511	12.05	3.9	4.64	8.42	8.48	3	2.22	2.49	1.23				
NT2RP2003513	5.02	4.48	4.09	4.53	1.64	2.04	2.58	1.55	3.7		*		-
NT2RP2003517	3.09	1.94	2.24	4.01	1.27	1.81	1.81	0.62	1.53				
NT2RP2003522	5.79	5.52	8.11	4.61	3.87	1.76	1.31	4.96	5.44				
NT2RP2003525	12.34	13.08	16.44	6.02	5.34	4.08	6.04	6.6	5.02	**	**	-	-
NT2RP2003533	88.01	167.21	169.95	95.54	157.31	89.62	178.82	120.18	151.89				
NT2RP2003541	3.67	3.34	5.25	3.35	1.69	1.26	1.11	0.78	0.47		**		-
NT2RP2003543	6.02	7.31	6.9	4.81	3.89	1.42	3.96	1.71	3.06	*	**	-	-
NT2RP2003545	16.66	28.91	37	10.57	5.83	7.38	9	7.02	10.57	*	*	-	-
NT2RP2003559	24.73	30.59	37.42	18.05	13.28	13.04	17.81	5.8	6.39	*	*	-	-
NT2RP2003564	4.21	3.5	2.84	5.11	2.21	2.76	1.47	1.11	1.54		**		-
NT2RP2003565	5.56	6.05	9.75	8.3	2.97	4.12	3.13	4.62	3.34				
NT2RP2003567	52.47	49.61	31.71	25.62	16.56	16.12	8.17	19.23	14.83	*	*	-	-
NT2RP2003575	228.18	422	264.34	79.35	234.74	114.07	248.45	399.29	319.2				
NT2RP2003576	12.51	13.48	14.93	11.41	10.35	7.47	9.35	12.38	11.58	*		-	
NT2RP2003579	6.35	14.72	8.69	5.77	5	3.85	5.14	3.96	3.9				
NT2RP2003581	5.18	8.39	5.74	5.34	1.72	1.57	1.66	0.89	1.73		**		-
NT2RP2003587	5.23	4.31	3.93	4.85	1.48	2.81	2.91	3.12	2.6		*		-
NT2RP2003590	10.26	7.56	7.31	8.22	4.4	10.25	8.81	5.02	6.24				
NT2RP2003593	30.36	26.83	29	16.89	17.04	17.86	10.43	21.71	15.35	**	*	-	-
NT2RP2003596	9.32	8.79	11.25	13.55	9.73	9.49	8.79	14.74	9.47				
NT2RP2003599	23.27	13.17	35	8.05	27.81	6.94	3.86	4	10.53				
NT2RP2003600	19.86	30.4	31.86	22.5	9.14	19.7	15.99	13.53	9.08		*		-
NT2RP2003604	5.88	9.89	7.47	5.4	1.89	1.85	3.39	3.16	2.76	*	*	-	-
NT2RP2003629	8.19	7.7	5.26	5.58	3.64	2.51	3.1	3.51	2.87		*		-
NT2RP2003630	4.6	3.1	1.8	4.67	0.47	1.48	1.43	1.9	2.02				
NT2RP2003643	14.26	14.44	12.75	14.01	7.67	9.12	19.42	10.04	13.07				
NT2RP2003655	7.62	6.24	7.73	7.33	2.44	6.8	2.97	5.19	4.57		*		-
NT2RP2003664	8.96	13.57	11.03	11.23	17.02	7.98	3.52	3.83	3.73		**		-
NT2RP2003668	5.83	2.7	3.35	6.14	1.92	4.61	2.43	9.15	4.25				
NT2RP2003687	2.45	2.75	3.32	4.63	0.64	2.77	0.71	2.3	0.91				
NT2RP2003691	2.86	0.41	1.55	4.29	1.06	2.07	1.69	2.35	1.51				
NT2RP2003702	7.99	4.44	8.03	9.77	1.89	6.56	5.26	5.52	3.42				
NT2RP2003704	6.11	9.87	8.33	7.33	6.55	3.79	6.43	2.95	5.24				
NT2RP2003706	7.36	9.13	9.09	6.95	3.88	3.8	6.16	3.16	4.56	*	*	-	-
NT2RP2003713	10.55	5.71	14.4	8.75	4.92	4.56	5.34	3.61	4.08				
NT2RP2003714	8.27	4.37	12.63	8.63	2.38	6.34	8.02	5.56	6.23				
NT2RP2003727	13.72	9.91	16.65	14.5	8.49	5.28	4.4	3.92	5.54		*		-
NT2RP2003737	5.45	5.17	12.85	7.76	3.42	3.25	3.61	5.76	7.42				
NT2RP2003751	4.58	1.12	4.62	4.58	0.42	0.71	2.16	1.87	0.69				
NT2RP2003760	5.71	6.37	7.89	7.16	2.44	3.65	5.58	4.39	4.01				
NT2RP2003764	4.38	3.82	3.93	5.42	1.13	2.52	3.39	1.74	2.45		*		-
NT2RP2003769	20.81	10.06	18.85	16.88	9.37	7.83	5.73	10.32	7.17				
NT2RP2003770	46.73	23.49	36.27	27.58	17.68	15.16	13.53	17.82	25.92				
NT2RP2003777	15.17	10.4	15.63	9.4	5.35	5.3	5.51	8.22	8.17	*	*	-	-
NT2RP2003781	85.09	53.2	80.23	44.9	32.89	44.6	88.34	75.84	75.38	*		-	
NT2RP2003785	11.62	18.04	20.61	13.78	15.2	6.96	6.32	9.84	5.9		*		-
NT2RP2003793	16.4	16.91	28.84	17.84	16.4	19.5	8.6	5.86	10.58		*		-
NT2RP2003806	22.61	30.87	30.72	19.98	15.24	17.95	21.46	20.85	31.8	*		-	
NT2RP2003825	121.72	69.01	127.36	108.65	103.08	122.02	106.86	101.92	114.26				
NT2RP2003840	11.66	9.2	14.49	9.94	6.01	4.99	5.06	8.29	6.32		*		-
NT2RP2003857	12.37	17.33	20.12	13.2	12.38	5.39	3.92	13.14	19.37				
NT2RP2003859	19.27	8.66	21.11	12.54	7.05	8.25	8.14	9.73	13.41				
NT2RP2003871	24.21	21.74	19.35	11.95	9.6	10.67	5.81	8.41	8.75	**	**	-	-
NT2RP2003876	10.53	11.98	18.66	19.02	25.1	11.05	7.68	10.36	8.8				
NT2RP2003878	8.32	9.1	10.32	8.36	3.76	3.6	4.02	3.95	3.32		**		-
NT2RP2003885	6.08	8.46	6.77	5.72	4.33	2.2	4.11	3.32	4.21		*		-
NT2RP2003898	16.47	22.78	20.73	12.55	8.77	11.94	7.99	8.27	7.33	*	**	-	-
NT2RP2003902	21.99	10.54	20.36	16.69	8	10.58	8.28	15.68	15.89				
NT2RP2003912	35.16	73.65	32.26	21.86	23.82	12.49	13.87	18.46	19.33				
NT2RP2003931	16.31	15.84	40.63	15.98	12.61	14.09	15.19	20.43	45.95				
NT2RP2003940	26.29	28.19	28.81	19.73	11.64	14	20.12	28.2	22.66	**		-	
NT2RP2003950	10.42	7.47	13.08	10.4	5.75	5.62	6.83	8.37	6.11				

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Table 431

NT2RP2003952	8.61	6.4	10.47	5.99	3.42	3.14	3.11	4	4.05	*	*	-	-
NT2RP2003968	14.45	22.39	24.81	11.6	25.12	6.38	6.57	9.01	14.39				
NT2RP2003976	33.5	36.02	32.14	28.15	26.29	22.25	25.49	23.11	18.45	*	**	-	-
NT2RP2003981	10.38	7.73	15.47	7.98	3.66	7.9	3.93	9.3	6.45				
NT2RP2003984	21.86	17.33	21.82	17.29	10	7.7	4.79	10.99	18.59				
NT2RP2003986	29.04	20.99	42.5	17.22	10.08	14.95	20.31	27.16	19.47				
NT2RP2003988	17.98	13.51	22.96	15.07	9.71	10.14	10.31	12.25	15.8				
NT2RP2004013	76.9	66.49	68.74	48.94	44.57	34.09	28.41	25.31	32.75	**	**	-	-
NT2RP2004014	12.05	10.78	9.86	7.34	4.69	5.32	4.75	6.66	7.06	**	**	-	-
NT2RP2004035	38.11	34.32	48.47	33.97	30.52	34.54	23.89	26.94	32.83				
NT2RP2004041	15.68	9.6	13.65	12.24	6.88	6.29	9.46	7.39	4.47				
NT2RP2004042	10.47	6.9	14.24	8.26	4.18	4.2	3.12	8.29	6.46				
NT2RP2004049	50.08	29.35	58.86	54.03	47.21	47.08	23.48	30.4	35.04				
NT2RP2004060	14.43	11.83	19.24	13.07	7.66	8.82	6.25	9.01	6.7		*		-
NT2RP2004066	9.22	7.65	15.12	7.14	3.11	3.37	2.62	3.51	3.15		*		-
NT2RP2004069	13.07	11	19.34	9.29	5.59	3.82	4.85	6.14	4.78		*		-
NT2RP2004076	7.23	8.97	8.94	6.15	5.2	2.62	3.55	3.66	4.01	*	**	-	-
NT2RP2004080	16.76	19.32	21.22	10.81	7.94	4.93	7.71	6.49	6.54	**	**	-	-
NT2RP2004081	12.13	9.06	12.95	7.67	4.89	5.2	4.76	5.29	3.41	*	**	-	-
NT2RP2004098	14.04	9.1	18.6	7.17	4.55	6.94	5.74	6.96	7.08				
NT2RP2004108	15	13.48	22.62	10.06	6.21	6.99	5.4	7.73	10.17	*	*	-	-
NT2RP2004124	8.21	9.75	17.19	8.66	5.64	4.42	4.13	6.1	2.63				
NT2RP2004130	14.54	18.18	16.71	14.91	10.54	10.38	6.64	6.32	8.03		**		-
NT2RP2004133	9.17	7.74	14.55	6.02	4.47	1.66	3.8	2.83	1.86		*		-
NT2RP2004141	13.91	6.7	8.65	9.25	5.97	4.12	2.68	2.87	3.2		*		-
NT2RP2004142	20.24	20.66	23.15	12.58	8.99	0.11	7.76	8.1	8.83	*	**	-	-
NT2RP2004152	12.94	17.34	28.22	13.04	12.79	7.85	8.66	8.13	4.02				
NT2RP2004165	23.06	20.1	27.11	14.41	8.19	16.16	10.91	12.82	15.14	*	*	-	-
NT2RP2004170	14.84	22.1	21.27	11.56	5.42	12.52	7.64	14.97	10.1	*		-	
NT2RP2004172	11.82	8.43	19.13	9.78	6.86	6.4	5.08	5.49	3.29				
NT2RP2004176	16.04	24.68	27.17	14.08	13.85	12.56	15.42	21.18	13.53				
NT2RP2004179	11.06	11.88	18.99	6.12	3.68	3.62	3.12	4.46	3.04	*	*	-	-
NT2RP2004187	10.62	14.3	17.05	10.83	6.49	6	6.3	3.3	5.65		*		-
NT2RP2004190	11.44	13.08	11.65	11.65	16.98	5.99	14.27	4.91	8.09				
NT2RP2004194	34.23	32.85	35.34	19.96	14.64	15.16	22.5	12.25	14.92	**	**	-	-
NT2RP2004196	30.83	39.33	27.33	12.84	5.98	11.23	10.98	13.1	14.08	**	**	-	-
NT2RP2004205	29.01	29.84	37.62	20.1	10.4	15.74	17.25	16.98	24.08	*	*	-	-
NT2RP2004207	8.99	13.88	16.49	8.05	7.02	4.72	8.6	7.78	25.16				
NT2RP2004226	17.66	11.75	16.67	11.25	9.6	5.13	9.93	6.52	8.04		*		-
NT2RP2004232	9.38	7.39	12.33	6.45	7.37	3.57	6.49	3.42	8.98				
NT2RP2004239	9.12	12.33	10.22	7.52	5.19	3.55	2.71	5.07	3.29	*	**	-	-
NT2RP2004240	34.67	45.84	33.56	20.39	18.64	6.67	14.35	6.97	4.81	*	**	-	-
NT2RP2004242	15.64	15.83	16.65	14.76	9.29	9.76	10.22	6.01	6.98		**		-
NT2RP2004245	7.49	8.21	10.79	7.33	2.04	4.45	4.33	4.59	4.95		*		-
NT2RP2004270	62.73	47.21	68.41	46.4	33.04	45.75	50.52	75.49	70.49				
NT2RP2004300	12.51	8.53	13.1	8.54	9.07	5.04	6.79	9.38	7.79				
NT2RP2004304	16.04	25.81	28.38	10.74	8.89	6.86	7.57	8.7	9.4	*	*	-	-
NT2RP2004313	5.32	5.55	8.05	4.79	1.11	1.27	2.98	2.46	2.35		*		-
NT2RP2004316	7.59	19.66	19.22	7.37	4.16	2.63	3.4	2.3	5.68		*		-
NT2RP2004321	11.35	10.01	12.72	6.18	1.74	2.16	3.62	2.37	4.34	**	**	-	-
NT2RP2004336	6.56	6.01	5.01	7.15	3.83	3.55	3.86	1.85	3.64		*		-
NT2RP2004339	86.87	54.65	64.97	50.21	27.02	70.75	73.53	111.22	98.32				
NT2RP2004347	9.56	12.29	15.81	9.78	3.94	5.75	4.47	6.18	9.27				
NT2RP2004364	17.82	15.18	19.6	11.98	7.62	12.3	9.63	15.21	13.78	*		-	
NT2RP2004365	16.43	16.15	23.6	8.67	8.61	4.88	6.23	5.81	4.59	*	**	-	-
NT2RP2004366	6.71	10.58	9.59	7.66	3.53	5.17	5.46	3.22	3.29		*		-
NT2RP2004373	12.26	11.21	11.74	7.26	2.71	4.58	3.35	3.56	4.51	**	**	-	-
NT2RP2004375	63.47	77.52	81.72	36.96	16.48	21.89	34.46	29.81	18.56	**	**	-	-
NT2RP2004388	11.31	16.36	12.26	9.91	2.21	4.95	5.82	4.38	4.02	*	**	-	-
NT2RP2004392	57.13	31.73	43.78	20.38	16.25	19.24	10.86	16.27	14.58	*	*	-	-
NT2RP2004396	13.42	9.2	11.06	9.69	3.89	7.39	5.67	7.43	7.76		*		-
NT2RP2004399	25.77	19.74	26.11	15.91	12.56	15.11	9.21	12.21	10.01	*	**	-	-
NT2RP2004400	10.29	9.25	9.33	9.9	4.17	8.44	7.31	8.61	9.43				
NT2RP2004404	142.91	126.47	123.47	87.01	85.43	109.26	171.94	127.81	174.94	*		-	

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Table 432

NT2RP2004410	39.53	65.74	46.52	39.11	16.74	16.36	21.28	23.23	25.45		*		-
NT2RP2004412	14.74	10.36	20.72	26.06	1.96	8.17	8.89	4.91	6.36				
NT2RP2004414	8.26	7	7.21	7.75	3.36	2.32	8.71	6.3	5.47				
NT2RP2004425	10.2	6.28	19.09	7.43	2.9	4.39	7.1	5.14	4.24				
NT2RP2004447	7.9	4.2	15.6	7.23	1.76	4.51	4.43	8.04	6.17				
NT2RP2004463	53.44	48.94	45.23	51.07	39.96	24.66	38.74	19.02	17.11		*		-
NT2RP2004476	18.45	12.59	23.94	14.93	16.73	11.7	16.21	16.49	14.59				
NT2RP2004488	10.21	10.37	13.58	8.53	5.46	7.65	8.97	6.18	4.15	*	*	-	-
NT2RP2004490	6.88	9.48	11.96	10.41	4.06	3.06	6.4	5.15	3.37				
NT2RP2004495	59.84	40.86	52.11	47.08	29.44	39.52	53.9	45.74	40.44				
NT2RP2004512	17.42	8.07	18.38	11.03	4.08	6.19	1.75	5.77	3.87		*		-
NT2RP2004523	26.61	22.99	26.09	20.55	9.56	18.73	12.96	22.93	30.09				
NT2RP2004524	21.22	18.85	29.36	17.14	12.55	10.77	11.27	10.59	14.51		*		-
NT2RP2004536	39.58	17.04	37.57	26.29	26.05	14.38	14.91	28.86	19.32				
NT2RP2004538	145.51	113.79	134.59	95.27	89.81	81.41	118.33	103.7	132.33	*		-	
NT2RP2004548	21.33	25.87	20.88	16.6	11.36	9.17	14.62	15.2	15	*	**	-	-
NT2RP2004551	8.55	11.05	18.95	8.38	5.63	4.59	5.77	5.04	6.54				
NT2RP2004556	107.44	116.09	115.34	100.64	83.01	68.21	138.61	66.34	73.2	*		-	
NT2RP2004568	25.54	15.99	32.04	18.77	7.42	18.63	9.21	19.06	44.48				
NT2RP2004580	28.48	22.84	30.46	23.04	12.01	15.3	24.34	30.63	24.49				
NT2RP2004585	104.19	75.97	102.59	102.16	96.71	82.97	64.51	65.78	63.06		*		-
NT2RP2004587	7.64	7.71	10.73	6.38	2.94	4.03	2.08	3.66	11.64	*		-	
NT2RP2004594	9.49	13.7	13.53	10.94	10.06	5.96	7.18	7.17	14.25				
NT2RP2004600	11.79	11.86	12.42	9.8	6.39	8.89	9.84	7.14	9.81	*	*	-	-
NT2RP2004602	16.85	24.33	21.89	13.29	12.49	8.02	12.27	7.59	7.04	*	*	-	-
NT2RP2004606	282.85	252.35	268.41	181.43	249.55	245.26	257.06	189.04	158.13				
NT2RP2004614	9.31	7.04	11.06	6.07	2.67	4.48	3.52	3.61	6.4	*	*	-	-
NT2RP2004648	12.5	37.87	41.62	14.38	8.31	11.65	10.13	8.24	22.59				
NT2RP2004655	27.02	40.5	41.28	26.01	23.69	13	4.9	10	13.87		**		-
NT2RP2004664	12.3	12.14	15.06	9.64	6.17	5.52	2.65	4.39	2.54	*	**	-	-
NT2RP2004670	9.81	11.79	9.6	6.17	5.86	2.45	3.26	4.14	2.42	*	**	-	-
NT2RP2004675	22.26	31.4	25.45	19.55	10.99	11.73	17.4	17	31.58	*		-	
NT2RP2004681	11.82	17.49	14.89	8.26	5.82	3.58	5.62	7.61	5.68	*	**	-	-
NT2RP2004689	5.34	26.14	16.38	15.38	9.9	10.44	10.84	15.98	14.64				
NT2RP2004709	38.28	22.19	35.75	22.32	11.28	19.42	7.33	20.31	16.27				
NT2RP2004710	23.78	32.41	33.69	19.19	16.47	14	10.16	17.13	21.44	*	*	-	-
NT2RP2004721	16.3	9.83	18.51	7.64	2.48	4.31	3.84	6.3	2.86	*	*	-	-
NT2RP2004736	12.51	12.2	14.69	12.94	8.12	6.27	5.93	10.36	6.34		*		-
NT2RP2004743	18.86	18.19	16.11	11.52	9.54	6.56	6.31	8.72	9.61	**	**	-	-
NT2RP2004750	59.2	56.12	63.52	47.6	43.74	38.38	59.22	63.07	62.81	**		-	
NT2RP2004755	27.3	33.26	34.09	17.59	21.76	19.12	17.05	12.23	8.96	**	**	-	-
NT2RP2004767	16.81	19.28	18.07	14.61	10.15	10.32	11.83	8.67	9.96	*	**	-	-
NT2RP2004768	39.27	17.22	28.44	49.02	23.23	30.46	23.63	20.93	17.76				
NT2RP2004775	10.4	6.35	15.81	7.59	3.37	4.94	1.86	3.35	3.03		*		-
NT2RP2004791	35.3	37.93	43.25	33.95	20.1	16.04	17.4	29.11	27.1		*		-
NT2RP2004794	54.46	52.25	59.56	37.23	24.39	16.04	14.21	17.04	17.83	*	**	-	-
NT2RP2004795	16.82	13.04	16.28	12.97	8.52	3.96	6.33	6.26	8.64		**		-
NT2RP2004799	16.76	14.17	14.52	9.03	7.47	5.55	2.73	2.76	3.58	**	**	-	-
NT2RP2004802	42.99	46.43	41.16	46.78	39.32	30.76	28.53	29.92	38.26		*		-
NT2RP2004810	18.3	18.68	17.35	9.03	6.57	4.19	8.85	4.21	4.39	**	**	-	-
NT2RP2004816	30.61	34.82	43.2	16.85	15.68	3.1	5.7	11.84	0.57	*	**	-	-
NT2RP2004837	55.01	32.88	59.21	31.78	19.92	27.08	12.99	11.53	9.41		*		-
NT2RP2004841	12.28	19.6	17.04	13.83	8.03	5.66	4.26	5.92	8.44		*		-
NT2RP2004847	56	45.24	59.59	31.54	30.59	31.44	43.02	39.63	29.66	**		-	
NT2RP2004861	6.61	6.78	10.74	6.21	2.52	2.33	3.42	5.23	3.33				
NT2RP2004897	8.06	8.52	10.02	7.86	4.8	3.34	2.33	3.07	4.66		**		-
NT2RP2004932	11.96	10.46	13.81	9.34	4.73	6.48	4.87	3.86	6	*	**	-	-
NT2RP2004933	6.78	7.42	14.62	6.21	3.1	2.23	3.41	1.97	1.54		*		-
NT2RP2004936	9.66	18.67	21.72	10.34	4.39	7.29	2.62	3.9	3.25		*		-
NT2RP2004951	8.57	7.11	15.72	9.26	2.32	5.42	3.11	6.13	4.04				
NT2RP2004958	12.5	13.69	22.18	6.53	5.09	6.63	3.92	5.67	5.43	*	*	-	-
NT2RP2004961	15.97	14.64	23.99	12.05	7.35	8.71	10.28	8.72	8.04		*		-
NT2RP2004962	15.99	15.58	20.13	13.9	10.21	9.93	9.78	10.65	9.69	*	**	-	-
NT2RP2004966	6.94	8.72	7.55	5.31	3.88	2.7	4.34	2.81	2.89	*	**	-	-

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Table 433

NT2RP2004967	18.8	14.08	15.99	13.12	6.04	9.98	11.43	12.91	9.85		*		-
NT2RP2004974	8.02	8.78	7.74	5.74	3.27	3.73	5.44	2.35	2.1	**	*	-	-
NT2RP2004978	14.12	27.31	13.7	11.96	4.65	6.79	4.16	9.57	4.35				
NT2RP2004982	4.88	6.54	10.22	4.28	1.48	0.85	1.99	1	1.83		*		-
NT2RP2004985	209.85	195.75	215.75	166.58	153.94	208.41	198.37	224.84	192.82				
NT2RP2004999	16.04	12.97	26.42	17.44	8.41	10.32	9.65	18.31	9.11				
NT2RP2005000	9.18	10.25	11.07	6.99	2.87	3.26	5.46	4.95	3.42	*	**	-	-
NT2RP2005001	18.08	20.79	40.06	15.62	11.69	13.08	12.25	15.19	13.27				
NT2RP2005003	15.88	14.42	15.05	11.32	5.53	6.52	11.83	11.19	8.75	*	*	-	-
NT2RP2005012	40.61	57.66	43.61	20.05	11.76	16.65	21.02	13.16	20.53	**	**	-	-
NT2RP2005018	6.29	10.32	12.32	7.2	3.34	4.91	3.54	5.22	4.18		*		-
NT2RP2005020	138.98	109.02	105.29	97.72	59.61	79.54	117.66	175.16	138.64				
NT2RP2005022	8.77	8.01	12.34	8.19	7.74	5.07	4.96	7.16	9.74				
NT2RP2005027	53.46	62.9	53.33	58.43	50.24	56.5	33.74	38.11	31.82		**		-
NT2RP2005031	6.85	8.81	9.58	5.73	4.02	3.36	3.46	3.48	3.14	*	**	-	-
NT2RP2005037	16.82	18.46	19.47	6.47	4.36	2.93	2.65	3.66	6.14	**	**	-	-
NT2RP2005038	6.96	8.98	11.09	7.2	2.46	3.49	4.34	2.45	1.1		*		-
NT2RP2005048	39.21	28.46	29.89	31.24	22.21	43.14	32.34	46.11	37.29				
NT2RP2005069	79.3	47.14	64.37	36.64	18.08	20.34	23.96	33.08	29.72	*	*	-	-
NT2RP2005073	67.78	54.66	62.54	70.16	48.08	81.7	55.95	55.76	57.19				
NT2RP2005097	10.25	7.51	14.59	6.49	1.21	4.7	3.75	2.8	2.35		*		-
NT2RP2005108	13.57	11.63	13.11	6.87	5.69	6.68	5.31	6.56	5.73	**	**	-	-
NT2RP2005116	11.75	10.87	12.14	10.24	4.17	4.29	7.43	5.88	6.2		**		-
NT2RP2005126	21.43	28.84	28.25	14.77	6.89	5.64	7.77	5.68	5.93	*	**	-	-
NT2RP2005135	10.21	11.92	11.29	12.06	3.02	7.4	9.29	7.72	6.92		*		-
NT2RP2005139	4.47	5.9	6.41	5.94	3.02	9.46	4.16	4.52	4.09				
NT2RP2005140	10.93	7.52	7.44	7.58	3.55	5.44	3	4.22	2.26		*		-
NT2RP2005144	13.73	10.54	13.89	8.29	4.49	7.83	1.84	3.98	2.4	*	**	-	-
NT2RP2005147	22.69	15.06	21.74	11.07	5.61	11.36	5.53	13.64	8.82	*	*	-	-
NT2RP2005148	19.34	14.98	12.3	16.32	7.5	14.47	18.68	18.99	24				
NT2RP2005159	9.52	7.06	9.83	13.34	5.14	7.92	4.36	3.56	6.05		*		-
NT2RP2005162	14.54	12.5	16.31	14.53	7.94	8	8.72	9.34	7.02		**		-
NT2RP2005163	25.5	37.52	33.86	15.82	13.92	18.66	24.95	23.28	21.32	*		-	
NT2RP2005168	10.58	6.62	14.16	11.05	5.89	4.43	4.83	6.74	4.36				
NT2RP2005181	4.05	2.99	8.75	6.74	2.11	1.29	1.74	3.19	2.03				
NT2RP2005204	14.87	10.24	20.73	15.12	7.06	10.51	11.01	6.88	10.24				
NT2RP2005219	24.24	19.15	32.19	26.01	12.29	15.28	21.03	18.69	23.06				
NT2RP2005227	12.24	9.75	17.91	17.67	5.27	7.45	11.51	12.06	11.25				
NT2RP2005237	103.35	89.54	103.29	128.64	70.44	96.83	81.16	75.84	83.42		*		-
NT2RP2005239	4.86	6.22	9.52	8.57	2.23	3.55	3.5	4.01	4.35				
NT2RP2005247	22.45	26.01	32.27	32.43	14.24	19.04	34.79	31.96	33.52				
NT2RP2005254	36.5	15.86	25.1	17.04	11.36	15.24	5.51	13.65	13.69				
NT2RP2005270	25.5	13.21	29.5	13.51	9.93	13.53	11.24	14.21	22.67				
NT2RP2005276	40.6	21.43	40.17	20.18	14.43	16.86	10.58	8.43	8.36		*		-
NT2RP2005287	16.9	10.22	25.14	13.6	9.12	7.29	8.33	9.76	8.8				
NT2RP2005288	6.35	8.09	8.85	7.18	3.2	3.43	4.54	4.39	3.3		*		-
NT2RP2005289	19.76	15.26	21.43	14.2	10.57	10.92	15.53	14.93	15.73	*		-	
NT2RP2005293	9.79	11.07	10.95	8.57	5.47	3.14	6.98	5.79	5.74	*	**	-	-
NT2RP2005315	15.84	21	21.65	20.97	8.72	12.4	13.48	9.21	11.44		*		-
NT2RP2005322	33.55	31.7	65.28	25.82	25.53	26.43	14.38	22.11	31.46				
NT2RP2005325	54.2	44	55.99	38.68	30.92	29.07	18.94	27.07	30.65	*	**	-	-
NT2RP2005336	20.36	12.98	27.96	11.35	7.87	9.01	10.99	13.9	14.17				
NT2RP2005343	12.61	22.98	14.15	9.9	5.77	8.7	7.81	10.19	10.12				
NT2RP2005344	6.04	8.8	10.41	6.82	3.18	3.71	4.76	3.86	3.88		*		-
NT2RP2005347	7.59	13.3	8.99	7.33	4.35	4.03	4.9	3.27	3.77		*		-
NT2RP2005354	41.58	40.59	43.7	31.3	21.57	29.41	26.2	24.6	22.64	**	**	-	-
NT2RP2005358	43.39	32.77	43.03	61.06	32.41	50.49	63.9	54.2	58.54		*		+
NT2RP2005360	11.79	10	18.74	11.01	6.71	7.24	3.72	6.21	9.76				
NT2RP2005378	29.24	21.46	29.8	11.99	9.12	7.48	6.73	9.68	15.33	**	*	-	-
NT2RP2005391	8.87	18.64	25.48	15.21	9.76	9	4.05	7.34	6.04				
NT2RP2005393	18.88	11.72	17.99	12.44	7.52	10.75	12.61	18.43	12.16				
NT2RP2005407	7.79	10.99	12.03	9.14	5.76	6.4	4.56	6.12	6.26		*		-
NT2RP2005419	14.03	13.17	13.95	13.78	13.3	12.37	11.42	9.28	10.02		**		-
NT2RP2005425	22.13	23.63	29.77	16.49	17.86	16.5	26.07	23.18	23.95	*		-	

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Table 434

NT2RP2005429	20.77	21.25	24.75	28.87	19.9	22.9	31.5	41.11	27.5				
NT2RP2005436	21.72	21.01	36.27	15.82	10.49	11.17	6.19	10.76	15.31				
NT2RP2005441	12.34	10.42	16.43	6.82	3.95	2.88	3.88	5.58	7.88	*	*	-	-
NT2RP2005442	100.99	76.34	97.05	85.22	107.34	64.16	56.06	96.44	76.81				
NT2RP2005444	44.56	42.84	50.52	45	41.48	37.39	33.32	34.33	40.3		*		-
NT2RP2005453	6.3	5.27	7.3	6.26	2.81	2.81	2.27	2.79	2.65		**		-
NT2RP2005457	65.08	106.4	103.3	51.25	79.76	59.93	40.37	56.9	47.82		*		-
NT2RP2005458	19.63	18.76	13.48	12.24	12.61	6.33	8.23	12.39	11.01		*		-
NT2RP2005463	26.71	23.66	25.36	21.35	13.39	12.75	11.08	11.67	8.93	*	**	-	-
NT2RP2005464	28.8	25.9	35.07	16.26	12.23	8.38	4.05	11.36	13.81	**	**	-	-
NT2RP2005465	8.44	13.41	18.06	10.55	9.11	6.34	5.69	6.77	5.88				
NT2RP2005472	156.47	127.25	179.85	146.2	122.26	139.88	141.98	194.05	159				
NT2RP2005476	18.49	17.23	18.61	16.08	8.51	7.62	10.76	9.58	6.82		**		-
NT2RP2005490	38.19	48.01	41.98	41.4	60.4	46.27	36.8	25.85	27.98		*		-
NT2RP2005491	79.97	62.21	87.46	43.7	46.69	33.15	42.26	41.55	39.38	*	**	-	-
NT2RP2005495	8.67	12.67	12.73	8.05	5.23	3.12	3.29	2.22	4.63	*	**	-	-
NT2RP2005496	40.82	33.68	40.13	35.53	16.36	22.99	49.27	41.88	52.93				
NT2RP2005498	14.64	10.07	20.28	8.15	3.71	0.94	3.15	5.06	7.24	*	*	-	-
NT2RP2005501	15.01	11.26	15.06	10.4	6.02	5.78	5.37	7.88	6.8	*	**	-	-
NT2RP2005506	386.46	291.76	402.21	469.63	426.17	208.66	248.04	333.44	241.6				
NT2RP2005509	12.93	15.67	24.29	8.78	9.8	9.01	11.69	14.68	14.73				
NT2RP2005514	15.12	18.77	16.43	9.09	7.1	7.44	5.07	6.13	3.95	**	**	-	-
NT2RP2005520	125.71	88	119.54	107.31	84.59	104.73	102.45	122.23	104.75				
NT2RP2005525	11.61	19.18	16.45	11.91	8.22	5.77	3.77	4.63	4.84		**		-
NT2RP2005531	6.49	2.54	4.37	5.65	2.65	0.74	1.72	1.38	1.4				
NT2RP2005535	28.78	24.33	27.3	18.42	7.97	16.95	13.78	20.87	16.38	*	*	-	-
NT2RP2005539	7.33	11.94	18.75	8.51	6.39	4.26	3.51	3.63	4.88				
NT2RP2005540	16.33	11.75	18.94	9.77	17.11	5.41	9.79	8.14	4.41		*		-
NT2RP2005541	14.69	11.15	19.91	13.02	7.16	8.12	7.95	8.57	7		*		-
NT2RP2005549	11.12	11.63	18.04	9.08	7.83	5.49	4.23	4.44	5.21		*		-
NT2RP2005555	16.74	21.24	18.63	10.59	10.43	7.67	9.05	5.08	3.67	**	**	-	-
NT2RP2005557	15.1	14.02	12.36	10.06	7.31	4.94	4.63	4.36	4.73	*	**	-	-
NT2RP2005581	28.08	26.29	29.21	26.59	10.92	19.41	31.86	21.24	23.29				
NT2RP2005586	16.13	21.05	17.82	8.84	4.94	6.39	4.6	7.07	6.9	**	**	-	-
NT2RP2005597	6.89	6.97	9.77	7.01	1.89	3.66	2.71	4.02	1.82		*		-
NT2RP2005600	10.61	7.34	12.5	8.41	8.29	5.16	5.14	5.97	3.47		*		-
NT2RP2005605	53.68	52.91	55.5	30.27	27.97	29.06	25.09	21.21	26.25	**	**	-	-
NT2RP2005614	9.49	10.07	16.9	6.5	3.69	4.19	2.85	3.64	2.63	*	*	-	-
NT2RP2005620	17.66	10.99	8.05	7.1	2.87	3.18	7.89	3.09	3.37				
NT2RP2005622	16.16	16.55	15.71	9.98	5.85	5.98	5.01	2.43	3.54	**	**	-	-
NT2RP2005632	24.79	21.59	16.99	24.01	11.37	16.72	22.78	10.85	12.69				
NT2RP2005635	41.82	31.3	47.35	47.22	30.84	66.01	30.58	31.82	30.82				
NT2RP2005637	8.32	23.19	12.21	8.57	5.9	4.47	3.6	7.75	5.54				
NT2RP2005640	15.46	12.6	16.31	14.33	9.36	13.4	14.45	17.32	12.67				
NT2RP2005645	23.93	18.08	21.54	10.6	8.02	9.84	11.24	9.09	9.15	**	**	-	-
NT2RP2005651	27.47	30.93	34.21	15.98	10.8	18.12	23.48	20.74	24.88	**	*	-	-
NT2RP2005654	13.13	10.24	14.43	6.36	4.26	2.41	3.56	3.27	5.28	**	**	-	-
NT2RP2005666	12.61	72.48	13.27	7.56	5.9	4.42	7.43	6.32	9.59				
NT2RP2005669	15.23	15	15.44	12.86	8.17	11.55	8.81	7.49	8.17	*	**	-	-
NT2RP2005670	7.59	11.17	16.69	7.09	6.37	6.24	3.98	5.41	8.38				
NT2RP2005671	8.66	9.38	12.5	6.17	4.27	6.41	3.39	7.42	4.35	*	*	-	-
NT2RP2005675	53.41	58.69	56.21	73.47	47.08	88.08	46.13	47.46	45.27		**		-
NT2RP2005683	12.5	14.86	22.54	12.03	8.9	11.13	12.51	11.13	11				
NT2RP2005690	7.16	9.78	9.15	7.31	2.58	3.76	6.01	4.75	5.81		*		-
NT2RP2005694	13.45	13.78	12.27	8.68	4.9	4.46	6.63	6.81	8.01	**	**	-	-
NT2RP2005701	21.29	27.54	24.8	13.54	7.14	7.23	9.96	8.67	7.38	**	**	-	-
NT2RP2005712	5.67	6.5	6.73	7.41	2.31	3.04	4.59	2.86	2.66		*		-
NT2RP2005719	17.92	12.64	12.02	8.92	5.92	13.08	4.64	11.29	9.06				
NT2RP2005722	24.17	15.94	25.68	22.5	8.47	9.89	8.38	12.95	9.48		*		-
NT2RP2005723	11.76	19.91	11.37	8.9	4.43	7.12	5.8	6.31	6.59		*		-
NT2RP2005726	13.16	8.51	18.51	13.17	7.93	10.58	7.85	8.96	10.35				
NT2RP2005729	20.35	17.21	20.34	11.64	9.52	5.78	12.25	8.44	10.44	**	**	-	-
NT2RP2005731	4.25	2.53	4.11	5.17	0	0.69	1.06	1.65	0.86		*		-
NT2RP2005732	54.72	53.14	65.72	91.69	67.12	83.97	67.17	50.47	67.53	*		+	

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Table 435

NT2RP2005737	61.08	46.51	54.73	57.66	30.52	54.9	80.55	70.19	69.8		*		+
NT2RP2005741	8.17	4.22	11.68	8.13	3	5.42	3.62	4.85	3.95				
NT2RP2005748	8.36	5.27	13.52	8.19	3.71	6.33	3.46	4.51	7.44				
NT2RP2005752	31.75	22.62	38.43	14.99	13.75	18.04	15.51	16.74	18.45	*	*	-	-
NT2RP2005753	34.44	30.95	46.77	33.24	26.02	18.11	26.19	25.32	15.55				
NT2RP2005763	8.78	7.62	12.88	6.76	3.85	3.68	4.32	5.6	4.17		*		-
NT2RP2005767	8.89	8.69	15.86	7.42	5.16	5.67	6.13	4.89	5.16				
NT2RP2005773	53.73	61.68	69.19	40.66	32.98	33.21	37.38	30.92	21.66	**	**	-	-
NT2RP2005774	13.75	12.5	18.48	16.31	7.06	7.63	18.33	17.56	17.06				
NT2RP2005775	12.13	7.53	22.24	13.73	4.82	6.66	4.04	6.6	5.74				
NT2RP2005781	39.68	23.61	38.05	24.73	22.45	22.65	9.91	16.91	23.06				
NT2RP2005784	30.34	20	41.77	17.54	13.38	14.34	11.13	13.26	15.12				
NT2RP2005789	16.92	16.55	24.71	17.16	13.64	7.39	8.95	14.02	9.78				
NT2RP2005799	11.23	8.75	9.48	10.01	3.28	4.24	3.37	6.03	3.88		**		-
NT2RP2005804	106.7	97.93	105.55	76.62	70.98	67.98	110.4	84.7	108.91	**		-	
NT2RP2005812	6.56	9.52	8.36	6.62	4.2	4.89	5.32	2.9	2.58		*		-
NT2RP2005815	2.76	4.98	5.71	6.34	2.94	2.66	4.39	4.52	4.97				
NT2RP2005835	26.87	25.04	37.02	18.31	16.79	16.79	10.34	14.43	39.55	*		-	
NT2RP2005841	22.25	27.56	27.52	20.49	14.43	16.92	11.4	11.65	19.51	*	*	-	-
NT2RP2005853	18.13	15.89	21.67	12.41	10.18	1.04	9.88	13.51	11.3		*		-
NT2RP2005857	11.03	8.75	10.83	7.42	4.51	1.32	4.21	5.92	5.5	*	**	-	-
NT2RP2005859	12.15	11.97	15.23	11.24	7.93	4.86	8.29	8.94	6.43		*		-
NT2RP2005860	0.96	5.77	2.68	4.74	2.31	1.31	1.34	1.77	1.13				
NT2RP2005863	8.01	8.99	7.06	7.45	6.66	5.32	7.67	5.36	4.12				
NT2RP2005868	5.66	10.09	8.76	11.28	4.39	6.75	7.63	5.42	5.14				
NT2RP2005876	29.94	9.36	44.21	25.04	19.27	15.81	14.52	17.33	37.26				
NT2RP2005878	17.4	21.07	28.07	15.86	10.5	10.77	9.96	17.05	21.58				
NT2RP2005883	9.58	9.62	13.3	8.93	6.54	7.61	3.43	11.45	8.28				
NT2RP2005886	109.48	86.27	131.02	108.7	95.74	145.77	77.39	72	86.69				
NT2RP2005887	12.65	18.34	15.15	9.59	5.47	2.19	3.8	5.68	5.07	*	**	-	-
NT2RP2005890	11.6	13.15	14.84	6.76	5.32	5.53	4.7	5.77	4.32	**	**	-	-
NT2RP2005901	11.96	15.27	14.95	10.18	6.55	8.12	6.42	5	5.8	*	**	-	-
NT2RP2005902	4.82	5.49	5.62	9.24	3.69	5.72	4.9	8.33	5.18				
NT2RP2005908	24.41	23.56	59.06	23.37	17.17	15.35	18.41	25.09	27.9				
NT2RP2005927	7.88	6.48	15.44	8.31	4.33	4.46	3.45	5.76	4.29				
NT2RP2005933	14.92	15.67	28.13	12.37	6.74	6	4	6.32	4.28		*		-
NT2RP2005941	10.69	8.58	13.22	7.84	3.9	3.96	2.9	4.82	2.65	*	**	-	-
NT2RP2005942	10.35	10.52	11.7	8.52	4	3.46	3.66	4.6	2.9	*	**	-	-
NT2RP2005946	8.12	19.6	14.91	5.77	6.58	2.97	4.94	4.86	6.09				
NT2RP2005970	73.5	72.19	81.01	50.77	49.15	40.53	67.44	62.72	62.64	**	*	-	-
NT2RP2005980	7.01	5.07	5.9	6.68	2.11	2.14	3.31	3.86	4.51		*		-
NT2RP2005994	12.99	9.14	13.53	7.59	4.09	0.3	2.32	3.71	4.52	*	**	-	-
NT2RP2006004	7.54	4.47	13.06	6.53	2.59	2.1	2.72	2.9	3.13				
NT2RP2006013	11.06	6.58	20.3	11.12	5.96	2.47	2.76	11.94	3.04				
NT2RP2006023	79.4	60.83	74.67	51.53	34.64	38.07	64.39	76.12	79.93	*		-	
NT2RP2006028	23.13	26.87	22.92	16.89	12.58	6.73	6.52	8.45	15.41	*	**	-	-
NT2RP2006038	4.35	4.75	6.83	4.07	1.31	0.83	1.09	0.16	1.4		**		-
NT2RP2006042	15.45	13.74	13.53	9.24	8.86	3.55	5.34	6.22	7.22	*	**	-	-
NT2RP2006043	17.81	13.76	15.29	13.7	7.47	8.55	9.41	5.9	6.89		**		-
NT2RP2006052	12.36	8.55	16.5	5.69	3	4.31	2.78	3.7	3.31	*	*	-	-
NT2RP2006057	7	6.58	13.05	6.99	3.77	3.67	1.75	3.57	2.95		*		-
NT2RP2006064	31.45	32.66	33.8	25.4	15.66	8.71	6.36	7.35	7.36	*	**	-	-
NT2RP2006068	7.85	6.5	16.27	7.3	3.64	3.64	2.88	4.02	3.43				
NT2RP2006069	10.49	8.04	9.64	6.75	2.89	1.65	2.28	1.16	1.94	*	**	-	-
NT2RP2006071	12.09	22.31	12.61	10.26	7.27	0.85	3.44	3.17	3.04		*		-
NT2RP2006090	10.61	10.59	22.59	7.62	4.75	0.57	5.24	4.28	5.3				
NT2RP2006092	15.25	7.07	12.08	13.1	8.69	10.62	13.15	8.79	8.66				
NT2RP2006097	52.21	101.2	64.35	48.63	48.31	38.97	25.59	53.43	52.7				
NT2RP2006098	13.67	12.41	21.3	14.85	6.15	8.49	5.13	8.68	3.6		*		-
NT2RP2006099	65.92	60.33	80.23	76.5	49.76	0.24	73.49	73.17	78.2				
NT2RP2006100	14.09	12.17	17.63	9.6	8.02	0.77	4.01	5.07	4.89		**		-
NT2RP2006103	6.26	4.22	7.72	5.83	3.58	2.06	2.74	2.72	2.55		*		-
NT2RP2006106	48	36	55.68	34.38	35.82	35.56	24.01	21.59	18.79		*		-
NT2RP2006127	6.5	4.86	5.96	5.76	1.93	3.45	3.78	1.37	2.06		*		-

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Table 436

NT2RP2006134	9.57	6.53	12.45	11.76	2.26	6.54	9.28	6.55	5.96				
NT2RP2006141	13.6	10.51	20.75	11.91	8.44	5.24	5.17	8.6	15.73				
NT2RP2006166	43.39	37.58	47.62	23.75	15.94	0.88	44.65	56.53	70.7	*		-	
NT2RP2006176	17.92	13.68	20.98	13.87	7.31	8.84	7.42	10.41	8.82		*		-
NT2RP2006181	4.75	8.83	6.23	3.92	1.81	1.35	3.97	2.81	2.8	*		-	
NT2RP2006184	64.52	54.32	63.63	42.14	32.28	42.22	63.72	47.39	43.75	**		-	
NT2RP2006186	8.19	11.92	9.4	6.19	2.49	2.83	2.18	2.13	1.87	*	**	-	-
NT2RP2006196	22.53	23.16	21.9	14.52	7.82	10.37	16.26	11.79	10.32	**	**	-	-
NT2RP2006199	9.01	9.11	8.26	8.72	4.43	4.65	6.19	4.21	5.05		**		-
NT2RP2006200	7.28	4.32	9.53	5.05	3.47	3.37	3.59	4.46	2.65				
NT2RP2006210	90.78	69.8	53.22	55.44	37.83	25.49	20.22	40.51	30.76		*		-
NT2RP2006219	11.28	20.39	17.51	8.1	14.35	6.63	11.34	9.44	19.6				
NT2RP2006224	12.75	19.13	21.38	12.72	10.81	3.64	17.87	16.61	1.85				
NT2RP2006237	7.47	20.77	9.96	5.08	2.48	0.88	3	2.56	0.6				
NT2RP2006238	10.52	14.31	12.03	6.19	1.38	2.03	2.55	2.62	2.66	**	**	-	-
NT2RP2006258	10.05	20.38	11.9	6.71	3.4	2.58	5.8	4.54	6.64	*		-	
NT2RP2006261	8.38	9.18	5.31	9.6	2.51	4.78	2.42	4.07	4.58		*		-
NT2RP2006269	17.03	14.29	15.32	11	5.59	7.26	3.86	12.06	5.85	*	*	-	-
NT2RP2006275	46.12	39	46.05	70.83	38.96	80.2	37.5	48.02	38.3				
NT2RP2006282	18.4	26.43	24.55	13.47	12.52	6.62	5.66	6.21	6.64	*	**	-	-
NT2RP2006302	17.18	26.6	32.5	13.26	6.56	8.01	5.28	4.17	5.65	*	*	-	-
NT2RP2006312	31.59	23.04	41.51	9.42	5.96	4.21	6.1	4.79	7.53	*	**	-	-
NT2RP2006320	41.28	41.71	36.93	24.86	13.12	15.23	28.98	37.1	32.63	**		-	
NT2RP2006321	10.41	9.33	12.86	10.26	2.43	5.6	7.6	9.6	8.78				
NT2RP2006323	7.58	5.4	4.29	6.62	1.35	3.01	7.41	4.95	4.91				
NT2RP2006333	5.03	7.52	4.99	6.18	1.44	5.34	2.1	4.81	3.82				
NT2RP2006334	7.94	8.71	7.64	8.5	4.46	6.47	2.3	4.34	3.32		**		-
NT2RP2006338	12.7	9.34	36.56	7.32	2.93	4.16	2.16	2.04	3.64				
NT2RP2006339	6.41	4.31	4.61	6.37	3.36	3.67	2.31	2.9	2.66		*		-
NT2RP2006355	6.78	12.38	3.94	6.81	1.66	2.59	2.74	4.14	2.84				
NT2RP2006365	5.27	2.38	4.32	5.39	0.85	1.53	2.13	3.92	2.48				
NT2RP2006374	123.01	124.5	151.43	183.62	144.52	148.4	137.08	112.64	166.86				
NT2RP2006393	22.69	18.53	23.1	17.79	6.84	13.61	27.67	23.54	25.74				
NT2RP2006394	15.6	11.55	17.73	16.97	12.66	13.34	9.59	13.69	11.86				
NT2RP2006400	8.82	4.99	12	10.48	4.15	11.24	9.88	11.64	10.5				
NT2RP2006411	4.42	4.9	11.08	5.28	2.3	3.07	2.25	3.04	3.21				
NT2RP2006429	2.69	1.8	8.38	6.1	1.17	1.68	2.03	2.68	1.46				
NT2RP2006435	1.14	1.44	3.96	3.86	0	1.28	1.25	0.25	0.25				
NT2RP2006436	18.89	25.65	29.36	23.03	10	15.2	18.88	16.71	17.66				
NT2RP2006441	3.24	5.37	8.45	6.78	2.17	3.47	5.5	2.69	1.87				
NT2RP2006447	19.2	14.3	18.35	21.17	15.45	16.45	6.09	13.77	11.65				
NT2RP2006454	8.01	2.56	13.95	6.26	3.2	3.65	3.95	4.09	2.96				
NT2RP2006455	37.87	46.16	39.71	20.34	20.45	22.87	31.23	29.73	37.11	**		-	
NT2RP2006456	12.66	10.34	20.88	11.22	5.29	5.49	7.54	4.09	3.92				
NT2RP2006464	49.31	38.6	70.84	30.42	38.8	32.65	22.89	19.33	15.74		*		-
NT2RP2006467	7.41	7.72	13.37	8.13	6.48	4.56	10.4	4.81	8.63				
NT2RP2006472	17.27	35.33	39.96	36.59	25.1	29.12	15.84	31.69	29.65				
NT2RP2006474	5.31	10.55	8.31	9.45	5.79	7.02	7.91	11.16	8.64				
NT2RP2006475	14.67	7.33	18.42	13.4	5.52	5.53	5.81	10.03	7.38				
NT2RP2006476	21.17	14.25	23.98	17.93	10.29	15.83	16.59	21.36	17.75				
NT2RP2006501	80.64	47.79	67.54	47.86	36.74	36.28	29.87	41.76	52.91				
NT2RP2006512	10.73	9.4	12.56	6.68	7.05	5.5	3.87	4.91	5.32	*	**	-	-
NT2RP2006526	12.09	17.75	22.2	19.62	16.43	13.33	17.31	20.34	13.23				
NT2RP2006527	4.41	6.17	7.16	7.48	1.84	1.55	3.51	2.56	2.84		*		-
NT2RP2006534	4.37	9.41	7.99	5.05	4.19	2.96	4.68	2.83	2.5				
NT2RP2006537	5.9	9.98	11.68	11.28	5.12	7.83	10.34	5.58	8.5				
NT2RP2006543	12.11	8.37	13.04	12.23	3.26	11.04	6.8	5.53	9.23				
NT2RP2006554	7.01	5.37	13.82	7.47	2.64	2.23	3.56	4.89	9.98				
NT2RP2006565	14.34	12.69	22.07	6.94	4.33	4.74	3.36	7.61	8.3	*	*	-	-
NT2RP2006571	65.34	49.49	69.38	45.6	41.55	34.63	47.98	65.86	43.88	*		-	
NT2RP2006573	12.86	9.58	16.76	8.82	7.97	5.87	5.7	4.86	5.46		*		-
NT2RP2006598	5.92	15.24	10.14	5.39	4.48	3.2	2.52	3.49	4.84				
NT2RP2006601	5.92	8.92	7.57	6.45	4.69	2.53	4.15	3.79	3.98		*		-
NT2RP3000002	17.28	31.41	14.62	22.94	26.64	18.92	27.08	23.91	17.49				

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Table 437

NT2RP3000011	14.9	6	15.29	9.33	4.35	7.79	4.33	10.84	6.28				
NT2RP3000014	108.09	109.54	95.92	98.76	68.18	81.91	47.71	112.2	132.8				
NT2RP3000016	14.35	13.63	24.71	7.65	8.46	5.45	3.86	7.49	4.11	*	*	-	-
NT2RP3000022	7.65	10.24	13.67	9.49	4.92	2.16	2.89	2.32	2.03		*		-
NT2RP3000024	12.64	12.37	14.37	11.32	5.72	6.81	6.24	6.05	6.52	*	**	-	-
NT2RP3000031	77.24	79.76	145.67	144.42	128.63	86.96	77.23	69.72	83.66				
NT2RP3000034	6.27	6.62	8.74	6.38	3.4	3.43	4.64	3.79	2.96		*		-
NT2RP3000037	17.58	19.44	20.81	11.72	11.55	13.9	18.45	10.67	14.15	**		-	
NT2RP3000040	27.59	16.23	24.01	13.53	7.79	10.55	2.51	8.1	6.81	*	*	-	-
NT2RP3000041	5.08	4.46	12.76	6.9	3.15	3.65	6.44	3	1.87				
NT2RP3000046	7.63	5.75	15.27	8.29	3.02	2.83	2.71	4.54	5.05				
NT2RP3000047	5.93	4.81	14.06	5.49	2.34	2.87	0.9	3.18	1.51				
NT2RP3000049	6.45	8.2	10.35	6.13	1.6	1.78	2.62	3.99	1.9		*		-
NT2RP3000050	11.72	13.02	12.95	7.97	7.04	4.74	3.27	4.45	3.93	**	**	-	-
NT2RP3000051	20.55	9.33	16.87	14.09	17.37	4.84	3.99	4.5	4.21		*		-
NT2RP3000054	6.46	5.61	6.8	6.67	3.52	2.38	1.52	2.23	2.77		**		-
NT2RP3000055	18.47	13.61	17.33	12.33	8.89	12.37	7.71	11.31	9.35	*	*	-	-
NT2RP3000056	1.67	2.36	8.51	3.35	1.42	1.09	0.81	1.36	0.36				
NT2RP3000059	7.89	7.9	22.29	10.9	7.16	5.13	2.59	4.88	2.31				
NT2RP3000063	1.84	4.14	7.63	4.56	1.09	0.43	0.47	0.97	0				
NT2RP3000068	6.17	8.89	16.21	5.26	4.81	2.29	6.13	4.42	2.89				
NT2RP3000069	9.15	8.31	8.75	6.58	4.56	4.92	4.17	3.76	6.03	**	**	-	-
NT2RP3000072	32.05	40.26	39.15	31.11	26.2	25.34	26.47	26.26	26.37	*	*	-	-
NT2RP3000080	25.2	23.2	22.56	18.48	15.53	13.5	21.79	14.38	13.52	**		-	
NT2RP3000085	67.96	43.89	70.79	53.46	33.71	65.94	52.26	69.62	62.27				
NT2RP3000087	111.9	96.79	117.72	81.88	54.53	62.52	49.82	71.54	66.46	*	**	-	-
NT2RP3000092	9.87	12.43	24.83	8.97	4.39	4.92	2.95	7.36	3.67				
NT2RP3000109	10.57	9.88	12.54	8.31	8.64	5.99	6.65	6.37	5.22	*	**	-	-
NT2RP3000119	8.08	6.85	10.03	6.29	4.73	2.45	4.69	3.89	2.89		*		-
NT2RP3000125	6.75	8.13	6.71	5.47	2.88	2.09	0.61	2.51	2.19	*	**	-	-
NT2RP3000131	13.6	16.29	13.49	12.52	5.73	6.16	5.37	4.48	4.22		**		-
NT2RP3000134	18.43	21.97	18.23	9.28	9.9	8.55	6.96	2.89	3.6	**	**	-	-
NT2RP3000137	10.23	18.11	17.39	15.98	4.55	11.71	4.48	6.98	5.44		*		-
NT2RP3000142	35.53	27.58	35.61	21.77	15.45	19.48	21.05	30.25	26.9	*		-	
NT2RP3000148	26.32	39.38	34.66	19.53	19	15.35	18.54	17.46	14.71	*	*	-	-
NT2RP3000149	32.9	38.83	27.1	14.1	20.26	8.54	10.04	7.73	9.34	*	**	-	-
NT2RP3000163	8.85	9.04	13.21	8.67	3.56	5.95	3.7	3.77	3.35		**		-
NT2RP3000168	15.39	20.39	19.23	9.48	11.8	5.55	7.63	15.26	9.88	*		-	
NT2RP3000169	15.25	12.33	13.06	7.58	7.27	4.09	8.07	3.27	4.36	**	**	-	-
NT2RP3000171	6.75	12.8	10.62	11.26	6.03	4.95	8.98	2.23	5.04				
NT2RP3000172	40.04	25.12	32.12	25.17	9.97	24.6	26.83	33.18	37.52				
NT2RP3000186	16.1	16.13	19.67	12.39	6.63	8.09	5.65	10.05	10.55	*	*	-	-
NT2RP3000197	50.94	62.27	70	34.47	33.63	20.62	34.62	48.18	55.04	*		-	
NT2RP3000201	14.53	11.88	22.5	7.11	4.59	3.11	5.14	5.79	5.41	*	*	-	-
NT2RP3000204	4.16	4.96	6.59	4.48	1.18	2.3	2.66	1.7	2.27		*		-
NT2RP3000207	95.59	249.91	234.63	30.21	59.19	29.76	35.62	12.46	31.91	*	*	-	-
NT2RP3000216	7.95	7.31	6.95	6.17	2.69	2.5	2.94	3.29	3.98	*	**	-	-
NT2RP3000220	22.18	29.86	28.92	10.43	5.88	15.01	13.77	5.33	14.12	**	*	-	-
NT2RP3000221	10.31	9.17	11.73	12.25	5.03	10.36	5.52	10.77	5.91				
NT2RP3000232	46.66	42.43	53.26	15.69	8.2	7.9	5.53	11.37	6.25	**	**	-	-
NT2RP3000233	8.3	12.35	2.97	7.16	16.65	2.19	9.24	3.42	2.51				
NT2RP3000234	3.63	3.88	5.86	5.35	3.32	2.04	1.6	2.52	2.2		*		-
NT2RP3000235	9.35	15.39	13.27	13.07	5.58	8.43	10.72	9.32	10.97				
NT2RP3000238	18.63	25.23	22.23	15.58	11.06	7.77	9.06	9.28	12.71	*	**	-	-
NT2RP3000247	32.06	44.16	41.62	22.89	17.24	20.67	24.3	20.29	19.85	**	*	-	-
NT2RP3000251	44.56	41.2	38.69	25.94	14.62	23.41	43.42	39.09	44.51	**		-	
NT2RP3000252	21.9	16.55	21.84	18.88	16.64	19.17	13.44	23.92	18.04				
NT2RP3000255	18.67	16.02	17.43	18.73	10.56	14.35	9.36	10.73	8.47		**		-
NT2RP3000262	17.74	15.84	18.49	25.1	16.29	24.75	12.36	12.76	13.36		**		-
NT2RP3000266	37.8	22.61	54.63	46.91	29.06	37.64	30.75	39.28	44.8				
NT2RP3000267	5.43	5.61	4.39	6.25	5.05	2.74	3.18	2.68	2.59		**		-
NT2RP3000271	4.92	10.2	10.62	7.08	4.11	3.49	3.88	5.36	2.72				
NT2RP3000278	5.77	11.93	8.85	9.67	5.55	4.79	8.29	7.56	5.48				
NT2RP3000281	32.19	29.94	32.48	16.28	8.76	14.6	16.94	10.41	13.64	**	**	-	-

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Table 438

NT2RP3000292	73.41	53.56	62.96	43.77	42.72	40.98	49.91	45.23	84.29	*		-	
NT2RP3000299	6.1	3.92	13.07	7.5	3.65	4.11	4.21	4.47	3.64				
NT2RP3000304	25.73	24.35	31.49	22.39	17.08	15.95	20.38	9.68	10.08	*	*	-	-
NT2RP3000310	21.09	16.82	33.26	14.15	13.15	10.27	8.12	6.37	6.54		*		-
NT2RP3000312	0.99	6.75	7.52	6.17	1.98	0.95	3.63	3.7	0.46				
NT2RP3000320	11.54	11.91	24.03	15.6	10.14	7.39	6.78	13.07	6.3				
NT2RP3000322	6.3	10.23	13.74	8.18	5.89	5.4	11.65	9.13	4.6				
NT2RP3000324	3.35	4.35	17.76	5.33	3.9	3.91	1.03	4.83	1.94				
NT2RP3000326	64.19	41.44	38.83	20.52	19.15	16.6	15.62	30.96	63.08	*		-	
NT2RP3000329	11.55	11.02	22.98	13.53	7.92	12.17	10.06	11.03	12.62				
NT2RP3000330	7.65	5.98	10.92	7.41	2.84	4.65	3.07	4.04	3.9		*		-
NT2RP3000333	5.32	5.01	9.94	8.43	4.88	3.17	4.98	3.48	4.27				
NT2RP3000341	13.68	14.31	17.57	13.78	9.61	9.9	9.7	9.67	11.82		*		-
NT2RP3000344	45.81	52.79	53.7	28.28	29.87	22.15	36.08	31.27	32.79	**	**	-	-
NT2RP3000345	9.05	22.29	17.79	14.81	9.64	10.42	11.7	5.94	6.21				
NT2RP3000348	152.75	76.47	143.51	181.96	103.16	145.4	96.65	108.56	99.33				
NT2RP3000350	14.44	9.79	17.94	12.6	7.91	9.69	10.66	15.9	13.61				
NT2RP3000359	12.38	12.66	23.75	11.88	10.77	13.58	14.05	17.04	16.51				
NT2RP3000361	30.21	20.92	25.69	12.5	10.99	10.9	7.28	12.88	9.35	**	**	-	-
NT2RP3000366	69.71	53.96	58.74	44.82	38.68	40.33	27.58	41.09	30.61	*	*	-	-
NT2RP3000378	5.8	12.66	6.1	6.74	3.98	3.58	4.72	5.63	5.68				
NT2RP3000384	26.45	19.42	18.46	13.21	9.98	7.79	8.34	6.32	5.93	*	**	-	-
NT2RP3000389	22.1	25.13	28.16	17.61	19.95	18.45	23.81	18.85	25.81	*		-	
NT2RP3000393	33.85	14.06	19.19	10.32	8.44	17.76	6.01	7.4	12.32				
NT2RP3000395	24.46	28.99	21.1	13.42	10.29	14.47	9.05	14.21	24.87	**		-	
NT2RP3000397	24.89	21.35	36.91	14.31	14.82	16.14	17.25	23.74	23.2				
NT2RP3000398	9.55	10.75	17.31	7.25	6.82	4.6	4.16	4.17	3.99		*		-
NT2RP3000403	93.32	64.65	56.89	57.84	43.74	45.93	35.74	40.63	30.88		*		-
NT2RP3000418	14.37	22.01	20.2	11.88	12.29	11.51	7.67	14.89	12.11	*		-	
NT2RP3000424	40.86	56.6	51.72	39.57	32.99	30.24	31.05	29.26	23.73	*	*	-	-
NT2RP3000427	19.59	24.95	16.59	14.3	10.74	15.64	9.16	9.9	12.52		*		-
NT2RP3000431	16.18	14.67	25.82	11.73	10.4	20.33	8.15	16.47	13.08				
NT2RP3000433	25.31	54.08	36.8	35.67	31.56	27.85	24.04	39.4	34.85				
NT2RP3000436	9.62	10.09	16.49	6.56	4.89	5.29	2.88	5.01	2.75	*	*	-	-
NT2RP3000439	44.72	47.78	44.4	50.96	50.94	30.43	33.38	44	42.05				
NT2RP3000441	10.82	8.96	14.82	10.83	6.19	5.02	6.65	8.63	7.39				
NT2RP3000444	17.45	14.75	26.3	14.55	11.35	9.32	12.21	11.85	12.68				
NT2RP3000448	6.61	7.47	11.97	6.37	5.01	4.15	4.85	3.6	5.55				
NT2RP3000449	17.38	26.19	23.45	8.67	7.34	7.86	3.61	4.2	2.92	**	**	-	-
NT2RP3000451	31.29	40.71	35.46	10.79	20.02	15.29	13.25	22.78	15.67	**	**	-	-
NT2RP3000456	6.24	4.2	13.64	8.03	3.84	0	2.84	3.63	2.55				
NT2RP3000460	10.33	10.39	17.07	7.27	4.9	3.93	5.19	5.56	4.78	*	*	-	-
NT2RP3000471	11.88	7.85	23.63	10.17	6.71	3.54	3.68	5.28	5.09				
NT2RP3000477	49.73	54.72	58.77	38.09	33.82	22.58	25.2	26.62	28.76	*	**	-	-
NT2RP3000478	6.95	4.02	8.07	5.51	2.95	1.38	1.83	1.8	1.91		*		-
NT2RP3000481	11.03	7.58	11.93	11.71	8.13	6.39	6.65	9.77	6.96				
NT2RP3000484	25.46	33.21	34.57	19.56	15.47	13.67	14.97	11.89	12.9	*	**	-	-
NT2RP3000487	21.14	29.38	33.76	13.62	12.2	14.9	5.33	12.46	12.14	*	*	-	-
NT2RP3000512	12.44	14.88	14.98	11.55	7.87	5.16	5.05	7.04	5.14	*	**	-	-
NT2RP3000523	93.94	104.88	80.32	71.64	44.61	35.48	20.12	30.84	18.65	*	**	-	-
NT2RP3000526	7.94	7.79	12.87	7.19	2.92	3.56	4	5.42	4.09		*		-
NT2RP3000527	42.97	38.74	42.72	25	28.15	22.19	19.81	21.07	11.92	**	**	-	-
NT2RP3000531	20.64	13.92	14.48	12.89	10.75	4.81	8.04	4.79	4.56		*		-
NT2RP3000532	5.33	6.65	5.17	4.82	3.38	2.17	2.24	1.62	4.13		*		-
NT2RP3000542	21.28	18.32	16.2	8.3	8.11	6.12	3.53	3.83	3.8	**	**	-	-
NT2RP3000554	11.71	17.67	14.03	9.45	3.02	6.99	4.57	4.9	5.09	*	**	-	-
NT2RP3000561	21.04	16.88	23.96	14.27	9.57	9.4	4.67	15.18	7.79	*	*	-	-
NT2RP3000562	56.42	51.6	61.28	47.36	46.18	42.62	32.74	44.25	48.68	*		-	
NT2RP3000578	19.29	21.22	25	14.6	13.72	9.4	9.07	9.7	10.06	*	**	-	-
NT2RP3000582	9.4	7.64	13.09	8.29	5.67	6.43	5.12	6.71	5.65				
NT2RP3000584	22.71	44.85	35.97	15.47	26.23	10.78	9.11	11.41	6.79		*		-
NT2RP3000586	8.23	4.88	7.14	6.37	3.31	2.97	3.91	1.9	2.63		*		-
NT2RP3000590	7.21	5.97	5.97	5.32	2.92	1.94	4.92	2.84	1.77		*		-
NT2RP3000592	69.63	37.92	90.02	128.75	103.66	125.15	70.02	69.72	60.26	*		+	

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Table 439

NT2RP3000596	8.71	11.87	13.23	5.92	4.35	3.28	4.65	3.35	4	*	**	-	-
NT2RP3000599	39.3	60.28	67.05	35.1	44.12	24.38	35.82	36.31	35.96				
NT2RP3000603	69.47	91.4	87.14	91.5	86.56	93.49	64.94	61.32	72.5				
NT2RP3000605	22.45	27.45	25.73	13.14	8.89	13.46	17.63	11.14	9.76	**	*	-	-
NT2RP3000607	10.48	11.53	16.41	10.77	7.11	9.56	5.29	9.79	8.32				
NT2RP3000616	11.96	13.13	17.29	7.98	6.33	4.22	6.69	4.25	4.27	*	**	-	-
NT2RP3000621	218.49	188.17	246.49	222.59	168.47	221.1	202.08	168.53	186.24				
NT2RP3000622	11.99	8.26	9.27	9.15	3.89	5.28	6.73	6.59	3.57				
NT2RP3000624	27.07	18.6	22.96	16.72	12.03	13.8	17.33	23.33	18.89	*		-	
NT2RP3000628	27.69	34.41	73.45	22.73	20.51	22.18	15.98	19.75	18.56				
NT2RP3000631	6.03	12.91	11.07	11.79	9.91	5.14	4.52	6.12	7.95				
NT2RP3000632	16.5	21.72	26.01	18.26	13.03	16.89	15.73	14.14	13.67				
NT2RP3000638	31.94	42.93	38.07	22.76	17	20.23	24.56	32.44	30.42	**		-	
NT2RP3000644	26.66	26.83	24.84	16.68	14.97	15.79	28.13	27.03	30.11	**		-	
NT2RP3000645	12.37	13.95	21.96	14.87	10.1	8.68	7	6.44	7.2		*		-
NT2RP3000652	20.17	23.26	25.45	12.67	9.39	13.26	9.11	9.19	15.37	**	*	-	-
NT2RP3000658	6.96	4.69	8.52	6.05	2.7	4.41	2.15	3.59	3.85		*		-
NT2RP3000660	21.94	12.21	11.63	11.36	9.42	9.56	9.02	8.73	8.05				
NT2RP3000661	15.39	18.23	27.58	11.62	4.78	9.25	6.26	7.03	6.07	*	*	-	-
NT2RP3000665	34.94	43.07	59.18	27.69	16.86	21.15	16.2	20.9	14.32	*	*	-	-
NT2RP3000676	11.53	4.79	8.95	6.6	4.34	2.4	4.94	2.78	3.68				
NT2RP3000677	12.19	14.6	7.18	13.97	4.51	9.55	9.82	11.58	12.06				
NT2RP3000681	7.72	7.98	7.04	6.12	2.54	4.33	4.62	3.23	3.26	*	**	-	-
NT2RP3000683	16.43	8.63	13.69	14.68	12.94	13.49	5.83	9.27	7.59				
NT2RP3000685	8.41	6.46	7.19	10.24	3.04	4.6	5.55	3.8	3.45		*		-
NT2RP3000690	11.52	7.55	10.23	15.03	9.13	13.25	14.85	17.96	14.92		*		+
NT2RP3000698	6.94	6.35	7.8	8.41	2.13	5.63	3.39	7.51	5.51				
NT2RP3000708	9.74	10.33	12.77	11.25	8.14	10.39	9.73	10.17	12.86				
NT2RP3000719	9.86	16.24	14.31	8.23	2.38	5.7	5.89	3.68	4.39	*	*	-	-
NT2RP3000721	8.23	3.7	5.33	7.95	1.94	5.33	6.54	5.47	6.13				
NT2RP3000728	4.68	4.59	4.86	7.19	1.44	3.15	5.16	3.82	3.57				
NT2RP3000730	14.89	15.22	17.78	16.76	11.05	11.99	16.08	10.04	9.6				
NT2RP3000733	62.46	50.63	81.88	55.7	39.3	45.85	39.59	39.01	40.88				
NT2RP3000735	4.91	3.22	9.89	6.52	1.99	3.91	2.03	3.65	2.09				
NT2RP3000736	6.36	3.45	10.98	8.89	2.09	4.31	3.75	3.03	2.56				
NT2RP3000739	40.42	44.03	40.83	24.77	27.39	34.23	25.37	20.3	32.14	*	*	-	-
NT2RP3000742	4.84	6.47	8.58	7.03	4.15	2.9	3.28	5.74	3.55				
NT2RP3000753	8.3	6.8	12.66	10.6	4.35	5.47	5.99	5.75	7.45				
NT2RP3000759	36.84	70.63	56.01	36.02	19.41	27.88	8.09	6.25	5.44		**		-
NT2RP3000789	45.54	27.39	34.07	33.12	27.39	34.54	20.51	27.67	27.21				
NT2RP3000815	22.33	13.62	22.75	12.02	10.68	14.79	18.74	20.82	19.96				
NT2RP3000818	30.57	21.11	33.63	24.24	17.69	21.68	13.73	17.32	15.5		*		-
NT2RP3000820	35.87	28.12	43.92	32.81	27.98	25.05	21.15	26.93	23.2				
NT2RP3000821	3.51	4.2	7.15	6.21	2.3	3.01	3.82	2.8	1.62				
NT2RP3000825	16.22	23.18	33.6	11.67	17.67	13.25	9.13	8.99	16.22				
NT2RP3000826	57.22	56.7	80.61	55.4	48.67	48.17	57.78	64.97	54.17				
NT2RP3000836	3.1	3.53	3.85	7.53	2.33	2.42	3.69	4.81	2.68				
NT2RP3000838	14.56	14.22	18.93	20.92	12.46	10.78	11.08	17.41	54.13				
NT2RP3000839	45.25	36.9	44.36	35.78	27.32	20.79	19.28	33.14	25.15	*	*	-	-
NT2RP3000841	12.21	10.37	21.1	12.42	10.04	9.18	8.34	11.21	7.12				
NT2RP3000845	8.59	31.26	15.5	9.69	12.93	10.25	5.37	12.21	8.92				
NT2RP3000847	12.91	10.6	18.85	11.06	8.9	9.57	6.7	5.47	6.54		*		-
NT2RP3000848	11.47	16.2	11.34	8.1	7	4.83	3.86	7.4	3.83	*	*	-	-
NT2RP3000850	21.09	31.1	29.31	19.76	12.79	16.25	10.7	10.54	5.19	*	**	-	-
NT2RP3000852	2.73	3.9	3.17	7.51	3.17	2.39	4.15	2.97	3.66				
NT2RP3000859	32.3	21.43	36.02	18.9	21.77	13.31	16.61	18.23	32.52				
NT2RP3000861	15.56	12.49	16.59	9.02	5.36	4.49	4.53	5.88	27.25	**		-	
NT2RP3000862	12.15	10.89	17.99	10.36	6.14	6.17	5.59	8.92	5.21		*		-
NT2RP3000865	9.02	6.17	10.68	7.46	4.29	4.01	2.73	4.35	3.2		*		-
NT2RP3000866	43.46	38.1	57.47	39.52	40.18	44.87	37.48	37.57	27.56				
NT2RP3000868	10.55	23.22	17.15	7.33	6.65	4.58	6.64	9.1	10.81	*		-	
NT2RP3000869	5.78	11.8	14.52	9.41	10.86	7.13	6.87	5.05	7.12				
NT2RP3000871	194.48	190.18	141.72	252.15	170.88	170.92	247.35	193.7	214.46				
NT2RP3000875	14.37	14.46	23.84	13.76	12.05	11.47	7.45	6.27	6.52		*		-

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Table 440

NT2RP3000895	2.84	2.51	12.27	4.16	1.17	2.03	1.28	3.4	1.59				
NT2RP3000900	10.4	8.3	14.31	18.92	3.45	5.38	4.15	13.51	4.93				
NT2RP3000901	14.3	18.5	22.78	13.03	13.47	11.77	11.97	9.53	14.53				
NT2RP3000903	5.01	6.85	6.69	5.82	1.64	3.35	1.28	1.92	1.35		**		-
NT2RP3000904	108.6	100.47	123.83	118.07	108.3	100.81	97.74	77.69	108.28				
NT2RP3000907	84.64	90.19	89.66	84.77	80.01	92.59	125.26	82.21	80.83				
NT2RP3000913	19.19	19.49	20.62	24.35	9.57	18.44	17.39	14.75	19.21				
NT2RP3000917	16.28	18.3	30.01	16.96	15.22	12.11	11.68	16.63	14.88				
NT2RP3000919	9.33	7.65	14.92	9.52	7.41	6.8	4.46	8.2	5.92				
NT2RP3000921	112.89	136.59	133.65	119.03	103.41	74.11	25.71	35.79	29.01		**		-
NT2RP3000942	67.7	68.21	86.84	75.24	51.25	30.13	38.31	52.76	48.83		*		-
NT2RP3000968	50.83	31.86	37.11	29.89	24.92	14.66	9.86	11.81	12.71		**		-
NT2RP3000974	8.96	8.74	9.35	9.04	12.66	5.51	4.39	4.92	2.99		**		-
NT2RP3000980	52.51	65.55	64.13	24.76	40.04	30.49	19.39	8.08	16.43	**	**	-	-
NT2RP3000984	21.27	24.19	17.57	32.72	12.14	21.58	18.47	14.77	17.87				
NT2RP3000994	13.76	10.35	18.12	10.02	5.77	7.25	4.5	8.07	7.2		*		-
NT2RP3001001	26.43	28.79	25.4	17.26	14.54	13.11	11.19	38.41	33.45	**		-	
NT2RP3001004	4.86	4.98	10.62	7.73	3.07	4.03	3.13	4.4	2.41				
NT2RP3001007	7.65	8.96	16.59	12.13	9.28	3.44	5.05	6.53	5.77				
NT2RP3001012	29.74	22.53	33.06	15.24	16.46	13.42	12.28	11.59	13.53	*	**	-	-
NT2RP3001042	8.82	8.59	12.15	8.9	5.69	3.5	3.15	4.09	3.65		**		-
NT2RP3001044	9.07	11.65	10.99	8.25	9.28	5.59	7.83	7.51	5.88		*		-
NT2RP3001048	6.16	7.8	4.48	10.05	2.76	3.93	4.91	5.32	6.21				
NT2RP3001050	13.37	10.61	15.08	10.7	4.83	9.6	6.34	11.26	9.4				-
NT2RP3001055	13.05	10.48	21.89	13.3	7.76	7.17	10.39	12.83	10.26				
NT2RP3001057	402.89	324.38	250.29	272.31	285.99	209.38	216.17	328.86	144.63				
NT2RP3001061	7.38	5.55	10.57	7.56	3.5	2.09	3.67	3.84	2.18		*		-
NT2RP3001069	5.39	4.71	9.6	4.84	1.4	2.62	2.39	2.57	3.49				
NT2RP3001074	12.1	8.82	12.25	8.96	3.61	6.95	9.25	6.39	6.94				
NT2RP3001078	13.01	11.28	14.67	14.05	9.24	8.9	10.46	7.65	9.46		*		-
NT2RP3001081	8.54	6.06	5.96	10.22	3.89	7.03	6.21	3.36	4.4				
NT2RP3001084	37.48	37.33	40.93	15.51	10.29	21.45	23.22	30.25	29.17	**	*	-	-
NT2RP3001095	7.76	24.69	13.38	9.04	3.7	5.9	3.38	7.52	4.23				
NT2RP3001096	10.65	10.08	12.53	7.44	5.06	4.16	3.27	5.66	3.18	*	**	-	-
NT2RP3001097	16.83	38.99	30.48	15.02	9.07	10.26	12.7	8.94	6.97		*		-
NT2RP3001107	28.61	24.48	44.48	22.05	25.16	18.26	10.04	8.83	11.02		*		-
NT2RP3001109	17.96	17.48	18.06	10.7	9.3	6.66	7.73	5.5	3.91	**	**	-	-
NT2RP3001111	10.67	15.58	14.57	9.33	6.41	6.38	8.41	3.97	4.53	*	*	-	-
NT2RP3001112	31.69	26.22	26.11	22.8	9.31	16.42	16.88	9.36	14.31		**		-
NT2RP3001113	14.44	9.43	17.91	10.99	5.21	10.46	6.16	6.79	9.04				
NT2RP3001115	254.68	276.58	258.3	135.39	153.31	123.7	118.47	299.67	339.02	**		-	
NT2RP3001116	5.38	8	8.83	6.23	4.02	2.69	4.29	3.33	3.99		*		-
NT2RP3001119	18.64	22.98	19.35	7.26	6.2	5.92	8.84	7.37	8.08	**	**	-	-
NT2RP3001120	6.46	9.54	10.55	5.21	2.06	2.39	3.48	2.35	2.85	*	**	-	-
NT2RP3001126	20.13	19.18	15.24	6.77	6.2	4.55	4.46	2.87	5.52	**	**	-	-
NT2RP3001127	348.14	574.68	264.45	161.21	220.83	168.52	563.89	269.72	342.5				
NT2RP3001133	93.42	110.06	112.43	156.23	89.96	123.37	108.06	86.85	85.22				
NT2RP3001140	96.94	96.61	111.2	55.83	46.1	51.01	55.61	103.28	84.66	**		-	
NT2RP3001147	4.72	7.64	8.71	6.37	2.09	3.65	2.74	3.66	2.93		*		-
NT2RP3001150	11.47	12.3	12.64	9.98	10.24	3.21	4.96	7.94	6.36		**		-
NT2RP3001152	36.54	72.08	61.62	66.57	55.9	58.11	48.19	41.6	53.56				
NT2RP3001155	19.7	23.76	17.71	11.79	7.15	8.62	14.02	11.36	10.16	**	*	-	-
NT2RP3001156	19.46	20.53	21.5	20.77	20.49	12.08	20.09	17.5	18.2				
NT2RP3001159	18.55	19.29	22.76	15.71	9.43	11.61	19.86	20.4	20.19	*		-	
NT2RP3001170	16.8	14.86	12.69	11.85	4.5	6.68	9.82	3.85	4.53	*	*	-	-
NT2RP3001176	17.96	17.32	14.24	8.81	7.86	12.88	9.17	14.49	11.22	*		-	
NT2RP3001195	197.73	229.27	190.42	299.15	260.22	386.11	194.62	191.1	184.16	*		+	
NT2RP3001209	74.83	67.88	81.64	88.53	60.41	90.53	81.32	84.97	83.11				
NT2RP3001214	17.39	13.69	27.12	17.15	13.89	13.51	7.67	14.21	13.2				
NT2RP3001216	18.74	16.38	19.13	19.54	12.84	10.16	26.01	26.17	21.52		*		+
NT2RP3001221	6.31	7.39	8.65	9.62	5.18	6.37	8.56	6.05	7.92				
NT2RP3001226	22.75	26.78	31.16	8.49	9.07	6.76	11.49	9.21	9.9	**	**	-	-
NT2RP3001230	6.51	6.56	3.99	9.46	3.93	5.31	7.3	6.36	5.9				
NT2RP3001232	6.36	3.81	12.04	7.09	3.34	3.56	1.97	4.41	3				

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Table 441

NT2RP3001236	30.11	19.17	30.67	17.48	11.33	17.05	7.98	12.61	12.49		*		-
NT2RP3001239	12.58	7.93	16.69	7.8	5.43	5.92	7.31	5.36	3.8				
NT2RP3001240	16.64	15.42	32.69	20.34	13.57	11.75	7.09	11.44	8.12				
NT2RP3001245	8.04	12.54	22.57	10.74	8.24	10.53	7.27	7.75	6.31				
NT2RP3001253	5.41	9.93	13.75	5.39	2.74	1.6	4.68	3.73	2.31				
NT2RP3001259	278.9	310.98	327.25	256.7	262.84	274.28	334.89	289.89	242.91				
NT2RP3001260	18.94	14.44	22.33	34.17	17.19	23.22	21.96	25.77	20.83				
NT2RP3001264	67.04	56.89	77.24	82.42	71.22	82.52	43.6	44.18	61.74				
NT2RP3001268	54.13	43.25	63.3	45.53	25.93	35.18	39.08	48.29	54.07				
NT2RP3001271	7.61	5.79	12.88	6.16	2.76	3.69	3.87	7.7	5.38				
NT2RP3001272	23.18	22.6	31.48	18.93	15.25	15.77	18.56	19.39	20.08	*		-	
NT2RP3001274	143.91	121	164.35	135.41	115.24	154.69	133.08	136.37	139.51				
NT2RP3001275	7.03	7.19	20.08	7.2	8.45	4.21	4.17	4.56	3.94				
NT2RP3001280	14.64	18.72	19.46	9.93	11.17	5.67	7.5	8.91	6.46	*	**	-	-
NT2RP3001281	0.38	2.63	0.7	4.71	1.73	1.17	1.88	0.77	0.6				
NT2RP3001288	43.86	21.34	42.34	25.62	18.43	26.29	27.01	32.19	37.1				
NT2RP3001297	77.1	64.75	81.93	35.55	27.23	38.6	12.09	28.24	29.77	**	**	-	-
NT2RP3001300	9.48	9.06	13.81	7.61	5.56	4.66	4.6	5.82	8.28				
NT2RP3001301	5.4	3.52	7.37	3.86	1.62	1.26	1.66	3.26	1.26				
NT2RP3001307	13.22	10.36	15.55	10.66	10.08	6.04	5.09	8.17	7.35		*		-
NT2RP3001310	9.88	12.87	16.58	11.85	7.95	6.71	4.27	4.42	3.89		*		-
NT2RP3001318	7.4	8.54	9.21	7.25	6.79	6.73	5.34	5.32	3.43		*		-
NT2RP3001322	11.09	11.38	14.04	15.94	12.19	11.47	14.66	6.17	7.73				
NT2RP3001325	1201.7	1025	1099	286.93	377.86	405.84	75.05	206.06	219.63	**	**	-	-
NT2RP3001338	162.73	132.54	198.96	171.74	181.83	241.04	134.27	161.16	143.19				
NT2RP3001339	16.04	11.7	17.8	11.35	7.84	6.88	2.83	5.64	4.58	*	**	-	-
NT2RP3001340	35.84	31.42	47.79	30.03	31.99	45.26	31.54	27.19	27.6				
NT2RP3001341	37.44	66.22	47.17	33.31	24.96	24.34	25.96	38.56	34.37				
NT2RP3001354	42.85	32.23	43.99	23.31	23.56	19.16	13.01	13.77	11.4	*	**	-	-
NT2RP3001355	2.26	7.76	10.15	5.3	3.13	3.72	4.66	3.96	2.91				
NT2RP3001356	43	54.12	51.32	62.98	37.84	46.81	81.45	50.61	59.12				
NT2RP3001359	34.72	29.05	42.17	41.55	33.32	37.07	21.86	23.34	24.66		*		-
NT2RP3001364	19.26	26.46	29.33	17.86	11.52	13.89	13.78	18.18	15.95	*	*	-	-
NT2RP3001373	16.79	12.24	26.6	10.58	10.1	9.34	9.17	17.19	12.49				
NT2RP3001374	95.59	73.12	108.77	136.19	114.69	107.19	68.33	56.48	69.32				
NT2RP3001383	12	19.08	15.5	12.1	5.75	6.51	13.27	9.62	6.82				
NT2RP3001384	22.91	17.21	30.7	33.57	22.7	20.56	19.13	14.74	15.12				
NT2RP3001388	9.38	9.17	7.78	9.06	5.69	4.27	7.73	5.71	5.18		*		-
NT2RP3001392	4.64	4.2	2.65	5.43	2.03	2.78	2.37	2.94	3.1				
NT2RP3001396	47.27	37.6	60.04	23.62	14.23	34.71	12.93	30.54	38.42				
NT2RP3001398	13.09	9.85	15.48	8.92	6.22	7.1	4.4	8.04	6.53	*	*	-	-
NT2RP3001399	17.91	14.49	24.37	16.05	7.15	6.8	6.07	7.51	6.62		*		-
NT2RP3001402	30.22	31.51	33.24	60.13	23.85	9.5	15.21	24.77	23.82		*		-
NT2RP3001407	72.56	60.86	88.74	96.01	74.06	85.12	43.61	63.39	61.28				
NT2RP3001416	18.88	22.22	16.48	16.79	17.16	5.73	3.31	4.98	5		**		-
NT2RP3001420	5.88	3.11	4.79	4.91	2.62	1.74	1.34	1.67	2.52		*		-
NT2RP3001425	11.74	10.47	11.8	11.91	6.37	9.11	8.4	4.94	6.04		*		-
NT2RP3001426	12.17	11.79	16.88	9.1	9.64	6.43	5.51	9.62	7.81		*		-
NT2RP3001427	10.81	11	21.59	12.3	6.43	8.87	17.63	22.78	19.89				
NT2RP3001428	7.7	10.58	20.16	8.58	3.38	6.04	5.05	8.84	8.9				
NT2RP3001429	4.55	6.04	12.09	5.05	1.79	1.93	2.26	1.46	1.89				
NT2RP3001432	20.32	18.99	30.96	16.39	14.24	12.25	16.49	28.23	11.89				
NT2RP3001439	31.43	37.32	28.95	26.93	25.44	19.21	14.96	11	10.21		**		-
NT2RP3001441	34.77	41.28	46.38	53.64	42.72	50.36	30.69	23.25	24.74		*		-
NT2RP3001446	4.24	2.49	4.94	4.53	3.01	2.2	2.82	2.01	1.51				
NT2RP3001447	22.35	21.24	25.11	13.3	8.65	15.94	13.67	37.08	14.99	*		-	
NT2RP3001449	139.79	126.76	203.02	199.4	166.47	178.45	131.32	106.74	139.38				
NT2RP3001453	31.6	35.5	49.48	34.98	29.3	36.04	28.49	31.86	35.69				
NT2RP3001457	13.38	17.23	17.13	11.75	10.12	6.15	5.98	6.75	6.92	*	**	-	-
NT2RP3001459	11.29	13.84	13.09	7	3.75	5.3	5.53	4.44	5.41	**	**	-	-
NT2RP3001463	6.65	4.84	3.81	4.67	1.94	1.07	1.96	2.08	0.69		*		-
NT2RP3001466	5.28	4.9	5.4	5.77	2.51	1.55	2.18	1.94	1.06		**		-
NT2RP3001472	5.37	5.26	7.06	12.24	7.01	3.59	1.12	2.87	2.9		*		-
NT2RP3001475	230.39	301.8	150.57	92.73	106.13	95.77	29.54	68.35	93.78	*	*	-	-

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Table 442

NT2RP3001479	6.51	3.77	10.27	6.45	4.18	2.2	2.6	4.56	5.3				
NT2RP3001490	15.72	6.25	23.45	15.28	5.31	6.47	7.24	7.84	8.04				
NT2RP3001492	14	14.91	21.99	13.76	7.53	9.81	14.28	13.21	12.48				
NT2RP3001495	18.56	21.11	19.03	12.08	9.76	9.93	15.89	18.33	21.35	**		-	
NT2RP3001497	36.57	27.99	40.31	47.7	28.75	36.07	23.59	21.43	24.3		*		-
NT2RP3001501	16.76	28.67	29.3	12.62	8.54	7.31	11.78	2.93	8.97	*	*	-	-
NT2RP3001527	5.54	5.56	5.02	7.34	2.65	3.31	4.71	3	2.59		*		-
NT2RP3001529	21.9	27.01	22.29	20.64	12.59	16.78	7.77	18.39	18.96				
NT2RP3001538	80.06	67.26	76.24	89.51	76.4	114.47	59.99	77.08	72.65				
NT2RP3001539	4.24	4.99	8.09	6.1	3.34	4.14	3.58	5.72	3.56				
NT2RP3001542	17.53	25.89	26.44	14.74	14.15	8.68	14.26	12.41	17.97	*		-	
NT2RP3001549	6.14	6.2	5.77	5.79	1.73	1.92	2.67	2.05	1.89		**		-
NT2RP3001554	28.4	40.66	43.76	10.47	10.16	7.96	15.92	6.96	13.22	**	**	-	-
NT2RP3001560	79.18	91.03	86.96	84.47	48.32	76.97	115.31	93.32	84				
NT2RP3001561	3.47	3.93	2.29	6.28	2.06	3.29	2.23	2.16	2.49				
NT2RP3001564	34.74	32.97	34.99	17.25	16.65	19.41	10.11	30.58	15.23	**		-	
NT2RP3001568	23.08	14.44	30.67	16.92	14.73	6.11	7.97	12.05	7.85				
NT2RP3001575	34.43	18.91	39.8	19.69	12.66	21.53	16.47	22.21	25.65				
NT2RP3001580	17.53	21.3	27.37	11.9	7.8	11.25	7.5	7.41	8.67	*	**	-	-
NT2RP3001587	14.32	16.9	20.18	11.06	6.6	9.89	19.28	18.65	20.31	*		-	
NT2RP3001589	6.31	5.44	5.39	5.29	2.4	2.48	2.34	4.87	3.41				
NT2RP3001592	37.3	61.22	57.18	30.41	23.17	28.18	46.3	38.66	32.65	*		-	
NT2RP3001607	11.49	11.68	9.02	7.34	3.49	8.45	5.15	2.53	3.96		**		-
NT2RP3001608	30.61	24.16	28.98	15.14	18	18.45	9.66	10.92	10.91	**	**	-	-
NT2RP3001613	55.34	46.31	54.71	81.86	48.17	86.77	51.11	48.11	44.78				
NT2RP3001619	162.64	181.38	185.09	152.03	118.43	125.85	144.48	167.59	158.06	*		-	
NT2RP3001621	29.97	24.25	25.08	33.83	16.83	30.34	32.22	27.66	24.11				
NT2RP3001629	28	13.33	26.21	16.28	12.69	19.85	19.79	23.48	12.56				
NT2RP3001630	3.51	2.38	4.56	4.63	1.01	2.11	3.79	2.64	3.67				
NT2RP3001631	64.16	51.12	67.22	112.91	65.5	60.67	59.38	50.82	71.84				
NT2RP3001634	3.71	4.65	2.94	7.85	2.25	2.09	4.62	2.51	1.18				
NT2RP3001642	29.24	22.78	34.25	25.21	18.32	21.46	34.78	35.92	40.14				
NT2RP3001645	18.72	13.31	23.84	17.34	7.46	8.49	11.13	12.12	12.05				
NT2RP3001650	4.88	6.33	12.48	7.77	5.89	4.37	3.47	3.76	3.82				
NT2RP3001667	17.36	19.67	39.76	21.84	7.89	10.07	11.81	14.81	13.16				
NT2RP3001671	13.32	10.22	13.86	10.05	5.86	9.27	7.9	6.32	3.97		*		-
NT2RP3001672	56.18	72.22	87.94	28.72	18.36	21.55	10.7	4.04	14.95	**	**	-	-
NT2RP3001676	11.94	10.66	12.76	8.88	5.99	6.36	7.09	3.31	6.98	*	*	-	-
NT2RP3001678	368.4	207.45	268.13	268.3	249.2	237.9	189.86	337.31	274.16				
NT2RP3001679	19.45	8.41	17.68	13.47	5.77	7.99	3.71	6.54	7.99				
NT2RP3001682	115.37	82.43	118.94	71.89	66.26	91.02	56.88	114.15	137.5				
NT2RP3001685	4.91	3.52	11.94	5.16	2.78	2.73	5	2.99	2.91				
NT2RP3001688	4.75	1.41	4.66	3.33	0.27	0.64	0.99	2.07	0				
NT2RP3001690	8.33	10.1	11.83	11.07	4.69	5.02	5.74	5.13	6.32		*		-
NT2RP3001693	2.22	6.17	10.5	5.55	2.56	2.65	2.84	2.33	2.39				
NT2RP3001696	7.34	11.29	11.31	6.93	5.94	11.43	6.97	3.31	6.44				
NT2RP3001698	780.45	572.31	725.4	616.13	658.96	0.94	533.83	1241.6	1289.4				
NT2RP3001708	348.43	297.84	257.74	514.57	355.27	1.82	148.2	628.13	519.33				
NT2RP3001712	32.9	21.37	35.65	18.32	14.72	16.28	22.44	33.16	22.67	*		-	
NT2RP3001716	13.86	9.55	15.36	8.27	11.28	8.27	5.55	15.45	9.22				
NT2RP3001724	28.26	21.7	18.91	32.47	31.93	25.73	16.65	23.86	18.15				
NT2RP3001727	27.92	15.82	33.03	16.01	12.47	12.24	8.97	9.14	8.89		*		-
NT2RP3001729	2.64	5.64	5.12	5.09	2.61	2.56	2.6	2.88	1.65				
NT2RP3001730	421.81	524.98	490.91	328.42	274.16	316.08	179.32	117.74	101.94	**	**	-	-
NT2RP3001733	1.54	1.62	4.9	4.53	0	1.49	0.54	0.39	1.87				
NT2RP3001737	7.85	25.52	17.42	10.76	4.14	4.59	3.35	7.04	17.36				
NT2RP3001738	28.07	24.45	41.36	18.76	13.82	15.18	12.56	15.63	32.84	*		-	
NT2RP3001739	2.19	2.42	9.16	4.78	1.8	1.62	1.06	2.07	0.9				
NT2RP3001742	11.1	11.43	14.41	9.77	5.51	6.65	7.73	6.52	8.12	*	*	-	-
NT2RP3001751	1.19	1.87	3.32	5.53	0.3	1.67	1.29	0.92	0.82				
NT2RP3001752	2.48	4.8	2.87	3.47	0.21	1.52	1.75	2.38	0.9				
NT2RP3001753	3.96	5.83	5.77	7.82	4.31	2.86	4.73	5.28	2.61				
NT2RP3001754	3.14	1.28	9.55	3.89	0.47	2.48	0.99	1.82	0.86				
NT2RP3001756	4.67	4.56	13.42	7.12	2.77	3.58	2.62	4.94	3.56				

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Table 443

NT2RP3001764	3.84	4.67	12.85	4.07	1.87	1.79	1.19	3.02	2.08				
NT2RP3001771	10.53	6.71	15.52	12	8.69	4.55	2.42	4.06	4.07		*		-
NT2RP3001777	40.65	47.79	33.95	47.7	28.57	21.63	29.91	18.82	40.09				
NT2RP3001782	18.47	18.59	14.66	13.14	8.87	10.49	5.89	13.23	9.56	*	*	-	-
NT2RP3001792	51.98	43.73	63.18	42.18	33.54	33.35	80.48	61.45	65.58				
NT2RP3001799	7.5	9.23	9.91	6.52	4.07	3.35	7.42	5.61	3.54	*		-	
NT2RP3001819	9.21	8.05	11.94	7.62	3.17	5.23	2.57	7.27	6.12				
NT2RP3001829	0.79	0.98	6.7	3.6	0.17	1.25	3.26	1.13	0.11				
NT2RP3001836	16.84	18.26	30.32	14.13	7.32	15.63	6.9	7.75	7.46		*		-
NT2RP3001839	6.81	9.19	13.79	8.6	4.4	4.34	2.3	5.79	3.54				
NT2RP3001844	5.94	4.03	11.89	5.39	1.37	2.09	2.04	1.24	1.53				
NT2RP3001848	53.13	36.02	38.27	40.15	39.26	28.02	46.65	51.58	51.5				
NT2RP3001854	53.05	46.79	83.54	47.02	38.11	28.76	72.37	61.23	74.82				
NT2RP3001855	8.77	9.33	11.43	9.53	8.22	8.62	9.1	7.34	5.15				
NT2RP3001857	2.78	1.95	7.57	5.8	0.8	2.63	1.53	2.14	0.95				
NT2RP3001858	1.48	1.77	7.55	6.01	1.18	1.83	0	1.41	1.37				
NT2RP3001861	4.86	3.76	12.83	6.03	2.09	1.54	1.75	2.42	0.53				
NT2RP3001866	4.29	4.19	8.56	7.38	2.36	3.86	2.27	2.97	2.71				
NT2RP3001871	4.11	2.37	11.14	4.75	0.71	0.4	0.62	1.36	0.06				
NT2RP3001874	10.44	5.38	11.3	5.07	2.46	1.93	2.08	3.65	5.3	*		-	
NT2RP3001878	6.84	8.82	7.25	6.09	2.26	2.81	4.01	2.14	3.46	*	**	-	-
NT2RP3001885	6.75	5.91	9.28	7.33	5.82	5.26	4.29	3.86	3.96		*		-
NT2RP3001896	15.8	9.61	18.78	10.19	5.77	12.23	2.88	7.21	8.15				
NT2RP3001898	10.12	6.81	17.59	9.29	3.83	4.48	2.35	4.36	3.15				
NT2RP3001899	4.46	3.48	9.66	6.74	4	4.77	3.33	4.46	3.02				
NT2RP3001901	2.97	2.49	8.51	4.89	2.11	2.05	1.6	0.22	0.74				
NT2RP3001915	21.98	18.4	24.23	18.83	15.46	12.75	6.48	6.95	5.98		**		-
NT2RP3001926	42.5	70.22	59.74	46.58	37.18	35.96	45.08	32.42	25.88				
NT2RP3001929	7.68	7.59	9	5.33	1.89	5.28	3.26	1.47	1.63	*	**	-	-
NT2RP3001931	7.03	5.58	8.39	8.57	1.83	4.32	4.68	3.69	4.06		*		-
NT2RP3001938	0.69	0.54	7.42	4.87	0	1.52	0	1.16	0.26				
NT2RP3001943	188.81	183.6	152.87	80.5	86.76	128.25	85.31	121.73	115.26	*	*	-	-
NT2RP3001944	17.12	20.99	26.58	14.69	15.73	4.63	10.12	15.18	9.75		*		-
NT2RP3001945	39.73	40.32	37.82	24.74	26.96	28.23	17.61	14.81	14.26	**	**	-	-
NT2RP3001947	47.48	38.36	48.19	30.55	15.52	22.26	24.69	18.23	25.96	*	**	-	-
NT2RP3001949	37.29	38.85	47.2	29.25	26.76	28.05	30.76	28.58	28.74	*	*	-	-
NT2RP3001952	10.17	10.07	6.99	3.68	1.57	0.37	2.44	1.18	1.17	**	**	-	-
NT2RP3001954	9.56	18.54	17.64	8.37	4.32	7.01	11.86	5.36	4.75	*		-	
NT2RP3001956	3.88	4.98	8.37	7.17	1.4	2.11	0.35	2.86	1.91				
NT2RP3001967	7.48	3.68	9.02	8.89	3.53	3.86	3.05	4.36	2.97				
NT2RP3001969	2.15	1.05	4.78	4.72	1.42	2.2	1.63	2.56	0.82				
NT2RP3001976	1.89	2.22	5.25	5.93	1.38	2.82	1.33	1.09	1.87				
NT2RP3001986	3.89	3.3	6.39	4.22	1.46	2.65	3.43	6.44	2.42				
NT2RP3001989	6.56	8.64	5.36	8.05	1.81	1.73	3.37	1.97	1.12		*		-
NT2RP3002002	7.76	11.38	8.57	5.38	2.01	2.22	6.25	3.04	6.16	*		-	
NT2RP3002004	7.76	12.41	12.06	6.85	3.16	4.05	3.73	2.48	3.6	*	**	-	-
NT2RP3002007	14.2	10.34	19.96	11.2	4.92	6.67	4.6	9.34	6.75				
NT2RP3002014	2.11	1.84	5.64	7.64	3.81	2.33	1.74	3.76	3.1				
NT2RP3002015	10.24	10.71	16.79	11.66	11.36	10.59	8.67	8.67	11.36				
NT2RP3002033	8	5.97	11.92	6.98	3.29	5.92	6.91	8.34	9.48				
NT2RP3002045	7.45	16.7	16.88	5.97	3.53	4.5	4.78	3.11	3.05	*	*	-	-
NT2RP3002054	292.36	495.82	456.61	206.09	224.87	171.66	441.79	291.3	543.12	*		-	
NT2RP3002056	3.09	3.6	0.88	3.45	0.32	0.79	0.92	1.02	0.67				
NT2RP3002057	10.26	15.21	13.61	7.78	1.9	3.69	9.33	6.11	3.21	*	*	-	-
NT2RP3002061	3.7	2.82	3.37	5.14	1.22	2.6	0	1.37	0.53		**		-
NT2RP3002062	14.95	11.22	12.96	12.28	11.33	13.44	7.88	11.32	11.12				
NT2RP3002063	3.07	0.91	3.18	5.76	3.45	2.53	1.35	2.57	1.94				
NT2RP3002064	4.75	4.07	6.06	8.44	3.11	3.26	2.69	6.61	3.66				
NT2RP3002071	2.99	2.02	2.84	4.58	1.41	2.26	2.09	2.02	0.69				
NT2RP3002073	4.16	1.73	3.01	5.39	0.35	0	3.4	1.98	3.29				
NT2RP3002074	3.97	4.7	9.59	5.64	1.52	1.74	2.26	2.79	1.06				
NT2RP3002075	115.61	136.72	152.03	61.15	60.41	66.84	138.08	127.44	140.01	**		-	
NT2RP3002077	1.88	1.37	7.12	4.73	0	2.99	1.52	0.95	1.4				
NT2RP3002081	9.52	4.64	17.43	9.04	2.14	3.36	6.77	6.6	8.59				

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Table 444

NT2RP3002086	9.1	5.64	14.68	7.72	4.13	4.75	9.35	9.69	7.69				
NT2RP3002094	3.34	2.83	6.44	4.61	2.06	2.3	2.41	5.92	1.29				
NT2RP3002096	12.33	8.92	11.73	8.59	3.97	5.5	5.94	5.18	4.01	*	**	-	-
NT2RP3002097	23.91	20.85	34.1	19.75	11.2	19.57	12.95	19.73	14.4				
NT2RP3002098	5.03	5.84	6.49	7.72	2.61	2.62	5.48	4.78	3.63				
NT2RP3002102	13.2	5.06	15.39	11.41	5.66	7.42	3.96	4.11	3.36				
NT2RP3002106	10.36	7.3	14.64	10.63	8.57	6.26	3.35	4.87	10.6				
NT2RP3002108	4.96	2.64	12.49	5.65	1.44	2.35	2.54	2.99	5.43				
NT2RP3002109	40.98	15.02	38.55	15.39	16.89	11.31	8.11	16.82	8.14				
NT2RP3002110	5.34	2.87	6.32	5.23	2.17	1.37	2.33	2.43	0.38				
NT2RP3002113	9.48	7.75	15.49	10.55	5.09	3.01	6.14	4.67	6.08				
NT2RP3002120	7.73	8.74	11.8	6.57	3.91	2.89	5.04	3.74	4.99	*	*	-	-
NT2RP3002121	1.11	4.94	1.77	5.17	1.32	0.68	2.8	1.37	1.2				
NT2RP3002126	64.09	54.26	55.37	40.43	28.8	44.09	33.92	65.97	39.23	*		-	
NT2RP3002128	8.94	4.6	9.8	7.18	4.51	3.23	4.1	5.32	11.38				
NT2RP3002130	45.15	21.81	38.29	25.97	19.96	17.62	5.74	23.29	23.75				
NT2RP3002133	713.78	729.07	666.05	842.53	766.78	697.72	544.62	1065.2	813.76				
NT2RP3002136	99.29	50.26	79.88	69.55	58.35	39.45	17.4	37.71	52.59				
NT2RP3002140	3.69	7.52	7.94	5.4	2.45	3.08	2.99	3.81	3.42				
NT2RP3002142	9.07	12.94	11.89	8.33	6.6	5.19	5.4	5.06	2.64	*	**	-	-
NT2RP3002146	9.3	10.61	11.18	9.37	7.32	7.23	12.19	11.03	8.72				
NT2RP3002147	11.07	11.26	19.71	10.63	7.44	5.02	4.38	6.88	4.67		*		-
NT2RP3002151	15	10.97	25.17	14.01	7.18	7.82	7.02	15.09	18.04				
NT2RP3002155	53.25	66.04	47.55	73.17	43.36	52.61	36.35	94.67	86.47				
NT2RP3002156	3.79	2.7	6.74	4.59	0.75	1.4	1.04	0.59	1.13		*		-
NT2RP3002160	9.08	10.25	12.47	12.87	7.96	7.04	2.86	3.65	6.87		*		-
NT2RP3002163	13.64	21.03	16.3	10.69	7.06	4.19	9.73	11.32	12.78	*		-	
NT2RP3002165	6.75	7.58	8.41	6.08	1.96	1.96	2.6	3.84	1.9	*	**	-	-
NT2RP3002166	5.43	5.03	4.69	5.27	1.55	0.67	2.88	6.31	2.47				
NT2RP3002173	517.9	446.69	509.69	297.97	240.6	253.29	44.66	135.22	128.7	**	**	-	-
NT2RP3002174	130.22	107.95	156.75	150.48	138.99	121.68	76.48	86.96	88.77		*		-
NT2RP3002181	5.97	4.69	12.81	5.8	2.39	3.23	1.84	5.23	1.34				
NT2RP3002185	44.31	38.54	51.77	25.79	16.42	22.4	38.06	52.39	48.7	**		-	
NT2RP3002193	7.33	7.63	13.87	8.26	3.71	3.99	4.19	5.78	8.23				
NT2RP3002204	41.05	45.66	52.03	45.02	28.36	25.63	28.31	47.28	47.76				
NT2RP3002244	12.8	20.63	18.31	13.33	15.24	10.05	9.17	7.08	5.13		*		-
NT2RP3002248	7.98	7.8	12.04	10.57	4.97	3.5	9.37	6.63	3.98				
NT2RP3002253	17.21	11.16	18.79	9.56	7.33	7.05	3.72	10.84	9.39	*		-	
NT2RP3002255	3.26	2.63	8.57	4.41	1.55	2.02	1.36	3.59	1.93				
NT2RP3002264	81.68	74.91	64.3	98.72	70.97	43.12	54.37	98.78	53.26				
NT2RP3002267	2.25	3.31	8.07	3.82	0.82	1.41	0.79	1.35	0.88				
NT2RP3002273	20.4	16.49	19.5	15.02	8.97	5.71	10.11	9.27	13.28	*	**	-	-
NT2RP3002276	3.97	2.93	8.36	4.35	0.7	1.55	1.24	0.89	0.84				
NT2RP3002281	13.35	12.31	15.77	11.45	7.06	7.28	10.16	10.76	11.32	*	*	-	-
NT2RP3002286	16.62	19.5	20.21	12.28	6.1	7.69	4.25	3.16	1.57	**	**	-	-
NT2RP3002297	94.9	98.81	132.4	64.72	33.84	39.98	11.41	37.45	29.98	*	**	-	-
NT2RP3002301	11.34	12.34	18.57	7.11	3.98	4.21	2.56	4.64	4.68	*	*	-	-
NT2RP3002303	7.54	10.15	16.1	7.32	5.62	4.17	5.05	6.82	7.85				
NT2RP3002304	91.67	49.25	50.79	81	77.65	34.95	31.29	39.07	25.04				
NT2RP3002309	4.32	3.35	10.38	4.01	1.44	1.07	2.59	1.36	0.22				
NT2RP3002311	9.65	9.45	12.73	9.08	6.57	4.41	3.9	4.09	5.31		**		-
NT2RP3002315	16.31	24.1	16.79	7.96	7.42	8.29	9.67	8.19	10.65	*	*	-	-
NT2RP3002318	8.49	14.45	9.47	9.99	3.2	4.43	5.43	3.04	5.3		*		-
NT2RP3002324	18.48	20.79	21.07	16.08	9.05	11.92	2.66	9.16	8.78	*	**	-	-
NT2RP3002330	14.44	26.39	29.36	13.92	12.3	11.42	5.88	11.72	10.72		*		-
NT2RP3002333	41.51	67.04	49.57	36.81	41.81	35.64	33.68	44.76	37.87				
NT2RP3002337	4.44	8.96	11.93	5.8	1.82	3.91	2.32	2.11	2.55		*		-
NT2RP3002342	25.61	22.15	24.13	19.61	11.87	9.75	11.85	13.94	20.4	*	*	-	-
NT2RP3002343	3.99	7.39	7.92	5.18	2.92	2.42	2.4	1.77	3.64		*		-
NT2RP3002351	20.96	17.51	19.58	6.79	4.97	3.6	9.93	4.83	3.54	**	**	-	-
NT2RP3002352	29.92	68.54	51.75	25.45	36.1	22.42	47.8	10.88	7.27				
NT2RP3002353	26.94	28.46	26.72	23.44	18.05	15.48	14.2	29.02	22.52	*		-	
NT2RP3002362	18.42	12.38	24.27	11.02	6.28	7.66	12.53	15.38	16.92				
NT2RP3002363	11.71	14.02	21.35	9.9	11.24	7.29	10.05	11.93	6.97				

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Table 445

NT2RP3002377	20.63	15.78	16.8	13.04	9.6	12.99	16.42	23.7	18.15	*		-	
NT2RP3002397	5.32	9.77	13.16	6.81	2.98	3.19	4.39	2.85	3.63				
NT2RP3002404	6.54	8.21	7.65	4.33	1.3	1.29	2.68	0.69	1.15	*	**	-	-
NT2RP3002410	7.62	4.7	8.02	3.73	3.33	1.2	3.81	3.45	2.67	*	*	-	-
NT2RP3002414	5.43	4.93	6.03	6.64	1.85	2.91	4.09	1.68	3.33		*		-
NT2RP3002430	5.86	5.44	9.44	4.78	1.52	1.85	3.2	1.23	1.16		*		-
NT2RP3002448	12.97	9.25	9.52	5.21	1.95	1.81	2.67	2	4.7	**	**	-	-
NT2RP3002454	12.06	19.92	16.37	13.74	7.64	12.02	13.75	9.17	8.67				
NT2RP3002455	4.76	3.53	5.11	6.77	1.51	4.71	3.7	5.48	5.26				
NT2RP3002456	58.03	38.92	43.81	27.96	14.69	15.06	14.57	36.86	33.26	*		-	
NT2RP3002462	20.18	13.39	21.5	10.24	9.33	4.6	3.9	5.28	3.19	*	**	-	-
NT2RP3002469	3.83	1.84	6.7	6.03	3.37	1.62	2.45	1.7	0.82				
NT2RP3002470	35.44	35.5	72.47	34.81	21.72	19.39	33.8	20.85	19.08				
NT2RP3002484	3.62	2.13	4.4	4.15	1.03	1.2	2.28	1.6	1.75				
NT2RP3002491	13.97	21.34	15.21	12.05	5.93	4.04	5.95	7.05	7.23	*	*	-	-
NT2RP3002494	24.09	40.78	35.02	15.6	8.77	12.21	26.54	16.61	15.03	*		-	
NT2RP3002497	1.45	2.72	2.12	3.96	0.95	2.47	1.03	1.64	2.67		-		
NT2RP3002500	16.58	14.89	20.26	24.82	15.49	27.1	14.57	11.42	19.8				
NT2RP3002501	32.52	29.62	45.43	41.64	21.97	31.25	12.71	18.89	18.63		*		-
NT2RP3002512	5.61	3.7	5.13	8.12	4.35	5.53	3.81	5.5	5.08				
NT2RP3002529	570.71	676.56	723.55	824.94	401.81	698.08	438.95	899.52	707.21				
NT2RP3002533	33.09	38.94	36.28	44.79	15.69	31.1	9.54	21.79	17.75		**		-
NT2RP3002539	6.02	8.36	9.74	6.07	3.74	0.01	2.47	0	0.12		**		-
NT2RP3002540	4.32	7.97	5.52	9.08	2.78	5.47	9.44	4.32	6.18				
NT2RP3002543	12.62	4.6	12.88	12.84	5.24	6.49	9.1	11.85	10.42				
NT2RP3002545	2.99	1.16	9.33	6.12	1.46	2.25	2.07	3.55	0.82				
NT2RP3002549	6.99	4.28	13.6	7.32	1.84	2.44	4.48	4.56	2.91				
NT2RP3002552	4.39	5.59	10.04	7.03	1.31	2.23	3.66	3.6	2.29				
NT2RP3002558	34.53	21.49	27.53	25.41	11.35	21.08	37	39.71	40.69		*		+
NT2RP3002565	13.64	7.8	14.18	11.1	3.88	9.31	11.41	13.37	16.44				
NT2RP3002566	7.8	8.76	13.33	16.41	6.98	8.51	6.63	7.76	8.89				
NT2RP3002571	8.13	11.03	10.93	9.57	4.89	4.39	4.63	2.67	3.9		**		-
NT2RP3002572	74.15	45.74	56.76	41.43	36.41	30.38	19.06	45.1	46.35				
NT2RP3002573	32.62	15.75	29.51	19.71	16.82	14.99	13.13	13.23	21.22				
NT2RP3002577	47.28	29.36	41.83	19.87	14.5	21	17.59	15.85	17.3	*	*	-	-
NT2RP3002579	8.63	6.06	12.6	7.23	3.12	4.38	5.33	4.66	5.1				
NT2RP3002582	6.19	3.82	10.45	7.84	3.56	3.38	4.87	4.78	3.74				
NT2RP3002587	10.07	10.45	15.76	10.84	6.77	7.46	4.8	4.74	3.88		*		-
NT2RP3002590	544.94	699.14	857.26	489.72	627.82	453.24	363.97	273.66	582.87				
NT2RP3002602	7.18	7.63	10.58	10.16	7.38	6.68	4.87	4.34	6.16		*		-
NT2RP3002603	14.44	13.52	18.75	16.38	10.66	15.03	8.16	15.4	88.12				
NT2RP3002621	6.81	5.15	9.83	8.56	3.04	3.97	3.12	5.17	6.09				
NT2RP3002622	6.75	5.01	13.82	8.8	3.27	3.73	2.74	4.44	11.45				
NT2RP3002624	26.96	16.99	21.5	17.24	10.36	13.21	17.97	25.27	18.08				
NT2RP3002628	6.59	5.38	9.7	6.43	2.65	4.46	4.24	5.21	2.97				
NT2RP3002629	5.76	11.73	14.59	10	6.43	5.93	6.71	4.48	3.96				
NT2RP3002631	48.35	45.23	46.18	26.1	22.1	27.75	26.27	23.38	21.25	**	**	-	-
NT2RP3002647	12	15.89	13.32	16.2	15.29	15.81	10.24	7.5	7.23		*		-
NT2RP3002649	9.3	7.92	12.59	9.96	4.23	5.01	3.45	5.1	5.57		*		-
NT2RP3002650	26.86	18.53	27.47	18.25	9.68	13.45	17.35	20.46	18.82				
NT2RP3002652	5.52	5.57	14.03	5.61	3.76	3.01	2.75	4.84	3.27				
NT2RP3002654	20.14	13.49	14.7	11.91	10.11	6.69	5.42	7.8	5.1		*		-
NT2RP3002657	16.5	15.29	20.85	14.05	6.31	13.07	15.2	14.6	14.98				
NT2RP3002659	15.92	19.34	18.66	13.66	10.7	8.74	4.85	10.09	6.73	*	**	-	-
NT2RP3002660	5.66	10.19	9.81	8.43	3.68	4.95	6.72	4.39	3.92				
NT2RP3002663	10.53	17.57	11.68	14.14	15.43	9.53	19.1	11.04	8.75				
NT2RP3002664	28.81	23.63	39.16	18.72	11.43	13.27	7.92	17.21	15.51	*	*	-	-
NT2RP3002667	32.83	27.15	33.62	23.94	18.84	19.81	15.18	21.3	26.19	*		-	
NT2RP3002671	38.88	30.21	40.39	24.11	16.4	14.74	30.8	35.93	33.74	*		-	
NT2RP3002682	8.45	6.51	13.68	7.64	3.93	4.02	2.41	3.04	2.62		*		-
NT2RP3002684	20.03	14.16	18.81	8.9	9.81	5.51	4.13	6.96	4.79	*	**	-	-
NT2RP3002687	9.25	11.21	13.71	14.12	8.33	10.78	7.86	7.74	7.01		*		-
NT2RP3002688	168.35	106.47	188.15	190.36	164.88	199.08	153.97	87.55	117.43				
NT2RP3002698	8.07	8.3	9.14	8.34	5.8	6.56	5.59	5.87	4.73		**		-

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Table 446

NT2RP3002701	11.4	8.8	15.19	9.64	4.21	7.04	4.79	10.11	7.18				
NT2RP3002705	30.23	29.89	43.68	30.05	23.71	23.42	20.15	25.03	27.52				
NT2RP3002708	25.52	23.92	35.27	19.02	13.81	19.8	19.34	22.92	17.32				
NT2RP3002711	87.34	128.24	131.86	149.35	126.88	84.65	16.56	37.78	36.54		**		-
NT2RP3002712	11.51	9.81	14.14	7.18	5.15	2.41	5.29	7.06	4.76	*	*	-	-
NT2RP3002713	17.13	13.75	17.42	8.41	9.55	4.36	13.41	9.28	8.38	*	*	-	-
NT2RP3002721	70.06	117.72	122.3	101.88	70.22	94.12	113.7	122.46	107.46				
NT2RP3002722	20.45	20.54	15.56	16.97	11.11	10.65	14.55	10.8	10.74		*		-
NT2RP3002723	12.21	14.76	21.14	7.75	4.55	7.76	4.96	7.72	6.61	*	*	-	-
NT2RP3002737	4.67	4.9	12.9	7.24	2.22	4.66	2.62	1.49	3.15				
NT2RP3002738	122.73	88.31	164.33	156.37	134.11	152.93	81.07	85.63	82.42				
NT2RP3002742	4.62	5.31	8.06	6.59	2.59	2.11	2.29	3.26	2.78		*		-
NT2RP3002744	11.76	7.9	17.24	10.03	4.45	6.38	6.88	8.18	6.87				
NT2RP3002756	8.91	6.64	6.82	7.81	5.13	2.63	2.84	1.31	1.38		**		-
NT2RP3002757	18.22	14.86	15.65	13.62	6.41	8.83	10.99	9.29	10.38	*	**	-	-
NT2RP3002758	16.5	15.69	16.85	13.98	8.17	9.33	15.83	11.78	10.47	*		-	
NT2RP3002762	6.55	8.17	14.93	9.13	2.38	7.36	4.56	5.11	6				
NT2RP3002763	6.01	4.94	14.86	7.96	3.26	4.46	4.15	2.77	3.35				
NT2RP3002770	13.79	15.86	20.19	13.26	7.67	4.65	6.38	6.79	5.16		**		-
NT2RP3002771	6.48	3.94	12.36	8.16	4.01	1.77	3.51	4.07	2.45				
NT2RP3002785	7.93	7.61	12.09	7.52	4.23	4.31	4.14	3.39	4.41		*		-
NT2RP3002790	12.74	8.68	16.54	10.03	4.49	9.67	11.67	8.3	11.43				
NT2RP3002799	44.32	36.15	61.61	71.32	40.17	61.97	38.77	29.46	32.11				
NT2RP3002801	9.13	7.96	8.02	8.82	3.17	7.55	6.99	2.43	2.63		*		-
NT2RP3002802	6.6	5.16	13.06	9.48	2.83	4.69	3.71	3.1	3.55				
NT2RP3002810	21.61	13.43	30.89	15.94	9.02	13.72	15.57	16.49	23.18				
NT2RP3002818	12.26	21.33	22.29	12.03	10.84	9.9	12.06	10.85	7.02				
NT2RP3002821	3.08	2.76	7.5	5.13	0.98	2.74	3.88	1.7	1.96				
NT2RP3002823	5.94	5.9	9.87	7.27	1.84	2.08	2.79	3.12	3.09		*		-
NT2RP3002825	46.16	68.1	69.32	16.84	16.8	11.22	9.52	7.53	4.62	**	**	-	-
NT2RP3002829	36.39	46.01	39.22	22.92	16.02	11.21	24.02	7.98	9.64	**	*	-	-
NT2RP3002831	9.11	9.95	10.41	14.39	9.89	8.12	9.96	4.98	9.9				
NT2RP3002836	16.68	11.51	17.27	10.91	4.09	9.65	4.06	4.72	7.36		**		-
NT2RP3002845	38.76	32.47	30.9	12.04	7.1	5.17	5.18	12.27	9.29	**	**	-	-
NT2RP3002852	27.07	21.18	24.92	24.24	10.22	18.18	20.47	22.49	18.97				
NT2RP3002861	6.45	10.44	9.71	7.81	2.41	4.65	6.77	4.65	5.14				
NT2RP3002869	6.19	9.1	10.7	6.8	3.23	3.7	4.89	3.27	3.99		*		-
NT2RP3002874	12.63	13.11	17.2	9.07	5.37	6.1	8.08	3.93	8.06	*	*	-	-
NT2RP3002876	143.63	148.27	181.51	254.93	163.87	216.77	137.83	99.6	141.63				
NT2RP3002877	16.65	19.83	22.97	18.33	13.19	15.19	13.02	8.47	12.29		*		-
NT2RP3002887	11.91	8.65	14.58	12.86	6.78	9.6	8.16	11.65	6.83				
NT2RP3002900	24.9	40	47.49	50.72	36.64	57.77	42.16	46.86	41.82				
NT2RP3002902	50.68	50.65	61.54	17.78	28.94	15.05	19.17	20.83	23.73	**	**	-	-
NT2RP3002909	5.43	3.6	6.73	6.91	1.07	4.91	4.39	3.43	4.07				
NT2RP3002911	32.27	38.37	39.37	37.75	22.31	32.66	41.96	41.35	47.38				
NT2RP3002948	97.24	122.54	134.73	183.88	103.17	110.98	109.55	85.09	95.2				
NT2RP3002953	130.69	155.36	174.07	145.08	99.42	98.1	201.22	181.14	165.58				
NT2RP3002955	11	13.27	12.07	9.74	5.71	6.63	7.47	5.75	5.17	*	**	-	-
NT2RP3002958	11.7	7.18	10.81	11.8	6.8	11.76	8.8	13.15	14.41				
NT2RP3002969	10.47	5.67	11.5	11.46	3.57	3.82	2.62	3.28	4.09		*		-
NT2RP3002972	9.18	3.34	9.31	7.48	3.85	0.87	5.21	5.53	7.19				
NT2RP3002978	17.8	13.14	17.07	16.61	7.47	16.55	15.56	17.59	21.66				
NT2RP3002983	14.39	16.02	14.98	15.99	6.52	11.68	18.52	16.38	19.45		*		+
NT2RP3002985	4.55	5.27	7.26	6.46	1.04	3.38	4.84	3.07	3.43				
NT2RP3002988	8.52	6.19	9.46	9	4.1	8.27	7.55	8.24	9.04				
NT2RP3003000	3.67	3.71	3.5	6.2	1.26	2.48	2.37	2.4	2.73		**		-
NT2RP3003008	10.96	2.67	10.84	10.43	9.08	7.16	5.31	8.35	5.42				
NT2RP3003012	2.33	3.47	10.69	4.62	0.4	1.73	0.84	1.69	1.54				
NT2RP3003015	94.04	42.5	71.87	52.22	37.75	51.79	66.36	44.43	66.31				
NT2RP3003018	4.14	3.97	9.63	5.98	1.6	1.48	2.56	2.43	2.26				
NT2RP3003028	3.8	4.39	9.49	7.13	4.25	1.98	3.07	2.68	1.64				
NT2RP3003029	10.59	12.64	16.85	9.46	5.29	7.18	11.38	8.45	12.28				
NT2RP3003032	18.44	16.02	27.77	16.77	11.22	12.42	15.36	17.44	10.46				
NT2RP3003041	9.55	9.82	9.95	12.39	5.66	4.67	6.47	4.02	3.62		**		-

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Table 447

NT2RP3003044	20.51	12.05	18.28	17.95	10.92	17.93	12.47	17.92	24.95				
NT2RP3003047	318.58	233.21	307.78	283.91	158.8	215.31	289.99	339.63	305.02				
NT2RP3003050	6.01	3.67	13.67	6.04	1.27	2.97	2.45	4.04	3.78				
NT2RP3003053	4.73	4.39	9.42	5.4	1.52	3.2	1.65	2.69	4.02				
NT2RP3003059	3.4	2.18	5.45	4.75	1.77	1.03	2.8	1.96	1.97				
NT2RP3003061	3.92	4.63	10.62	7.14	5.71	3.17	3.68	3.67	3.35				
NT2RP3003068	13.64	16.72	19.09	13.94	11.08	9.11	15.51	9.65	9.79				
NT2RP3003071	501.47	582.68	529.35	407.82	335.95	447.01	379.51	122.11	170.7	*	*	-	-
NT2RP3003076	11.52	4.82	12.85	9.77	5.93	5.76	7.19	9.4	27.45				
NT2RP3003078	14.69	14.12	17.86	9.88	7.71	7.1	3.81	7.38	11.24	**	*	-	-
NT2RP3003081	14.34	14.21	20.22	13.69	9.02	9.23	12.85	17.91	10.55				
NT2RP3003090	4.38	6.96	9.84	6.19	3.29	2.43	4.26	4.05	2.94				
NT2RP3003097	14.02	15.06	14.8	11.66	5.57	6.77	8.05	9.19	6.11	*	**	-	-
NT2RP3003098	6.1	7.46	9.23	6.48	4.67	4.01	3.99	4.01	3.93		*		-
NT2RP3003101	11.04	12.95	14.52	11.99	6.27	8.65	11.09	9.21	8.98				
NT2RP3003109	27.77	29.32	24.18	32.49	26.06	31.9	22.67	12.21	14.33		*		-
NT2RP3003121	14.74	6.75	15.15	12.65	4.66	5.96	4.11	5.09	12.75				
NT2RP3003133	8.34	7.45	12.11	8.93	5.28	6.18	2.52	4.07	7.32				
NT2RP3003137	4.53	5.11	11.1	4.41	2.55	1.77	1.57	3.58	2.61				
NT2RP3003138	14.49	14.02	31.57	15.47	8.83	7.42	8.07	6.92	9.16				
NT2RP3003139	17.72	13.28	16.88	11.32	8.97	7.87	7.6	10.95	5.4	*	*	-	-
NT2RP3003145	29.81	27.36	41.27	37.92	28.86	28.23	19.57	16.3	17.5		*		-
NT2RP3003150	3.07	5.2	3.99	5.23	1.85	1.66	3.17	2.46	1.85				
NT2RP3003157	36.91	28.34	31.25	37.59	20.43	24.91	16.55	12.31	12.99		**		-
NT2RP3003185	12.88	12.16	22.32	13.29	10.08	11.04	7.56	13.67	13.84				
NT2RP3003193	56.79	51.34	61.74	61.27	47.04	47.44	61.96	79.57	80.02				
NT2RP3003197	14.34	9.96	23.45	8.85	5.2	5.54	6.63	9.8	4.5				
NT2RP3003203	13.42	14.29	19.75	14.19	7.85	8.04	8.52	12.56	10.13				
NT2RP3003204	19.08	17.04	30.4	16.33	10.47	7.75	7.19	12.58	11.16				
NT2RP3003210	6.33	8.19	12.29	9.16	9.84	6.29	6.27	7.36	5.46				
NT2RP3003212	8.37	8.5	11.56	8.16	5.18	3.57	6.2	5.26	6.14		*		-
NT2RP3003213	5.67	4.05	5.85	6.17	2.96	2.21	4.78	3.56	3.34				
NT2RP3003224	55.68	53.67	56.74	16.3	18.72	16.37	11.98	29.14	26.24	**	**	-	-
NT2RP3003226	4.57	3.58	10.67	6.47	2.35	3.36	2.91	2.15	2.81				
NT2RP3003230	7.29	5.28	14.91	8.17	2.63	3.43	3.72	2.45	3.81				
NT2RP3003235	79.63	66.15	103.5	95.3	92.56	60.75	55.64	70.39	55.23				
NT2RP3003242	73.44	66.48	77.54	45.7	33.8	25.86	41.52	43.2	38.85	**	**	-	-
NT2RP3003251	104.1	73.55	126.64	135.43	95.34	99.58	79.05	81.02	71.32				
NT2RP3003252	10.37	11.27	12.13	9.17	5.92	6.54	5.47	5.61	2.73	*	**	-	-
NT2RP3003258	15.2	11.75	13.65	15.47	7.62	6.38	7.6	4.08	5.36		**		-
NT2RP3003260	20.33	21.23	23.55	13.01	8.75	11.13	14.98	15.72	16.47	**	**	-	-
NT2RP3003264	39.02	33.18	49.85	37.17	29.58	23.32	18.19	26.52	25.18		*		-
NT2RP3003273	4.51	4.91	15.07	7.81	4.36	2.59	2.42	2.45	2.99				
NT2RP3003278	10.07	13.81	15.32	10.69	5.74	4.93	4.88	5.26	3.08		**		-
NT2RP3003280	8.01	8.36	9.74	5.35	2.41	1.56	1.8	2.02	2.23	*	**	-	-
NT2RP3003282	6.34	4.14	6.3	6.51	1.72	3.27	3.2	1.42	0.91		*		-
NT2RP3003290	5.35	4.64	5.82	6.64	2.67	3.3	2.13	0.74	2.31		**		-
NT2RP3003301	10.24	13.13	10.58	8.04	5.22	4.9	4.68	1.19	1.93	*	**	-	-
NT2RP3003302	44.6	31.52	44.49	25.69	16.4	28.65	36.54	47.16	60.3	*		-	
NT2RP3003311	4.75	4.55	11.5	8.43	3.14	4.46	2.2	3.71	1.64				
NT2RP3003312	24.36	35.16	29.14	9.01	9.9	12.13	5.11	5.46	5.49	**	**	-	-
NT2RP3003313	11.85	10.76	12.83	7.95	5.85	3.91	3.77	4.31	3.7	*	**	-	-
NT2RP3003327	9.48	7.49	11.81	7.32	3.83	2.99	4.61	4.57	4.3		*		-
NT2RP3003330	28.77	45.14	40.86	24.02	22.59	18.95	15.05	12.99	8.77	*	**	-	-
NT2RP3003344	7.42	9.51	10.17	9.56	3.26	4.53	3.31	3.26	4.42		**		-
NT2RP3003346	7.58	7.33	10.55	7.96	3.11	4.95	5.04	6.17	6.71				
NT2RP3003349	77.06	82.34	60.61	59.72	39.01	41.31	20.2	47.64	67.66	*		-	
NT2RP3003353	5.79	9.35	12.49	5.84	3.66	3.54	2.78	3.58	3.64		*		-
NT2RP3003354	50.09	93.38	122.44	53.2	56.67	30.98	100.88	61.77	52.32				
NT2RP3003368	10.01	14.26	18.12	8.66	5.26	5.87	4.9	3.64	2.35	*	*	-	-
NT2RP3003375	13.81	11.33	19.09	11.92	5.85	11.47	12.29	9.6	11.66				
NT2RP3003377	8.13	11.7	14	6.42	2.73	1.97	7.35	4.71	8.09	*		-	
NT2RP3003384	15.97	18.59	24.94	10.9	5.8	5.57	11.93	4.66	4.64	*	*	-	-
NT2RP3003385	10.44	16.16	15.37	14.39	15.35	10.89	10.54	6.35	9.2				

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Table 448

NT2RP3003396	16.4	12.74	16.94	16.32	6.79	16.93	14.73	19.34	18.49				
NT2RP3003403	3.1	2.78	7.09	5.18	1.78	3.29	1.96	3.43	3.41				
NT2RP3003409	7.35	11.81	12.63	9.44	12.96	4.77	6.95	7.18	6.37				
NT2RP3003411	11.06	12.25	14.86	7.42	4.83	5.8	7.12	7.74	6.44	**	**	-	-
NT2RP3003420	19.06	32.9	36.55	21.71	11.78	14.57	23.43	20.87	21.3				
NT2RP3003425	6.27	5.68	8.42	5.84	2.62	3.03	4.29	2.39	4.38		*		-
NT2RP3003426	7.48	8.53	6.3	7.22	3.59	4.34	6.93	6.05	8.2				
NT2RP3003427	28.71	32.12	28.4	30.38	20.54	27.6	31.57	21.98	21.07				
NT2RP3003433	4.33	3.61	3.8	5.72	1.58	3.56	2.47	5.63	2.76				
NT2RP3003437	3.79	2.73	8.27	7.3	2.16	3.14	2.83	3.31	4.36				
NT2RP3003448	50.3	43.28	42.61	71.29	41.3	73.4	51.67	39.73	51.96				
NT2RP3003455	10.05	10.38	13.46	9.15	4.03	7.96	7.2	5.64	6.56		*		-
NT2RP3003462	10.37	9.93	17.25	9.92	5.42	4.43	5.52	5.56	5.82		*		-
NT2RP3003464	14.66	13.89	13.26	12.87	7.49	6.91	18.26	16.54	18.68		**		+
NT2RP3003469	17.22	14.94	13.68	14.5	4.68	9.94	19.05	18.28	19.4		*		+
NT2RP3003473	10.99	11.83	10.53	13.09	12.46	13.39	10.9	7.59	8.71	*		+	
NT2RP3003474	3.37	3.95	4.83	6.73	2.05	5.69	2.42	1.56	2.61		*		-
NT2RP3003475	25.58	23.74	27.15	19.96	21.31	0.35	11.64	10.85	19.52		*		-
NT2RP3003490	6.09	2.59	4.63	5.62	1.54	3.26	2.21	16.1	3.36				
NT2RP3003491	18.8	17.56	17.3	22.58	14.42	27.63	10.64	13.18	15.87		*		-
NT2RP3003493	4.17	0.67	1.27	6.14	0.62	2.97	3.62	2.46	1.88				
NT2RP3003500	5.9	4.89	5.02	7.76	1.8	6.18	6.6	5.32	6.99				
NT2RP3003527	7.67	4.85	6.47	6.19	2.35	4.17	6.12	6.18	4.88				
NT2RP3003532	10.61	16.22	14.72	12.47	4.81	8.89	14.42	12.45	12.15				
NT2RP3003535	38.7	29.85	32.07	25.66	21.86	25.49	14.16	14.9	18.19	*	**	-	-
NT2RP3003536	5.83	2.22	11.18	6.74	1.99	4.05	4.69	4.1	3.31				
NT2RP3003543	83.01	76.4	71.54	99.52	61.99	69.1	35.13	38.35	47.54		**		-
NT2RP3003549	5.05	3.61	9.39	4.68	1.49	3.34	2.95	6.92	3.73				
NT2RP3003552	5.72	3.03	6.03	6.81	1.98	1.74	4.06	3.11	1.34				
NT2RP3003555	7.3	5.08	11.06	9.46	2.64	6.2	9.1	6.02	7.32				
NT2RP3003559	16.08	18.05	20.35	13.82	7.72	7.64	10.69	7.28	10	*	**	-	-
NT2RP3003564	21.9	11.18	19.14	32.64	13.35	24.42	5.9	11.04	13.84				
NT2RP3003572	4.45	3.71	12.53	6.23	1.91	3.3	2.99	5.76	5.28				
NT2RP3003576	10.13	4.39	10.89	7.2	4.48	6.35	2.89	3.48	6.99				
NT2RP3003587	4.99	3.94	10.87	4.59	3.45	2.48	4.61	2.31	2.5				
NT2RP3003589	8.81	6.29	8.93	5.98	6.78	3.45	8.93	5.16	5.31				
NT2RP3003592	16.97	13.2	13.23	12.11	9.09	12.9	9.83	6.59	9.69		*		-
NT2RP3003593	8.95	15.57	14.21	12.38	7.8	13.05	6.6	6.07	15.06				
NT2RP3003614	16.19	15.38	25.69	16.13	12.3	18.94	17.5	16.33	15.44				
NT2RP3003621	23.31	9.78	21.55	19.16	8.76	10.65	10.2	15.44	18.25				
NT2RP3003625	30.15	13.92	27.9	27.09	17.35	16.31	10.08	25.7	26.09				
NT2RP3003627	13.85	10.22	17.05	10.88	8	10.73	7.14	16.59	27.58				
NT2RP3003636	43.56	19.06	24.94	24.57	26.12	25.77	9.71	16.11	10.76				
NT2RP3003642	9.55	5.41	10.21	6.42	5.7	4.71	4.31	4.84	5.36				
NT2RP3003645	11.93	7.13	13.91	10.67	5.31	7.85	4.02	4.25	4.25		*		-
NT2RP3003648	6.56	6.34	9.24	8.44	4.41	4.52	4.4	2.95	3.73		*		-
NT2RP3003649	26.09	26.77	29.81	22.55	18.26	23.64	34.18	24.81	32.1	*		-	
NT2RP3003650	12.61	11.46	21.64	12.68	5.46	10.24	6.28	12.27	13.31				
NT2RP3003656	6.54	4.65	10.33	8.68	1.7	4.51	3.42	4.72	11.15				
NT2RP3003659	9.46	5.9	15.28	7.57	5.1	6.1	4.35	6.43	5.32				
NT2RP3003662	8.5	8.39	10.9	5.37	1.92	5.94	1.35	3.6	1.87	*	**	-	-
NT2RP3003664	4.6	5.97	8.27	6.79	3.03	4.25	2.14	1.93	3.82		*		-
NT2RP3003665	11.75	13.45	13.25	12.32	5.11	5.74	4.75	7.06	5.47		**		-
NT2RP3003671	70.45	72.23	46.58	69.47	88.76	53.27	45.85	13.94	22.44		*		-
NT2RP3003672	12.42	9.87	13.46	13.04	14.86	11.85	11.18	14.12	13.48				
NT2RP3003673	8.49	4.06	14.72	9.56	1.98	4.91	4.97	6.88	5.68				
NT2RP3003679	10.33	6.46	20.68	8.71	5.36	8.11	4.9	8.58	8.08				
NT2RP3003680	13.23	15.82	26.63	9.67	11.59	10.92	6.46	10.89	9.67				
NT2RP3003686	3.02	3.35	12.97	5.63	1.59	1.88	2.06	1.47	1.07				
NT2RP3003688	9.23	7.33	11.82	8.17	6.77	3.83	2.32	5.97	3.24		*		-
NT2RP3003697	6.83	7.26	6.91	7.08	5.61	6.06	2.11	3.71	4.84		*		-
NT2RP3003701	9.67	9.01	11.76	7.31	4.84	5.19	3.31	2.62	4.46	*	**	-	-
NT2RP3003704	10.73	9.76	12.38	10.7	7.93	10.02	15.67	9.66	12.47				
NT2RP3003714	6.87	2.51	9.56	7.86	2.41	3.23	1.8	2.83	0.8				

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Table 449

NT2RP3003716	7.01	8.27	14.18	5.47	2.75	3.52	6.58	5.29	3.83				
NT2RP3003721	13.04	10.15	23.8	10.64	5.81	9.58	11.26	11.19	10.89				
NT2RP3003722	3.89	8.42	15.57	8.33	6.34	5.67	3.09	6.47	3.17				
NT2RP3003726	9.91	10.2	12.37	9.7	5.8	5.18	6.04	11.22	5.51				
NT2RP3003729	15.24	10.41	15.84	9.27	8.89	4.46	6.77	7.5	6.93		*		-
NT2RP3003731	21.75	24.76	24.08	12.03	11.65	6.88	4.57	8.08	5.08	**	**	-	-
NT2RP3003740	6.25	8.21	13.85	9.2	5.84	6.01	5.86	5.22	4.61				
NT2RP3003746	8.07	4.76	18.45	7.1	1.15	4.58	3.94	4.56	4.9				
NT2RP3003749	12.41	10.83	19.25	6.47	8	6.02	6.17	7.75	8.42				
NT2RP3003754	6.51	6.89	16.88	6.39	6.73	2.6	13.69	10.54	7.77				
NT2RP3003759	5.04	4.82	10.4	5.36	1.64	1.95	2.96	2.71	1.17				
NT2RP3003764	37.79	25.83	53.35	42.39	40.22	42.13	25.68	27.55	28.87				
NT2RP3003766	53.84	52.07	31.23	39.67	26.34	21.22	14.6	22.88	28.5		*		-
NT2RP3003767	8.01	8.08	7.88	8.43	4.34	4.24	4.39	2.88	4.34		**		-
NT2RP3003778	24.16	27.96	20.47	21.14	16.84	15.25	32.15	22.31	26.7				
NT2RP3003779	12.68	5.29	15.64	10.68	4.35	10.53	3.1	5.95	4.41				
NT2RP3003783	21.6	12.18	19.59	7.99	4.9	7.06	6.28	6.7	5.9	*	*	-	-
NT2RP3003787	6.7	5.75	13.41	6.04	3.64	1.85	4.2	4.99	1.46				
NT2RP3003789	8.11	11.36	13.5	7.92	6.55	6.67	5.52	5.69	3.28		*		-
NT2RP3003795	28.23	17.85	14.78	13.94	17.1	12.18	13.09	11.24	13.99				
NT2RP3003799	7.73	3.87	9.64	5.67	2.6	3.17	2.83	1.93	2.55				
NT2RP3003800	80.77	76.75	98.8	62.18	49.64	73.93	101.61	58.63	58.22				
NT2RP3003805	19.72	20.08	15.07	17.29	8.51	14.67	17.48	12.39	11.94				
NT2RP3003809	8.63	14.84	28.37	7.81	4.06	5.86	6.78	7.04	6.7				
NT2RP3003819	19.91	12.71	21.8	8.29	12.89	15.12	8.35	11.58	14.32				
NT2RP3003824	4.44	5.34	16.42	6	3.26	2.18	5.16	4	3.14				
NT2RP3003825	15.83	8.99	17.57	10.52	9.35	8.99	8.88	7.14	8.67				
NT2RP3003828	7.18	6.66	13.27	7.4	5.95	4.81	5.75	3.03	3.24				
NT2RP3003831	49.77	38.05	46.92	12.19	13.59	13	11.7	8.2	8.68	**	**	-	-
NT2RP3003833	7	12.76	5.52	6.51	1.52	3.02	3.01	1.46	3.08				
NT2RP3003836	22.92	45.16	37.16	16	14.78	18.49	26.73	7.91	11.58	*		-	
NT2RP3003842	3.09	1.45	4.55	4.66	0.91	2.25	1.5	2.49	0.97				
NT2RP3003843	23.17	13.66	18.94	21.62	11.25	18.44	16.81	22.17	19.21				
NT2RP3003844	11.64	8.51	12	9.56	4.9	7.1	7.94	10.02	13.51				
NT2RP3003845	11.56	8.88	8.25	8.42	3.89	7.04	8.15	6.21	10.88				
NT2RP3003849	5.16	5.61	9.2	5.16	1.5	2.43	2.36	2.09	1.97		*		-
NT2RP3003862	8.43	6.43	11.03	6.94	2.53	2.38	2.84	2.47	3.72		*		-
NT2RP3003870	9.39	14.91	15.6	7.42	3.58	2.61	4.29	2.22	5.4	*	*	-	-
NT2RP3003874	8.27	8.06	7.54	6.09	3.19	3.65	2.59	2.64	5.21	*	**	-	-
NT2RP3003876	6.84	5.28	7.66	10.08	2.52	6.72	2.11	6.22	4.3				
NT2RP3003880	11.2	8.02	13.91	8.47	2.77	7.12	3.7	8.83	6.95				
NT2RP3003889	6.9	11.63	11.35	8.75	7.41	9.51	7.37	8.06	5.22				
NT2RP3003891	13.51	11.29	17.94	8.42	7.04	7.49	10.43	12.21	12.8	*		-	
NT2RP3003914	2.72	1.62	6.58	5.33	2.56	2.54	2.7	1.4	2.69				
NT2RP3003915	13.41	9.97	16.94	9.16	3.98	5.29	7.39	4.87	7.36	*	*	-	-
NT2RP3003918	7.35	6.41	5.09	8.06	2.84	2.93	4.26	2.94	4.43		*		-
NT2RP3003920	10.75	6.92	10.79	7.41	1.85	6.22	6.71	4.36	3.03		*		-
NT2RP3003924	33.52	17.52	18.55	12.63	9.6	13.46	9.41	16.84	13.76				
NT2RP3003932	13.16	5.83	7.58	6.21	2.22	4.38	1.9	2.22	2.59		*		-
NT2RP3003939	11.85	14.76	15.54	9.97	7.98	8.34	3.34	3.94	3.84	*	**	-	-
NT2RP3003940	12.22	9.19	12.29	11.49	8.56	4.42	7.78	12.51	10.79				
NT2RP3003943	7.2	4.68	6.57	7.12	5.58	5.18	4.42	3.92	6.05				
NT2RP3003959	7.72	13.55	11.27	9.14	1.71	5.64	6.69	7.88	9.75				
NT2RP3003963	75.69	75.77	72.03	129.26	82.85	106.1	81.78	51.98	65.78				
NT2RP3003965	18.74	14.24	13.95	14.48	9.03	12.62	20.67	19.68	26.47				
NT2RP3003972	4.57	5.37	14.74	8.17	2.14	5.46	5	3.91	5.17				
NT2RP3003973	6.48	6.48	12.61	7.2	3.25	3.55	3.26	4.26	5.78				
NT2RP3003979	4.45	3.72	9.63	4.82	2.41	2.62	1.15	1.72	1.66				
NT2RP3003980	146.06	117.79	158.74	103.46	88.31	102.32	155.94	132.47	147.6	*		-	
NT2RP3003982	7.33	5.76	16.01	6.18	2.48	3	4.61	2.79	5.02				
NT2RP3003989	10.71	10.02	27.87	8.13	4.12	8.61	5.84	9.52	13.56				
NT2RP3003992	46.04	43.58	55.68	31.62	22.83	36.4	32.87	30.71	18.85	*	*	-	-
NT2RP3004000	75.38	38.37	57.12	93.25	54.67	51.6	36.78	36.39	33.4				
NT2RP3004001	14.94	10.16	22.03	15.95	8.73	15.13	13.16	15.23	21.06				

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Table 450

NT2RP3004005	23.75	15.81	26.46	14	10.64	14.12	16.28	18.58	18.43				
NT2RP3004013	22.54	11.33	21.98	6.11	3.13	3.73	3.05	4.94	3.43	*	*	-	-
NT2RP3004016	7.39	7.18	13.3	10.92	9.82	5.35	6.27	5.44	4.76				
NT2RP3004025	22.82	15.93	25.25	22.37	10.03	12.12	21.2	17.91	21.7				
NT2RP3004030	4.66	4.65	8.61	4.83	3.44	3.8	4.36	2.41	1.96				
NT2RP3004041	4.1	2.26	3.06	5.03	2.28	1.57	2.62	0.7	0.71				
NT2RP3004042	2602.1	1724.7	1778.2	2098.3	1690	1795.1	1947.3	2828.9	2085.3				
NT2RP3004044	32.34	21.11	30.01	12.91	11.29	11.35	7.18	15.29	26.2	**		-	
NT2RP3004051	19.22	22.27	34.06	33.29	21.4	25.83	12.31	39.18	27.89				
NT2RP3004052	20.9	17.89	21.89	18.39	15.57	16.97	13.27	17.39	19.16				
NT2RP3004053	19.14	11.65	20.87	15.13	10.18	12.84	3.1	7.99	5.77		*		-
NT2RP3004055	5.06	6.81	8.6	5.35	3.54	2.7	2.8	3.03	2.13		*		-
NT2RP3004059	26.03	28.01	36.98	19.3	19.54	21.1	20.16	18	15.03	*	*	-	-
NT2RP3004063	29.14	22.42	34.14	23.83	23.28	19.51	31.01	26.64	12.72				
NT2RP3004067	7.95	8.62	20.76	10	4.39	4.65	3.75	4.12	8.39				
NT2RP3004070	905.61	934.59	965.28	291.19	622.85	595.78	278.31	1360.6	1279.5	*		-	
NT2RP3004075	11.59	15.27	23.01	8.7	5.82	8.89	3.95	5.77	5.73		*		-
NT2RP3004078	13.83	11.53	17.13	13.53	5.08	9.69	12.68	11.48	12.45				
NT2RP3004083	33.39	27.25	43.84	12.1	13.49	7.53	6.38	6.07	6.79	*	**	-	-
NT2RP3004084	25.34	24.44	39.2	27	15.25	16.2	38.67	47.1	47.33				
NT2RP3004087	13.47	17.06	17.12	15.44	8.85	8.53	10.22	10.37	8.13		*		-
NT2RP3004090	72.24	81.09	78.4	57.09	57.97	55.36	77.78	70.88	90.98	**		-	
NT2RP3004093	28.49	18.68	45.95	14.41	12.09	18.33	8.92	23.19	25.5				
NT2RP3004095	33.26	26.66	48.11	23.16	21.66	33.49	19.24	23.44	21.47				
NT2RP3004102	34.73	35.32	40.77	25.98	17.76	24.22	15.74	23.36	12.18	*	**	-	-
NT2RP3004110	7.05	4.57	10.07	7.67	1.49	3.89	2.25	3.65	1.62		*		-
NT2RP3004119	11.05	7.96	13.76	6.77	3.42	4.11	3.84	3.73	1.51	*	*	-	-
NT2RP3004125	3.06	3.32	9.52	6.05	1.93	1.78	1.81	1.49	1				
NT2RP3004129	11.05	13	16.54	13.66	11.08	8.18	7.67	3.97	5.87		*		-
NT2RP3004130	6.85	5.7	8.22	6.11	4.3	3.04	1.91	3.1	2.41		**		-
NT2RP3004133	8.31	5.24	20.22	8.3	3.21	4.09	3.33	4.08	3.29				
NT2RP3004145	5.99	4.29	13.16	5.33	2.78	2.69	2.63	4.11	3.14				
NT2RP3004148	53	37.5	49.88	32.7	23.92	15.17	30.82	36.4	44.13	*		-	
NT2RP3004155	8.18	8.86	12.7	12.14	3.98	4.25	2.59	2.94	3.13		**		-
NT2RP3004165	77.97	53.41	68.62	51.37	46.12	31.89	49.51	25.55	55.19				
NT2RP3004179	9.55	6.18	11.2	6.95	2.94	2.88	4.01	3	3.7		*		-
NT2RP3004185	6.31	5.21	6.12	9.04	2.95	2.38	1.55	0.61	2.3		**		-
NT2RP3004188	6.31	7.01	6.86	7.94	4.08	2.67	3.74	2.3	1.82		**		-
NT2RP3004189	15.63	7.3	21.16	9.58	5.21	8.89	4.83	8.4	6.14				
NT2RP3004190	64.52	34.39	57.67	48.45	40.38	53.55	47.37	42.21	45.49				
NT2RP3004191	122.58	123.5	136.79	74.78	46.86	44.19	48.51	70.16	47.4	**	**	-	-
NT2RP3004202	18.55	13.31	21.41	14.01	15.47	6.42	10.97	12.13	10.67				
NT2RP3004205	10.59	7.33	14.79	6.1	4.73	2.92	2.52	2.35	2.6		*		-
NT2RP3004206	15.55	12.16	17.94	7.47	8.64	7.63	5.69	7.13	12.18	*		-	
NT2RP3004207	8.65	8.42	9.24	5.53	2.88	3.67	2.31	1.22	2.02	**	**	-	-
NT2RP3004209	27.4	23.65	14.82	17	13.67	16.8	19.95	17.39	12.49				
NT2RP3004215	22.45	23.53	27.86	11	7.75	10.82	4.22	8.07	7.54	**	**	-	-
NT2RP3004219	5.58	5.12	13.51	6.61	2.08	4.81	3.19	3.17	3.09				
NT2RP3004242	4.18	6.26	13.02	6.15	3.05	4.41	4.72	3.98	3.45				
NT2RP3004246	3.85	4.1	9.37	4.89	2.24	1.94	1.48	3.04	2.11				
NT2RP3004253	7.46	3.55	9.07	5.38	2.69	1.44	2.57	2.47	3.21				
NT2RP3004258	8.43	4.33	9.6	7.18	4.84	3.38	6.14	4.76	3.41				
NT2RP3004262	5.75	6.49	6.12	6.38	2.36	2.74	4.69	0.6	2.65		*		-
NT2RP3004275	5.37	6.56	6.47	6.33	1.33	2.3	2.5	1.89	3.75		**		-
NT2RP3004282	4.86	27.86	18.63	6.39	3.74	5.05	2.71	3.54	3.27				
NT2RP3004289	6.43	5.13	10.92	5.92	2.79	3.35	2.25	2.59	3.21				
NT2RP3004294	4.71	4.44	6.56	4.95	2.62	3.32	2.88	6.45	3.88				
NT2RP3004298	64.72	55.93	73.74	63.66	58.3	70.43	70.1	51.46	68.44				
NT2RP3004309	10	7.69	11.97	7.21	2.5	3.75	5.84	3.48	5.36	*	*	-	-
NT2RP3004321	23.29	38.14	42.57	12.44	16.53	8.76	14.14	5.43	9.71	*	*	-	-
NT2RP3004322	4.19	4.29	4.98	4.8	1.3	0.91	2.93	1.84	2.18		**		-
NT2RP3004332	9.53	11.83	11.13	7.92	3.85	4.05	4.3	2.24	2.92	*	**	-	-
NT2RP3004334	14.9	13.13	17.93	15.28	11.06	7.25	6.62	11.71	9.43		*		-
NT2RP3004336	9.94	8.5	13.66	9.26	7.37	6.68	4.73	8.17	4.32				

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Table 451

NT2RP3004338	20.15	16.11	15.61	11.35	11.45	16.93	14.61	18.8	16.46				
NT2RP3004341	45.52	46.06	66.9	30.5	32.86	24.48	35.75	44.1	42.23	*		-	
NT2RP3004345	5.41	7.27	12.03	7.28	2.26	2.19	5.01	3.58	4.59				
NT2RP3004348	8.2	11.9	19.15	6.37	5.32	6.29	9.92	4.97	6.08				
NT2RP3004349	46.27	44.89	52.77	25.21	14.4	28.82	51.32	39.58	50.42	**		-	
NT2RP3004355	13.69	17.95	13.45	12.62	8.18	11.72	10.41	5.58	7.23		*		-
NT2RP3004356	6.56	4.92	9.79	7.46	3.18	5.93	2.87	5.09	3.61				
NT2RP3004360	11.41	7.43	12.2	11.26	4.38	7.34	4.62	4.39	7.23		*		-
NT2RP3004361	22.43	16.96	27.29	12.91	14.7	16.73	18.55	21.02	26.27				
NT2RP3004374	6.08	4.11	5.92	5.52	2.91	4.87	2.31	2.56	2.6		*		-
NT2RP3004378	50.03	39.45	48.92	39.78	39.18	55.24	61.97	46.46	63.83				
NT2RP3004399	25.24	30.84	27.39	23.98	13.72	17.1	23.05	19.32	24.46	*		-	
NT2RP3004405	5.46	2.89	3.95	6.86	3.8	2.54	2.58	3.57	3.49				
NT2RP3004406	48.02	80.1	76.06	27.26	18.49	29.22	40.17	40.49	25.13	*	*	-	-
NT2RP3004411	21.84	13.45	15.39	11.3	8.55	12.78	6.83	10.8	17.8				
NT2RP3004424	12.83	9.11	14	10.53	6.29	12.31	8.49	6.86	11.07				
NT2RP3004428	9.06	4.59	7.61	7.92	3	6.19	2.13	2.45	2.73		*		-
NT2RP3004432	41.77	40.01	43.16	46.87	29.7	37.75	43.11	55.91	45.48				
NT2RP3004434	6.59	6.36	9.2	19.42	10.09	11.41	8.35	8.97	10.87				
NT2RP3004446	5.55	1.31	2.23	5.8	1.27	2.52	2.84	1.81	2.66				
NT2RP3004451	28.05	27.38	35.9	43.9	34.57	29.99	27.84	20.66	27.06				
NT2RP3004454	3.04	4.95	3.07	5.17	2.65	2.97	3.32	1.95	4.76				
NT2RP3004466	17.88	12.48	17.63	17.19	13.76	19.32	8.38	10.38	11.73		*		-
NT2RP3004470	6.58	4.48	12.1	9.37	2.81	3.83	6.66	6.76	5.57				
NT2RP3004472	4.96	8.32	13.71	7.25	5.54	4.58	2.83	3.65	3.08				
NT2RP3004475	9.27	6	11.18	8.66	2.73	3.48	3.79	5.2	3.34		*		-
NT2RP3004480	22.33	15.69	32.46	17.18	10.83	15.46	12.05	10.67	10.95				
NT2RP3004481	7.51	6.36	10.91	7.96	3.04	6.85	8.17	5.21	5.83				
NT2RP3004490	1.96	3.67	4.31	5.07	2.67	3.48	2.86	2.05	1.78				
NT2RP3004496	29.05	43.68	52.3	32.37	24.7	28.45	17.59	12.79	20.95		*		-
NT2RP3004498	6.1	6.29	10.2	8.29	5.15	5.43	3.36	4.35	5.77				
NT2RP3004503	13.34	8.17	15.98	13.28	6.98	13.95	9.69	13.04	16.21				
NT2RP3004504	26.86	13.87	24.17	16.13	11.34	13.03	8.55	9.71	9.3		*		-
NT2RP3004505	60.88	42.22	65.16	60.93	61.18	59.93	38.93	40.66	35.92				
NT2RP3004507	6.96	5.95	8.15	5.81	3.02	3.27	2.74	2.78	2.24		**		-
NT2RP3004519	3.09	3.32	8.34	4.29	1.92	0.77	1.76	0.64	1.58				
NT2RP3004524	22.27	16.91	24.46	12.8	14.38	10.78	10.59	7.77	17.02	*		-	
NT2RP3004527	31.26	36.6	41.52	32.19	22.11	22.1	23.08	21.05	18.57		**		-
NT2RP3004534	1954.5	1225.4	1438.4	1526.7	1505.7	1779.6	777.34	2507.5	2418.6				
NT2RP3004539	4.71	4.69	10.04	5.61	3.18	4.71	4.15	5.52	6.25				
NT2RP3004541	14.72	10.14	22.05	12.49	7.26	9.05	8.78	11	10.96				
NT2RP3004544	17.32	13.37	16.21	16.43	8.76	13.79	6.55	10.61	10.66		*		-
NT2RP3004551	12.43	7.15	13.73	9.94	5.53	6.65	10.18	9.42	7.62				
NT2RP3004552	19.37	11.98	21.3	18.2	12.57	16.98	18.98	16.22	18.63				
NT2RP3004557	11.18	12.99	15.15	12.15	8.14	12.54	12.08	12.56	14.07				
NT2RP3004561	2.52	4.37	4.66	6.9	2.44	3.94	3.97	3.31	3.2				
NT2RP3004566	16.46	13.14	29	10.83	7.99	8.15	3.35	6.43	21.27				
NT2RP3004569	20.41	16.28	28.7	14.13	11.71	13.43	13.97	16.78	16.75				
NT2RP3004572	12.48	13.38	19.74	11.19	9.39	9.67	3.98	9.35	8.35		*		-
NT2RP3004578	6.49	6.06	8.06	7.21	4.59	4.3	5.13	4.76	4.1		*		-
NT2RP3004584	8.34	6.1	9.57	5.07	2.29	4.9	3.85	3.5	2.08	*	*	-	-
NT2RP3004588	4.64	4.62	7.46	7.78	2.88	3.22	3.01	5.54	3.28				
NT2RP3004594	18.77	25.61	21.44	21.59	19.15	22.94	29.86	27.19	18.84				
NT2RP3004603	4.79	6.26	5.77	8.8	3.9	4.9	5.46	7.72	5.82				
NT2RP3004612	6.46	6.92	12.58	12.71	4.69	5.32	2.31	10.42	14.75				
NT2RP3004617	8.05	8.14	15.39	8.87	3.8	5.79	3.78	6.88	7.16				
NT2RP3004618	36.56	23.11	37.29	24.87	25.7	22.47	22.39	33.72	29.91				
NT2RP3004625	19.69	16.42	18.21	11.76	10.91	14.71	6.25	8.76	11.12	*	**	-	-
NT2RP3004635	11.6	9.72	13.73	7.06	5.4	4.21	3.68	2.39	2.94	*	**	-	-
NT2RP3004640	4.25	10.31	12.87	7.49	7.74	5.34	4.28	3.2	9.33				
NT2RP3004642	15.02	23.4	27.93	15.96	15.92	16.39	17.49	17.88	14.1				
NT2RP3004647	10.52	11.7	14.69	13.69	6.27	6.34	18.22	14.86	18.18		*		+
NT2RP3004652	28.1	24.38	41.76	13.95	14.47	12.02	4.02	12.27	12.65	*	*	-	-
NT2RP3004669	7.74	7.41	20.24	7.31	6.69	6.49	4.02	6.68	4.21				

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Table 452

NT2RP3004670	5.78	5.9	15.55	5.95	8.77	4.78	1.73	4.19	3.14				
NT2RP4000008	4.28	3.76	9.74	7.01	3.13	2.8	0.87	1.61	1.16				
NT2RP4000018	777.26	720.79	779.71	458.85	552.02	180.81	608.14	341.39	573.73	*	*	-	-
NT2RP4000023	12.08	13.49	11.95	6.59	4.27	3.03	5.43	2.46	2.58	**	**	-	-
NT2RP4000025	10.92	10.01	10.19	8.87	3.46	6.52	5.55	3.38	7.2		*		-
NT2RP4000035	13.64	12.06	18.1	13.28	10.2	10.62	12.01	14.28	15.16				
NT2RP4000041	7.95	4.85	12.17	6.47	2.4	5.6	2.83	2.55	3.55				
NT2RP4000049	5.5	8.69	14.31	6.89	4.49	2.04	3	3.25	4.73				
NT2RP4000050	7.92	6.2	13.4	9.91	4.4	3.61	2.52	5.2	2.39				
NT2RP4000051	11.64	12.9	17.08	9.37	6.75	7.7	7.83	11.79	8.18	*		-	
NT2RP4000063	9.36	7.43	9.4	6.21	2.66	4.7	2.12	2.88	2.29	*	**	-	-
NT2RP4000065	8.57	5.45	7.62	5.43	1.38	3.74	3.79	2.44	1.14		*		-
NT2RP4000070	8.9	10.6	11.32	10.92	5.17	4.74	3.9	3	5.41		**		-
NT2RP4000074	7.09	6.56	7.33	6.07	3.64	2.14	2.7	1.95	3.11		**		-
NT2RP4000078	10.64	7.98	15.22	9.04	4.02	9.72	4.12	7.85	6.44				
NT2RP4000080	39.53	29.48	35.07	14.73	7.78	7.51	7.13	12.84	8.56	**	**	-	-
NT2RP4000099	17.27	15.29	21.59	9.54	12.81	6.62	5.87	6.72	3.64	*	**	-	-
NT2RP4000102	8.52	8.93	15.05	7.45	6.98	5.31	5.6	5.59	5.12				
NT2RP4000103	20.66	29.01	31.17	15.7	16.08	13.47	20.04	13.58	12.68	*	*	-	-
NT2RP4000108	10.35	7.66	11.54	5.11	5.39	5.22	4.96	2.69	3.44	*	**	-	-
NT2RP4000109	9.73	11.84	8.78	8.41	4.9	6.21	6.7	3.67	4.98		*		-
NT2RP4000111	9.68	7.22	7.83	10.68	5.18	7.24	9.51	4.5	2.88				
NT2RP4000112	16.91	11.4	24.28	20.79	19.36	22.3	16.09	13.49	17.44				
NT2RP4000115	7.34	4.25	10.98	5.53	2.81	4.32	2.76	2.51	2.27				
NT2RP4000129	24.84	25.48	33.51	13.19	12.49	13.21	12.38	15.5	12.9	**	**	-	-
NT2RP4000137	20.7	16.54	14.08	10.11	6.13	6.89	9.81	6.38	10.47	*	*	-	-
NT2RP4000138	7.91	6.25	8.72	5.36	2.95	3.73	3.09	3.11	5.54	*	*	-	-
NT2RP4000141	11.63	7.1	7.39	5.05	2.2	2.55	3.83	2.34	1.67	*	*	-	-
NT2RP4000147	7.8	8.75	6.46	5.67	2.45	1.71	3.71	1.66	2.95	*	**	-	-
NT2RP4000150	22.83	40.43	32.64	26.18	18.45	19.86	24.1	13.63	20.82				
NT2RP4000151	5.35	2.77	7.92	5.7	2.57	4.58	2.81	1.73	3.64				
NT2RP4000157	5.03	3.17	7.55	5.12	2.41	3.03	2.61	4.59	2.88				
NT2RP4000159	7.7	6.21	14	7.81	5.43	9.16	5.02	7.93	7.16				
NT2RP4000163	11.36	16.35	22.24	7.82	6.7	5.1	11.58	8.66	14.17	*		-	
NT2RP4000167	5.72	10.76	11.28	6.86	1.93	2.94	6.09	1.64	2.98				
NT2RP4000171	17.67	20.8	16.76	13.24	7.81	11.48	17.22	11.6	13.85	*		-	
NT2RP4000175	7.68	11.5	9.21	7.19	5.94	7.44	5.84	4.86	6.71		*		-
NT2RP4000180	8.25	9.87	9.45	8.5	4.86	7.21	9.47	6.55	7.72				
NT2RP4000185	3.44	9.69	9.07	5.25	3.82	5.08	3.89	5.51	9.51				
NT2RP4000192	3.66	2.3	7.85	7.16	4.58	3.22	2.99	2.89	2.84				
NT2RP4000194	4.94	3.92	6.27	5.67	6.92	4.33	4.73	3.32	6.3				
NT2RP4000196	4.44	3.86	8.22	4.42	2.19	1.89	2.14	2.44	1.01				
NT2RP4000210	4.32	3.9	5.46	5.03	2.17	1.97	3.56	2.52	3.91				
NT2RP4000212	10.41	10.12	9.74	6.43	6.54	3.07	4.86	4.69	2.44	*	**	-	-
NT2RP4000214	21.41	28.56	31.47	14.93	12.43	12.75	14.71	10.53	11	*	**	-	-
NT2RP4000216	18.56	17.54	17.8	9.05	3.32	6.3	7.12	4.66	4.69	**	**	-	-
NT2RP4000218	20.76	13.22	21.73	16.85	12.17	21.91	12.16	18.58	23.33				
NT2RP4000223	11.85	6.5	8.31	9.5	4.18	9.75	8.04	7.05	11.84				
NT2RP4000243	10.56	9.93	12.96	11.2	9.86	11.7	8.64	9.69	10.23				
NT2RP4000246	7.12	5.86	5.64	5.65	4.43	4.42	2.37	2.31	3.27		**		-
NT2RP4000250	11.29	8.98	12.39	10.04	3.49	5.45	5.46	5.81	5.67		**		-
NT2RP4000256	3.26	5.13	6.67	4.51	2.18	2.56	3.11	2.41	2.48				
NT2RP4000257	23.54	23.13	30.8	34.24	27.3	37.51	26.44	19.58	27.22				
NT2RP4000259	5.19	5.55	3.54	8.67	2.13	4.17	4.34	3.84	5.01				
NT2RP4000261	4.72	2.05	7.37	6.8	1.48	3.76	2.37	3.23	3.88				
NT2RP4000262	2.93	2.46	11.12	5.21	1.63	2.61	2.49	2.62	2.71				
NT2RP4000263	8.03	5.82	13.8	7.33	4.75	4.76	8.35	4.63	5.93				
NT2RP4000280	36.69	25.69	34.43	21.81	13.93	11.89	23.3	25.5	21.75	*		-	
NT2RP4000286	7.96	5.71	10.34	8.48	4.4	5.47	4.56	4.72	2.93				
NT2RP4000290	6.28	5.27	10.35	7.67	3.77	4.58	5.45	2.24	4.35				
NT2RP4000291	23.37	31.04	45.88	29.65	20.44	28.9	16.58	13.08	6.43		*		-
NT2RP4000301	9.06	21.31	16.13	18.84	21.42	12.52	13.04	8.64	8.86				
NT2RP4000312	7.37	5.86	10.71	6.75	4.45	5.45	4.08	4.23	5.32				
NT2RP4000321	14.11	6.64	13.51	10.77	5.65	7.11	6.38	8.75	12.76				

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Table 453

NT2RP4000323	42.99	31.25	39.68	23.73	23.52	24.08	25.22	26.31	20.02	*	*	-	-
NT2RP4000324	28.87	20.72	25.53	23.74	16.73	21.66	28.32	24.57	21.68				
NT2RP4000334	11.51	10.77	15.15	9.55	9.47	9.13	6.39	6.12	5.89		**		-
NT2RP4000343	20.88	12.62	32.18	18.49	14.22	8.72	14.98	17.89	14.7				
NT2RP4000348	12.35	14.21	17.96	11.42	8.77	9.63	12.1	7.85	8.02				
NT2RP4000349	8.77	16.24	12.89	11.44	12.7	9.21	11.37	7.34	11.23				
NT2RP4000355	253.25	117.6	189.34	264.37	149.78	254.47	257.02	316.08	192.79				
NT2RP4000356	61.98	36.7	79.91	60.03	57.95	82.79	39.95	40.28	37.12				
NT2RP4000360	38.52	30.1	36.81	28.77	30.27	34.86	22.5	29.04	23		*		-
NT2RP4000367	5.32	7.72	13.11	9.15	7.75	6.58	5.65	7.52	4.05				
NT2RP4000370	6.13	3.8	7.29	7.4	4.81	4.6	4.29	3.27	2.44				
NT2RP4000373	52.16	35.56	49.83	33.3	22.86	20.18	8.95	13.1	7.55	*	**	-	-
NT2RP4000376	4.35	4.76	3.85	5.98	2.55	3.6	3.64	2.24	1.76		*		-
NT2RP4000381	4.21	7.62	7.46	8.53	4.41	5.48	6.16	4.44	4.11				
NT2RP4000388	15.3	8.64	28.13	9.56	6.37	8.78	3.98	7.28	10.59				
NT2RP4000390	9.32	12.91	21.1	9.57	7.3	6.9	4.45	8	7.73				
NT2RP4000393	4.73	6.04	14.2	5.91	3.76	3.4	2.49	4.28	1.61				
NT2RP4000398	15.1	12.32	17.4	15.43	7.99	12.09	10.09	7.98	7.95		*		-
NT2RP4000406	6.93	7.1	10	7.22	4.81	7.48	4.73	7.43	4.16				
NT2RP4000407	14.2	8.65	18.88	9.39	7.38	7.23	8.05	7.66	8.08				
NT2RP4000413	6.36	8.44	8.74	7.32	6.23	4.25	14.9	11.64	8.91				
NT2RP4000415	5.58	6.36	5.25	8.19	3.66	6.69	6.61	5.43	4.11				
NT2RP4000417	4.81	3.78	14.82	6.27	2.89	2.95	1.78	3.56	2.97				
NT2RP4000423	8.56	11.85	52.11	7.59	6.28	6.14	5.59	8.25	4.46				
NT2RP4000424	5.63	6.45	12.56	7.04	3.08	2.9	3.66	4.14	1.14				
NT2RP4000447	7.22	11.02	14.44	6.8	2.54	3.42	2.02	2.94	1.68		*		-
NT2RP4000448	10.44	4.78	12.49	7.44	5.19	4.9	2.34	3.11	4.18				
NT2RP4000449	14.23	13.95	15.79	8.35	8.81	8.15	9.09	11.62	7.03	**	*	-	-
NT2RP4000453	9.01	6.07	14.02	7.74	5.15	4.89	6.56	4.27	8.08				
NT2RP4000455	9.03	10.34	8.68	7.99	5.45	3.17	4.44	4.36	4.13		**		-
NT2RP4000456	7.04	6.17	17.02	5.76	3.52	4.72	1.66	2.58	3.46				
NT2RP4000457	13.26	8.71	17.6	8.13	4.23	7.52	11.15	9.14	8.56				
NT2RP4000461	55.44	37.43	46.46	34.13	24.48	24.96	29.53	26.44	29.5	*	*	-	-
NT2RP4000462	42.85	30.75	56.94	75.69	50.54	40.64	52.98	43.57	42.53				
NT2RP4000463	85.58	62.21	92.77	65.01	52.99	43.38	67.48	75.6	83.4				
NT2RP4000471	25.28	34.12	24.81	15.24	25.16	15.87	19.6	16.58	11.2		*		-
NT2RP4000472	7.71	9.85	9.52	10.37	5.54	5.62	6.84	6.67	3.82				
NT2RP4000476	14.81	18.77	16.55	11.79	4.98	3.82	5.79	4.35	2.67	*	**	-	-
NT2RP4000480	12.42	10.39	22.37	9.71	8.11	7.69	2.98	6.14	7.56				
NT2RP4000481	7.17	5.4	16.93	6.71	1.97	4.16	2.54	3.59	3.12				
NT2RP4000483	21.87	12.5	29.34	14.63	7.41	9.82	17.08	21.67	14.93				
NT2RP4000487	11.87	8.84	15.81	9.26	6.43	6.73	8.06	10.31	7.08				
NT2RP4000496	16.33	41.67	19.05	11.91	7.25	5.15	7.41	10.6	17.63				
NT2RP4000497	5.81	3.81	10.08	3.87	3.09	2.81	2.48	1.77	2.22				
NT2RP4000498	26.54	11.6	46.3	21.94	11.56	20.83	11.71	6.48	8.74				
NT2RP4000500	16.19	14.2	13.24	21.4	11.25	11.2	15.02	6.9	5.02				
NT2RP4000507	14.47	9.74	21.49	11.59	12.91	17.96	12.44	18.01	18.95				
NT2RP4000515	34.88	29.88	36.21	23.73	25.4	27.6	24.2	28.54	29.19	*		-	
NT2RP4000516	8.8	4.78	15.95	7.22	3.73	6.26	5.56	4.23	5.23				
NT2RP4000517	6.93	4.39	11.92	5.6	2.28	2.95	2.26	2.51	3.47				
NT2RP4000518	5.66	5.23	9.62	6.13	3.29	2.14	2.66	2.57	2.25		*		-
NT2RP4000519	11.25	13.8	9.43	7.22	5.12	6.11	9.96	4.77	2.74	*		-	
NT2RP4000524	3.66	2.61	3.66	4.66	0.22	1.66	1.44	0.06	0.23		**		-
NT2RP4000528	9.85	11.61	11.68	7.98	5.49	4.94	7.65	1.72	3.24	*	*	-	-
NT2RP4000537	22.62	26.04	23.49	9.39	8.19	12.07	6.5	9.43	12.67	**	**	-	-
NT2RP4000541	6.77	5.01	14.31	6.57	5.43	3.77	2.53	4.6	6.37				
NT2RP4000543	7.3	6.98	11.29	8.27	7.56	3.29	6.55	3.66	5.22				
NT2RP4000545	22.52	30.13	32.57	13.3	16.56	19.62	18.71	21.42	13.96	*	*	-	-
NT2RP4000546	4.78	4.57	9.21	6.74	1.72	3.53	3.64	0.82	4.41				
NT2RP4000549	11.61	18.79	20.98	6.99	2.21	3.33	4.79	2.09	3.96	*	*	-	-
NT2RP4000556	15.54	16.2	17.27	7.73	3.7	5.61	5.6	2.76	4.84	**	**	-	-
NT2RP4000557	11.07	12.42	10.89	8.61	4	8.57	12.02	7.59	12.85				
NT2RP4000558	14.08	10.84	18.04	10.75	6.08	12.87	11.5	16.9	20.52				
NT2RP4000560	6.31	4.01	7.32	5.77	2.76	5.36	5.37	6.37	4.62				

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Table 454

NT2RP4000568	23.22	25.79	25.36	10.18	10.21	8.47	12.24	9.65	11.67	**	**	-	-
NT2RP4000583	5.85	2.98	7.97	6.46	2.06	2.6	3.62	4.57	3				
NT2RP4000585	9.33	19	28.37	6.6	3.13	5.64	10.5	7.96	7.04				
NT2RP4000588	7.43	10.21	10.68	6.68	2.44	1.85	5.44	2.87	5.6	*	*	-	-
NT2RP4000590	6.55	7.08	8.76	6.12	1.79	2.53	5.82	2.45	2.62		*		-
NT2RP4000599	40.85	42.1	36.12	25.51	13.35	23.08	24.88	16.83	13.91	*	**	-	-
NT2RP4000603	16.26	11.07	12.79	9.86	5.09	7.92	5.61	11.76	8.02	*		-	
NT2RP4000607	18.04	30.52	24.32	19.53	17.65	25.01	23.84	28.13	28.14				
NT2RP4000614	10.28	8.25	15.91	8.83	8.89	11.93	10.16	9.95	16.38				
NT2RP4000634	6.36	4.3	5.27	7.5	2.83	3.42	3.64	2.83	2.88		*		-
NT2RP4000638	23.34	31.48	44.47	17.42	11.63	10.92	16.58	9.75	15.96	*	*	-	-
NT2RP4000648	20.24	25.67	26.97	19.17	9.45	12.88	31.67	25.66	31.95	*		-	
NT2RP4000657	29.17	33.57	37.98	49.46	41.57	42.06	36.04	23.15	32.67	*		+	
NT2RP4000691	5.59	4.16	3.63	5.96	2.37	3.18	5.01	2.34	4.68				
NT2RP4000697	6.38	8.16	10.53	9.34	4.77	12.75	6.26	6.22	8.11				
NT2RP4000704	1.95	1.59	2.11	5.91	1.47	3.12	1.95	2.78	2.48				
NT2RP4000710	20.97	14	15.55	13.68	8.51	18.99	7.53	9.31	11.22		*		-
NT2RP4000713	4.84	3.26	2.49	5.57	2.13	4.31	3.32	1.62	2.08				
NT2RP4000724	3.62	3.53	2.74	6.31	1.65	2.66	3.33	4.03	5.81				
NT2RP4000725	3.89	2.42	3.21	6.35	1.7	3.24	4.75	1.9	3.76				
NT2RP4000728	11.56	10.9	20.97	12.34	10.22	7.45	16.8	22.52	15.47				
NT2RP4000737	13.76	11.71	16.21	12.21	6.25	7.06	13.63	12.39	10.01				
NT2RP4000739	8.74	4.93	10.91	9.95	3.76	6.63	5.46	5.27	7.1				
NT2RP4000749	16.46	11.21	22.1	13.84	13.31	13.35	10.75	11.02	11.19				
NT2RP4000769	9.99	10.26	18.79	12.18	3.6	7.13	3.73	5.86	5.05				
NT2RP4000774	9.26	8.05	14.72	7.64	2.48	6.01	4.16	4.89	5.59				
NT2RP4000781	4.81	3.97	6.84	6.54	2.43	3.37	3.39	2.48	3.03				
NT2RP4000783	17.33	30.73	35.46	25.7	13.51	13.28	15.68	13.86	21.97				
NT2RP4000788	24.76	10.56	23.27	26.79	17.17	17.48	11.21	13.65	10.18				
NT2RP4000792	5.04	4.94	10.96	8.67	1.86	4.24	2.65	4.16	5.52				
NT2RP4000809	342.08	122.2	157.03	126.01	165.45	173.36	118.64	164.8	122.66				
NT2RP4000817	8.94	6.91	14.48	7.71	3.01	5.35	5.37	3.63	4.85				
NT2RP4000821	136.37	90.35	131.55	91.69	114.89	72.17	100.95	73.86	85.69				
NT2RP4000822	14.55	12.26	20.9	11.12	8.44	15.29	16.17	13.27	18.76				
NT2RP4000823	2939.8	2567.2	3305.2	1530.8	2690.7	2293.4	1706.4	1550.9	2562.9				
NT2RP4000831	78.61	54.25	90.69	72.05	94.12	99.31	70.64	58.37	82.02				
NT2RP4000833	27.77	14.49	23.94	22.19	7.07	21.11	19.12	24.88	29.44				
NT2RP4000837	6.72	4.87	9.85	8.02	2.92	3.66	2.57	4.16	7.79				
NT2RP4000839	145.23	125.82	232.83	173.61	169.29	177.66	124.91	117.96	102.54				
NT2RP4000846	29.27	18.32	20.88	21.05	17.61	12.28	9.05	14.78	13		*		-
NT2RP4000848	18.2	11.65	15.75	19.15	9.44	13.53	19	14.72	12.39				
NT2RP4000855	6.13	7.14	11.29	10.66	4.62	6.62	4.65	3.21	3.53				
NT2RP4000863	6.72	6.6	6.48	8.17	4.81	5.97	4.42	5.29	3.77		**		-
NT2RP4000865	45.32	26.52	38.54	39.71	38.1	49.51	43.48	35.35	41.09				
NT2RP4000873	144.06	68.9	135.34	139.48	79.72	155.93	87.22	97.84	116.06				
NT2RP4000874	10.17	6.06	16.44	7.29	2.79	4.52	3.81	5.9	8.53				
NT2RP4000875	14.13	12.82	21.34	9.26	7.3	7.14	8.99	11.91	13.22	*		-	
NT2RP4000878	36.06	33.12	27.77	33.84	31.46	17.83	20.58	24.01	24.14		*		-
NT2RP4000879	8.38	6.53	9.14	6.87	3.51	3.32	2.85	3.36	3.88		**		-
NT2RP4000880	35.09	26.71	47.85	50.74	42.76	41.2	29.03	30.06	33.07				
NT2RP4000891	701.32	715.69	430.85	696.54	840.24	746.75	898.32	324.76	792.55				
NT2RP4000894	21.41	14.41	21.14	15.13	8.85	12.55	11.08	19.34	17.24				
NT2RP4000898	2.97	2.72	11.52	4.95	1.01	2.82	2.18	3.29	4.66				
NT2RP4000899	44.53	41.78	65.07	39.31	37.51	42.09	31.81	35.26	42.89				
NT2RP4000907	4.19	4.02	10.25	6.24	3.94	2.33	1.69	3.11	0.94				
NT2RP4000908	14.45	17.63	18.1	10.04	7.21	5.31	4.66	6.8	4.87	**	**	-	-
NT2RP4000910	216.22	171.01	317.29	253.37	286.44	240.15	188.21	180.84	183.37				
NT2RP4000918	3.56	6.94	4.06	7.07	6.01	6.69	5.32	2.08	2.17				
NT2RP4000925	5.57	5.14	8.28	6.79	4.75	4.89	3.2	5.18	4.02				
NT2RP4000927	3.1	2.26	4.02	4.89	1.52	0.68	2.5	1.38	1.2				
NT2RP4000928	9.4	7.34	14.03	9.56	4.86	8.73	4.09	5.17	5.52				
NT2RP4000929	3.84	3.91	13.46	5.95	2.85	3.04	2.12	4.29	1.99				
NT2RP4000946	6.59	6.92	14.08	8.15	4.03	3.77	3.48	3.97	1.29				
NT2RP4000947	3.36	4.07	10.59	4.84	0.29	0.97	0.36	0.58	0				

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Table 455

NT2RP4000949	10.71	9.2	16.65	6.86	2.65	3.74	2.78	1.39	2.41	*	*	-	-
NT2RP4000955	5.81	4.35	6.4	6.28	2.77	1.08	2.31	3.19	3.37		*		-
NT2RP4000959	46.28	46.79	57.49	28.43	49.02	25.11	20.47	30.52	16.93		**		-
NT2RP4000962	11.98	9.47	12.39	11.59	10.69	8.83	6.01	4.92	5.77		**		-
NT2RP4000973	21.72	16.11	23:28	13.29	14.47	13.18	9.73	13.42	15.34	*		-	
NT2RP4000975	12.7	11.46	22.76	9.51	5.19	6.19	5.82	10.95	9.25				
NT2RP4000979	15.15	9.34	21.99	15.27	12.98	9.04	9.28	10.97	8.24				
NT2RP4000984	6.41	8.08	14.46	6.57	1.97	3.73	2.22	3.31	3.09				
NT2RP4000986	6.86	5.41	12.86	6.12	4.31	1.27	1.5	2.5	1.16		*		-
NT2RP4000988	17.65	11.88	13.93	10.42	7.43	7.63	9.24	12.28	11.72	*		-	
NT2RP4000989	4.65	7.43	6.1	6.61	2.52	1.81	2.98	2.09	3.85		*		-
NT2RP4000990	6.25	7.92	5.23	9.42	4.63	4.12	5.36	2.51	2.44				
NT2RP4000994	8.9	9.21	16.92	10.87	4.94	9.69	11.79	23.69	21.99				
NT2RP4000996	77.3	49.17	79.6	45.61	34.69	39.35	32.71	38.95	46.1	*	*	-	-
NT2RP4000997	122.55	129.24	107.05	94.09	70.8	26.94	46.25	80.17	57.14		**		-
NT2RP4001001	12.46	18.44	15.8	14.39	8.88	9.17	8.14	8.28	5.33		*		-
NT2RP4001004	5.22	3.76	7.06	6.01	1.06	2.64	1.83	1.39	1.05		*		-
NT2RP4001006	13.89	13.25	17.25	8.9	7.61	7.07	7.25	6.36	7.3	**	**	-	-
NT2RP4001009	16.48	20.86	24.07	12.83	13.33	10.38	13	7.19	7.56	*	*	-	-
NT2RP4001010	12.07	13.64	9.65	9.47	5.84	7.62	5.8	4.44	3.25		**		-
NT2RP4001013	109.49	147.49	90.54	50.6	80.74	63.83	38.95	52.28	51.67		*		-
NT2RP4001029	20.54	17.68	29.5	9.58	9.72	9.68	7.27	4.7	8.7	*	*	-	-
NT2RP4001036	9.27	12.23	13.79	8.52	7.63	4.92	8.03	6.75	4.44		*		-
NT2RP4001041	36.4	40.27	32.69	14.35	15.64	11.72	23:48	9.92	16.78	**	*	-	-
NT2RP4001042	15.67	10.3	17.88	10.18	7.53	8.42	5.86	5.84	7.9		*		-
NT2RP4001046	36.69	45.09	54.4	22.18	26.84	16.1	31.95	24.71	14.49	*	*	-	-
NT2RP4001050	14.02	22.04	12.83	10.97	2.91	3.84	9.37	3.59	3.94		*		-
NT2RP4001051	21.06	26.13	23.41	17.4	11.41	16.25	15.66	11.32	18.06	*	*	-	-
NT2RP4001057	5.02	3.25	6.98	7.18	2.13	3.82	4.33	2.83	3.14				
NT2RP4001063	6.13	4.37	7.2	7.29	2.91	4.39	2:87	3.18	3.35		*		-
NT2RP4001064	9.3	9.96	15.17	12.02	5.98	5.07	7.19	9.48	7.97				
NT2RP4001067	10.58	14.37	13.96	6.93	4.54	4.48	7.26	9.16	8.36	**	*	-	-
NT2RP4001078	4	5.51	5.6	4.49	1.94	2.06	3.66	2.7	1.04		*		-
NT2RP4001079	8.77	14.47	11.97	8.98	3.49	1.98	7.36	2.56	7.44				
NT2RP4001080	8.56	8.71	5.39	7.24	5.74	5.86	5.43	5.54	6.58				
NT2RP4001086	8.1	13.85	11.2	8.73	5.59	7.65	7.59	3.27	6.54				
NT2RP4001095	21.9	10.2	20.98	20.1	8.21	22.42	25.97	28.91	25.72				
NT2RP4001098	9.87	7.14	14.73	8.69	4.17	6.42	4.56	7.67	4.16				
NT2RP4001100	87.64	83.13	87.53	54.87	47.17	71.93	63.14	104.74	100.86	*		-	
NT2RP4001105	4.62	5.85	6.18	8.6	3.1	3.62	2.72	2.96	3.35		**		-
NT2RP4001110	4.35	3.52	3.95	6.4	1.65	2.39	2.86	1.95	2.46		*		-
NT2RP4001115	9.9	15.92	16.54	12.73	4.3	5.05	12.1	7.78	11.14				
NT2RP4001117	47.61	50.63	46.56	30.24	19.2	17.67	37.4	37.77	12.69	**		-	
NT2RP4001122	7.49	13.49	11.17	8.93	3.06	4.64	5.55	4.07	4.81		*		-
NT2RP4001123	15.99	10.87	15.29	13.96	11.8	8.64	4.92	11.31	11.27				
NT2RP4001126	32.2	22.75	27.43	23.25	13.48	17.12	8.86	11.87	13.23		**		-
NT2RP4001127	5.7	5.54	5.37	7.61	3.72	4.66	3.57	2.2	3.61		**		-
NT2RP4001138	6.95	3.88	7.12	9.78	5.56	5.09	4.09	4.44	3.91				
NT2RP4001143	12.5	11.65	11.43	11.35	7.29	7.76	9.34	8.18	11.45				
NT2RP4001148	6.15	6.48	10.09	9.86	3.88	5.87	3.55	2.98	4.94				
NT2RP4001149	10.56	12.29	14.62	14.76	6.44	4.57	8.21	6.46	7.23		*		-
NT2RP4001150	2.08	2.58	2.6	5.53	2.21	2.02	2.86	2.61	5.29				
NT2RP4001159	28.55	18.86	30.75	17.14	15.33	13.97	7.91	12.94	18.83				
NT2RP4001162	19.05	7.92	22.71	10.51	6.28	6.36	7.29	6.36	7.28				
NT2RP4001170	4.82	3.9	7.97	5.23	1.81	3.87	2.53	3.13	2.09				
NT2RP4001174	28.66	24.87	30.19	18.62	12.05	22.33	28.65	25.07	34.84	*		-	
NT2RP4001175	41.57	44.74	48.16	32.54	33.99	41.64	26.8	24.72	38.38		*		-
NT2RP4001176	940.52	839.83	1091.9	860.36	509.5	960.82	721.44	858.51	780.83				
NT2RP4001184	63.86	45.01	63.95	60.3	52	64.4	59.44	58.17	76.19				
NT2RP4001198	36.14	14.18	33.12	25.99	15.11	24.84	10.23	17.15	15.95				
NT2RP4001199	7.47	5.66	10.86	10.65	3.07	4.16	4.96	7.07	8.52				
NT2RP4001206	64.73	49.7	69.67	51.07	49.14	54.08	37.12	41.91	43.36		*		-
NT2RP4001207	7.32	3.58	10.38	7.77	2.4	3.4	3.22	3.79	1.65				
NT2RP4001210	10.03	7.34	12.93	9.04	5.66	7.56	3.96	6.73	5.83				

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Table 456

NT2RP4001213	7.81	5.05	8.73	8.57	3.73	3.8	4.8	3.72	3.86				
NT2RP4001214	3.93	5.31	4.9	6.79	4.2	2.68	6.35	2.95	4.56				
NT2RP4001219	16.88	22.36	19.11	23.96	11.89	15.23	12.2	5.76	8.23		*		-
NT2RP4001228	31.68	26.26	28.99	28.25	18.75	24.21	24.62	30.13	29.4				
NT2RP4001235	19.17	16.01	20.65	14.75	7.88	8.31	4.98	7.75	11.8	*	*	-	-
NT2RP4001256	7.87	5.89	15.98	8.52	4.59	3.98	3.22	7.66	6.44				
NT2RP4001257	10.17	7.29	12.91	9.33	4.43	6.16	4.58	7.66	4.3				
NT2RP4001260	9	7.35	9.45	7.52	2.82	3.63	1.87	4.5	2.81		**		-
NT2RP4001261	14.73	14	19.92	14.97	13.67	11.83	31.07	30.65	37.38		**		+
NT2RP4001274	46.98	48.98	34.12	11.26	8.82	9.09	7.45	6.66	5.77	**	**	-	-
NT2RP4001276	24.77	28.67	28.03	20.15	20.05	19.84	15.05	9.27	8.86	**	**	-	-
NT2RP4001283	274.25	154.44	255.86	208.49	145.59	283.17	127.22	121.38	88.24		*		-
NT2RP4001299	70.57	64.2	62.96	46.39	43.31	37.19	12.59	32.14	14.83	**	**	-	-
NT2RP4001313	1.97	3.19	11.08	5.06	1.72	1.96	1.4	3.15	1.49				
NT2RP4001315	13.31	15.88	15.77	13.24	9.24	10.09	4.21	7.24	8.5	*	**	-	-
NT2RP4001320	57.94	46.23	43.52	51.85	61.21	49.26	36.69	35.49	37.13		*		-
NT2RP4001325	218.13	214.83	355	324.95	260.73	208.15	240.45	201.7	209.88				
NT2RP4001336	66.24	37.07	61.11	58.79	61.6	67.7	54.66	37.6	43.21				
NT2RP4001339	6.71	9.24	9.26	9.34	4.49	4.79	2.82	4.96	4.68		*		-
NT2RP4001343	117.66	66.55	122.62	134.91	97.85	136.86	58.06	81.43	87.93				
NT2RP4001344	93.3	59.49	108.06	106.25	89.38	122.67	65.91	65.77	78.19				
NT2RP4001345	8.99	7.64	17.74	11.99	4.82	6.81	4.98	6.9	5.71				
NT2RP4001351	19.43	14.61	27.02	22.21	10.47	17.51	14.3	12.05	12.26				
NT2RP4001353	3.32	5.15	8.01	5.72	0.75	1.22	1.09	1.47	0.82		*		-
NT2RP4001355	4.79	4.23	4.91	4.97	2.19	1.13	2.63	2	2.13		**		-
NT2RP4001367	14.2	16.94	22.96	11.42	11.61	7.99	7.87	8	4.49		*		-
NT2RP4001372	4.19	2.77	5.41	7.79	3.55	1.91	2.83	1.62	2.32				
NT2RP4001373	51.47	33.24	43.9	16.16	26.86	13.77	10.57	24.44	16.81	*	*	-	-
NT2RP4001375	4.45	4.59	11.77	7.62	2.36	2.63	2.14	3.81	2.97				
NT2RP4001379	5.44	4.91	12.41	7.76	2.24	3.26	2.93	5.12	3.63				
NT2RP4001381	28.02	25.15	21.15	23.38	16.12	13.96	17.03	26.57	24.23				
NT2RP4001386	29.66	19.44	36.04	29.56	18.78	18.25	18.75	24.44	26.66				
NT2RP4001389	11.24	11.58	9.67	9.26	6.9	5.34	3.69	2.72	3.74	*	**	-	-
NT2RP4001396	5.21	4.67	8.34	6.72	2.25	1.78	3.47	3.22	1.99				
NT2RP4001407	5.66	5.49	6.51	7.81	4.54	1.79	3.65	1.8	5.23				
NT2RP4001409	8.48	7.57	16.74	7.93	2.96	5.53	4.77	6.78	4.46				
NT2RP4001410	76.31	89.86	99.62	25.06	52.86	47.85	42.92	82.06	57.7	*		-	
NT2RP4001414	30.84	57.5	63.9	31.08	20.37	24.44	13.71	23.74	21.51		*		-
NT2RP4001424	11.24	11.55	15.27	11.2	4.99	6.97	6.22	6.82	6.88		**		-
NT2RP4001433	19.8	14.14	16.87	12.54	11.03	6.56	10.55	8.89	6.43	*	*	-	-
NT2RP4001438	69.21	52.84	81.07	58.91	49.01	54.6	39.37	44.33	43.61		*		-
NT2RP4001442	7.93	5.58	7.34	6.34	2.77	3.09	4.34	2.59	3.24		*		-
NT2RP4001447	7.95	6.53	5.53	6.92	3.73	3.72	3.38	1.74	2		**		-
NT2RP4001466	26.98	30.25	30.96	13.22	11.9	17.04	5.41	8.17	9.81	**	**	-	-
NT2RP4001467	56.03	66.43	78.02	42.37	52.35	39.87	17.7	35.75	26.38	*	**	-	-
NT2RP4001472	23.78	41.35	30	13.57	13.9	13.93	11.58	12.27	10.38	*	*	-	-
NT2RP4001474	7.87	8.46	14.35	7.2	5.31	5.23	4.32	3.7	3.69		*		-
NT2RP4001483	6.68	4.49	11.62	7.08	3.5	3.8	3.02	2.79	3.04				
NT2RP4001488	25.21	54.85	68.99	28.07	36.56	22.06	36.35	46.46	23.9				
NT2RP4001492	10.33	5.85	8.11	7.33	2	4.79	7.35	5.55	5.24				
NT2RP4001498	7.69	4.58	4.14	7.14	3.13	3.73	4.3	3.05	2.12				
NT2RP4001502	209.76	206.24	150.31	118.11	105.88	95.3	44.44	56.95	57.25	*	**	-	-
NT2RP4001503	7.44	8.32	13.64	9.66	7.22	6.9	4.97	6.76	6.61				
NT2RP4001507	13.79	9.83	18.56	10.78	5.48	8.77	10.23	16.21	17.48				
NT2RP4001510	5.75	3.91	6.87	6.33	3.38	4.41	4.72	4.9	4.63				
NT2RP4001516	8.14	6.69	9.41	7.53	2.26	3.8	4.88	3.25	3.25		*		-
NT2RP4001520	131.31	173.55	237.05	131.12	129.89	116.61	94.53	82.4	103.86				
NT2RP4001523	33.88	38.97	38.29	18.41	8.08	12.46	21.96	12.77	13.03	**	**	-	-
NT2RP4001524	21.05	28.36	29.26	13.82	9.16	8	8.02	5.86	9.68	**	**	-	-
NT2RP4001529	19.64	17.51	18.7	21.14	10.37	22.92	12.83	17.42	17.09				
NT2RP4001531	12.2	10.44	17.59	14.87	8.44	10.35	9.15	12.78	10.56				
NT2RP4001546	200.55	317.08	217.26	217.42	252.35	233.58	165.76	290.78	247.68				
NT2RP4001547	50.85	72.72	70.29	50.48	41.66	51.65	70.8	75.31	63.14				
NT2RP4001551	5.28	7.23	6.07	6.96	2.03	2.81	2.74	2.79	2.73		**		-

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Table 457

NT2RP4001555	5.61	4.66	4.4	6.85	1.41	2.54	5.43	2.64	2.46				
NT2RP4001567	14.43	18.57	12.18	9.17	4.93	4.07	5.01	3.84	5.68	*	**	-	-
NT2RP4001568	20.92	33.87	32.23	19.47	17.65	14.08	25.04	13.01	8.31				
NT2RP4001569	38.32	29.49	40	37.57	26.2	39.13	21.18	30.23	30.47				
NT2RP4001571	15.01	7.71	15.89	14.4	7.44	9.88	7.38	9.18	8.27				
NT2RP4001574	25.53	25.21	25.8	22.48	16.52	21.02	13.78	20.38	15.43	*	*	-	-
NT2RP4001575	5.89	6.11	13.99	11.72	4.86	9.13	5.91	5.72	3.19				
NT2RP4001578	138.32	156.83	176.17	106.73	98.03	117.94	140.07	117.64	162.41	*		-	
NT2RP4001592	9.9	23.21	17.14	17.16	3.08	11.08	13.53	10.53	12.39				
NT2RP4001593	39.07	48.78	46.75	25.68	17.84	15.12	20.23	20.2	20.66	**	**	-	-
NT2RP4001605	8.89	11.75	9.28	6.36	2.98	4.4	4.38	3.06	5.09	*	**	-	-
NT2RP4001606	18.77	11.14	16.78	12.15	11.21	15.99	4.83	13.12	16.6				
NT2RP4001607	6.86	5.47	8.59	11.52	4.98	6.05	4.83	4.03	5.51				
NT2RP4001610	3.61	1.38	4	7.17	1.24	4.9	2.72	3.85	3.06				
NT2RP4001614	9.32	7.4	5.36	10.94	2.88	8.46	8.3	5.56	6.1				
NT2RP4001623	4.1	3.9	7.53	8.2	4.59	6.06	6.02	5.72	5.27				
NT2RP4001626	25.96	32.39	24.45	30.25	8.64	19.85	8.25	9.34	7.78		**		-
NT2RP4001634	5.5	5.13	5.73	8.25	3.86	4.21	6.58	3.67	4.85				
NT2RP4001638	6.66	10.41	10.2	8.73	4.08	5.57	10.07	5.59	6.69				
NT2RP4001644	54.14	31.27	53.6	60.84	32.15	47.2	22.38	29.74	30.92				
NT2RP4001646	19.49	10.73	26.93	21.07	12.28	14.22	11.82	16.28	16.41				
NT2RP4001656	13.27	8.07	17.13	8.91	6.79	8.31	7.24	7.86	6.43				
NT2RP4001666	5.12	4.37	7.8	6.14	1.29	4.07	3.21	5.08	2.86				
NT2RP4001670	3.97	4.22	8.36	10.93	2.63	2.89	3.57	4.05	2.82				
NT2RP4001677	60.48	67.97	86.27	37.88	33.85	40.42	60.13	40.04	66.44	*		-	
NT2RP4001679	63.4	46.03	74.85	69.08	70.96	72.54	80.35	59.3	58.1				
NT2RP4001695	25.41	48.09	50.45	43.83	20.99	24.93	40.69	28.74	39.61				
NT2RP4001696	10.8	7.02	11.48	9.54	3.39	6.61	2.58	6.02	6.23				
NT2RP4001699	7.34	4.14	12.45	8.78	2.82	5.44	4.48	5.75	8.17				
NT2RP4001717	14.1	8.06	13.01	8.07	5.02	5.29	6.3	4.01	4.24		*		-
NT2RP4001719	12.35	7.72	11.2	8.9	5.51	7.17	4.84	7.79	6.21				
NT2RP4001725	3.63	2.94	5.27	5.13	1.69	2.36	2.09	2.38	2.12				
NT2RP4001726	27.43	19.04	36.39	17.49	15.05	17.67	16.15	9	13.24				
NT2RP4001730	17.07	14.23	28.12	18.8	22.34	22.39	15.23	16.15	19.5				
NT2RP4001739	13.08	27.52	18.78	28.99	19.24	16.38	17.13	15.51	14.38				
NT2RP4001741	36.21	33.9	43.76	24.77	17.24	19.76	19.65	43.11	31.46	**		-	
NT2RP4001753	17.2	14.59	16.48	7.48	4.99	6.73	3.91	7.96	13.47	**		-	
NT2RP4001760	8.36	7.54	12.21	7.55	2.73	5.75	3.77	6.5	5.81				
NT2RP4001787	449.13	316.48	382.02	579.25	624.67	556.76	483.34	493.96	418.4	**		+	
NT2RP4001790	7.47	3.89	8.52	8.8	3.39	5.62	4.59	3.58	5.07				
NT2RP4001795	63.42	46.97	73.29	43.26	32.42	28.05	20.69	20.32	20.73	*	**	-	-
NT2RP4001803	8.84	7.88	10.54	9.34	4	5.93	4.96	3.55	3.59		**		-
NT2RP4001805	5.95	5.69	10.38	8.15	3.79	5.46	9.95	6.17	7.95				
NT2RP4001809	55.79	43.66	54.44	43.11	38.36	44.76	37.5	36.54	53.86				
NT2RP4001817	34.65	23.28	22.77	22.82	15.26	16.99	9.01	16.13	16.73		*		-
NT2RP4001822	6.52	3.81	10.26	6.23	2.19	2.7	2.67	9.77	2.8				
NT2RP4001823	3.6	2.46	7.23	4.29	1.65	1.68	0.91	2.7	2.37				
NT2RP4001827	92.63	82.49	90.1	26.32	25.71	23.6	20.01	17.73	25.06	**	**	-	-
NT2RP4001828	61.47	38.75	56.29	48.73	53.93	46.7	40.24	45.94	36.84				
NT2RP4001836	44.8	31.89	48.09	43.58	41.3	52.3	39.14	27.95	48.98				
NT2RP4001838	6.15	7.83	5.55	9.67	6.83	6.27	7.38	14.64	4.59				
NT2RP4001841	120.68	83.99	187.16	139.43	130.99	191.28	92.44	82.4	82.84				
NT2RP4001849	5.44	4.67	11.88	5.66	3.18	2.21	2.03	4.71	2.38				
NT2RP4001861	120.57	86.96	121.65	102.03	95.48	118.7	109.17	140.23	134.58				
NT2RP4001877	47.77	41.26	29.9	28.86	24.84	22.31	17.4	14.34	21.88		*		-
NT2RP4001879	28.67	26.1	20.85	19.88	15.94	14.99	7.59	15.66	4.85	*	*	-	-
NT2RP4001889	38.95	24.39	36.19	23.27	20.66	27.73	35.61	41.13	33.21				
NT2RP4001893	6.77	9.6	11.58	7.5	6.4	5.73	3.91	4.94	4.11		*		-
NT2RP4001896	20.14	21.68	20.53	23.47	19.99	18.99	15.61	11.88	13.51		**		-
NT2RP4001898	54.69	54.01	78.1	65.64	57.05	63.77	28.3	45.74	52.57				
NT2RP4001901	17.19	14.63	24	14.51	10.05	13.25	15.49	18.92	20.72				
NT2RP4001910	121.38	105.48	128.54	129.33	152.14	104.65	69.31	116.85	87.82				
NT2RP4001925	17.35	19.33	26.78	14.34	7.91	7.52	5.99	7.67	6.41	*	**	-	-
NT2RP4001926	13.94	13.08	14.09	14.02	5.92	2.48	4.72	6.01	4.66		**		-

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Table 458

NT2RP4001927	22.95	20.54	20.03	14.02	11.73	7.04	7.86	6.56	6.03	*	**	-	-
NT2RP4001931	31.71	30.66	39.53	15.12	11.86	11.1	6.42	8.14	7.84	**	**	-	-
NT2RP4001933	124.92	135.92	123.56	117.23	83.52	79.43	61.4	54.06	63.46		**		-
NT2RP4001938	21.23	9.61	28.3	17.33	8.99	14.74	12.02	19.38	17.02				
NT2RP4001942	40.71	46.99	41.11	32.73	26.67	27.19	19.11	35.23	32.36	**		-	
NT2RP4001945	3.45	3.93	9.62	6.08	1.55	2.05	2.15	2.81	1.6				
NT2RP4001946	10.3	8.04	13.38	10.29	3.79	3.79	3.46	4.08	3.41		*		-
NT2RP4001947	16.45	15.77	21.11	11.34	9.6	7.02	4.68	3.24	4.94	*	**	-	-
NT2RP4001950	5.04	4.87	6.27	6.87	2.41	1.7	3	2.63	1.3		*		-
NT2RP4001953	26.47	19.18	22.05	22.48	9.35	15.94	17.83	14.03	17.8				
NT2RP4001966	6.74	6.56	3.55	6.86	3.2	2.07	1.97	1.5	1.8		*		-
NT2RP4001970	7.84	6.46	14.19	9.16	3.49	5.37	2.96	4.43	3.21				
NT2RP4001975	16.36	22.03	28.3	17.31	12	7.09	9.7	16.29	13.08				
NT2RP4001988	38	36.95	48.12	29.2	31.09	30.9	21.07	21.03	23.16	*	**	-	-
NT2RP4001996	24.73	23.55	24.27	15.39	14.66	5.03	8.32	9.1	9.68	*	**	-	-
NT2RP4002014	11.39	15.95	16.62	10.15	7.55	6.98	8.4	7.61	5.52	*	*	-	-
NT2RP4002018	16.73	14.11	11.76	12.16	9.31	11.09	15.09	12.65	8.98				
NT2RP4002035	5.82	5.03	4.44	7.72	3.9	4.37	5.69	2.8	2.78				
NT2RP4002043	18.95	25.2	14.18	17.22	10	14.87	15.39	7.04	10.89				
NT2RP4002046	24.11	28.29	25.84	19.27	12.78	20.33	11.41	17.55	17.78	*	*	-	-
NT2RP4002052	12	15.65	20.88	9.3	9.08	6.85	4.02	3.61	4.24	*	**	-	-
NT2RP4002056	153.48	150.03	95.32	64.65	34.92	59.97	51.1	38.55	53.86	*	*	-	-
NT2RP4002057	40.68	39.2	39.83	19.31	30.56	26.73	27.83	37.55	52.18	*		-	
NT2RP4002058	17.65	14.46	13.17	10.87	3.28	4.52	5.26	2.89	2.9	*	**	-	-
NT2RP4002064	5.15	7.64	7.19	5.68	1.88	1.94	2.82	1.16	2.09		**		-
NT2RP4002071	19.67	23.04	16.87	12.91	7.48	6.56	8.07	4.85	9.75	*	**	-	-
NT2RP4002075	4.49	2.91	8.1	6.42	3.43	5.27	3.76	2.11	2.28				
NT2RP4002078	19.28	11.77	21.52	11.04	6.62	7.49	7.2	13.73	14.2	*		-	
NT2RP4002081	26.93	23.81	24.19	19.25	16.65	23.73	20.7	21.48	20.63		*		-
NT2RP4002083	12.48	9.47	12.44	9.18	6.34	7.57	7.79	10.15	9.98	*		-	
NT2RP4002099	4.69	4.27	5.09	6.55	1.89	1.66	2.86	2.04	1.79		**		-
NT2RP4002106	48.22	85.51	111.5	22.9	29.06	16.21	28.91	8.21	26.28	*	*	-	-
NT2RP4002111	21.8	28.93	25.95	13.09	13.73	11.32	21.21	10.01	16.62	**		-	
NT2RP4002112	18.8	22.05	20.04	17.73	8.26	13.72	15.37	6.12	8.09		*		-
NT2RP4002116	131.42	129.9	145.31	124.89	86.8	130.87	116.59	193.03	130.26				
NT2RP4002122	9.21	7.05	12.08	10.75	5.68	5.1	3.65	7.4	5.23				
NT2RP4002126	16.25	10.45	26.23	9.01	12.04	10.44	10.14	17.51	8.7				
NT2RP4002133	59.92	73.72	76.92	61.59	43.1	56.16	80.78	84.66	86.01				
NT2RP4002136	12.24	16.73	29.34	16.04	8.23	7.86	20.93	16.43	17.62				
NT2RP4002139	65.39	168.51	135.79	98.21	29.79	27.09	86.97	65.15	29.84				
NT2RP4002174	10.15	13.02	11.19	12.5	4.36	7.32	8.88	11.55	11.53				
NT2RP4002185	23.38	25.82	19.72	13.23	6.3	10.39	10.9	7.33	11.09	**	**	-	-
NT2RP4002186	16.88	7.65	12.65	11.9	7.3	14.74	12.63	14.19	17.64				
NT2RP4002187	28.59	22.57	36.35	26.74	19.36	12.02	11	23.37	23.58				
NT2RP4002188	5.08	7.53	8.31	11.66	6.59	7.86	4.55	4.87	6.3				
NT2RP4002199	5.25	3.74	5.62	11.93	2.92	3.8	2.79	4.05	2.9				
NT2RP4002206	3.81	1.86	2.83	8.57	1.99	1.73	3.4	4.64	3.09				
NT2RP4002210	5.45	3.2	5.65	5.42	1.97	2.98	3.71	3.22	3.36				
NT2RP4002222	6.38	6.14	7.04	6.83	3.57	3.25	6.5	5.55	8.67				
NT2RP4002241	19.38	17.71	14.08	18.19	11.3	8.8	22.47	17.63	22.91				
NT2RP4002248	35.82	21.31	27.47	30.46	20.08	26.03	19.35	24.1	27.06				
NT2RP4002250	1.58	1.78	7.25	3.8	1.3	0.25	0.61	0.65	1.92				
NT2RP4002259	5.84	5.18	13.48	7.69	2.79	5.42	4.19	2.88	3.6				
NT2RP4002268	35.43	25.77	32.22	22.21	30.41	16.71	15.9	32.72	23.26				
NT2RP4002288	22.95	20.57	22.28	19.59	16.95	19.16	16.63	15.69	17.98	*	**	-	-
NT2RP4002290	13.7	13.76	25.96	11.44	11.61	14.66	7.05	8.48	10.18				
NT2RP4002298	10.23	12.39	16.74	11.6	8.3	6.18	9.56	4.97	3.02				
NT2RP4002306	15.16	15.97	20.14	18.18	10.48	11.51	13.4	11.06	13.62				
NT2RP4002308	8.45	5.65	13.02	8.55	4	9.83	3.47	4.84	5.83				
NT2RP4002336	36.27	19.86	28.84	13.28	11.25	15.46	7.56	12.49	16.8	*	*	-	-
NT2RP4002340	2.84	2.81	9.7	4.27	0.88	0.87	1.22	1.79	3.04				
NT2RP4002361	9.6	7.94	13.29	10.99	5.46	5.57	5.78	8.11	5.48				
NT2RP4002367	2.79	2.98	7.18	5.28	1.95	2.56	3.24	1.85	1.33				
NT2RP4002368	24.08	18.92	33.22	37.33	27.57	13.68	19.74	22.15	15.46				

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Table 459

NT2RP4002377	39.07	34.91	52.74	47.19	54.21	38.25	54.01	36.88	39.01				
NT2RP4002408	8.23	10.17	7.33	8.55	4.11	5.54	5.29	2.67	3.53		*		-
NT2RP4002425	16.72	9.87	22.95	18.36	10.72	16.61	14.74	22.3	29.56				
NT2RP4002432	134.52	97.55	162.62	149.32	142.05	170.39	110.43	102.21	77.71				
NT2RP4002447	15.99	16.51	16.61	15.14	7.55	8.09	7.58	13.4	16.29				
NT2RP4002451	15.11	13.46	19.12	12.6	10.1	7.99	7.15	14.07	11.51				
NT2RP4002461	94.61	109.24	116.21	78.57	91.21	74.75	80.34	65.93	74.08	*	*	-	-
NT2RP4002486	16.89	12.32	16.5	14.11	11.37	5.17	6.32	4.06	4.63		**		-
NT2RP4002517	13.38	14.55	13.22	12.72	9.03	11.46	10.8	6.18	8.61		*		-
NT2RP4002556	14.42	18.7	14.04	18.8	13.59	13.31	16.09	6.06	5.52				
NT2RP4002569	16.26	11.41	27.18	13.33	6.98	10.11	3.13	6.78	11.56				
NT2RP4002587	4.28	5.9	13.49	5.9	21.35	3.55	2.37	3.48	4.03				
NT2RP4002591	11.21	8.73	16.61	10.63	3.25	5.39	2.62	6.98	4.42		*		-
NT2RP4002607	7.19	4.54	8.62	7.82	4.54	6.78	3.93	3.64	3.85				
NT2RP4002627	129.04	84.31	131.91	123.08	121.1	113.29	100.69	103.33	117.09				
NT2RP4002628	23.42	19.42	25.54	15.3	10.07	9.36	10.28	14.93	5.74	*	*	-	-
NT2RP4002630	34.52	45.14	38.61	24.65	19.47	21.97	38.2	24.12	21.41	**		-	
NT2RP4002639	69.58	58.92	77.5	92.97	83.99	82.67	76.62	44.55	74.09	*		+	
NT2RP4002641	10.87	7.59	20.93	9.6	5.64	6.42	5.77	9.03	8.9				
NT2RP4002658	167.82	202.75	171.29	210.71	275.39	155.29	113.71	313.1	177.93				
NT2RP4002669	11.89	14.59	18.31	13.81	8.54	6.37	6.6	13.8	11.32				
NT2RP4002677	38.73	39.84	49.87	21.84	19.97	14	8.4	12.92	7.79	**	**	-	-
NT2RP4002715	60.14	28.66	66.85	78.28	49.48	49.64	41.22	48.79	51.15				
NT2RP4002750	5.11	4.54	6.02	5.02	2.86	2.29	1.61	2.5	1.93		**		-
NT2RP4002784	13.9	15.39	21.97	16.43	16.29	10.56	10.51	11.54	8.19				
NT2RP4002791	19.14	16.24	15.43	15.81	11.98	5.79	6.28	6.12	6.25		**		-
NT2RP4002811	7.07	4.03	15.62	8.02	4.02	6.88	1.73	4.87	5.66				
NT2RP4002830	22.24	23	26.1	14.14	12.81	9.89	5.49	12.55	7.49	**	**	-	-
NT2RP4002832	6.62	7.2	10.83	9.33	4.27	5.54	7.23	5.78	6.45				
NT2RP4002850	120.6	112.69	112.51	87.95	73.32	75.57	95.07	111.13	108.7	**		-	
NT2RP4002874	8.25	8.24	13.89	8.67	2.89	3.54	1.21	3.45	2.95		*		-
NT2RP4002884	89.55	83.99	93.99	87.7	70.28	83.78	63.11	54.66	68.06		**		-
NT2RP4002888	6.66	8.16	10.03	7.45	4.69	3.72	4.86	3.64	2.94		*		-
NT2RP4002891	19	20.18	21.15	16.8	8.39	11.91	12.08	8.99	11.53	*	**	-	-
NT2RP4002894	39.86	38.92	34.99	21.18	29.78	22.86	11.88	16.42	39.6	*		-	
NT2RP4002896	7.81	11.66	17.8	10.13	3.4	6.5	5.01	4.37	5.08				
NT2RP4002905	5.89	3.63	14.35	7.98	3.09	2.98	3	5.21	1.93				
NT2RP4002907	14.82	12.9	19.78	10.14	7.04	6.74	11.86	12.75	9.47	*		-	
NT2RP5003459	437.62	468.29	451.9	449.8	544.78	414.46	466.17	464	478.98				
NT2RP5003461	21.93	17.54	18.05	12	9.18	10.65	7.44	6.63	4.58	**	**	-	-
NT2RP5003471	52.72	62.97	42.21	31.11	21.1	25.12	46.83	20.37	35.04	*		-	
NT2RP5003477	5.7	3.4	3.74	5.93	3.44	2.66	3.17	2.23	2.28				
NT2RP5003487	1749.6	1957.3	1778.8	1241.4	1573.1	1807.7	1562.4	2343.9	2243.6				
NT2RP5003492	6.08	6.5	15.88	6.67	3.98	3.96	2.59	3.25	1.92				
NT2RP5003500	4.26	2.52	9.75	6.65	2.34	2.66	2.29	2.53	3.57				
NT2RP5003506	10.49	9.24	16.38	12.74	9.52	9.22	9.69	9.29	9.27				
NT2RP5003512	6.99	7.06	8.63	5.95	2.46	3.36	2.76	2.88	3.49	*	**	-	-
NT2RP5003522	10.07	9.26	8.55	5.18	3.12	3	5.35	1.85	3.07	**	**	-	-
NT2RP5003524	6.44	9.05	5.63	7.13	1.41	1.72	4.66	2.23	3		*		-
NT2RP5003527	117.46	141.32	115.3	136.41	95.19	117.09	134.61	57.44	67				
NT2RP5003531	24.59	24.67	34.31	22.85	17.67	26.56	12.06	25.82	35.99				
NT2RP5003534	6.96	7.88	13.1	6.91	5.36	2.92	2.47	4.02	3.38		*		-
NT2RP6000020	19.43	27.72	47.01	19.42	30.65	12.46	29.24	22.48	15.27				
NT2RP6000022	13.58	7.81	13.25	8.64	4.5	5.83	7.1	5.5	4.05		*		-
NT2RP6000050	5.27	8.58	7.67	6.81	3.59	4.26	5.19	3.06	5.18				
NT2RP6000063	5.9	4.93	5.56	6.03	1.07	1.6	2.56	2.13	3.15		**		-
NT2RP6000074	10.12	8.88	7.2	8.89	3.35	3.32	4.76	3.03	4.96		*		-
NT2RP6000083	36.48	50.53	36.06	34.94	19.9	25.84	29	16.57	36.99				
NT2RP6000100	9.33	8.85	11.79	8.7	3.93	5.47	3.33	5.54	5.88		*		-
NT2RP6000123	7.59	5.31	8.36	10.56	5.66	4.44	3.17	5.91	3.98				
NT2RP6000129	4.7	6.51	7.04	5.86	2.6	3.34	4.3	7.17	3.53				
NT2RP6000147	23.98	19.21	18.37	28.9	18.17	21.68	18.73	17.92	16.85				
NT2RP6000163	6.02	5.5	6.17	6.66	2.33	2.81	2.76	2.24	3.12		**		-
NT2RP6000181	31.82	37.36	38.55	11.76	5.01	6.27	13.35	6.28	18.64	**	**	-	-

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Table 460

NT2RP6000182	11.67	12.98	10.81	11.27	4.67	4.19	7.63	8.13	8.65		**		-
OVARC1000001	10.18	10.98	7.82	10.48	3.67	5.27	8.05	6.3	4.32				
OVARC1000003	19.46	16.04	21.53	24.56	18.39	28.35	24.31	27.93	25.27		*		+
OVARC1000004	154.65	161.68	111.37	257.56	204.62	269.89	148.7	142.43	153.8	*		+	
OVARC1000006	8.96	9.17	13.23	12.36	9.89	7.09	8.46	11.94	16.91				
OVARC1000013	12.84	15.42	21.83	13.5	7.52	11.75	8.01	7.31	7.45		*		-
OVARC1000014	9.51	5.51	9.75	8.67	3	2.57	4.2	4.5	5.23				
OVARC1000017	7.8	10.89	11.1	9.23	5.72	5.56	7.08	8.83	7.59				
OVARC1000026	39.97	98.56	58.17	35.12	21.04	21.52	23	21.16	19.52				
OVARC1000035	53.62	63.74	56.85	49.18	30.89	52.6	44.01	25.83	35.4		*		-
OVARC1000037	44.18	27.1	33.64	21.27	17.7	36.96	22.76	28.28	23.56				
OVARC1000058	21.2	16.03	18.93	19.43	6.93	18.25	18.85	19.08	20.93				
OVARC1000060	8.69	7.53	9.42	11.74	4.69	15.1	7.86	12.81	10.28				
OVARC1000068	11.63	6.29	9.06	11.58	8.06	9.18	6.71	8.97	7.36				
OVARC1000069	130.28	91.82	110.55	138.44	48.02	81.99	34.87	114.87	91.52				
OVARC1000071	4.7	2.59	5.56	6.14	1.28	3.78	7.5	3.79	3.09				
OVARC1000075	608.15	715.16	979.97	596.89	401.8	521.41	1505.9	1295.8	1454		**		+
OVARC1000083	31.41	22.53	32.47	28.89	10.2	12.73	23.7	17.6	16.65				
OVARC1000085	150.84	132.35	115.14	65.66	79.36	104.26	57.87	55.95	46.39	*	**	-	-
OVARC1000086	21.41	22.84	29.16	11.19	16.67	9.71	14.87	19.23	16.21	*	*	-	-
OVARC1000087	5.75	4.1	5.37	4.05	5.46	2.99	2.78	3.2	3.4		*		-
OVARC1000090	32.43	34.99	39.46	22.05	34.29	19.79	30.39	42.7	35.58				
OVARC1000091	19.21	16.58	18.4	9.39	12.78	9.69	3.97	5.82	3.09	**	**	-	-
OVARC1000092	12.38	12.28	20.09	9.9	9.89	8.91	11.14	12.55	9.97				
OVARC1000105	143.72	148.63	164.07	88.33	70.71	97.62	141.54	139.36	177.6	**		-	
OVARC1000106	56.13	50.31	43.64	33.71	26.64	28.64	25.97	22.43	26.91	**	**	-	-
OVARC1000109	41.67	37.23	42.5	18.44	22.06	21.86	20.05	26.41	16.1	**	**	-	-
OVARC1000113	24.72	16.19	25.29	12.07	22.86	8.51	9.56	13.5	7.9		*		-
OVARC1000114	20.78	17.23	18.89	9.6	15.6	9.38	19.16	20.46	17.77	*		-	
OVARC1000133	17.57	29.71	58.68	7.88	21.62	13.9	11.06	7.62	51.45				
OVARC1000137	26.29	21.24	32.71	19.41	23.84	21.06	17.64	15.76	21.29				
OVARC1000139	159.47	147.34	170.25	146.09	161.46	121.94	114.2	86.17	91.75		**		-
OVARC1000145	5.46	5.11	5.9	4.05	7.97	2.4	2.98	4.01	3.61		**		-
OVARC1000148	26.75	26.35	26.82	10.67	7.97	11.29	11.04	13.8	10.7	**	**	-	-
OVARC1000151	10.96	7.69	7.49	4.61	6.76	7.44	5.23	9.46	5.82				
OVARC1000157	131.87	72.71	159.16	28.64	46	29.09	32.55	30.3	35.03	*	*	-	-
OVARC1000162	5.48	6.74	10.66	5.09	8.45	3.6	3.17	7.57	4.35				
OVARC1000168	20.5	23.24	26.19	11.56	15.79	12.79	11.3	16.45	13.91	**	*	-	-
OVARC1000169	67.7	69.5	69.91	59.55	32.42	51.67	35.89	25.97	33.69		**		-
OVARC1000178	7.01	7.74	9.93	3.35	8.16	5.02	5.67	3.4	4.49		*		-
OVARC1000182	6.26	2.63	4.45	2.72	4.87	3.13	2.7	3.24	3.81				
OVARC1000186	14.26	11.19	12.68	6.9	8.25	3.97	5.99	5.56	7.72	*	**	-	-
OVARC1000188	19.42	11.08	15.15	6.26	7.14	4.44	6.66	6.47	9.02	*	*	-	-
OVARC1000191	10.3	6.61	7.55	5.45	7.49	3.47	4.08	6.65	4.21				
OVARC1000198	22.01	20.32	21.51	13.28	15.24	8.22	13.24	17.04	19.28	*		-	
OVARC1000208	131.85	125.05	141.2	106.48	130.32	109.42	107.54	141.64	112.43				
OVARC1000209	37.5	42.42	46.9	35.76	48.15	33.79	26.69	26.98	20.75		**		-
OVARC1000212	14.17	16.96	15.84	10.34	14.11	8.11	6.32	5.07	5.47		**		-
OVARC1000216	7.5	5.29	9.53	2.31	4.11	1.95	4.22	3.32	1.67	*	*	-	-
OVARC1000240	30.72	25.44	20.48	13.87	16.01	11.11	15.84	21.45	17.35	*		-	
OVARC1000241	9.83	9.47	8.6	4.52	5.75	4.08	4.87	6.55	6.44	**	**	-	-
OVARC1000249	12.5	10.38	14.17	6.99	8.18	4.94	7.53	30.07	10.99	*		-	
OVARC1000254	211.04	164.08	171.72	162.84	218.18	173	104.59	109.93	114.49		**		-
OVARC1000255	8.62	6.5	15.01	2.8	3.3	2.22	1.58	8.88	3.88	*		-	
OVARC1000267	41.48	57.68	54.05	22.69	31.39	23.55	19.25	29.77	21.42	*	**	-	-
OVARC1000275	6.58	9.72	13.14	1.2	3.21	1.15	3.78	4.58	2.47	*	*	-	-
OVARC1000287	20.12	19.59	19.09	8.41	13.5	9.21	9.7	16.66	9.51	**	*	-	-
OVARC1000288	34.41	32.21	34.44	10.93	20.1	12.59	9.34	11.6	15.85	**	**	-	-
OVARC1000298	37.89	35.05	40.4	26.93	41.61	26.19	16.03	19.69	20.76		**		-
OVARC1000302	10.27	8.52	8.63	3.64	6.33	2.17	4.38	8.26	6.64	*		-	
OVARC1000304	13.52	8.67	11.83	6.89	9.55	6.81	7.04	9.75	5.89				
OVARC1000307	9.2	9.65	13.33	4.99	7.9	7.07	7.34	4.85	4.2		*		-
OVARC1000309	10.77	7.81	10.14	3.65	4.52	3.3	3.45	4.14	3.51	**	**	-	-
OVARC1000312	38.52	63.36	48.96	16.29	39.99	22.16	11.44	23.2	11.33		*		-

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Table 461

OVARC1000313	31.08	25.28	22.97	16.65	33.34	16.32	7.95	14.64	16.92		*		-
OVARC1000321	95.57	70.17	108.42	49.21	78.85	36.91	71.72	84.76	66.41				
OVARC1000326	9.36	7.55	9.19	5.69	4.73	3.83	2.8	4.95	2.81	**	**	-	-
OVARC1000327	9.64	6.54	7.7	4.58	5.69	4.67	3.24	3.34	3.39	*	**	-	-
OVARC1000331	31.51	26.56	17.69	20.2	32.18	25.32	7.77	12.73	9.94		*		-
OVARC1000335	10.5	10.92	9.98	3.56	6.12	5.55	3.62	2.51	3.12	**	**	-	-
OVARC1000347	22.28	19.59	19.77	14.38	17.51	15.31	11.64	10.94	10.7	*	**	-	-
OVARC1000348	9.03	9.66	11.56	3.27	3.92	2.72	2.5	3.43	2.51	**	**	-	-
OVARC1000363	17.67	18.03	15.99	8.09	14.09	9.86	7.93	4.93	7.38	*	**	-	-
OVARC1000377	9.05	5.89	9.25	3.23	6.62	3.71	2.88	2.47	4.83		*		-
OVARC1000382	11.38	10.29	10.44	4.87	5.92	3.1	5	4.78	5.93	**	**	-	-
OVARC1000384	15.04	16.77	12.96	3.9	4.19	3.88	3.11	4.29	3.9	**	**	-	-
OVARC1000401	12.88	8.81	11.8	7.36	8.78	6.88	5.26	4.94	4.67		**		-
OVARC1000406	452.57	396.91	414.58	242.32	241.63	222.43	202.53	242.65	184.03	**	**	-	-
OVARC1000407	11.18	13.52	12.76	4.82	6.15	3.43	3.77	3.81	3.74	**	**	-	-
OVARC1000408	143.25	152.71	130.24	110.8	163.58	95.03	87.98	95.98	86.83		**		-
OVARC1000410	12.11	11.07	15.74	6.71	11.27	6.87	6.11	5.6	3.42		**		-
OVARC1000411	11.28	8.14	7.71	4.73	4.82	3.45	4.09	4.41	4.68	*	*	-	-
OVARC1000414	15.72	17.28	11.48	7.59	8.9	10.02	14.36	14.47	14.88	*		-	
OVARC1000420	11.3	11.1	10.67	5.43	7.49	5.25	8.15	6.28	6.64	**	**	-	-
OVARC1000421	21.51	18.12	14.96	8.46	10.6	6.1	8.22	6.83	7.06	*	**	-	-
OVARC1000427	255.84	237.66	229.09	230.15	286.16	201.09	155.75	128.13	139.78		**		-
OVARC1000431	86.97	107.76	104.05	53.83	76.2	48.18	31.1	18.06	18.56	*	**	-	-
OVARC1000437	18.7	18.85	16.29	10.2	15.26	9.01	9.96	5.69	8.45	*	**	-	-
OVARC1000439	14.55	21.25	13.48	9.92	17.37	9.21	5.86	5.66	4.06		*		-
OVARC1000440	37.93	36.45	33.24	14.99	19.86	14.94	10.14	8.93	10.09	**	**	-	-
OVARC1000442	47.65	39.77	34.86	17.92	25.44	19.14	36.52	26.4	37.91	*		-	
OVARC1000443	9.63	12.52	9.02	8.56	33.14	5.66	16.38	5.13	9.47				
OVARC1000461	8.43	5.22	4.46	4.04	5.64	3.64	3.41	4.7	3.49				
OVARC1000465	13.05	12.4	8.82	5.16	5.82	3.89	4.59	3.18	2.41	*	**	-	-
OVARC1000466	22.78	19.36	18.72	10.66	17.86	12.45	11.65	7.24	8.12		**		-
OVARC1000467	8.03	5.77	8.99	2.45	3.8	2.2	3.29	2.29	3.38	*	*	-	-
OVARC1000470	15.96	13.65	10.41	7.96	9.91	7.26	9.53	10.16	10.25				
OVARC1000473	12.49	10.05	10.69	6.2	7.49	6.37	10.6	7.2	9.15	**		-	
OVARC1000479	24.56	30.78	25.75	8.77	13.76	7.96	8.07	9.81	9.07	**	**	-	-
OVARC1000484	41.23	29.61	25.62	15.32	17.14	13.32	29.7	26.23	34.72	*		-	
OVARC1000486	15.8	17.22	17.4	11.06	13.85	9.12	14.13	11.53	12.18	*	*	-	-
OVARC1000496	6.74	8.5	5.88	2.96	8.22	5.46	2.84	3.93	3.9		*		-
OVARC1000520	8.86	5.17	6.53	2.16	5.01	3.05	4.06	3.97	5.92				
OVARC1000522	35.51	29.95	29.3	26.12	30.21	22.71	22.42	16.55	18.06		**		-
OVARC1000526	25.75	25.79	19.89	12.38	14.14	8.6	32.78	19.39	27.42	**		-	
OVARC1000529	17.7	16.61	13.49	7.72	9.26	6.61	12.03	7.5	12.39	**		-	
OVARC1000533	31.08	27.41	22.88	25.25	24.54	12.97	18.02	13.21	18.14		*		-
OVARC1000543	11.04	5.87	5.45	4.07	4.48	2.25	3.68	3.22	4.84				
OVARC1000550	9.45	7.02	5.98	3.29	4.46	2.66	4.35	2.47	4.43	*	*	-	-
OVARC1000553	34.95	36.44	34.04	16.33	24.77	21.97	31.22	31.95	33.2	**	*	-	-
OVARC1000556	22.37	23.81	26.15	14.72	11.54	9.38	19.99	16.63	22.58	**		-	
OVARC1000557	11.61	9.78	7.49	2.51	3.89	2.24	6.45	4.03	5.39	**	*	-	-
OVARC1000561	67.36	70.57	52.24	30.14	35.45	26.39	87.82	47.67	77.14	**		-	
OVARC1000564	79.74	89.59	94.8	35.3	37.73	54.01	49.59	52.84	37.26	**	**	-	-
OVARC1000573	11.41	12.83	14.29	6.97	10.13	6.51	5.93	10.17	8.55	*	*	-	-
OVARC1000576	235.06	210.51	199.48	203.8	258.47	200.46	142.26	126.19	115.56		**		-
OVARC1000578	15.29	13.44	14.45	8.15	12.93	8.56	9.81	12.76	11.9	*	*	-	-
OVARC1000581	5.46	3.63	4.65	3.12	3.25	1.85	1.84	1.64	2.35		**		-
OVARC1000586	99.11	90.08	96.7	58.86	53.54	48.9	78.17	82.33	62.01	**	*	-	-
OVARC1000588	5.04	6.16	5.9	2.73	4.3	3.79	4.96	4.69	3.2	*		-	
OVARC1000605	11.72	9.54	8.96	6.4	6.63	6.02	4.7	4.72	5.55	*	**	-	-
OVARC1000622	86.95	79.96	78.79	29.56	66.79	40.9	71.63	93.74	75.18	*		-	
OVARC1000636	9.18	7.82	11.99	5.56	6.68	4.67	5.37	6.74	3.7	*	*	-	-
OVARC1000640	9.32	12.02	12.8	8.63	10.33	8.57	6.08	8.89	7.4		*		-
OVARC1000649	137.37	159.82	123.65	116.33	170.6	128.38	91.38	85.12	81.65		**		-
OVARC1000661	14.89	15.01	20.86	11.94	15.89	11.61	9.31	9.27	13.9				
OVARC1000677	42.34	38.62	28.23	30.67	34.02	28.61	19.25	22.35	28.93				
OVARC1000678	18.66	21.84	18.64	9.55	15.51	8.53	9.3	11.98	8.4	*	**	-	-

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Table 462

OVARC1000679	17.17	15.32	16.17	8.84	11.11	9.5	8.07	11.07	12.27	**	*	-	-
OVARC1000681	8.2	7.24	6.7	4.69	3.61	5.03	3.58	6.1	3.97	**	*	-	-
OVARC1000682	113.12	97.53	93.09	104.53	135.81	99.85	59.24	48.57	73.95		*		-
OVARC1000689	57.01	42.21	46.96	44.44	54.09	47.18	30.34	27.71	26.26		*		-
OVARC1000700	15.99	15.69	20.71	10.16	14.93	8.67	10.07	14.65	13.84				
OVARC1000703	26.78	29.43	35.22	14.83	20.62	12.69	19.45	19.63	21.91	*	*	-	-
OVARC1000722	101.86	85.68	116.52	89.03	99.63	84.39	90.99	59.44	79.26				
OVARC1000726	14.33	9.39	12.54	8.8	8.89	8.63	5.72	6.56	7.04		*		-
OVARC1000727	10.18	7.75	13.09	5.79	7.58	4.18	6.38	6.81	6.67				
OVARC1000730	29.15	29.95	31.68	12.76	10.82	12.92	11.85	21.92	19.46	**	*	-	-
OVARC1000741	29.33	29.17	34.55	13.03	37.4	9.12	12.19	21.98	17.49		*		-
OVARC1000746	7.78	5.19	7.05	4.39	4.32	3.45	2.05	2.62	3.13	*	**	-	-
OVARC1000764	38.05	40.13	44.9	31.76	33.36	24.43	25.99	25.42	30.04	*	**	-	-
OVARC1000769	15.32	19.03	26.3	6.54	8.47	6.17	10.92	9.44	11.01	*	*	-	-
OVARC1000771	12.14	10.36	12.36	5.65	9.59	2.99	5.56	6.75	5.39		**		-
OVARC1000773	208.54	178.97	168.4	156.38	229.88	197.98	120.99	98.51	115.59		**		-
OVARC1000775	34.96	28.91	27.77	13.91	16.38	12.88	14.63	18.43	17.02	**	**	-	-
OVARC1000778	16.25	14.26	17.29	7.71	11.77	9.22	9.21	13.13	13.25	*		-	
OVARC1000779	5.51	4.08	7.92	1.14	3.76	1.42	1.72	21.49	16.55				
OVARC1000781	14.72	11.11	14.65	7.53	10.61	4.88	3.59	7.19	4.56	*	**	-	-
OVARC1000787	16.08	11.69	22.35	5.66	7.21	5.45	9	11.11	9.91	*		-	
OVARC1000789	23.78	29.78	21.78	12.72	20.51	12.99	10.1	11.61	10.12		**		-
OVARC1000800	37.24	52.19	47.92	15.44	23.62	15.47	18.1	25.22	22.47	**	**	-	-
OVARC1000802	10.69	12.79	19.22	5.61	8.97	4.92	12.57	10.26	7.88				
OVARC1000810	41.47	36.61	45.9	14.82	21.04	14.45	26.69	32.64	43.34	**		-	
OVARC1000811	19.55	15.32	20.3	9.11	11.03	10.04	5.82	8.76	8.16	**	**	-	-
OVARC1000814	47.61	40.61	47.27	21.78	30.43	20.51	28.06	40.57	35.2	**		-	
OVARC1000816	30.44	36.85	45.82	25.26	35.06	20.13	15.73	10.27	23.79		*		-
OVARC1000817	7.44	5.99	13.01	2.4	3.28	3.96	1.6	3.36	1.57		*		-
OVARC1000834	9.2	11.08	10.6	3.33	5.92	2.58	4.12	4.4	2.95	**	**	-	-
OVARC1000846	33.2	36.76	34.02	15.54	20.84	16.18	25.4	21.7	22.13	**	**	-	-
OVARC1000850	10.1	9.46	13.94	3.02	6.63	4.93	5.97	6.78	5.46	*	*	-	-
OVARC1000853	124.13	83.82	117.1	50.7	94.43	66.32	58.07	66.46	64.96		*		-
OVARC1000862	9.56	7.61	8.86	6.22	4.52	5.06	2.49	2.85	3.78	*	**	-	-
OVARC1000873	22.12	9.86	11.25	3.95	10.2	7.01	4.33	4	5.56				
OVARC1000875	25.32	18.88	20.49	9.43	11.13	12.13	10.43	9.71	12.19	**	**	-	-
OVARC1000876	14.43	11.76	13.8	4.33	8.64	6.48	3.87	5.38	3.7	**	**	-	-
OVARC1000883	16.65	14.83	22.63	10.71	10.46	10.25	4.07	3.52	3.44	*	**	-	-
OVARC1000885	14.94	15.72	15.2	7.47	13.49	6.08	8.84	6.87	4.31		**		-
OVARC1000886	13.43	12.39	14.55	7.87	12.43	7.38	15.33	6.54	7.36				
OVARC1000890	238.12	222.49	244.97	168.11	248.06	165.63	120.4	102.6	108.39		**		-
OVARC1000891	14.84	13	11.09	4.07	5.36	4.55	3.08	4.38	3.01	**	**	-	-
OVARC1000897	5.52	4.78	5.55	2.64	2.48	2.49	2.14	2.77	2.38	**	**	-	-
OVARC1000912	18.82	12.83	16.34	8.16	8.42	8.22	8.21	8.74	10.52	*	*	-	-
OVARC1000914	14.59	8.15	9.14	3.85	5.26	5.95	4.68	5.3	4.1		*		-
OVARC1000915	17.53	15.34	14.44	6.42	7.74	4.39	7.85	11.07	8.04	**	**	-	-
OVARC1000916	15.19	18.72	21.06	9.85	20.11	11.22	12.02	12.35	10.4		*		-
OVARC1000924	11.12	12.86	14.01	5.55	9.51	4.44	3.13	4.61	3.65	*	**	-	-
OVARC1000928	46.27	37.28	34.31	5.2	8.81	6.65	4.93	6.15	5.85	**	**	-	-
OVARC1000936	10.09	10.55	9.33	5.2	9.07	4.74	3.02	5.31	5.15		**		-
OVARC1000937	7.99	8.04	6.58	4.25	5.19	2.94	3.85	3.95	5.45	*	*	-	-
OVARC1000945	15	14.98	13.39	5.71	5.62	7.78	3.1	4.11	2.76	**	**	-	-
OVARC1000948	7.88	5.06	4.83	2.65	3.28	2.79	2.69	2.39	2.47	*	*	-	-
OVARC1000956	14.88	11.07	13.93	5.15	8.05	6.51	8.38	4.46	6.46	**	*	-	-
OVARC1000959	16.85	16.96	14.18	9.84	10.41	6.42	15.3	9.78	14.01	**		-	
OVARC1000960	47.32	52.37	41.49	22.16	32.89	19.82	46.28	34.15	44.56	*		-	
OVARC1000964	306.84	272.77	304.89	274.01	264.01	211.54	160.52	108.2	102.39		**		-
OVARC1000971	7.74	6.08	3.76	3.85	7.47	4.63	2.45	4.82	2.32				
OVARC1000975	109.05	95.15	91.82	89.45	126.14	83.84	54.44	48.09	54.61		**		-
OVARC1000976	6.41	7.34	5.63	3.4	4.98	2.89	5.48	3.56	2.85	*		-	
OVARC1000981	24.82	24.19	24.61	14.13	15.11	11.79	18.79	11.54	16.77	**	*	-	-
OVARC1000982	21.37	12.18	12.3	7.66	16.73	9.68	5.67	4.54	5.45		*		-
OVARC1000984	10.44	9.85	10.17	2.64	4.78	2.24	2.88	2.32	3.54	**	**	-	-
OVARC1000995	27.57	24.28	19.39	14.42	17.35	10.4	23.31	17.65	22.26	*		-	

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Table 463

OVARC1000996	12.75	15.42	13.22	7.58	7.82	4.86	10.5	9.45	10.8	**	*	-	-
OVARC1000999	77.92	64.11	52.33	34.61	41.57	26.78	51.13	38.47	53.84	*		-	
OVARC1001000	34.25	25.88	23.55	13.32	17.72	11.08	24.85	23.48	28.11	*		-	
OVARC1001004	4.45	4.47	4.74	3.56	4.7	2.11	3.94	2.09	3.24				
OVARC1001010	7.8	4.93	6.92	2.94	3.81	2.97	3.34	2.1	2.69	*	*	-	-
OVARC1001011	10.56	5.96	7.28	2.55	4.47	3.01	5.82	4.52	6.66	*		-	
OVARC1001030	135.15	261.75	227.94	119.93	118.81	67.28	114.11	94.32	117.34				
OVARC1001032	10.53	7.53	10.42	4.6	4.01	3.78	8.13	6.94	7.33	**		-	
OVARC1001034	10.83	11.24	8.27	5.28	4.2	4.55	7.53	5.89	7.35	**	*	-	-
OVARC1001038	36.07	37.32	30.24	14.88	24.71	11.8	14.41	10.88	16.24	*	**	-	-
OVARC1001040	40.95	33.02	36.27	20.4	24.74	15.2	38.11	31.08	34.73	**		-	
OVARC1001041	28.88	24.51	24.41	14.12	19.17	10.91	20.98	17.34	23.83	*		-	
OVARC1001044	8.66	8.02	6.34	3.74	2.76	3.79	6.52	3.05	4.17	**		-	
OVARC1001049	23.67	22.64	22.97	8.16	12.73	9.28	19.46	22.57	21.53	**		-	
OVARC1001051	381.08	484.89	350.06	354.62	546.22	323.29	741.7	383.07	703.22				
OVARC1001054	6.6	5.59	5.17	3.06	5.01	2.19	3.89	3.27	2.79		**		-
OVARC1001055	14.4	14.98	14.95	7.9	10.31	6.02	5.76	7.98	6.8	**	**	-	-
OVARC1001062	17.06	13.11	19.77	9.47	7.02	5.92	5.47	7.54	3.76	*	**	-	-
OVARC1001065	58.8	47.67	46.94	41.39	58.25	31.45	28.27	24.21	23.74		**		-
OVARC1001068	12.24	9.85	10	9.05	10.45	10.03	4.46	8.42	5.6		*		-
OVARC1001072	5.2	5.85	5.86	2.66	7.45	1.74	3.96	4.57	2.54		*		-
OVARC1001073	7.5	8.58	12.65	4.76	6.4	4.65	5.22	6.96	5.47				
OVARC1001074	4.7	5.22	6.88	3.02	6.61	3.48	7.1	3.06	2.4				
OVARC1001078	12.05	11.95	9	4.67	9.88	3.56	7.61	7.71	7.4		*		-
OVARC1001085	11.18	10.66	13.33	5.34	5.76	6.26	7.62	7.57	5.14	**	*	-	-
OVARC1001086	9.39	8.11	10.75	4.2	10	3.47	6.76	8.44	4.74				
OVARC1001091	241.22	186.8	193.81	163.03	271.86	178.86	140.22	106.42	112.84		*		-
OVARC1001092	18.15	15.63	18.59	22.78	28.04	21.17	13.63	16.45	14.87	*		+	
OVARC1001104	8.1	6.77	10.2	3.75	7.44	6.44	3.73	7.33	6.12				
OVARC1001107	107.49	92.87	112.02	98.9	125.4	90.42	58.37	49.66	59.61		**		-
OVARC1001113	4.26	4.3	6.18	3.48	7.31	2.59	2.8	2.95	2.48		*		-
OVARC1001117	14	17.53	15.78	9.22	10.42	7.27	18.6	16.88	12.72	**		-	
OVARC1001118	28.39	26.32	27.08	13.26	13.63	13.64	14.58	18.84	21.16	**	*	-	-
OVARC1001125	15.09	9.24	18.28	5.27	6.72	6.56	3.81	6.47	3.35	*	*	-	-
OVARC1001129	8.66	7.06	12.46	3.03	6.25	3.24	5.49	10.45	5.05				
OVARC1001132	9.08	13.23	15.1	8.86	15.2	9.07	5.57	13.13	8.52				
OVARC1001138	155.24	193.79	160.3	115.39	149.38	101.68	122.48	164.58	137.03				
OVARC1001141	12.99	10.8	12.94	7	9.03	7.57	7.48	10.75	7.3	**	*	-	-
OVARC1001154	128.63	107.01	106.33	119.46	158.63	83.66	81.42	78.16	83.39		*		-
OVARC1001161	17.68	27.92	21.1	11.55	22.82	12.42	16.84	15.27	15.42				
OVARC1001162	21.74	16.75	19.82	10.26	11.33	9.72	10.1	12.69	11.14	**	**	-	-
OVARC1001163	10.91	8.03	10.73	4.37	5.95	4.38	3.95	7.35	4.62	**	*	-	-
OVARC1001167	38.47	38	43.81	17.29	22.87	18.91	28.74	29.72	36.08	**	*	-	-
OVARC1001169	11.94	7.48	10.4	5.85	13.24	4.72	3.88	5.51	4.65		*		-
OVARC1001170	26.22	26.34	31.69	14.46	15.02	12.36	12.5	14.3	11.17	**	**	-	-
OVARC1001171	143.81	236.48	129.81	114.4	117.18	158.91	77.44	54.36	128.19				
OVARC1001173	24.91	33.6	36.93	11.93	16.26	13.53	26.95	27.14	25.91	**		-	
OVARC1001176	209.32	244.43	234.51	205.75	340.26	228.89	167.09	179.74	200.74		*		-
OVARC1001180	67.2	61.17	66.56	30.38	32.42	26.76	42.84	47.13	54.33	**	*	-	-
OVARC1001188	18.84	14.15	17.06	4.37	15.93	5.9	10.16	39.68	8.56				
OVARC1001200	14.51	7.89	14.82	6.11	7.72	3.65	4.16	15.56	6.11				
OVARC1001202	37.46	21.56	29.17	10.06	10.43	13.25	17.78	23.14	18.29	*		-	
OVARC1001206	6.83	6.97	11.31	3.06	5.96	2.9	2.03	8.52	4.3				
OVARC1001209	56.31	51.58	60.2	57.91	69.04	54.41	36.32	29.24	28.87		**		-
OVARC1001219	14.82	14.11	12.95	3.65	7.48	4.86	4.34	7.98	3.54	**	**	-	-
OVARC1001222	17.11	17.29	18.38	6.61	16.42	9.64	6.56	7.21	5.56		**		-
OVARC1001232	34.23	34.49	36.17	16.43	23.42	19.3	24.37	27.16	28.45	**	**	-	-
OVARC1001240	22.68	22.79	23.45	11.83	13.49	10.07	14	20.54	14.23	**	*	-	-
OVARC1001243	8.41	5.82	7.86	3.1	7.95	3.99	3.48	18.25	1.41				
OVARC1001244	43.29	22.42	33.3	20.02	23.25	15.87	15.69	21.46	15.18				
OVARC1001246	191.8	262.18	216.69	139.76	292.92	181.43	261.49	147.46	197.54				
OVARC1001247	33.18	25.43	26.03	8.87	21.81	17.23	8.61	11	7		**		-
OVARC1001260	10.58	9.81	13.5	4.35	12.46	3.56	7.06	8.38	13.07				
OVARC1001261	10.86	9.17	11.3	5.17	7	3.2	4.94	4.19	3.51	*	**	-	-

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Table 464

OVARC1001268	91.7	87.42	103.18	50.09	61.38	43.24	78.98	90.56	56.28	**		-	
OVARC1001270	7.04	6.65	7.37	4.89	4.4	3.37	2.36	3.78	2.58	**	**	-	-
OVARC1001271	19.59	14.31	19.8	9.15	12.99	7.59	10.4	9.45	13.28	*	*	-	-
OVARC1001282	9.08	5.35	8.29	3.47	3.89	2.86	2.79	2.02	1.62	*	*	-	-
OVARC1001296	8.37	7.88	7.76	3.73	3.83	3.51	3.2	2.52	1.42	**	**	-	-
OVARC1001306	8.13	8.36	10.06	2.51	4.13	1.61	1.91	3.24	2.11	**	**	-	-
OVARC1001314	6.35	7.88	10.42	5.15	6.88	5.6	5.8	2.73	3.16		*		-
OVARC1001316	9.21	9.19	7.4	3.28	5.15	2.41	2.09	2	2.6	**	**	-	-
OVARC1001329	66.76	60.97	62.75	30.71	36.83	28.85	49.5	54.71	56.06	**	*	-	-
OVARC1001330	6.94	7.09	6.08	3.83	3.92	2.72	1.52	3.71	2.62	**	**	-	-
OVARC1001336	20.53	13.52	17.21	8.37	10.93	7.02	7.67	13.22	12.66	*		-	
OVARC1001338	9.67	3.35	7.39	3.31	2.87	2.49	3.22	2.79	2.03				
OVARC1001339	93.84	87.95	84.06	45.91	66.98	50.22	43.37	46.73	40	**	**	-	-
OVARC1001340	6.83	5.17	8.34	3.19	3.73	1.7	2.64	3.21	3.16	*	*	-	-
OVARC1001341	30.38	40.21	33.21	15.81	17.56	16.77	23.98	16.89	14.16	**	*	-	-
OVARC1001342	319.96	384.64	298.02	528.73	514.44	449.66	353.76	251.2	152.62	*		+	
OVARC1001344	24.05	19.69	20.03	8.91	10.1	7.96	16.66	12.81	15.35	**	*	-	-
OVARC1001357	6.41	18.75	6.59	4.08	6.56	3.73	3.75	4.14	3.16				
OVARC1001359	59.32	54.06	31.23	23.17	43.75	45.21	51.59	26.81	37.78				
OVARC1001360	5.67	4	3.9	1.82	2.67	1.87	1.59	2.07	1.71	*	**	-	-
OVARC1001369	7.6	9.8	9.35	5.24	6.16	2.48	5.5	3.41	1.68	*	*	-	-
OVARC1001372	9.97	8.14	5.06	1.49	5.79	2.2	2.9	3.07	0.96		*		-
OVARC1001376	27	25.34	21.25	12.73	15.31	10.9	17.23	14.16	15.91	**	*	-	-
OVARC1001381	39.84	52.86	35.2	18.78	31.21	17.84	39.83	32.09	35.47	*		-	
OVARC1001391	4.35	4.74	4.59	3.41	5.61	3.07	2.93	3.15	1.97		**		-
OVARC1001392	11.01	13.87	11.26	7.11	8.72	6.36	4.32	4.97	3.08	*	**	-	-
OVARC1001399	7.11	9.27	5.73	3.62	4.78	3.62	4.04	3.29	4.7	*	*	-	-
OVARC1001417	8.65	8.11	7.05	3.69	5.18	3.15	2.59	2.11	3.11	**	**	-	-
OVARC1001419	9.55	7.34	7.59	3.69	5.75	3.4	4.52	2.92	1.58	*	**	-	-
OVARC1001425	13.5	5.66	6.59	3.04	5.54	5.43	3.66	1.31	1.7				
OVARC1001436	14.91	13.09	11.35	5.12	5.94	3.89	4.56	3.69	3.48	**	**	-	-
OVARC1001442	5.57	6.26	6.22	3.11	6.56	2.54	5.62	2.71	2.72				
OVARC1001451	30.68	20.35	20.93	10.57	21.04	10.84	19.07	21.71	23.53				
OVARC1001452	16.95	14.67	11.44	7.52	6.15	5.24	7.7	11.36	6.64	**		-	
OVARC1001453	7.86	6.06	6.61	4.22	6.52	4.39	4.72	4.86	4.79		*		-
OVARC1001476	20.63	24.57	30.44	15.92	22.32	7.34	11.05	12.16	16.07		*		-
OVARC1001480	7.35	4.8	7.98	3.71	4.84	5.16	2.87	2.08	3.16		*		-
OVARC1001489	11.25	5.88	6.53	8.16	19.5	4.38	4.69	2.8	2.81				
OVARC1001493	15.28	11.36	13.67	4.88	4.94	2.76	9.11	6.21	8.31	**	*	-	-
OVARC1001496	32.05	27.24	23.8	12.75	20.64	11	9.38	5.04	10.85	*	**	-	-
OVARC1001499	5.67	6.05	4.7	2.72	3.78	1.85	2.85	4.6	2.57	*	*	-	-
OVARC1001506	31.76	25.87	22.22	8.57	18.43	9.44	18.79	15.06	20.59	*		-	
OVARC1001509	17.78	13.64	12.09	7.06	8.79	5.76	15.13	14.75	21.14	*		-	
OVARC1001510	8.59	5.24	6.08	3.07	5.95	3.22	7.27	7.67	4.5				
OVARC1001516	10.81	12.88	13.12	5.8	9.08	6.34	8.79	7.64	9.61	*	*	-	-
OVARC1001525	7.75	5.51	6.34	3.13	4.32	3.66	4.26	3.77	3.8	*	*	-	-
OVARC1001542	30.12	29.23	28.39	14.89	25.03	14.49	18.26	13.2	26.28	*		-	
OVARC1001544	27.99	28.47	20.46	12.55	18.48	10.77	36.56	24.05	33.39	*		-	
OVARC1001546	6.07	8.98	10.22	3.38	5.35	8.68	3.38	3.45	4.28		*		-
OVARC1001547	4.36	6.21	6.19	3.96	3.95	1.63	2.77	2.7	2.24		**		-
OVARC1001555	137.04	110.5	136.25	120.36	174.1	119.31	90.66	69.83	70.87		*		-
OVARC1001560	10.54	9.21	9.05	6.2	10.38	4.19	4.33	6.13	2.34		*		-
OVARC1001569	28.34	25.69	28.31	17.71	19.82	21.58	15.15	17.9	16.82	**	**	-	-
OVARC1001570	9.57	12.59	13.54	7.21	9.92	6.14	6.01	6.08	8.45		*		-
OVARC1001577	10.2	13.78	13.09	13.59	16.75	9.11	10.56	8.87	5.25				
OVARC1001578	0	0.27	1.12	0.09	2	0.48	1.37	0.77	0				
OVARC1001596	18.44	38.66	31.49	14.48	23.49	16.88	13.34	13.82	12.27				
OVARC1001600	12.84	12.05	12.79	8.39	9.83	7.52	7.16	10.38	7.31	**	*	-	-
OVARC1001607	17.69	15.72	17.94	10.9	18.71	12.05	10.18	16.33	11.6				
OVARC1001610	7.42	7.24	11.17	5.09	7.94	4.34	2.78	4.22	3.55		*		-
OVARC1001611	3.52	5.78	9.33	2.82	5.44	3.47	2.68	4.9	2.76				
OVARC1001615	7.22	4.15	9.71	3.66	4.51	3.88	4.88	4.91	5.78				
OVARC1001636	5.13	4.74	6.26	4.34	6.6	4.17	6.58	6.24	9.12				
OVARC1001668	40.93	55.07	40.85	20.99	33.29	18.89	40.58	43.41	37.28	*		-	

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OVARC1001702	9.4	5.63	9.29	4.18	2.13	4.1	3.32	3.32	2.46	*	*	-	-
OVARC1001703	7.15	7.4	12.31	4.47	5.7	4.5	5.85	8.24	3.65				
OVARC1001710	18.66	12.34	27.68	8.37	10.17	11.06	8.89	17.12	13.23				
OVARC1001711	18.7	15.2	21.81	10.78	18.26	9.63	7.19	14.6	8.6		*		-
OVARC1001713	106.12	95.89	110.84	111.33	127.16	96.1	59.14	62.39	67.07		**		-
OVARC1001725	7.41	8.41	15.02	6.01	22.46	3.17	4.32	4.47	6.9				
OVARC1001726	9.14	11.76	13.16	5.3	10.91	4.63	7.72	5.13	7.08		*		-
OVARC1001727	6.13	4.36	5.44	2.42	3.92	3.64	2.37	4.79	3.09	*		-	
OVARC1001731	326.35	314.92	333.21	240.06	116.88	168.02	275.41	235.36	284.79	*	*	-	-
OVARC1001735	10.45	7.4	10.3	3.26	6.6	5.16	2.85	50.48	3.58	*		-	
OVARC1001741	51.89	35.06	44.69	30.3	40.05	30.18	29.82	27.49	31.74		*		-
OVARC1001745	48.03	48.42	50.14	20.26	24.89	18.25	35.38	41.14	42.19	**	*	-	-
OVARC1001759	8.58	9.79	14.25	4.9	9.68	2.54	3.21	5.87	3.66		*		-
OVARC1001762	15.44	18.76	16.88	4.99	8.2	5.87	5.45	4.57	3.61	**	**	-	-
OVARC1001766	83.39	85.91	87.93	59.55	79.17	53.32	53.78	49.12	57.96		**		-
OVARC1001767	7.04	5.21	8.42	2.96	5.88	2.78	2.97	1.63	2.74		*		-
OVARC1001768	14.52	13.49	18.22	6.31	12.6	7.55	3.97	6.24	6.88		**		-
OVARC1001770	26.33	28.28	29.2	13.86	20.54	11.13	6.52	15.1	8.61	*	**	-	-
OVARC1001776	7.09	4.63	7.55	4.18	5.49	2.76	2.6	3.29	2.71		*		-
OVARC1001791	10.39	7.82	10.63	6.37	4.38	3.31	3.58	4.2	5.4	*	**	-	-
OVARC1001795	7.98	5.23	12.47	1.59	4.12	3.1	3.31	4.76	7.14				
OVARC1001798	40.84	44.26	46	20.27	29.31	16.26	30.23	32.18	29.44	**	**	-	-
OVARC1001802	21.47	24.32	21.73	9.56	17	10.13	13.8	16.34	14.18	*	**	-	-
OVARC1001805	21.41	25.19	22.93	13.01	23.64	11.53	6.55	5.13	2.96		**		-
OVARC1001807	9.03	4.95	8.69	4.35	5.41	3.66	4.23	6.47	5.73				
OVARC1001809	149.46	129.89	172.57	133.13	197.68	130.62	61.18	73.6	73.85		**		-
OVARC1001812	14.81	11.9	18.98	7.06	7.79	6.77	7.18	8.19	7.69	*	*	-	-
OVARC1001813	16.16	13.4	12.96	5.79	9.88	6.64	9.17	11.83	7.83	*	*	-	-
OVARC1001820	13.24	13.12	21.66	6.46	7.84	7.81	9.43	11.92	8.26	*		-	
OVARC1001828	7.36	8.18	15.13	2.53	4.46	3.16	2.97	2.27	1.93		*		-
OVARC1001833	7.55	8	10.4	3.73	5.88	2.72	2.14	3.67	2.55	*	**	-	-
OVARC1001839	9.51	8.23	9.47	3.48	6.12	2.44	2.33	1.23	3.33	*	**	-	-
OVARC1001846	10.75	6.47	12.96	4.44	5.49	4.43	2.19	5.18	4.87		*		-
OVARC1001849	21.23	22.64	18.18	12.84	14.77	8.26	9.88	17.09	10.17	*	*	-	-
OVARC1001861	14.15	12.35	14.96	7.86	9.2	6.06	6.33	6.39	8.07	**	**	-	-
OVARC1001873	10.37	9.13	10.41	3.08	3.81	3.28	3.75	2.72	3.55	**	**	-	-
OVARC1001879	12.35	13.47	14.5	4.79	6.62	4.85	9.81	8.26	4.82	**	*	-	-
OVARC1001880	17.95	16.04	17.13	6.7	12.3	6.25	9.7	7.19	8.89	*	**	-	-
OVARC1001883	10.68	7.64	9.62	5.66	5.31	4.96	4.5	5.37	3.66	*	**	-	-
OVARC1001900	21.57	23.04	21.79	9.35	13.16	8.64	4.93	5.9	5.98	**	**	-	-
OVARC1001901	6.1	3.23	6.27	3.76	3.35	2.44	2	2.36	2.55		*		-
OVARC1001911	5.85	6.08	5.24	3.87	3.1	3.23	3.29	4.37	2.41	**	*	-	-
OVARC1001916	15.55	14.04	13.05	10.21	8.26	9.44	6.7	7.73	11.27	**	*	-	-
OVARC1001928	4.28	4.17	5.98	2.82	2.37	1.14	3.65	1.6	1.43	*	*	-	-
OVARC1001937	25.6	15.71	13.44	9.48	11.18	11.27	11.49	12.97	7.51				
OVARC1001940	8.76	8.78	8.37	2.83	3.28	2.84	2.16	2.96	2.02	**	**	-	-
OVARC1001942	20.24	15.16	17.14	7.55	9.31	5.48	5.3	6.71	7.34	**	**	-	-
OVARC1001943	29.68	32.41	20.55	12.97	22.62	15.27	4.34	4.72	5.72		**		-
OVARC1001949	14.19	11.75	10.33	3.19	5.85	4.46	2.89	6.47	5.47	**	**	-	-
OVARC1001950	13.94	15.9	10.94	6.19	9.29	6.75	8.04	7.58	9.81	*	*	-	-
OVARC1001952	122.9	130.05	103.73	90.55	135.58	102.89	79.11	70.36	72.15		**		-
OVARC1001954	7.45	6.81	6.15	3.11	3.63	2.91	2.32	2.33	2.18	**	**	-	-
OVARC1001963	12.44	11.79	17.61	6.04	6.32	5.28	6.38	9.47	7.04	*	*	-	-
OVARC1001983	25.71	30.08	25.81	12.15	15.68	10.47	16.02	11.31	11.87	**	**	-	-
OVARC1001987	13.81	15.75	12.25	6.15	7.8	4.37	5.37	6.61	4.93	**	**	-	-
OVARC1001989	18.41	16.89	13.96	7.74	13.38	8.71	14.94	11.39	11.29	*		-	
OVARC1001991	12.31	10.21	10.74	6.47	8.3	7.41	6.69	6.19	5.31	*	**	-	-
OVARC1002005	33.83	38.39	35.62	17.89	27.06	20.01	28.16	23.73	27.11	**	**	-	-
OVARC1002044	25.13	24.53	23.58	14.08	17.38	11.27	23.29	17.04	24.49	**		-	
OVARC1002046	79.06	107.27	86.51	49.53	77.97	65.8	68.65	65.46	67.43		*		-
OVARC1002050	9.22	6.62	10.19	4.05	4.76	4.15	4.13	2.81	4.5	*	*	-	-
OVARC1002058	18.18	16.91	17.55	13.19	18.87	6.99	24.17	22.71	28.4		*		+
OVARC1002066	67.02	72.72	47.65	37.79	39.59	35.74	62.17	50.77	51.33	*		-	
OVARC1002082	34.4	33.12	24.78	17.13	27.63	15.59	48.32	29.05	33.16				

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OVARC1002091	18.78	19.82	15.43	10.02	4.76	6.56	9.66	6.62	10.94	**	**	-	-
OVARC1002092	11.35	7.73	4.3	3.87	5.5	2.76	3.85	4.56	3.79				
OVARC1002093	11.71	8.5	20.66	4.96	14.44	7.82	5.85	5.4	7.08				
OVARC1002094	6.29	6.49	6.65	2.69	4.04	2.24	4.34	3.07	3.08	**	**	-	-
OVARC1002107	13.48	8.34	12.83	6.06	7.84	6.33	9.41	7.18	12.5	*		-	
OVARC1002112	26.38	33.01	27.23	12.79	21.35	12.35	12.54	9.82	14.29	*	**	-	-
OVARC1002126	65.16	69.33	51.38	44.56	51.62	38.84	65.71	52.52	60.89				
OVARC1002127	6.15	6.37	5.32	1.95	4.41	3.09	5.22	3.46	3.37	*	*	-	-
OVARC1002138	5.22	5.32	3.68	5.16	3.08	2.95	2.56	2.26	2.94		*		-
OVARC1002143	7.3	4.6	3.7	3.29	5.14	1.8	3.79	3.64	5.8				
OVARC1002156	14.33	13.86	13.02	10.03	12.28	6.78	8.59	6.29	5.67		**		-
OVARC1002158	9.15	5.03	4.65	3.18	3.11	2.41	3.88	2.86	4.37				
OVARC1002165	67.03	61.86	54.25	23.78	36.97	31.97	46.19	44.24	42.15	**	*	-	-
OVARC1002176	10.61	13.89	9.02	5.22	6.29	4.46	9.03	7.11	8.09	*		-	
OVARC1002178	11.02	11.22	6.01	3.16	5.47	2.82	6.17	3.48	3.57	*		-	
OVARC1002182	6.32	5.52	5.4	2.92	5.92	3.91	6.46	4.29	5.82				
OVARC1002185	13.32	14.59	15.01	5.81	10.11	6.86	7.78	7.13	8.82	**	**	-	-
PLACE1000004	9.74	9.21	11.61	4.85	7.73	5.01	4.83	8.27	4.93	*	*	-	-
PLACE1000005	27.12	18.01	21.46	13.29	16.54	9.78	14.01	13.75	13.04		*		-
PLACE1000006	91.12	57.04	55.23	34.88	52.28	43.96	6.98	11.96	13.8		**		-
PLACE1000007	7.26	8.75	8.28	8.37	10.72	8.06	3.04	5.48	2.7		*		-
PLACE1000014	2.23	2.04	4.15	1.42	4	3.02	1.88	2.43	1.7				
PLACE1000031	25.49	34.88	32.13	13.67	27.22	11.3	27.49	25.37	24.47				
PLACE1000033	18.11	15.97	17.95	12.01	14.01	16.72	14.29	10.78	15.77				
PLACE1000040	8.82	8.21	10.8	5.78	10.45	6.53	3.91	7.12	4.69		*		-
PLACE1000048	20.38	17.3	18.51	15.36	23.63	12.54	8.78	9.57	6.66		**		-
PLACE1000050	5.4	7.04	6.5	2.42	4.86	4.46	3.72	6.27	1.7				
PLACE1000061	9.33	8.61	17.26	5.67	11.39	8.55	3.23	9.76	4.54				
PLACE1000066	6.66	5.77	17.49	7.42	6.83	5.75	5.92	4.2	3.99				
PLACE1000075	12.56	13.3	14.47	10.46	23.06	11.81	12.58	8.36	7.76				
PLACE1000078	16.43	18.48	16.12	10.89	9.95	8.28	13.59	13.8	12.7	**	*	-	-
PLACE1000081	10.24	9.79	10.46	3.99	5.51	5	3.34	5.78	6.89	**	*	-	-
PLACE1000086	24.93	18.79	23.44	11.66	12.45	12.8	14.85	17.83	16.54	**	*	-	-
PLACE1000094	9.77	8.35	20.14	5.83	7.13	8.45	9.11	6.86	4.47				
PLACE1000101	13.24	13.69	14.14	7.47	11.68	8.08	3.54	8.15	5.57	*	**	-	-
PLACE1000121	13.12	18.46	20.42	15.19	20.27	14.52	7.88	10.58	8.77		*		-
PLACE1000133	9.91	9.72	12.83	7.9	8.22	8.5	5.09	6.11	8.25		*		-
PLACE1000142	9.88	8.89	10.42	4.19	7.46	3.72	7.05	4.74	5.82	*	**	-	-
PLACE1000146	26.84	30.96	24.74	12.94	22.4	10.59	30.36	28.2	29.92	*		-	
PLACE1000163	7.41	5.19	10.36	3.1	5	4.08	3.16	3.43	3.29		*		-
PLACE1000172	27.22	20.45	29.16	10.4	14.2	9.22	8.64	12.45	11.02	**	**	-	-
PLACE1000181	113.9	71.51	73.22	49.28	64.78	42.83	38.76	53.7	55.02				
PLACE1000184	17.72	15.27	19.8	11.79	14.01	13.85	9.11	9.87	10.76	*	**	-	-
PLACE1000185	16.19	14.48	17.72	7.66	7.1	6.34	4.1	6.59	4.27	**	**	-	-
PLACE1000198	9.65	11.81	15.71	11.09	11.55	8.4	6.38	19.65	7.03				
PLACE1000213	6.26	6.05	11.46	4.09	6.36	3.94	3.17	3.29	3.78				
PLACE1000214	9.15	11.17	11.68	8.73	8.08	4.64	3.79	6.02	5.34		**		-
PLACE1000220	25.57	22.54	23.7	11.03	13.14	7.79	10.18	10.81	12.09	**	**	-	-
PLACE1000231	14.42	18.43	23.26	5.64	9.79	6.68	7.36	7.88	9.82	*	*	-	-
PLACE1000236	7.58	6.02	8.68	1.98	6.24	5.31	3.56	10.92	5.78				
PLACE1000245	26.52	25.91	22.56	9.19	16.74	15.36	8.75	9.5	10.2	*	**	-	-
PLACE1000246	45.69	36.58	50.55	14.83	17.16	15.14	8.9	11.47	10.62	**	**	-	-
PLACE1000258	9.85	11.52	11.33	3.16	7.83	3.08	2.46	5.51	4.37	*	**	-	-
PLACE1000288	14.3	14.29	20.76	4.5	8.13	8.1	4.73	7.76	5.77	*	*	-	-
PLACE1000292	22.65	21.9	21.53	9.54	18.93	11.23	12.98	16.24	12.38	*	**	-	-
PLACE1000302	24.34	18.15	25.79	8.82	16.47	8.9	10.89	16.25	19.37	*		-	
PLACE1000304	9.25	6.15	7.74	5.54	8.18	3.68	3.39	11.18	2.7				
PLACE1000308	15.07	8.66	14.03	6.88	10.38	7.58	8.62	8.08	9.22				
PLACE1000309	50.33	32.12	45.32	24.2	31.82	23.11	35.7	38.12	29.88				
PLACE1000312	7.8	7.45	13.99	4.65	6.15	3.95	7.1	6.14	4.22				
PLACE1000330	37.2	43.13	26.2	23.56	30.84	17.96	20.8	28.35	14.01				
PLACE1000332	19.72	22.93	22.77	9.1	18.25	13.71	15.08	10.86	13.37	*	**	-	-
PLACE1000347	18.65	20.7	25.21	9.08	28.96	11.34	16.06	14.13	12.46		*		-
PLACE1000351	4.55	3.12	7.2	2.8	3.17	2.14	6.68	4.21	4.87				

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PLACE1000374	4.36	4.25	6.34	4.3	3.67	2.84	1.94	3.1	1.77		*		-
PLACE1000380	16.1	6.91	17.82	9.8	10.53	4.49	5.18	5.02	6.92				
PLACE1000383	6.36	4	6.16	2.37	2.92	2.52	2.89	0.95	0.87	*	*	-	-
PLACE1000397	11.59	7.26	11.9	2.79	5.06	5.01	6.09	6.59	6.48	*		-	
PLACE1000401	9.04	6.59	7.42	3.23	3.26	3.54	3.28	2.6	2.94	**	**	-	-
PLACE1000406	13.08	8.33	14.95	2.59	5.95	3.66	6.86	10.26	6.27	*		-	
PLACE1000412	8.51	7.48	7.35	3.42	4.96	3.44	3.84	4.02	2.52	**	**	-	-
PLACE1000420	18.93	23.33	27.28	7.24	14.78	9.32	4.07	6.78	6.75	*	**	-	-
PLACE1000421	17.83	12.09	14.21	5.67	5.38	4.01	4.24	5.77	6.73	**	**	-	-
PLACE1000423	9.91	10.66	9.25	5.17	5.46	3.16	3.23	3.33	2.82	**	**	-	-
PLACE1000424	6.41	4.46	8.86	3.52	3.38	1.84	2.63	2.91	2.34		*		-
PLACE1000430	9.9	7.48	10.47	5.49	5	3.45	3.57	3.09	3.55	*	**	-	-
PLACE1000433	8.1	6.1	7.11	1.95	4.44	2.14	2.34	1.88	2.11	*	**	-	-
PLACE1000435	28.95	26.53	24.32	14.09	14.79	9.09	16.84	11.65	12.23	**	**	-	-
PLACE1000437	13.7	9.76	13.69	6.32	11.96	9.08	8.69	6.76	4.42		*		-
PLACE1000442	4.21	4.33	5.54	1.97	3.93	1.28	2.62	4.3	2.3				
PLACE1000444	8.39	8.02	5.47	3.23	8.73	7.32	3.64	5.13	5.23				
PLACE1000453	8.24	8.08	7.4	2.64	6.34	3.96	5.87	6.05	5.1	*	**	-	-
PLACE1000456	9.14	8.93	7.88	4.6	6.83	3.55	4.93	5.65	3.15	*	**	-	-
PLACE1000465	29.59	27.02	24.71	10.66	16.38	9.53	7.25	7.03	4.61	**	**	-	-
PLACE1000481	10.19	8.45	9.18	6.24	5.2	4.46	5.55	2.41	2.95	**	**	-	-
PLACE1000492	14.54	13.99	15.18	6.98	17.38	5.81	5.24	4	6.05		**		-
PLACE1000508	8.74	6.29	6.02	2.46	6.75	1.48	4.68	3.01	3.04		*		-
PLACE1000512	4.85	3.74	3.65	2.37	3	3.01	2.27	2.44	1.75	*	*	-	-
PLACE1000540	12.96	8.47	7.79	4.5	9.85	7.03	5.75	9.5	3.54				
PLACE1000541	10.16	15.98	11.44	6.25	17.26	10.37	7.65	6.38	9.85				
PLACE1000546	13.1	11.96	11.32	7.18	10.25	10.48	6.08	5.2	6.25		**		-
PLACE1000547	8.49	5.52	7.86	5.49	10.6	14.98	5.43	2.62	3.64		*		-
PLACE1000560	22.37	15.31	18.14	8.36	10.85	7.86	6.26	3.35	3.9	*	**	-	-
PLACE1000562	8.22	7.18	9	4.62	4.33	3.02	4.18	2.13	2.7	**	**	-	-
PLACE1000564	17.41	14.24	11.35	10.42	10.44	10.34	8.72	6.17	6.09		*		-
PLACE1000583	11.44	8.04	7.49	4.72	4.9	3.91	5.24	5.95	5.26	*	*	-	-
PLACE1000587	7.15	6.59	3.7	3.14	3.88	4.15	3.78	3.64	4.07				
PLACE1000588	18.91	11.92	9.8	5.65	7.81	8.36	8.6	5.83	6.87				
PLACE1000596	11.7	13.56	11.65	8.47	13.84	9.08	10.58	5.53	9.44				
PLACE1000599	9.76	11.08	9.94	6.95	10.5	6.09	4.81	2.43	3.16		**		-
PLACE1000605	16.65	12.34	15.55	9.49	9.68	6.14	6.32	3.07	5.49	*	**	-	-
PLACE1000610	13.13	11.57	11.01	8.74	7.05	4.41	9.69	6.2	4.65	*	*	-	-
PLACE1000611	44.34	42.43	32.52	26.13	31.67	19.73	63.56	39.23	50.7				
PLACE1000626	7.16	6.36	6.63	3.54	3.14	2.93	5.25	5.57	5.32	**	**	-	-
PLACE1000633	7.75	6.07	5.61	4.09	5.95	4.33	4.51	3.72	5.54				
PLACE1000636	9.18	4.57	3.73	3.4	5.99	3.07	2.89	4.22	5.33				
PLACE1000653	13.52	15.36	9.28	7.56	11.63	7.5	6.22	4.09	7.58		*		-
PLACE1000656	16.45	24.27	20.78	6.6	13.98	8.95	13.7	10.63	9.13	*	*	-	-
PLACE1000663	17.59	14.23	11.72	6.71	8	7.43	15.75	11.07	16.5	*		-	
PLACE1000706	22.58	27.08	16.29	14.32	16.15	9.77	10.6	7.13	11.87		*		-
PLACE1000712	15.91	18.32	12.16	10.41	18.03	9.89	15.21	13.33	14.12				
PLACE1000716	9.51	6.38	10.32	4.38	8.28	5.91	5.52	6.18	6.28				
PLACE1000740	62.65	63.87	75.82	66.13	88.56	67.41	54.02	47.28	39.42		*		-
PLACE1000748	21.69	20.13	21.77	15.61	19.67	14.26	16.35	17.23	19.62		*		-
PLACE1000749	8.09	6.77	9.49	5.21	7.14	4.97	2.01	3.41	3.49		**		-
PLACE1000751	5.85	6.89	7.76	3.42	4.79	3.39	2.03	3.31	2.82	*	**	-	-
PLACE1000755	17.27	23.58	23.84	13.28	21.64	9.26	15.55	10.98	9.19		*		-
PLACE1000769	3.3	5.09	3.02	3.66	5.56	3.4	3.76	2.68	2.93				
PLACE1000778	43.25	43.09	44.83	22.77	18.03	27.54	20.87	24.08	21.65	**	**	-	-
PLACE1000785	31.35	17.11	31.03	9.35	9.07	8.25	11.86	8.82	7.46	*	*	-	-
PLACE1000786	5.99	3.18	7.12	2.4	4.01	1.88	2.45	4.94	6.92				
PLACE1000793	62.95	70.84	86.12	74.56	80.1	68.58	59.03	72.61	48.69				
PLACE1000795	170.82	165.32	165.81	123.39	175.42	137.1	104.41	82.02	95.27		**		-
PLACE1000798	34.34	30.96	28.31	19.04	23.22	14.81	22.05	22.97	28.25	*		-	
PLACE1000812	16.41	17.23	19.15	11.98	12.41	10.24	15.41	13.57	12.8	**	*	-	-
PLACE1000823	25.51	22.51	19.45	15.2	17.94	10.61	13.45	15.88	12.99	*	*	-	-
PLACE1000825	9.78	4.9	7.94	5.02	3.89	3.86	4.94	3.55	4.1				
PLACE1000838	37.15	32.03	40.12	17.98	18.59	17.35	19.92	15.21	15.97	**	**	-	-

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Table 468

PLACE1000841	7.87	7.94	8.8	7.6	12.23	10.86	5.33	4.89	4.56		**		-
PLACE1000843	16.04	20.1	24.44	8.07	13.38	10.99	7.02	9.18	7.59	*	**	-	-
PLACE1000849	5.43	7.23	9.29	4.99	5.8	4.19	3.26	3.96	2.16		*		-
PLACE1000856	209.98	229.07	253.03	209.39	256.66	183.75	147.93	119.29	119.6		**		-
PLACE1000863	16.12	16.52	27.27	10.41	12.7	10.18	13.62	16.56	12.54				
PLACE1000876	16.98	21.81	24.49	11.69	18.7	12.24	19.45	15.76	20.21				
PLACE1000899	225.37	148.25	253.61	106.96	112.25	68.21	130.08	130.64	120.26	*		-	
PLACE1000907	11.9	9.88	11.62	4.52	6.53	6.56	4.58	7.2	4.58	**	**	-	-
PLACE1000909	219.81	187.78	224.87	129.92	144.43	97.69	209.39	207.09	231	**		-	
PLACE1000912	4.53	4.31	6.11	1.98	4.16	2.65	2.79	1.25	1.4		*		-
PLACE1000914	13.65	11.52	16.16	6.76	9.53	7.59	5.22	5.53	2.91	*	**	-	-
PLACE1000918	13.18	11.98	16.82	5.88	9.64	8.52	8.09	14.67	8.16	*		-	
PLACE1000927	6.93	7.22	10.54	4.38	6.32	3.11	4.55	3.47	4.34		*		-
PLACE1000931	9.5	7.15	10.84	7.43	6.57	4.4	3.12	4.27	3.39		**		-
PLACE1000944	12.44	7.29	10.38	5.9	6.11	4.93	5.15	6.79	5.9	*		-	
PLACE1000948	15.03	15	16.76	7.56	11.29	7.62	5.5	9.31	6.83	**	**	-	-
PLACE1000958	5.27	4.99	7.38	2.51	5.7	3.99	1.85	6.23	4.43				
PLACE1000972	8.38	5.92	10.49	3.65	7.53	4.25	3.77	5.86	4.19				
PLACE1000977	11.29	8.32	15.95	5.04	5.25	7.02	2.5	10.48	3.14				
PLACE1000979	13.89	7.86	9.86	3.34	7.43	5.36	4.42	5.93	8.8				
PLACE1000986	30.12	30.53	34.37	25.05	28	23.07	15.94	15.63	18.52	*	**	-	-
PLACE1000987	19.26	23.97	21.74	13.41	21.5	10.91	16.26	13.02	12.47		*		-
PLACE1001000	4.37	7.15	10.87	3.42	3.04	2.14	2.69	2.93	3.43				
PLACE1001007	6.61	2.96	5.44	2.81	6.06	3.04	2.78	3.89	2.01				
PLACE1001010	9.46	6.18	10.43	5.02	5.52	3.2	5.18	3.73	3.91	*	*	-	-
PLACE1001015	7.99	5.3	8.03	6.19	7.65	4.6	3.26	3.31	2.3		*		-
PLACE1001016	17.51	11.26	16.44	6.61	7.04	6.42	3.95	3.27	2.38	*	**	-	-
PLACE1001022	14.42	12.9	14.76	4.97	7.37	5.56	7.11	8.21	7.4	**	**	-	-
PLACE1001024	11.18	12.76	12	5.14	10.39	4.2	4.43	3.88	2.99		**		-
PLACE1001036	105.59	109.4	58.51	52.8	114.22	89.89	113.54	86.02	137.21				
PLACE1001038	9.63	8.86	10.53	4.68	5.51	5.33	2.98	5.92	7.98	**		-	
PLACE1001048	7.22	3.94	6.41	5.19	5.21	3.49	3.25	3.01	2.83		*		-
PLACE1001054	17.12	18.15	23	21.95	14.11	11.96	6.57	6.82	6.81		**		-
PLACE1001062	7.69	5.86	7.49	3.03	6.18	4.98	5.6	1.77	1.91		*		-
PLACE1001063	11.82	13.23	13.09	8.34	8.29	7.45	3.15	3.88	2.78	**	**	-	-
PLACE1001076	17.46	15.27	22.58	9.61	12.22	10.09	9.5	6.93	10.2	*	*	-	-
PLACE1001081	8.04	6.12	10.01	3.34	3.8	3.43	2.11	2.93	3.84	*	*	-	-
PLACE1001088	1077.5	1434.9	897.35	706.08	898.84	874	835.46	1189	1173.1				
PLACE1001092	41.3	35.7	38.59	14.58	20.22	12.39	28.15	30.94	33.71	**	*	-	-
PLACE1001098	27.39	22.29	18.87	5.94	11.11	13.11	8.05	8.36	7.66	*	**	-	-
PLACE1001100	12.04	12.72	14.57	7.69	8.66	8.94	7.95	8.39	9.98	**	*	-	-
PLACE1001104	10.26	8.03	11.29	7.1	4.81	4.72	5.84	4.16	5.12	*	*	-	-
PLACE1001114	19.87	21.11	13.11	5.44	7.05	8.22	2.52	3.44	2.49	*	**	-	-
PLACE1001118	16.04	15.17	13.54	9.49	13.49	10.14	5.69	6.26	3.99		**		-
PLACE1001123	11.13	9.28	10.37	3.01	8.71	7.98	2.59	2.22	5.96		**		-
PLACE1001136	9.63	8.36	10.4	4.16	7.83	10.1	11.4	6.43	4.95				
PLACE1001144	22.24	18.89	18.24	5.11	10.59	8.11	16.88	14.03	17.77	**		-	
PLACE1001147	9.73	14.79	11.54	7.5	5.73	6.98	3.33	4.01	4.07	*	**	-	-
PLACE1001148	16.26	12.46	13.41	8.25	12.02	6.54	11.91	10.71	11.91				
PLACE1001159	5.83	2.18	9.14	5.55	4.85	2.75	3.37	5.16	1.28				
PLACE1001168	6.64	5.38	5	2.78	4.75	2.95	4.38	2.12	2.36		*		-
PLACE1001171	17.87	14.63	16.06	9.77	9.8	9.82	9.4	7.26	9.58	**	**	-	-
PLACE1001183	24.74	23.48	20.67	15.23	16.9	11.49	12.71	7.91	11.36	**	**	-	-
PLACE1001185	8.91	7.62	8.02	4.21	7.14	4.11	5.56	3.21	2.94	*	**	-	-
PLACE1001201	16.85	15.12	18.88	10.04	10.01	9	9.33	10.2	8.94	**	**	-	-
PLACE1001229	15.21	12.61	13.94	9.57	11.26	12.86	8.81	8.47	8.63		**		-
PLACE1001231	13.31	19.61	12.2	8.58	26.11	14.91	13.39	13.43	8.59				
PLACE1001238	6.16	6.8	5.78	3.46	6.45	5.07	3.57	1.84	3.63		**		-
PLACE1001241	7.81	12.55	8.77	4.56	8.8	2.29	6.75	1.69	5.45				
PLACE1001242	15.15	9.43	9.57	6.93	8.62	5.05	5.42	2.86	4.67		*		-
PLACE1001247	18.19	25.95	17.43	7.95	13.13	8.09	9.19	7.53	8.42	*	*	-	-
PLACE1001250	27.19	16.6	15.62	14.1	21.99	16.23	13.87	8.35	7.98				
PLACE1001257	5.07	4.07	3.3	6.21	3.6	2.05	3.64	3.01	2.62				
PLACE1001272	11.61	5.34	6.33	4.73	5.73	6.35	5.18	6.02	6.39				

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Table 469

PLACE1001279	20.66	18.57	13.78	9.04	11.1	8.58	6.47	4.72	6	*	**	-	-
PLACE1001280	13.73	13.22	15.63	11.44	10.47	6.22	11.2	7.22	13.37				
PLACE1001294	6.1	5.02	7.03	2.98	5.24	4.37	4.18	2.25	4.36				
PLACE1001295	9.52	6.34	5.73	4.11	5.38	4.8	4.66	3.72	5.16				
PLACE1001300	110.16	136.11	96.73	55.88	77.8	69.78	127.86	93.28	123.22	*		-	
PLACE1001304	22.83	23.35	19.82	13.09	11.18	12.56	8.64	8.3	14.22	**	**	-	-
PLACE1001311	22.93	29.08	18.33	13.63	11.98	8.91	18.15	14.72	19.17	*		-	
PLACE1001323	5.15	4.73	4.73	2.24	3.77	2.07	2.58	2.19	2.91	*	**	-	-
PLACE1001325	6.51	4.36	2.66	3.73	4.01	0.79	3.09	1.19	1.69				
PLACE1001340	12.71	9.9	7.91	5.93	10.17	3.62	8.49	5.49	7.3				
PLACE1001344	7.26	5.61	6.3	3.22	4.87	2.35	5.26	3.25	5.47	*		-	
PLACE1001351	10.82	9.34	9.06	4.54	4.04	2.83	5.68	5.94	6.17	**	**	-	-
PLACE1001366	16.46	16.32	12.21	7.96	10.61	8	10.02	6.25	6.08	*	*	-	-
PLACE1001377	10.72	11.21	8.12	8.14	11.01	6.18	7.03	5.07	5.96		*		-
PLACE1001383	8.47	7.74	7.34	7.01	7.31	9.16	4.38	4.51	5.67		**		-
PLACE1001384	5.51	3.13	4.87	2.26	4.64	2.12	1.25	1.77	2.28		*		-
PLACE1001387	3.71	2.66	5.28	2.18	4.13	3.15	1.31	2.35	1.76				
PLACE1001395	2.97	1.83	2.95	0.9	3.39	0.94	2.26	2.27	0.93				
PLACE1001399	43.48	36.95	39.47	25.54	39.02	28.91	11.4	22.35	12.37		**		-
PLACE1001401	8.85	12.13	13.82	4.1	7.84	5.28	5.15	5.58	4.43	*	*	-	-
PLACE1001407	6.42	8.95	6.88	3.19	5.6	3.04	3.23	2.38	2.93	*	**	-	-
PLACE1001412	4.65	3.97	3.56	2.52	8.46	2.63	3.1	2.07	4.54				
PLACE1001414	10.05	7.04	8.23	5.26	7.99	5.53	4.37	7.32	4.41				
PLACE1001416	18.05	14.76	21.75	8.21	15.69	7.54	12.66	14.94	10.13				
PLACE1001433	10.35	9.53	10.38	6.47	9.26	5.35	4.33	6.8	5.78		**		-
PLACE1001440	15.78	8.2	12.06	9.97	10.51	7.97	4.11	5.02	3.17		*		-
PLACE1001456	5.95	5.2	7.6	4.32	4.51	3.68	3.46	6.83	4.09				
PLACE1001464	7.17	7.13	12.08	4.46	13.26	4.47	2.92	3.59	4.74		*		-
PLACE1001468	5.87	5.89	7.51	4.49	7.19	3.15	4.98	3.89	5.45				
PLACE1001484	1.93	2.72	3.26	3.17	5.24	2.3	3.27	1.7	4.61				
PLACE1001500	5.55	5.43	7.47	3.4	4.88	4.91	3.43	5.41	4.22				
PLACE1001502	10.13	6.73	10.36	4.95	5.09	3.9	4.24	7.4	4.55	*		-	
PLACE1001503	18.94	15.22	23.11	6.62	14.6	9.42	9.19	12.06	11.69		*		-
PLACE1001505	14.33	11.5	15.08	6.94	9.91	8.35	5.05	5.21	4.29	*	**	-	-
PLACE1001513	9.76	7.84	14.27	4.51	12.01	5.72	4.02	6.18	4.23		*		-
PLACE1001516	12.33	10.13	14.29	6.5	8.85	7.91	5.4	6.92	6.78	*	*	-	-
PLACE1001517	22.78	28.63	26.65	15.6	22.43	12.49	25.55	23.34	19.3				
PLACE1001523	4.85	4.2	4.25	1.46	3.64	2.44	3.61	4.37	5.02	*		-	
PLACE1001526	15.63	6.8	12.63	5.9	5.99	8.7	6.38	8.18	11.68				
PLACE1001534	13.26	10.83	12.93	4.83	7.66	4.05	5.45	22.34	4.41	**		-	
PLACE1001536	12.35	10.07	11.17	5.95	10.51	7.42	7.47	10.57	7.69				
PLACE1001545	7.78	9.31	13.04	5.48	7.28	3.94	2.6	3.19	3.02		*		-
PLACE1001551	11.64	13.9	20.49	7.15	9.98	9.21	7.74	8.57	7.76				
PLACE1001564	5.33	7.01	11.33	5.64	6.02	6.32	3.9	3.45	6.93				
PLACE1001570	8.81	7.17	13.9	5.61	7.77	3.89	5.34	9.04	4.82				
PLACE1001571	30.16	29.44	29.76	18.26	25.49	9.78	12.94	16.78	20.12		**		-
PLACE1001595	49.16	53.02	65.48	26.84	29.86	29.28	20.63	17.19	22.48	**	**	-	-
PLACE1001602	17.93	20.86	26.59	9.8	15.66	12.03	25.23	43.22	27.97	*		-	
PLACE1001603	16	11.85	13.84	6.26	7.5	6.17	10.37	25.06	14.43	**		-	
PLACE1001608	313.79	262.26	299.49	248.62	194.58	212.51	255.55	259.42	224.33	*		-	
PLACE1001610	34.83	33.4	50.14	21.2	19.91	21.09	16.25	16.43	15.58	*	*	-	-
PLACE1001611	16.58	14.57	13.52	8.27	15.57	6.53	5.96	3.97	4.4		**		-
PLACE1001629	15.86	14.27	16.52	6.92	12.73	5.97	9.05	9.4	8.15	*	**	-	-
PLACE1001632	15.6	14.68	11.95	5.15	11.43	6.76	4.77	3.59	2.95	*	**	-	-
PLACE1001634	10.26	9.24	12.21	4.71	7.41	4.15	3.93	4.97	4.63	*	**	-	-
PLACE1001637	29.75	28.67	36.48	16.79	19.46	16.75	23.41	26.79	22.84	**		-	
PLACE1001640	28.95	18.03	24.89	16.93	21.97	12.71	8.91	11.62	9.32		*		-
PLACE1001655	8.24	5.56	6.83	4.09	4.25	2.93	2.13	3.7	1.34	*	*	-	-
PLACE1001672	8.94	18.15	13.66	4.81	11.29	4.01	5.1	4.86	14.47				
PLACE1001676	39.58	47.75	47.96	23.16	26.28	21.98	31.5	32.99	28.58	**	**	-	-
PLACE1001683	7.54	6.2	11.62	2.16	4.9	3.68	2.93	3.43	3.72		*		-
PLACE1001691	10.4	6.5	11.03	4.05	13.34	5.07	4.28	5.31	2.34		*		-
PLACE1001692	3.74	6.24	4.95	3.58	3.97	3.4	3.88	3.22	2.42				
PLACE1001705	11.04	7.84	13.66	10.64	5.83	6.51	5.2	5.34	3.62		*		-

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Table 470

PLACE1001716	13.89	6.26	12.85	5.68	7.61	3.53	6.17	4.09	5.84				
PLACE1001720	20.23	23.86	21.86	17.41	19.42	17.41	10.68	9.34	8.72	*	**	-	-
PLACE1001728	21.97	14.68	15.36	7.87	10.67	10.96	10.39	5.46	5.25	*	*	-	-
PLACE1001729	7.28	8.78	9.32	4.24	3.8	3.29	3.96	2.03	2.64	**	**	-	-
PLACE1001739	18.08	18.75	18.08	11.34	16.38	11.72	10.55	8.26	8.75	*	**	-	-
PLACE1001740	60.6	61.56	51.85	52.21	47.26	48.39	41.09	28.81	37.51		**		-
PLACE1001745	155.43	121.46	146.04	80.69	92.15	78.37	106.17	102.99	100.25	**	*	-	-
PLACE1001746	12.07	9.53	11.89	5.08	6.32	6.38	6.4	7.42	7.33	**	**	-	-
PLACE1001748	20.09	15.85	13.57	8.98	10.94	8.77	6.58	3.28	8.51	*	*	-	-
PLACE1001753	8	5.61	7.17	2.42	2.42	2.08	3.13	1.99	2.1	**	**	-	-
PLACE1001760	16.81	13.89	14.09	5.89	6.99	11.7	8.68	6.91	7.81	*	**	-	-
PLACE1001767	7.75	5.83	9.04	3.14	5.58	2.6	2.92	2.72	1.2	*	**	-	-
PLACE1001771	6.86	8.78	6.5	5.1	22.6	7.92	6.68	3.61	1.79				
PLACE1001775	10.25	8.72	8.89	5.62	4.98	4.94	5.79	4.51	5.33	**	**	-	-
PLACE1001777	55.87	33.24	46.38	19.69	26.37	22.71	26.45	22.89	29.83	*		-	
PLACE1001781	7.62	4.99	5.26	2.61	3.65	3.27	2.46	2.47	3	*	*	-	-
PLACE1001783	8.67	3.54	4.17	1.75	1.71	2.1	2.79	1.87	2.94				
PLACE1001786	10.13	7.03	6.19	5.28	7.53	4.48	4.3	2.57	2.1		*		-
PLACE1001788	9.62	8.2	7.79	2.13	3.02	3.67	3.87	1.93	2.04	**	**	-	-
PLACE1001795	12.86	13.57	11.91	3.76	6.82	4.77	2.63	4.68	2.65	**	**	-	-
PLACE1001799	15.19	12.46	11.73	6.44	10.22	5.84	11.66	9.72	12.14	*		-	
PLACE1001810	19.9	17.99	15.3	8.61	16.81	15.9	19.42	15.41	19.52				
PLACE1001817	9.2	10.03	10.24	5.73	12.6	6.09	4.49	4.6	5.41		**		-
PLACE1001821	8.12	9.65	9.24	5.34	5.81	5.22	5.09	4.7	3.49	**	**	-	-
PLACE1001836	14.74	10.74	8.7	7.59	8.81	4.93	6.55	5.02	5		*		-
PLACE1001844	8.12	5.11	7.16	1.96	5.82	2.85	3.18	2.67	1.5		*		-
PLACE1001845	13.24	11.82	8.77	7.59	7.48	3.74	4.84	2.2	2.42		**		-
PLACE1001858	9.06	7.62	7.23	4.16	3.93	3.22	7.66	3.49	3.91	**		-	
PLACE1001869	5.88	6.08	4.84	3.37	6.33	2.79	3.14	2.33	2.54		**		-
PLACE1001890	14.71	9.13	7.02	7.27	10.27	7.92	6.48	7.41	7.57				
PLACE1001897	21.63	13.66	12.13	7	10.58	7.47	6.17	7.42	7.81		*		-
PLACE1001902	25.9	24.36	23.51	11.89	19.02	13.01	23.32	19.87	28.51	*		-	
PLACE1001904	4.8	4.58	4.71	4.2	4.02	2.48	4	1.2	3.18				
PLACE1001907	11.99	11.09	12.77	4.36	7.42	4.55	5.4	2.81	6.4	**	**	-	-
PLACE1001910	17.55	13	11.78	10.79	10.86	3.78	8.75	3.34	6.51		*		-
PLACE1001912	16.99	20.76	18.01	10.56	10.89	7.91	12.99	8.39	12.1	**	*	-	-
PLACE1001918	10.35	11.16	9.4	5.64	8.81	4.76	8.14	4.97	7.28	*	*	-	-
PLACE1001920	3.62	1.84	1.09	2.06	2.78	2.12	0.89	2.37	2.67				
PLACE1001928	33.91	29.31	26.67	16.07	24.12	10.81	21.1	17.01	25.49	*		-	
PLACE1001930	13.35	8.41	9.7	5.16	9.65	8.14	5.7	4.65	9.73				
PLACE1001949	83.24	64.21	68.63	50.5	75.89	66.37	92.93	85.41	92.12		*		+
PLACE1001959	8.04	5.93	10.64	4.56	6.1	3.95	4.33	5.06	5.07				
PLACE1001969	8.52	5.51	4.9	2.62	4.36	2.04	3.84	2.43	3.2				
PLACE1001974	16.8	19.43	17.28	9.77	10.54	5.8	6.98	5.43	6.49	**	**	-	-
PLACE1001981	11.42	11.82	8.18	7.19	8.78	5.34	7.9	5.15	5.59		*		-
PLACE1001983	9.22	8.71	12.62	5.54	7.95	6.32	7.39	5.63	6.5				
PLACE1001989	27.47	22.77	28.46	13.3	18.78	12.49	12.35	16.17	10.35	*	**	-	-
PLACE1002004	8.73	7.48	9.33	6.79	9.77	5.49	6.57	6.13	4.33		*		-
PLACE1002008	10.54	8.97	12.2	6.77	11.46	10.25	3.74	7.33	3.11		*		-
PLACE1002015	12.37	10.1	13.36	6.64	10.58	8.15	7.89	14.69	9.22				
PLACE1002044	18.51	15.04	21.28	6.21	11.74	9.02	6.6	10.2	12.21	*	*	-	-
PLACE1002045	3.16	4.19	5.33	2.46	6.56	3.13	3.41	1.95	2.73				
PLACE1002052	4.29	2.34	2.47	1.89	4.94	1.55	4.09	3.83	3.62				
PLACE1002066	4.5	3.49	6.01	2.29	3.79	2.93	3.54	3.65	2.92				
PLACE1002072	6.4	5.54	6.91	3.66	5.16	4.7	3.95	6.12	2.07	*		-	
PLACE1002073	12.89	11.8	16.36	10.66	11.47	7.97	5.88	5.64	4.74		**		-
PLACE1002080	18.63	22.97	23.1	12.21	18.28	13.9	13.6	15	15.2	*	*	-	-
PLACE1002081	23.13	27.18	27.3	14.91	18.06	14.86	16.14	20.45	20.82	**	*	-	-
PLACE1002090	11.49	14.13	12.79	4.54	7.24	4.65	4.29	3.51	5.75	**	**	-	-
PLACE1002095	5.46	5.54	4.46	5.08	11.47	7.41	4.99	5.27	7.8				
PLACE1002102	8.22	13.54	14.09	8.11	14.1	7.74	9.04	16.2	14.08				
PLACE1002109	17.45	10.93	19.35	12.82	7.15	7.61	9.22	12.81	9.47				
PLACE1002115	6.48	5.79	9.09	2.86	4.39	3.56	3.32	3.75	3.44	*	*	-	-
PLACE1002119	3.98	5.58	7.03	2.87	6.47	3.2	3.72	4.12	4.62				

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Table 471

PLACE1002140	8.54	9.5	15.02	4.83	8.98	6.88	2.91	6.38	4.28		*	-
PLACE1002150	27.18	33.61	30.05	18.28	25.09	23.98	12.7	14.95	15.29	*	**	- -
PLACE1002153	173.25	217.95	284.37	422.44	424.65	291.99	262.39	242.27	220.74	*		+
PLACE1002157	7.42	5.99	8.84	3.16	6.59	2.52	3.59	2.5	5.34		*	-
PLACE1002163	9.5	10.33	17.51	4.81	9.35	4.71	6.61	8.07	8.46			
PLACE1002168	406.19	407.62	562.52	187.65	80.86	161.78	377.56	231.11	429.49	**		-
PLACE1002170	23.07	18.68	22.02	9.58	14.95	10.12	4.39	9.86	5.14	*	**	- -
PLACE1002171	118.3	86.27	82.5	107.58	135.49	96.73	60.2	59.88	56.63		*	-
PLACE1002180	12.53	12.02	17.4	11.66	15.77	12.8	11.61	13.11	10.84			
PLACE1002184	76.94	90.34	67.89	42.12	70.86	43.23	20.87	27.8	29.07		**	-
PLACE1002200	5.64	6.44	11.56	2.73	4.37	3.29	2.8	2.86	3.48			
PLACE1002205	5.47	5.6	9.09	2.28	6.05	2.28	3.51	2.6	1.9		*	-
PLACE1002213	11	9.68	7.88	3.37	8.5	3.33	5.73	2.26	4.33		*	-
PLACE1002219	30.67	24.88	33.1	11.7	18.03	17.11	5.85	10.58	12.01	*	**	- -
PLACE1002227	5.38	6.1	6.51	3.19	5.95	3.48	3.48	8.52	2.37			
PLACE1002253	7.93	4.46	10.74	3.51	5.52	2.84	4.18	3.76	3.24			
PLACE1002256	10.19	4.49	11.42	3.66	5.44	3.17	1.81	4.48	5.21		-	
PLACE1002259	6.68	9.14	16.04	2.32	8.56	3.26	2.76	5.45	13.61			
PLACE1002285	15.21	20.2	16.69	10.84	18.4	10.19	8.14	7.95	6.12		**	-
PLACE1002301	11.84	7.92	13.87	3.5	5.75	4.91	3.98	8.04	4.04	*		-
PLACE1002310	9.3	8.21	7.36	1.56	5.25	3.56	3.57	2.81	3.34	*	**	- -
PLACE1002311	6.47	4.93	7.42	3.5	5.65	2.75	2.49	2.97	1.32		*	-
PLACE1002319	23.43	17.43	19.83	7.96	14.77	10.74	10.78	13.23	11.96	*	*	- -
PLACE1002329	7	4.89	6.25	3.06	3.73	2.65	1.68	2.85	1.64	*	**	- -
PLACE1002333	16.35	14.3	13.78	9.29	11.1	10.53	8.49	6.32	5.51	**	**	- -
PLACE1002342	14.18	15.16	20.35	5.96	11.78	6.24	4.58	8.15	6.84	*	**	- -
PLACE1002343	9.54	8.56	16.64	3.45	4.23	3.21	2.86	1.85	3.18	*	*	- -
PLACE1002355	8.47	11.34	12.23	4.32	8.27	5.65	2.98	2.78	4.19	*	**	- -
PLACE1002358	6.25	5.01	7.85	2.33	4.09	1.66	2.63	1.27	2.04	*	**	- -
PLACE1002359	94.59	64.3	78.26	42.47	26.68	29.68	51.17	53.76	59.14	**		-
PLACE1002374	11.64	7.08	11.73	4.84	7	4.57	3.23	3.62	3.66		*	-
PLACE1002376	10.84	6.42	7.57	6.56	6.2	4.93	8.79	6.04	6.62			
PLACE1002379	14.26	10.82	12.17	6.95	8.14	6.98	5.34	4.44	3.6	**	**	- -
PLACE1002386	7.89	3.52	7.76	1.91	2.26	2.95	2.4	2.03	2.94			
PLACE1002395	17.68	20.65	22.77	6.45	9.6	7.04	4.3	2.63	2.39	**	**	- -
PLACE1002399	9.59	8.59	10	4	5.08	4.5	2.83	2.8	3.46	**	**	- -
PLACE1002407	14.84	17.54	12.15	4.78	9.29	6.64	6.32	3.95	6.87	*	**	- -
PLACE1002433	18.89	14.68	17.11	8	12.47	6.81	12.74	12.61	16.41	*		-
PLACE1002437	6.94	5.04	7.88	4.77	3.72	3.8	1.97	3.5	4.81	*		-
PLACE1002438	8.47	9.76	8.93	6.11	6.03	2.52	3.69	3.74	4.55	*	**	- -
PLACE1002446	61.22	60.91	53.35	35.08	40.23	34.18	52.04	54.81	48.63	**		-
PLACE1002447	50.06	38.25	48.75	30.92	38.93	28.36	26.38	23.5	18.47		**	-
PLACE1002450	8.68	4.18	8.14	2.56	3.07	3.06	3.45	3.27	1.66	*		-
PLACE1002462	20.62	21.36	20.69	8.83	13.93	7.63	14.57	11.43	17.67	**	*	- -
PLACE1002465	6.3	10.21	4.45	2.37	6.62	4.25	3.41	1.81	3.99			
PLACE1002474	8.9	10.86	8.01	5.33	8.28	3.73	2.36	3.29	4.22		**	-
PLACE1002477	10.23	12.91	13.31	8.45	8.55	11.89	12.5	6.6	14.96			
PLACE1002493	5.44	5.3	4.56	4.99	2.63	4.56	5.81	1.5	1.86			
PLACE1002497	9.23	6.42	6.03	5.54	3.94	3.18	4.77	3.01	2.42		*	-
PLACE1002499	28.78	23.91	22.93	13.59	10.19	9.79	16.45	7.7	12.71	**	*	- -
PLACE1002500	9.83	6.14	9.08	4.34	6.18	2.49	5.4	1.41	3.42		*	-
PLACE1002514	57.39	61.96	51.39	31.16	36.96	26.56	53.37	39.47	40.85	**		-
PLACE1002518	7.97	7.12	4.14	3.92	5.36	3.52	3.58	1.82	2.65		*	-
PLACE1002529	14.35	10.84	8.84	6.09	12.13	6.95	3.37	3.6	3.7		**	-
PLACE1002532	6.92	6.97	5.35	4.94	5.47	4.76	4.62	5.36	3.19			
PLACE1002536	9.3	12.32	10.38	5.35	4.64	5.41	7.12	5.91	4.59	**	*	- -
PLACE1002537	7.11	8.85	6.37	5.99	5.45	6.3	4.25	3	3.53		**	-
PLACE1002539	7.92	6.45	7.28	2.97	5.46	7.97	2.07	2.63	4.82		*	-
PLACE1002547	14.65	14.48	12.7	9.78	11.89	6.33	5.01	4.47	6.38		**	-
PLACE1002571	27.85	40.71	17.49	16.84	14.71	12.01	13.72	7.48	9.31			
PLACE1002578	11.7	10.9	10.03	8.42	11.59	6.31	11.22	5.24	9.68			
PLACE1002583	12.45	8.98	8.93	4.7	6.58	5.37	8.92	7.31	10.13	*		-
PLACE1002591	14.95	9.64	30.65	14.99	14.6	1.99	10.65	10.99	7.37			
PLACE1002598	134.77	135.3	115.7	105.05	127.67	81.8	77.51	75.71	89.77		**	-

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Table 472

PLACE1002604	8.27	3.87	5.87	4.56	4.62	4.03	4.08	2.97	4.32				
PLACE1002612	7.74	6.07	5.48	4.79	5.04	4.26	2.87	1.84	4.68		*		-
PLACE1002625	8.98	7.38	5.26	3.91	6.23	4.29	4.63	2.42	5.37				
PLACE1002638	10.71	6.82	9.31	4.39	4.89	3.67	4.86	2.91	4.12	*	*	-	-
PLACE1002655	20.05	17.22	10.12	8.15	9.62	8.61	4.45	4.4	4.69		*		-
PLACE1002665	2.85	2.11	1.16	1.34	3.18	0.77	1.36	1.74	1.47				
PLACE1002685	40.11	36.95	37.09	21.27	32.67	18.25	35	28.12	33.61	*		-	
PLACE1002692	10.4	8.99	7.49	3.22	6.32	3.77	7.61	3.76	6.83	*		-	
PLACE1002714	16.77	11.38	9.27	6.42	9.93	4.45	11.48	11.6	13.87				
PLACE1002721	75.97	53.95	40.28	41.2	57.12	33.39	36.52	34.39	33.55				
PLACE1002722	22.13	17.93	14.21	5.69	15.15	8.22	22.92	15.1	22.19				
PLACE1002726	7.85	7.95	6.76	3.03	4.47	1.55	5.1	2.92	3.72	**	**	-	-
PLACE1002755	11.64	12.77	9.75	6.41	12.37	7.42	9.89	7.27	9.98				
PLACE1002768	14.14	13.66	17.41	6.96	8.91	8.35	8.23	12.96	13.43	**		-	
PLACE1002772	11.58	12.05	13.28	5.34	9.18	5.42	7.04	6.7	6.74	*	**	-	-
PLACE1002775	3.87	3.22	3.82	4.05	3.19	0.98	1.6	5	2.48				
PLACE1002780	8.73	8.1	8.81	2.91	6.16	2.92	3.15	6.37	4.26	*	*	-	-
PLACE1002782	15.09	16.8	18.22	6.13	9.37	3.95	11.73	13.03	12.96	**	*	-	-
PLACE1002794	41.39	43.8	46.4	31.76	35.79	20.44	25	22.44	21	*	**	-	-
PLACE1002795	26.08	25.22	25.57	11.54	12.89	13.19	17.32	17.1	14.49	**	**	-	-
PLACE1002811	45.78	45.63	45.46	25.72	32.56	23.15	17.78	22.39	22.66	**	**	-	-
PLACE1002815	15.82	13.42	19.22	7.58	7.46	5.69	11.61	7.34	8.29	**	*	-	-
PLACE1002816	4.86	2.68	5.34	8.68	10.83	8.75	3.44	3.56	2.71	**		+	
PLACE1002822	12.2	11.93	11.07	6.15	11.75	10.16	7.41	12.24	8.12				
PLACE1002833	9.14	11.66	12.33	5.57	7.46	7.07	4.75	8.35	4.08	*	*	-	-
PLACE1002834	6.07	5.81	8.84	3.09	3.53	4.27	1.8	2.98	2.41	*	*	-	-
PLACE1002835	58.22	46.91	63.08	49.95	62.63	44.56	42.91	35.34	35.49		*		-
PLACE1002839	20.38	22.46	21.91	8.31	11	7.79	15.07	14.42	13.25	**	**	-	-
PLACE1002851	24.75	15.11	15.09	7.91	14.09	8.63	20.69	22.56	25.92				
PLACE1002853	17.64	15.34	22.8	5.52	6.45	6.1	6.28	8.18	4.17	**	**	-	-
PLACE1002881	24.86	14.92	26.75	13.38	16.28	13.04	14.2	20.46	17.04				
PLACE1002901	14.25	14.06	17.74	6.8	8.96	8.66	8.78	4.53	4.12	**	**	-	-
PLACE1002904	18.88	26.12	22.33	14.53	22.41	13.83	9.21	13.95	10.54		*		-
PLACE1002905	4.41	8.93	12	2.54	8.87	4.07	3.83	5.83	4.18				
PLACE1002908	13.22	16.1	15.63	15.4	12.99	11.14	8.47	5.63	8.35		**		-
PLACE1002911	10.97	9.2	9.02	6.7	11.96	7.89	5.04	4.71	5.5		**		-
PLACE1002941	15.88	10.4	17.73	6.14	8.22	5.77	14.58	18	12.89	*		-	
PLACE1002950	23.65	20.5	17.79	16.96	17.44	5.49	24.31	14.61	17.93				
PLACE1002955	5	5.58	7.97	3.29	6.71	3.61	3.06	3.96	2.19		*		-
PLACE1002958	88.1	92.98	103.56	90.74	91.81	78.41	59.31	53.18	47.63		**		-
PLACE1002962	3.13	4.33	9.15	0.9	4.01	2.47	0.8	0.76	1.87				
PLACE1002967	35.4	50.14	51.41	21.55	34.48	29.97	31.98	26.21	37.19				
PLACE1002968	4.93	4.01	6.65	3.18	3.05	1.93	2.74	2.46	2.95	*	*	-	-
PLACE1002976	59.32	76.52	110.97	52.57	103.04	77.15	42.49	35.2	48.8				
PLACE1002991	6.98	4.41	7.57	2.11	5.56	3.18	2.77	5.13	6.66				
PLACE1002993	13.31	16.98	19.44	6.54	17.73	10.56	9.53	20.73	7.89				
PLACE1002996	33.54	26.83	25.33	24.84	36.88	25.62	15.5	28.74	20.59				
PLACE1003010	5.97	5.37	8.7	4.68	3.28	4.88	3.8	4.41	3.12				
PLACE1003025	19.13	20.65	29.6	10.42	22.81	11.62	14.02	22.04	12.57				
PLACE1003027	4.81	4.57	8.94	2.3	4.47	0.55	3.14	5.14	2.31				
PLACE1003044	13.45	13	13.59	5.33	7.16	6.74	3.17	4.52	2.59	**	**	-	-
PLACE1003045	16.2	13.12	16.27	11.21	14.83	10.08	8.58	7.66	5.73		**		-
PLACE1003052	15.26	13.65	16.48	5.57	12.75	6.74	15.39	12.34	13.31	*		-	
PLACE1003083	26.86	32.06	29.46	16.75	26.42	15.92	23.57	20.32	20.14		*		-
PLACE1003085	11.46	7.5	13.4	5.76	9.36	4.66	6.66	6.58	5.57				
PLACE1003092	13.44	11.78	13.5	8.16	11.43	7.08	8.07	7.87	6.9	*	**	-	-
PLACE1003097	6.17	6.46	16.32	3.05	5.89	3.08	3.13	5.88	4.77				
PLACE1003100	36.23	40.39	38.56	32.04	32.87	28.75	26.62	23.05	18.02	*	**	-	-
PLACE1003108	11.34	8.75	20.83	7.36	13.72	5.15	3.96	4.75	4.82				
PLACE1003115	7.34	6.75	7.41	3.32	6.32	2.75	1.65	0.73	1.92		**		-
PLACE1003120	12.49	11.78	16.03	7.63	9.21	4.76	11.87	11.32	7.77	*		-	
PLACE1003135	7.09	5.05	7.89	3.8	2.81	2.79	2.64	3.42	1.44	*	*	-	-
PLACE1003136	68.81	77.15	81.76	65.96	72.38	60.39	44.74	39.52	47.1		**		-
PLACE1003141	9.02	4.98	11.12	4.59	4.76	5.17	4.62	5.32	3.84				

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Table 473

PLACE1003145	12.65	9.94	12.43	3.74	5.65	4.53	6.94	8.05	4.35	**	*	-	-
PLACE1003147	26.48	26.41	26.84	11.9	16.38	12.11	16.22	18.19	14.71	**	**	-	-
PLACE1003153	10.51	10.55	11.78	2.97	6.22	4.35	5.52	7.01	3.61	**	**	-	-
PLACE1003163	8.08	7.83	4.23	1.17	6.16	2.64	1.92	2.39	2.29		*		-
PLACE1003172	11.82	10	15.87	6.77	13.23	9.45	7.97	8.79	7.46				
PLACE1003174	15.37	9.05	12.28	9.12	4.76	2.9	4.07	4.06	4.97		*		-
PLACE1003176	5.18	3.89	6.16	2.81	3.31	2.68	2.96	3.04	2.06	*	*	-	-
PLACE1003181	9.36	6.29	8.52	1.78	2.48	3.42	2.28	1.97	1.19	**	**	-	-
PLACE1003184	23.08	18.89	20.23	9.3	11.84	12.17	13.78	13.13	10.63	**	**	-	-
PLACE1003190	8.27	8.79	9.4	3.25	4.54	3.59	4.27	2.82	4.68	**	**	-	-
PLACE1003200	9.79	7.56	9.39	2.41	6.08	2.83	2.42	1.72	3.3	*	**	-	-
PLACE1003205	126.72	130.26	137.95	113.01	122.92	109.79	99.16	86	89.92	*	**	-	-
PLACE1003209	2.16	16.18	2.48	0.47	10.18	0.97	2.71	3.36	3.16				
PLACE1003214	22.58	19.76	20.17	11.54	15.74	15.47	11.96	12.4	14.5	*	**	-	-
PLACE1003229	11.83	11.81	10.65	4.92	4.84	3.94	7.34	5.53	5.38	**	**	-	-
PLACE1003238	8.67	6.17	6.07	3.06	1.84	4.56	1.99	2.39	2.01	*	**	-	-
PLACE1003249	64.47	55.31	48	33.64	42.61	31.3	33.47	28.86	18.94	*	*	-	-
PLACE1003256	18.3	25.49	17.26	10.97	13.36	18.51	17.3	11.04	4.08				
PLACE1003258	49.07	49.35	44.47	34.46	50.32	29.75	23.51	18.19	23.43		**		-
PLACE1003279	10.3	14.58	7.71	5.42	10.68	4.9	6.28	3.11	11.78				
PLACE1003294	21.78	16.35	23.18	6.69	11.5	6.25	12.62	8.7	9.35	*	*	-	-
PLACE1003296	42.17	40.86	35.97	38.78	41.16	32.25	23.79	17.48	17.34		**		-
PLACE1003297	49.69	50.94	40.2	15.98	31.29	21.96	19.68	11.27	24.02	*	**	-	-
PLACE1003302	25.32	31.25	29.06	9.93	15.98	12.55	24.23	16.15	20.93	**	*	-	-
PLACE1003334	185.2	152.92	141.49	146.89	154.17	125.41	110.94	69.78	76.19		*		-
PLACE1003337	48.98	43.27	41.6	31.2	33.91	22.01	17.95	11.14	16.35	*	**	-	-
PLACE1003342	33.19	37.72	34.03	17.42	45.69	20.1	23.58	17.03	23.28		**		-
PLACE1003343	6.84	5.22	10.11	7.16	4.99	3.86	5.46	2.81	3.26				
PLACE1003344	11.02	7.76	2.99	1.99	8.29	3.43	7.57	2.34	3.75				
PLACE1003353	19.54	21.69	17.69	8.25	8.74	5.2	10.76	10.8	13.5	**	**	-	-
PLACE1003361	44.83	37.64	33.66	33.83	37.42	32.13	26.59	20.73	23.72		*		-
PLACE1003366	12	18.42	15.82	7.6	12.12	4.37	10.36	5.92	5.45		*		-
PLACE1003369	4.81	3.43	3.93	0.94	3.73	1.31	1.63	1.07	0.84		**		-
PLACE1003372	13.64	7.8	10.54	3.88	10.47	3.36	4.52	1.77	3.52		*		-
PLACE1003373	8.88	8.18	9.38	3.94	3.76	0.99	4.29	2.31	3.38	**	**	-	-
PLACE1003375	22.91	23.46	16.65	11.55	17.67	11.28	29.27	13.77	19.27				
PLACE1003378	1.92	0.43	0.47	1.45	0.86	1.22	0.77	0.97	0.76				
PLACE1003383	15.75	12.58	10.55	7.3	8.49	3.81	2.43	7.46	2.15	*	*	-	-
PLACE1003394	19.46	13.29	10.26	6.3	12.66	5.09	11.98	10.6	17.14				
PLACE1003401	8.87	6	5.04	3.66	4.75	2.93	5.66	3.3	5.47				
PLACE1003405	7.6	8.07	5.91	3.39	5.27	4.58	4.12	1.47	2.3	*	*	-	-
PLACE1003407	10.24	7.49	7.79	2.43	3.28	2.12	4.16	2.37	3.5	**	**	-	-
PLACE1003420	7.71	5.57	6.39	3.78	6.36	2.21	2.89	1.88	2.26		**		-
PLACE1003428	6.55	5.9	4.45	2.19	4.16	0.9	3.49	2.31	8.87	*		-	
PLACE1003432	51.6	69.55	75.77	36.76	44.92	44.22	42.27	64.14	52.55	*		-	
PLACE1003438	1.98	2.35	1.48	2.21	4.73	1.43	4.08	0.93	0.7				
PLACE1003452	3.01	3.41	4.3	1.8	3.84	2.08	2.34	2.25	1.64		*		-
PLACE1003454	3.87	4.87	5.58	2.54	4.5	3.92	2.57	2.43	1.33		*		-
PLACE1003455	2.92	2.41	4.04	1.6	1.9	1.64	1.75	0.8	1.88	*	*	-	-
PLACE1003456	2.36	4.17	3.63	2.06	10.37	2.22	2.4	1.94	0.64				
PLACE1003460	4.76	5.09	4.73	4.08	6	2.64	6.38	3.46	2.92				
PLACE1003478	6.15	2.11	2.66	1.92	3.96	2	5.39	1.91	4.04				
PLACE1003484	6.84	8.17	8.98	4.36	6.73	3.1	4.12	4.68	4.63		**		-
PLACE1003493	83.14	41.9	88.74	60.01	72.45	45.07	64.55	71.53	53.96				
PLACE1003503	7.36	5.03	5.29	1.12	3.91	3.51	2.36	3.64	2.4		*		-
PLACE1003505	32.2	45.22	38.51	20.24	36.17	23.66	24.44	34.5	27.01				
PLACE1003516	7.02	7.8	7.71	2.88	5.85	3.76	2.24	2.98	3.86	*	**	-	-
PLACE1003519	4.06	1.81	5.55	3.83	3.85	1.91	2.58	1.64	0.34				
PLACE1003520	12.72	16.96	9.15	8.71	16.58	8.45	4.85	6.39	5.22		*		-
PLACE1003521	14.95	10.13	14.17	6.02	7.53	5.56	6.77	8.38	4.75	*	*	-	-
PLACE1003525	20.17	19.13	25.59	15.85	14.55	12.63	20.97	18.71	22.36	*		-	
PLACE1003528	35.65	25.12	43.38	21.63	30.38	28.64	16.02	24.64	18.65				
PLACE1003529	11.19	16.69	21.6	20.8	16.66	31.76	18.24	15.7	15.44				
PLACE1003537	3.15	4.02	8.21	3.24	3.64	3.89	1.76	2.65	2.32				

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Table 474

PLACE1003549	16.21	19.52	27.74	11.72	18.71	13.09	12.65	15.02	13.74				
PLACE1003553	12.63	20.69	18.89	10.17	18.28	8.51	8.12	9.44	8.9		*		-
PLACE1003566	9.49	12.35	9.77	7.53	10.49	7.08	3.77	4.66	6.9		*		-
PLACE1003568	5.3	4.9	19.78	3.8	7.59	3.87	5.3	6.3	4.21				
PLACE1003573	32	27.25	37.46	17.52	23.28	16.23	15	18.28	19.13	*	**	-	-
PLACE1003575	66.07	60.03	70.99	42.8	62.9	38.6	75.17	59.46	62.58				
PLACE1003583	8.33	4.65	6.88	3.47	6.26	5.07	2.38	3.4	4.1		*		-
PLACE1003584	12.09	10.66	18.02	7.17	8.48	19.2	8.54	7.15	2.79				
PLACE1003592	29.77	33.55	28.89	21.34	26.31	15.85	12.59	8.49	12.12	*	**	-	-
PLACE1003593	7.15	3.54	8.27	3.34	2.24	1.83	3.11	5.19	5.45				
PLACE1003594	7.18	8.49	9.31	5.03	6.61	3.38	4.99	3.18	2.37	*	**	-	-
PLACE1003596	5.11	3.13	4.25	2.82	5	3.14	3.75	4.1	3.76				
PLACE1003598	31.57	29.75	31.55	14.81	20.6	17.31	5.31	17.81	7.34	**	**	-	-
PLACE1003602	6.51	2.47	7.47	1.84	4.91	0.98	2.4	4.6	2.56				
PLACE1003605	10	6.14	7.29	5.28	8.85	3.75	6.45	5.07	2.93				
PLACE1003611	15.94	16.54	24.25	11	9.1	12.46	10.14	10.62	12.83	*		-	
PLACE1003618	7.78	7.74	12.1	3.49	6.12	2.68	4.58	5.29	6.93	*		-	
PLACE1003625	14.19	21.53	18.27	11.53	22.81	17.82	13.8	9.54	11.86				
PLACE1003626	11.55	14.38	14.6	5.94	11.97	7.26	4.57	4.49	2.04		**		-
PLACE1003630	3.86	4.65	3	4.62	4.58	3.02	3.68	3.68	1.66				
PLACE1003635	8.33	7.29	10.19	5.35	5.59	4.6	3.51	4.48	4.17	*	**	-	-
PLACE1003638	4.33	3.09	4.93	3.86	6.02	2.38	2.01	3.6	1.35				
PLACE1003644	35.03	24.77	24.25	19.14	20.11	17.95	8.77	10.6	6.97		**		-
PLACE1003654	75.56	74.57	74.52	77.61	72.17	67	35.39	33.92	31.06		**		-
PLACE1003656	7.81	5.19	8.37	3.06	4.32	3.8	1.16	1.63	2.96	*	**	-	-
PLACE1003660	16.26	21.8	21.11	12.32	17.1	13.06	14.44	12.72	12.99		*		-
PLACE1003669	12.05	8.79	12.65	4.93	9.33	7.48	3.9	4.69	4.41		**		-
PLACE1003670	110.15	83.05	76.99	55.55	52.05	50.36	48.6	63.39	52.6	*	*	-	-
PLACE1003671	11.47	3.49	4.69	7.13	4.59	4.35	3.71	2.69	2.22				
PLACE1003697	9.65	10.83	16.05	9.21	10.08	8.25	6.51	4.97	6.76		*		-
PLACE1003704	10.59	7.92	10.14	6.15	6.81	6.51	4.22	3.63	3.86	*	**	-	-
PLACE1003709	9.06	8.99	10.78	5.34	6.7	5.47	3.53	3.36	1.83	**	**	-	-
PLACE1003711	28.05	31.28	32.33	21.12	31.77	27.07	16.12	16.73	14.21		**		-
PLACE1003723	27.32	34.97	28.91	18.16	26.8	21.24	17.63	17.4	10.81		**		-
PLACE1003724	29.33	36.12	25.65	19.94	34.26	21.71	26.66	13.83	15.71				
PLACE1003737	8.24	6.31	9.31	2.89	4.06	2.72	3.31	2.56	3.28	**	**	-	-
PLACE1003738	5.02	4.71	5.03	8.76	2.78	9.43	1.8	2.2	2.93		**		-
PLACE1003742	17.85	18.69	20.82	14.24	7.57	8.14	10.49	8.98	8.16	*	**	-	-
PLACE1003744	5.48	2.82	3.4	0.66	1.04	1.08	1.74	1.94	0.38	*		-	
PLACE1003758	23.32	22.73	21.79	9.9	15.26	16.38	15.29	14.75	13.36	*	**	-	-
PLACE1003760	40.1	57.96	44.54	28.85	37.15	22.14	11.09	14.54	11.41		**		-
PLACE1003762	65.35	58.09	77.98	35.3	88.27	46.92	46.48	32.75	38.3		*		-
PLACE1003765	93.01	107	70.69	55.75	97.14	46.35	33.33	44.53	44.51		*		-
PLACE1003768	34.07	21.23	23.34	10.87	13.6	6.67	25.2	17.43	28.3	*		-	
PLACE1003771	5.38	5.57	5.27	3.47	7.27	2.71	1.77	1.77	2.44		**		-
PLACE1003772	5.63	7.96	4.89	1.17	7.74	2.12	3.12	2.24	2.28		*		-
PLACE1003783	5.15	3.84	3.95	2.36	3.83	1.92	1.65	1.17	0.84		**		-
PLACE1003784	5.59	6.96	5.68	2.81	4.01	2.73	3.1	2.42	1.88	**	**	-	-
PLACE1003788	34.98	33.59	27.31	19.49	15.1	21.27	12.2	5.92	10.73	*	**	-	-
PLACE1003795	26.48	33.02	23.72	12.5	28.84	12.28	23.33	16.94	16.45				
PLACE1003827	9.74	8.51	10.55	21.41	16.48	10.33	5.7	3.14	1.91		**		-
PLACE1003833	14.14	10.78	12.27	5.74	8.62	5.66	5.59	6.29	7.37	*	**	-	-
PLACE1003839	259.31	241.18	222.89	217.52	173.45	205.17	163.55	139.4	151.61		**		-
PLACE1003845	69.72	60.2	118.04	40.89	28.14	26.89	48.08	43.86	45.73				
PLACE1003850	9.53	11.45	9.42	3.3	8.43	5.88	6.51	3.87	5.97		*		-
PLACE1003852	32.49	28.32	26.73	21.76	30.69	26.63	18.45	14.12	17.92		**		-
PLACE1003858	19.9	13.83	13.86	8.03	12.82	5.24	7.08	4.19	7.71		*		-
PLACE1003861	40.22	66.3	33.51	12.47	57.37	18.72	33.23	18.67	19.13				
PLACE1003864	34.51	84.76	122.59	61.83	70.16	55.03	69.32	56.31	42.37				
PLACE1003870	9.43	6.5	5.9	2.94	3.32	3.4	5.69	3.86	5.74	*		-	
PLACE1003885	10.07	6.76	3.91	3.5	6.22	3.91	3.49	3.72	6.33				
PLACE1003886	12.66	12.76	10.57	6.28	9.54	3.51	13.66	8.88	12.28	*		-	
PLACE1003888	15.48	13.6	17.45	7.94	12.36	6.23	14.56	8.73	9.07	*		-	
PLACE1003892	6.59	4.85	8.21	5.64	7.14	2.75	3.77	2.15	4.24				

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Table 475

PLACE1003900	9.05	5.59	5.53	3.41	9.33	4.49	4.41	6.87	4.79				
PLACE1003902	9.43	6.06	7.46	2.35	3.67	1.76	3.96	1.76	3.05	*	*	-	-
PLACE1003903	17.33	19.36	14.55	9.42	10.87	10.03	9.08	6.56	7.77	**	**	-	-
PLACE1003915	14.67	18	11.19	12.64	10.36	9.98	8.5	5.29	8.8		*		-
PLACE1003918	10.58	6.62	8.73	7.34	5.29	3.45	7.05	5.69	4.94				
PLACE1003923	11.24	8.95	4.47	2.95	4.6	4.65	4.65	3.26	3.87				
PLACE1003932	9.02	5.88	4.39	2.18	9.39	4.8	6.3	4.31	5.14				
PLACE1003936	11.92	7.46	8.85	2.47	4.23	4.36	9.51	9.11	10.65	*		-	
PLACE1003966	11.6	10.3	9.01	5.2	6.1	4.37	6.77	5.83	6.22	**	**	-	-
PLACE1003968	4.88	5.07	4.71	0.66	3.28	0.8	3.51	1.87	0.72	*	*	-	-
PLACE1004018	4.89	2.45	2.55	4.7	8.1	2.19	2.99	1.85	1.89				
PLACE1004020	12.24	14.87	17.86	7.54	8.19	5.65	7.35	9.99	10.06	*	*	-	-
PLACE1004028	2.49	1.88	2.35	1.78	7.14	2.28	1.01	1.49	0.82		*		-
PLACE1004034	6.5	4.91	7.64	2.7	5.45	2.86	3.71	3.07	1.75		*		-
PLACE1004042	5.94	2.98	4.53	2.04	4.08	3.55	3.58	3.9	2.95				
PLACE1004078	6.26	4	5.13	2.35	3.57	1.92	1.94	3.66	4.31	*		-	
PLACE1004103	4.16	6.73	8.68	2.05	3.45	2.36	1.89	0.91	3.01	*	*	-	-
PLACE1004104	0.6	1.12	3	1.89	7.2	1.01	1.88	2.79	1.52				
PLACE1004113	0.85	1	0.69	0.62	4.18	1	1.54	0.77	1.59				
PLACE1004114	12.27	11.63	12.84	9.04	6.13	6.15	17.17	8.3	11.59	**		-	
PLACE1004118	25.56	29.6	34.14	10.69	22.13	12.84	16.2	19.15	19.4	*	*	-	-
PLACE1004128	6.77	8.44	8.16	3.47	7.23	7.78	2.81	3.08	3.14		**		-
PLACE1004130	9.36	4.88	10.96	8.2	7.53	9.87	4.28	6.71	6.1				
PLACE1004149	2.51	2.43	6.21	2.78	5.35	2.6	3.3	3.26	2.01				
PLACE1004156	13.06	9.08	13.29	7.39	11.05	6.74	9.05	9.4	10.62				
PLACE1004160	20.97	19.94	23.27	14.03	30.3	7.33	16.97	16.65	14.66		*		-
PLACE1004161	7.06	8.18	8.06	5.83	7.98	4.77	4.77	4.44	4.99		**		-
PLACE1004166	41.1	39.11	42.06	19.36	22.19	21.87	24.56	28.32	30.02	**	**	-	-
PLACE1004168	32.92	30.07	31.55	16.2	15.66	13.35	21.23	25.32	27.11	**	*	-	-
PLACE1004170	14.53	21.92	19.94	10.32	12.85	10.61	11.03	18.31	8.2	*		-	
PLACE1004178	2.75	3.62	3.97	2.55	6.19	3.35	0.34	1.55	0.72		**		-
PLACE1004183	36.95	43.53	45.99	27.78	51.84	25.82	21.25	25.43	23.92		**		-
PLACE1004197	5.75	5.24	7.84	2.14	4.97	3.74	3.04	2.49	3.28		*		-
PLACE1004199	21.75	27.66	12.12	12.42	24.13	11.64	10.47	10.88	12.46				
PLACE1004203	11	13.62	10.81	4.23	10.81	6.59	10.74	11.32	12.32				
PLACE1004242	20.49	16.48	21.11	6.81	6.93	13.71	6.23	11.27	9.24	*	**	-	-
PLACE1004249	6.73	11	11.25	4.47	10.26	6.2	5.79	8.22	6.09				
PLACE1004255	32.98	36.35	38.9	17.52	26.48	21.84	27.95	27.86	29.02	*	*	-	-
PLACE1004256	12.54	10.51	15.03	5.99	5.51	6.23	3.84	5.04	3.23	**	**	-	-
PLACE1004257	3.25	14.27	11.31	3.36	8.12	8.15	2.7	9.49	4.03				
PLACE1004258	11.89	26.37	21.62	8.76	18.18	12.25	12.69	13.44	9.66				
PLACE1004270	8.17	8.34	11.88	6.47	6.77	11.76	8.27	3.74	6.39				
PLACE1004272	1.52	1.56	3.17	1.04	3.51	0.46	1.56	1.06	1.78				
PLACE1004273	23.31	38.14	20.87	17.38	14.34	7.01	17.2	17.07	20.56				
PLACE1004274	12.13	13.19	15.06	6.12	12.19	6.04	6.47	11.78	6.75				
PLACE1004277	18.65	17.3	16.15	12.2	21.29	13	13.46	15.12	20.1				
PLACE1004279	20.99	17.87	19.27	8.96	30.05	13	8.21	11.3	11.19		**		-
PLACE1004282	12.55	12.53	16.59	4.95	9.12	5.25	6.7	6.34	5.89	*	**	-	-
PLACE1004284	9.58	14.66	15.53	8.95	7.35	5.65	6.2	6.82	3.1	*	*	-	-
PLACE1004289	11.29	10.79	11.74	3.16	5.71	3.35	2.35	6.14	2.14	**	**	-	-
PLACE1004298	19.52	18.15	16.36	8.87	22.44	9.43	11.73	9.62	8.57		**		-
PLACE1004302	6.5	4.57	6.26	4.18	7	3.55	1.56	4.16	0.55		*		-
PLACE1004305	7.16	4.88	7.78	4.02	11.98	4.38	3.44	4.62	2.94		*		-
PLACE1004316	21.08	20.32	25.43	14.83	15.07	12.7	13.59	13.17	12.8	*	**	-	-
PLACE1004322	9.54	3.44	10.02	13.05	22.34	1.36	2.52	7.35	3.43				
PLACE1004325	13.79	15.32	21.15	8.25	8.41	6.63	10.63	11.11	9.78	*		-	
PLACE1004332	13.76	26.81	27.83	10.52	16.97	4.86	9.28	8.37	7.2		*		-
PLACE1004336	9.25	9.04	10.31	3.17	5.77	3.05	2.53	4.29	2.93	**	**	-	-
PLACE1004346	11.14	15.86	16.19	8.6	6.7	8.17	14.67	2.81	3.65	*		-	
PLACE1004358	4.9	6.6	5.3	4.66	3.48	2.52	2.87	2.07	1.85		**		-
PLACE1004376	4.37	7.66	6.28	3.82	16.23	3.24	18.46	3.42	3.06				
PLACE1004384	20.82	15.88	20.1	10.2	14.54	11.76	10.47	11.55	9.77	*	**	-	-
PLACE1004385	16.21	25.32	29.3	6.24	11.85	7.12	18.49	9.57	9.67	*		-	
PLACE1004388	13.03	15.64	14.98	6.26	11.49	8.38	7.85	6.97	4.61	*	**	-	-

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PLACE1004405	6.83	7.82	8.42	1.74	2.87	2.17	1.79	1.77	1.06	**	**	-	-
PLACE1004407	11.75	11.43	14.16	6.35	10.59	6.28	6.13	6.07	6.47	*	**	-	-
PLACE1004424	6.94	8.4	8.66	2.02	6.19	2.66	3.43	3.43	2.34	*	**	-	-
PLACE1004425	15.08	13.72	13.35	6.65	11.37	7.31	11.7	10.39	11.17	*	*	-	-
PLACE1004427	9.79	7.13	8.53	5.79	4.82	4.58	2.31	1.96	2.72	*	**	-	-
PLACE1004428	8.46	5.33	5.57	3.25	3.29	3.21	2.85	2.65	3.1	*	*	-	-
PLACE1004433	6.57	5.12	7.26	2.15	3.61	2.86	2.76	2.36	3.32	*	**	-	-
PLACE1004435	5.31	5.07	8.8	2.76	3.41	3.61	2.83	0.69	1.36		*		-
PLACE1004437	123.66	158.84	144.08	116.56	167.95	86.05	49.84	88.42	68.77		**		-
PLACE1004441	10.02	12.73	11.55	5.63	11.08	5.24	5.14	4.56	2.63		**		-
PLACE1004446	4.95	5.73	4.69	2.19	3.83	1.62	2.79	2.61	2.66	*	**	-	-
PLACE1004450	17.21	13.77	11.35	7.43	9.82	10.35	13.72	15.81	15.38				
PLACE1004451	21.93	21.83	22.42	14.24	15.13	14.34	10.39	9.42	10.97	**	**	-	-
PLACE1004456	5.66	3.89	4.79	2.22	5.14	3.7	4.95	1.66	2.31				
PLACE1004458	6.57	4.16	7.77	2.1	5.75	2.16	2.41	3.03	1.54		*		-
PLACE1004460	6.93	5.13	4.79	2.01	4.85	1.65	3.61	2.54	1.12		*		-
PLACE1004467	10.11	11.82	9.53	2.74	4.49	5.1	3.12	1.44	1.55	**	**	-	-
PLACE1004471	14.09	22.14	14.79	8.38	18.33	11.21	5.81	8.78	5.83		*		-
PLACE1004473	8.27	14.31	9.86	3.42	8.92	3.77	4.46	5.47	8.39				
PLACE1004475	4.2	2.67	2.47	2.6	8.42	6.68	3.42	2.58	2.7				
PLACE1004482	42.46	39.9	32.17	18.98	31.24	19.51	41.1	31.66	45.4	*		-	
PLACE1004491	3.4	5.37	4.92	2.26	2.87	1.21	3.11	1.77	1.09	*	*	-	-
PLACE1004492	14.75	10.5	4.26	8.39	16.03	7.27	3.28	2.19	2.31				
PLACE1004506	18.11	19.82	21.23	12.46	23.49	16.62	17.33	12.61	13.21		*		-
PLACE1004507	14.62	14.01	19.19	12.21	20.75	13.12	5.25	3.93	6.09		**		-
PLACE1004510	8.27	7.11	7.77	4.2	4.81	1.36	5.06	2.94	3.49	*	**	-	-
PLACE1004516	5.75	6.67	3.83	4.51	8.48	2.72	4.69	2.56	3.06				
PLACE1004518	9.64	6.39	6.6	5.58	7.29	2.45	2.45	4.03	4.48		*		-
PLACE1004519	45.05	38.06	29.43	16.22	21.37	17.38	37.02	29.03	42.7	*		-	
PLACE1004520	5.65	5.88	4.83	5	23.3	3.26	7.89	2.48	5.32				
PLACE1004530	8.55	8.01	8.19	4.33	4.87	3.07	5.74	4.33	5.72	**	**	-	-
PLACE1004545	16.35	9.42	10.89	5.28	6.16	4.82	7.69	5.29	6.88	*		-	
PLACE1004547	8.88	4.99	7.28	3.79	10.69	2.44	2.07	2.03	2.03		*		-
PLACE1004548	8.06	7.34	7.17	1.99	3.55	1.53	3.36	1.74	4.09	**	**	-	-
PLACE1004550	9.29	4.74	4.57	6.39	7.24	2.64	11.12	3.11	5.12				
PLACE1004551	28.29	24.92	17.22	13.36	20.97	8.68	22.61	16.23	21.2				
PLACE1004559	38.64	25.35	19.12	16.44	15.14	16.5	25.43	24.95	33.62				
PLACE1004562	50.29	46.32	50.21	54.16	56.41	39.84	35.71	42.24	45.43				
PLACE1004564	12.01	9.86	9.29	4.62	9.04	5.79	9.27	6.54	10.21				
PLACE1004604	17.66	17.86	15.11	9.74	9.81	7.66	16.75	11.47	16.51	**		-	
PLACE1004611	6.51	3.64	4.04	1.34	7.9	1.38	3.77	0.9	3.89				
PLACE1004629	7.22	4.23	7.21	2.88	5.64	1.27	4	2.37	6.88				
PLACE1004630	5.71	5.71	5.05	2.41	3.38	0.92	6.59	3.07	5.19	*		-	
PLACE1004637	15.22	15.19	15.73	4.5	6.73	18.68	5.83	11.18	5.64		*		-
PLACE1004645	16.19	10.08	17.1	10.36	11.57	13.97	10.9	12.36	6.68				
PLACE1004646	4.97	5.64	4.39	4.13	5.71	3.39	2.58	3.34	2.67		**		-
PLACE1004648	5.49	4.11	3.96	3.64	5.16	4.29	1.91	1.5	0.14		**		-
PLACE1004655	3.31	1.36	2.13	1.15	3.39	0.72	0.74	1.06	1.47				
PLACE1004658	61.58	67.15	67	38.54	49.97	38.25	52.62	54.12	65.08	**		-	
PLACE1004664	1.19	4.36	2.93	2.86	5.73	2.7	1.85	2.13	1.51				
PLACE1004672	28.88	30.42	25.6	16.98	20.16	13.59	16.28	11.87	13.82	**	**	-	-
PLACE1004674	4.27	1.5	4.11	2.41	3.15	1.89	1.56	2.96	3.87				
PLACE1004681	6.54	6.41	13.08	7.27	21.72	12.91	4.64	4.9	3.36				
PLACE1004686	4.34	3.3	4.61	2.4	3.38	2.38	2.29	3.63	0.39				
PLACE1004690	6.4	6.12	8.6	4.32	13.96	8.66	2.73	4.56	2.78		*		-
PLACE1004691	12.44	14.52	17.78	7.94	13.42	7.13	8.04	12.14	11.56				
PLACE1004693	8.4	10.27	9.88	5.82	5.16	5.28	2.45	3.25	2.73	**	**	-	-
PLACE1004701	144.88	198.16	97.68	190.88	167.91	84.32	88.33	73.95	139.9				
PLACE1004705	3.47	3.01	2.93	2.39	3.96	1.27	1.92	3.49	3.87				
PLACE1004708	48.88	43.13	45.03	31.98	28.55	23.56	15.06	39.44	11.77	**		-	
PLACE1004716	20.04	14.83	24.39	8.19	12.11	8.27	8.37	8.78	9.57	*	*	-	-
PLACE1004722	5.57	7.39	10	4.45	6.54	3.93	3.57	3.69	3.48		*		-
PLACE1004736	16.71	17.15	24.67	12.34	13.91	6.89	9.19	22.16	13.53				
PLACE1004737	5.22	7.74	7.78	3.83	6.24	1.98	3.06	3.38	3.05		*		-

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PLACE1004740	5.7	7.45	13.2	8.48	9.7	6.78	5.51	4.01	4.39				
PLACE1004743	25.2	29.5	32.11	15.32	29.52	15.01	26.22	23.41	28.91				
PLACE1004751	26.3	37.3	36.23	17.86	40.34	16.49	27.84	27.38	23.37				
PLACE1004757	27.21	29.89	35.01	20.07	11.76	13.22	19.63	14.54	16.78	*	**	-	-
PLACE1004761	36.62	28.57	36.7	16.84	22.51	18.17	11.71	16.47	11.41	**	**	-	-
PLACE1004773	6.34	3	4.53	3.16	3.36	2.2	2.15	2.55	2.95				
PLACE1004775	6.98	4.5	11.09	2.47	5.26	2.58	2.74	2.24	1.32				
PLACE1004777	22.12	29.48	36.12	13.38	18.93	13.39	17.54	20.58	18.98	*		-	
PLACE1004793	38.61	50.6	39.99	29.77	37.64	25.63	24.47	24.63	21.5		**		-
PLACE1004796	8.45	9.48	8.63	3.38	9.79	3.2	3.16	2.68	3.41		**		-
PLACE1004804	5.96	3.66	3.88	1.07	6.07	2.59	2.15	2.35	2.21		*		-
PLACE1004813	7.54	8.6	8.99	4.2	5.66	4.51	4.87	4.35	4.23	**	**	-	-
PLACE1004814	4.13	4.9	5.89	3.27	11.52	2.25	2.11	31.08	4.24				
PLACE1004815	5.57	3.05	6.31	3.48	4.55	1.54	4.88	2.03	1.26				
PLACE1004816	10.65	12.52	15.46	46.16	13.59	7.88	11.01	6.49	24.95				
PLACE1004824	10.1	10.18	14.93	3.84	7.8	4.37	6.87	4.52	8.59	*		-	
PLACE1004827	6.33	6.31	10.2	1.77	3.73	0.89	1.94	4.36	3.45	*	*	-	-
PLACE1004836	18.51	24.59	14.94	5.86	11.83	5.72	3.63	5.6	4.83	*	**	-	-
PLACE1004838	32.68	37.85	26.97	17.25	33.96	16.53	18.4	22.65	17.82		*		-
PLACE1004840	26.67	33.84	24.99	11.9	21.32	10.63	17.68	19.77	20.11	*	*	-	-
PLACE1004842	29.36	29.36	36.71	26.03	17.22	20.39	11.25	16.65	13.58	*	**	-	-
PLACE1004850	12.96	12.93	15.16	9.69	10.5	6.77	8.83	9.34	8.77	*	**	-	-
PLACE1004868	19.8	16.22	20.8	8.53	16.93	9.03	11.19	11.11	9.47		**		-
PLACE1004885	7.93	7.22	6.94	1.5	3.78	3.6	1.94	2.3	1.73	**	**	-	-
PLACE1004886	8.48	8.07	17.49	4.04	4.63	2.9	4.53	4.47	2.5				
PLACE1004887	11.79	13.7	11.52	6.38	10.2	7	3.69	4.3	5.52	*	**	-	-
PLACE1004896	6.25	6.09	7.72	0.93	8.2	4.59	2.58	2.25	1.01		**		-
PLACE1004900	11.28	8.08	8.69	8.58	6.42	4.7	4.96	5.45	3.62		*		-
PLACE1004902	7.13	7.38	10.7	4.87	6.92	2.81	4.29	4.21	2.64		*		-
PLACE1004904	23.08	23.38	37.33	15.52	22.71	12.92	16.1	22.74	25.02				
PLACE1004911	11.74	10.67	12.36	7.47	12.66	7.84	6.28	5.55	4.09		**		-
PLACE1004913	12.82	12.15	14.37	4.58	7.86	4.67	7.24	7.07	6.68	**	**	-	-
PLACE1004918	17.31	18.68	18.94	7.36	10.01	6.44	8.32	5.56	6.18	**	**	-	-
PLACE1004930	6.79	6.06	5.6	1.3	2	3.65	2.19	1.6	1.33	**	**	-	-
PLACE1004934	14.99	19.19	12.29	5.42	10.92	8.11	4.61	8.66	7.47	*	*	-	-
PLACE1004937	18.93	13.85	13.4	11.81	10.98	11.51	15	13.14	16.45				
PLACE1004949	5	5.22	6.64	5.79	3.31	3.09	4.44	4.05	3.5		*		-
PLACE1004969	13.91	13.85	11.55	11.71	12.45	9.25	4.82	9.25	5.58		*		-
PLACE1004970	28.75	33.22	29.53	13.51	29.35	23.54	15.11	12.88	14.15		**		-
PLACE1004972	13.26	11.27	10.14	5.85	6.98	5.82	4.89	3.42	1.54	**	**	-	-
PLACE1004974	16.47	29.85	28.89	16.44	23.94	17.53	14.71	17.1	12.72				
PLACE1004975	12.92	11.66	12.08	5.89	13.8	6.88	5.54	3.55	3.43		**		-
PLACE1004979	7.78	7.47	6.98	3.07	7.65	3.76	4.2	4.56	6.5		*		-
PLACE1004982	30.58	23.61	26.29	14.3	19.23	11.42	16.82	24.16	30.51	*		-	
PLACE1004985	29.66	24.94	25.1	15.66	19.26	12.6	21.78	17.15	20.28	*	*	-	-
PLACE1005003	16.43	14.5	16.78	6.69	10.88	11.47	1.79	5.8	6.41	*	**	-	-
PLACE1005004	5.26	4.21	4.06	1.44	3.4	2.25	2.76	1.23	1.09	*	*	-	-
PLACE1005005	17.79	13.99	18.79	11.99	10.57	8.86	7.49	5.3	5.99	*	**	-	-
PLACE1005011	10.94	14.04	9.8	3.35	9.24	6.44	3.46	2.32	0.6		**		-
PLACE1005026	31.74	35.88	28.88	14.82	24.65	14.67	35.74	25.33	28.57	*		-	
PLACE1005027	26.29	29.23	15.87	7.97	19.55	9.09	25.84	19.81	24				
PLACE1005031	38.12	16.05	14.24	9.18	25.55	17.12	7.22	9.47	10.36				
PLACE1005036	13.86	12.84	17.42	8.68	15.64	10.29	11.23	7.16	6.77		*		-
PLACE1005041	111.13	87.66	72.07	36.83	51	43.47	99.34	93.97	97.87	*		-	
PLACE1005046	27.6	29	18.07	15.06	19.65	20.68	22.16	13.25	24				
PLACE1005047	50.64	34.98	35.58	25.13	37.56	21.77	26.01	15.91	25.77		*		-
PLACE1005052	10.39	12.55	10.8	4.67	15.46	6.61	10.9	9.05	16				
PLACE1005055	24.31	33.8	18.61	16.75	10.79	11.1	19.54	11.46	10.17				
PLACE1005066	7.67	8.41	7	12.21	61.68	20.27	25.44	4.84	8.48				
PLACE1005077	9.62	6.97	5.62	4.44	4.68	3.2	5.42	5.71	7.8				
PLACE1005085	10.11	4.46	3.84	3.42	3.7	2.05	2.8	5.01	2.86				
PLACE1005086	11.97	11.74	11.67	7.31	18.85	7.84	6.74	6.63	9.62		*		-
PLACE1005088	86.57	83.56	74.65	79.4	89.3	75.33	56.8	52.44	57.53		**		-
PLACE1005089	6.31	4.13	4.27	1.8	3.13	4.07	2.18	0.55	2.04		*		-

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PLACE1005101	11.5	9.29	11.94	9.18	4.8	5.47	5.22	3.69	6.78	*	**	-	-
PLACE1005102	22.17	25.98	27.54	6.07	7.69	6.94	7.15	5.65	7.82	**	**	-	-
PLACE1005108	10.15	7.73	6.02	2.99	6.05	3.33	4.8	7.23	6.47				
PLACE1005110	3.97	2.39	3.45	3.59	3.78	1.51	2.14	1.33	2.15				
PLACE1005111	23.94	21.69	16.98	14.04	21.5	8.57	20.32	16.74	23.71				
PLACE1005123	16.94	14.46	12.96	5.45	9.5	5	6.89	4.29	5.82	*	**	-	-
PLACE1005124	9.14	6.62	6.15	2.06	5.47	1.8	6.61	3.46	5.33	*		-	
PLACE1005128	6.83	4.81	4.87	1.09	3.42	1.91	3.3	3.63	2.82	*	*	-	-
PLACE1005130	12.43	17.68	12.68	4.58	11.05	5.79	12.55	5.44	10.87				
PLACE1005141	6.07	3.99	5.18	6.23	2.88	1.1	9.65	2.17	2.82				
PLACE1005146	10.52	9.7	6.88	6.24	10.69	5.88	5.25	8.14	5.49				
PLACE1005152	91.15	76.64	75.79	51.06	95.95	52.59	42.4	38.1	38.75		**		-
PLACE1005157	5.11	3.75	6.06	2.82	4.86	2.4	1.9	2.79	1.7		*		-
PLACE1005162	24.79	23.25	27.03	17.82	26.77	20.32	10.52	15.51	11.65		**		-
PLACE1005170	9.55	7.54	6.99	11.08	19.85	14.4	3.82	8.2	5.94				
PLACE1005176	5.55	5.17	6.85	2.52	4.13	3.01	2.09	2.54	1.26	*	**	-	-
PLACE1005181	10.56	18.07	15.09	7.46	9.06	8.01	10.91	12.85	10.11	*		-	
PLACE1005184	3.64	4.4	5.5	5.28	11.77	4.26	3.84	3.69	3.06				
PLACE1005186	5.96	5.07	5.66	2.88	2.54	3.26	3.64	4.33	4.72	**	*	-	-
PLACE1005187	20.53	14.71	18.55	9.5	10.66	10.36	12.23	12.87	7.61	*	*	-	-
PLACE1005189	8.28	7.72	11.92	4.24	7.19	3.99	6.84	7.52	5.99				
PLACE1005193	39.26	44.11	39.59	31.34	38.66	28.91	36.03	40.56	33.69				
PLACE1005200	1391.4	1317.2	1202.3	1770.3	2457.3	1744.3	1189.8	1397.9	586.38	*		+	
PLACE1005206	48.27	41.57	88.17	48.38	52.86	50.82	27.19	13.53	58.32				
PLACE1005216	10.1	9.74	10.26	5.79	10.41	5.95	3.4	3.26	4.05		**		-
PLACE1005223	35.86	44.94	37.06	23.02	25.39	16.59	23.41	26.05	19.76	*	**	-	-
PLACE1005225	5.34	5.81	6.83	4.25	3.02	5.27	2.59	3.79	3.7		*		-
PLACE1005232	37.45	31.95	45.29	20.08	17.68	11.81	24.42	25.92	23.95	**	*	-	-
PLACE1005239	7.93	6.66	12.45	5.29	3.66	4.36	3.81	3.89	4.86				
PLACE1005243	16.13	27.58	27.13	19.28	15.8	19.25	6.8	13.48	9.67		*		-
PLACE1005250	5.37	6.75	7.77	5.96	4.93	3.55	3.78	5.49	3.24				
PLACE1005261	61.12	61.95	56.67	47.53	36.14	42.92	20.88	23.52	21.14	**	**	-	-
PLACE1005266	7.03	6.91	9.71	5.82	8.14	5.96	4.18	3.69	5.53		*		-
PLACE1005271	8.47	8.61	6.86	4.77	7.74	3.27	3.65	3.57	3.35		**		-
PLACE1005277	20.92	15.1	22.31	9.09	13.8	9.19	14.68	15.64	18.36	*		-	
PLACE1005287	15.1	8.12	14.31	5.25	6.44	6.19	5.01	4.78	3.02	*	*	-	-
PLACE1005299	10.04	6.09	8.79	4.5	5.75	7.77	4.03	4.98	7.58				
PLACE1005305	8.97	7.38	9.77	4.47	3.45	4.18	3.14	3.99	3.81	**	**	-	-
PLACE1005307	12.01	9.78	33.93	6.5	6.01	6.92	5.78	5.91	8.37				
PLACE1005308	6.72	9.28	13.18	4.37	5.39	4.05	5.69	4.54	7.02				
PLACE1005313	8.46	6.04	10.79	5.16	6.95	3.74	4.51	3	4		*		-
PLACE1005320	9.29	12.54	14.31	7.32	9.29	5.14	4.92	4.65	5.56		**		-
PLACE1005327	31	25.4	35.29	16.09	17.4	11.88	9.82	14.36	14.83	**	**	-	-
PLACE1005331	13.95	13.36	13.69	9.09	7.58	7.27	7.77	10.5	7.36	**	**	-	-
PLACE1005335	11.38	7.64	13.28	5.94	7.87	3.65	8.18	25.07	9.78				
PLACE1005336	29.59	23.98	23.59	14.99	18	12.79	23.63	28.14	27.34	*		-	
PLACE1005351	11.96	8.58	19.03	4.6	4.51	3.68	3.27	6.24	4.61	*		-	
PLACE1005366	73.8	70.81	70.61	45.9	65.72	42.52	55.33	53.05	50.72	*	**	-	-
PLACE1005373	9.8	6.9	15.51	3.87	3.73	2.69	2.9	3.58	2.99	*	*	-	-
PLACE1005374	31.25	37.89	30.27	12.29	20.74	12.12	33.17	26.39	29.29	**		-	
PLACE1005383	9.15	7.91	6.27	5.38	5.79	4.82	3.77	5.77	7.02	*		-	
PLACE1005388	14.78	7.34	14.13	9.31	7.11	6.02	6.28	5.49	5.89				
PLACE1005409	11.86	10.31	14.09	4.95	5.84	5.2	5.09	4.29	5.35	**	**	-	-
PLACE1005410	13.35	9.74	14.55	5.14	6.18	4.53	6.86	5.79	5.13	**	*	-	-
PLACE1005426	10.65	4.8	11.31	4.23	3.51	3	2.46	6.49	1.78				
PLACE1005431	8.27	7.3	10.2	3.04	3.82	2.32	3.59	3.79	5.31	**	*	-	-
PLACE1005453	7.65	9.23	18.96	3.09	5.38	3.63	2.3	4.42	3.43				
PLACE1005467	10.75	11.01	23.28	4.33	7.93	7.46	6.29	7.36	5.29				
PLACE1005471	7.1	9.43	5.6	3.8	6.04	3.15	3.31	6.18	12.95				
PLACE1005476	29.52	27.39	29.6	15.57	12.74	15.37	14.04	14.17	16.52	**	**	-	-
PLACE1005477	9.37	7.91	13.74	3.68	6.31	4.63	5	3.74	6.24	*	*	-	-
PLACE1005480	7.1	8	8.36	5.61	4.81	4.45	4.92	2.94	2.27	**	**	-	-
PLACE1005481	10.21	6.44	10.18	3.66	4.76	4.41	5.76	4.63	3.43	*	*	-	-
PLACE1005494	9.19	9.94	10.69	3.34	4.05	3.41	4.87	3.69	4.02	**	**	-	-

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PLACE1005495	11.05	11.48	9.86	5.01	5.38	4.26	3.3	3.97	3.58	**	**	-	-
PLACE1005497	9.89	9.26	8.02	3.87	6.07	3.47	3.99	3.58	2.73	**	**	-	-
PLACE1005499	23.46	21.47	29.66	8.65	19.6	10.05	16	19.54	21.59	*		-	
PLACE1005502	9.18	6.48	6.37	3.45	3.87	4.29	4.21	4.81	4.94	*	*	-	-
PLACE1005513	33.31	27.28	25.19	10.65	9.46	7.45	5.15	5.68	9.33	**	**	-	-
PLACE1005515	11.7	9.47	10.48	3.66	3.88	4.7	6	4.7	5.35	**	**	-	-
PLACE1005519	8.43	6.62	7.72	4.49	2.77	2.81	3.1	2.36	5.05	**	*	-	-
PLACE1005526	8.8	10.4	11.16	2.78	4.21	2.23	3.21	3.51	3.18	**	**	-	-
PLACE1005528	26.91	22.55	23.87	12.32	10.17	9.81	19.08	11.09	17.43	**	*	-	-
PLACE1005530	20.34	15.73	21.3	12.14	14.27	9.82	8.49	8.49	4.49	*	**	-	-
PLACE1005536	18.12	14.92	18.89	3.17	4.7	3.13	5.93	4.22	4.19	**	**	-	-
PLACE1005539	42.25	35.31	35.69	15.02	20.49	15.33	32.11	27.06	37.95	**		-	
PLACE1005543	35.86	20.69	14.02	11.25	7.4	11.67	9.96	8.84	11.47				
PLACE1005544	4.98	5.73	4.38	2.31	2.15	3.58	3.94	2.43	3.09	*	*	-	-
PLACE1005550	26.58	26.63	19.78	16.15	16.36	16.32	11.17	10.41	11.67	*	**	-	-
PLACE1005554	23.49	15.23	16.27	7.02	8.22	4.71	11.04	7.45	10.06	*	*	-	-
PLACE1005557	10.41	9.97	10.58	3.15	3.37	2.55	4.57	1.9	2.76	**	**	-	-
PLACE1005563	10.87	11.46	9.72	4.64	6.41	6.88	7.08	5.98	5.9	**	**	-	-
PLACE1005569	27.85	17.24	16.24	8.47	8.97	6.39	9.6	5.75	9.27	*	*	-	-
PLACE1005574	29.21	21.31	10.09	12.87	15.06	14.88	14.12	11.93	13.7				
PLACE1005584	80.18	66.17	69.3	73.19	89.15	68.42	53.92	40.06	44.96		*		-
PLACE1005590	14.81	9.97	11.59	6.51	9.72	8.47	7.14	6.35	7.74		*		-
PLACE1005595	23.18	18.25	21.16	12.01	10.55	9.94	19.07	11.17	15.91	**		-	
PLACE1005601	11.31	7.51	15.39	5.61	6.28	8.37	7.21	9.02	6.01				
PLACE1005603	18.98	21.86	14.52	8.39	9.87	6.77	12.21	11.52	14.3	*		-	
PLACE1005604	8.92	8.05	5.89	5	4.08	4.67	3.54	2.41	2.72	*	**	-	-
PLACE1005611	33.68	22.2	29.76	11.8	16.07	9.26	20.54	21.42	26.07	*		-	
PLACE1005622	30.69	27.64	23.31	11.83	18.8	12.91	22.33	27.88	24.08	*		-	
PLACE1005623	9.95	5.8	5.03	2.69	3.21	2.46	4.37	5.18	4.94				
PLACE1005630	8.17	9.56	9.09	4.43	7.2	3.43	4.75	3.89	4.7	*	**	-	-
PLACE1005638	60.6	66.64	49.38	29.59	36.73	29.78	61.43	55.47	68.03	**		-	
PLACE1005646	17.8	13.84	15.64	9.47	9.48	7.41	6.37	4.37	5.79	**	**	-	-
PLACE1005647	13.8	11.09	12.51	5.66	5.78	5.71	6.46	4.42	5.24	**	**	-	-
PLACE1005648	28.95	31.24	20.78	11.15	9.99	10.48	23.48	13.79	10.43	**		-	
PLACE1005653	16.03	13.03	11.9	5.52	4.03	5.5	8.65	5.02	7.5	**	*	-	-
PLACE1005656	15.9	11.93	10.98	7.3	8.49	5.09	13.9	11.98	12.97	*		-	
PLACE1005659	10.5	8.34	6.31	5.3	4.01	3.82	4.61	3.03	4.74	*	*	-	-
PLACE1005660	12.82	10.45	9.32	4.78	5.95	3.56	5.23	2.26	5.04	**	**	-	-
PLACE1005664	23.43	27.28	25.73	6.86	20.98	19.65	21.23	13.1	15.7		*		-
PLACE1005666	12.43	11.64	13.67	7.79	10.52	6.99	11.1	12.9	13.47	*		-	
PLACE1005669	14.08	13.16	10.98	6.36	8.32	3.2	8.01	5.64	11	*		-	
PLACE1005682	22.57	20.73	18.81	7.71	10.55	7.1	12.18	6.07	11.14	**	**	-	-
PLACE1005698	7.18	6.68	8.02	7.04	5.88	4.02	4.11	5.29	4.18		**		-
PLACE1005708	17.69	17.02	22.05	11.44	15.51	9.8	12.59	9.64	8.25	*	*	-	-
PLACE1005725	9.73	11.27	13.97	7.09	8.31	6.27	4.4	6.46	6.4	*	*	-	-
PLACE1005727	10.04	8.34	11.08	6.79	10.76	10.55	4.59	6.83	6.56		*		-
PLACE1005730	13.44	12.68	11.77	6.36	7.19	8.47	5.04	7.92	8.47	**	**	-	-
PLACE1005736	5.83	5.5	7.74	3.15	14.38	1.73	4.63	3.09	3.33		*		-
PLACE1005739	7.01	13.06	9.75	7.43	7.8	5.14	2.96	4.16	3.47		*		-
PLACE1005745	8.04	6.14	6.43	4.26	4.82	5.89	4.13	2.63	4.39		*		-
PLACE1005752	128.36	102.07	139.38	89.6	72.86	89.83	103.85	94.56	103.55	*		-	
PLACE1005755	13.46	9.22	14.54	4.95	6.97	3.84	5.58	5.65	3.87	*	*	-	-
PLACE1005756	10.54	16.55	18.56	10.11	10.69	10.1	6.71	10.57	12.53				
PLACE1005760	5.36	6.71	8.64	9.33	6.58	7.47	2.74	8.03	2.74				
PLACE1005763	18.11	17.1	15.35	9.45	11.68	9.73	7.29	9.29	9.82	**	**	-	-
PLACE1005768	19.31	21.05	13.08	10.64	11.47	13.73	6.13	9.41	9.52		*		-
PLACE1005771	24.23	23.82	24.14	14.86	21.27	9.53	16.05	19.49	20.2		*		-
PLACE1005783	6.96	4.13	7.26	3.95	3.94	3.49	3.16	3.04	5.15				
PLACE1005799	43.95	40.56	57.56	28.57	25.86	15.96	30.85	26.7	32.18	*	*	-	-
PLACE1005802	18.73	15.75	12.71	10.65	14.22	15.85	21.48	13.68	14.38				
PLACE1005803	14.16	12.88	18.69	6.94	7.06	7.31	4.95	5.48	3.9	**	**	-	-
PLACE1005804	16.14	16.06	21.67	10.66	8.62	11.86	4.49	6.03	5.63	*	**	-	-
PLACE1005813	7.59	9.87	17.86	7.9	9.25	7.77	3.93	4.99	5.43				
PLACE1005815	17.11	19.5	18.51	7.94	18	6.6	9.57	8.13	8.77		**		-

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PLACE1005828	21.32	17.86	17.66	18.38	28.15	11	8.41	12.77	17.42				
PLACE1005833	19.04	15.23	17.55	13.68	13.86	12.16	11.62	13.97	12.02	*	*	-	-
PLACE1005834	31.23	40.41	42.31	19.53	15.14	12.45	22.97	22.37	27.18	**	*	-	-
PLACE1005835	8.38	4.15	8.95	3.69	3.05	3.25	2.72	13.93	4.26				
PLACE1005836	6.34	4.47	7.11	2.95	2.55	2.1	1.11	4.41	2.67	*		-	
PLACE1005845	7.96	5.73	10.94	3.26	4.7	1.75	3.2	4.47	3.62	*	*	-	-
PLACE1005850	7.12	8.63	11.96	4.89	4.51	3.39	2.96	4.97	6.83	*		-	
PLACE1005851	49.92	45.46	36.8	28.76	36.45	21.25	9.27	9.06	15.36		**		-
PLACE1005856	9.13	9.45	9.68	4.42	6.52	4.26	5.66	4.96	7.88	**	*	-	-
PLACE1005875	19.11	12.96	14.66	10.98	11.89	11.34	7.25	9.07	9.2		*		-
PLACE1005876	6.84	5.72	8.26	3.52	3.77	3.26	2.47	4.32	3	*	*	-	-
PLACE1005878	6.18	5.12	8.15	3.65	4.35	1.9	2.1	7.39	4.67				
PLACE1005880	10.13	10.1	15.44	15.29	7.51	5.59	11.17	12.56	8.92				
PLACE1005884	15.13	11.77	15.14	4.99	6.58	3.8	5.03	3.76	7.31	**	**	-	-
PLACE1005890	14.12	12.54	15.15	4.55	6.88	4.96	4.84	4.65	10.58	**	*	-	-
PLACE1005898	22.47	43.11	28.59	9.23	15.21	13.1	10.14	6.45	7.84	*	*	-	-
PLACE1005913	11.08	12.76	18.39	6.03	9.77	5.43	8.89	7.87	5.55				
PLACE1005921	38.7	26.83	45.11	14.95	20.53	13.93	14.46	15.3	19.69	*	*	-	-
PLACE1005923	35.55	28.6	35.14	8.99	9.9	10.33	7.55	9.92	9.16	**	**	-	-
PLACE1005926	9.28	6.52	9.69	4.22	6.79	3.62	4.36	4.97	3.85		*		-
PLACE1005927	8.32	7.66	16.91	2.68	3.86	2.87	2.78	4.08	4.5				
PLACE1005932	17.99	14.04	15.58	5.88	10.67	7.85	11.54	8.65	8.07	*	*	-	-
PLACE1005934	7.56	7.52	8.85	2.45	3.18	2.78	2.65	3.47	4.68	**	**	-	-
PLACE1005936	8.91	7.48	10.96	2.6	4	2.78	2.64	2.57	2.62	**	**	-	-
PLACE1005939	14.59	14.49	13.88	5.4	8.87	6.89	7.24	6.14	6.85	**	**	-	-
PLACE1005951	184.11	138.22	202.24	63.95	124.2	100.53	163.66	124.76	76.11	*		-	
PLACE1005953	4.12	2.98	5.89	2.81	3.65	1.89	1.88	2.73	1.8				
PLACE1005955	147.21	90.51	163.74	157.35	162.66	147.78	83.65	73.22	67.87				
PLACE1005966	21.58	17.57	18.88	12.22	12.03	11.48	18.97	16.95	19.33	**		-	
PLACE1005968	7.85	6.96	6.59	3.18	3.12	3.27	2.21	3.25	2.08	**	**	-	-
PLACE1005975	6.58	6.62	8.7	2.59	2.3	2.44	2.13	2.22	2.24	**	**	-	-
PLACE1005990	13.31	13.53	10.46	5.9	8.19	4.45	5.05	6.3	5.08	*	**	-	-
PLACE1005997	11.27	8.34	8.61	3.34	7.86	4.32	3.83	4.17	2.65		**		-
PLACE1006002	7.2	9.3	8.62	4.13	3.01	2.96	3.03	3.74	3.08	**	**	-	-
PLACE1006003	19.13	15.27	13.68	6.84	9.41	7.04	14.37	14.53	15.21	*		-	
PLACE1006011	14.53	12.13	13.55	5.17	8.37	6.39	12.92	13.32	12.8	**		-	
PLACE1006017	17.66	15.33	13.64	7.8	6.85	7.26	3.44	3.4	5.68	**	**	-	-
PLACE1006037	19.54	15.54	16.94	5.06	9.69	7.93	15.52	15.45	11.65	**		-	
PLACE1006040	21.73	18.19	20.02	8.22	10.07	7.19	9.12	8.1	8.15	**	**	-	-
PLACE1006063	18.04	22.51	29.29	15.12	25.84	15.72	12.74	9.35	9.64		*		-
PLACE1006071	24.45	22.47	19.59	9.7	14.01	7.6	15.44	10.65	16.68	**	*	-	-
PLACE1006073	38.01	25.19	30.05	16.58	19.75	14.04	20.88	12.98	14.52	*	*	-	-
PLACE1006074	21.69	19.68	21.99	13.65	9.89	8.37	10.34	8.49	11.16	**	**	-	-
PLACE1006076	6.98	23.32	28.44	3.28	24.98	6.58	8.27	11.5	12.4				
PLACE1006079	5.36	7.59	6.02	3.43	3.4	2.8	2.82	1.59	5.77	*		-	
PLACE1006093	17.29	20.55	15.5	11.28	11.48	8.91	6.51	3.34	7.24	*	**	-	-
PLACE1006116	6.66	4.88	6.43	2.05	2.48	1.97	3.15	0.18	1.1	**	*	-	-
PLACE1006119	9.01	6.23	8.79	2.16	3.34	2.75	3.83	1.45	4.03	**	*	-	-
PLACE1006129	11.8	19.99	13.49	6.74	8.91	6.37	6.93	6.6	9.52	*	*	-	-
PLACE1006139	11.03	9.2	11	5.5	4.05	3.54	5.37	5.2	8.18	**	*	-	-
PLACE1006143	34.11	32.02	23.21	13.95	17.22	16.38	5.72	10.56	8.1	*	**	-	-
PLACE1006157	20.08	16.11	21.21	6.21	8	10.58	9.26	6.55	9.67	**	**	-	-
PLACE1006159	22.74	19.17	16.53	5.42	7.39	5.18	11.09	3.24	9.93	**	*	-	-
PLACE1006164	10.4	12.06	12.25	3.81	6.89	2.98	4.98	2.08	3.84	**	**	-	-
PLACE1006167	150.43	130.54	128	105.79	82.45	55.54	118.18	93.17	93.5	*	*	-	-
PLACE1006170	12.04	9.61	11.88	3.48	3.73	3.68	2.75	2.82	3.04	**	**	-	-
PLACE1006181	14.32	10.9	10.36	5.74	6.23	4.42	6.29	2.91	4.76	**	*	-	-
PLACE1006187	23.98	21.9	19.46	7.26	12.29	5.92	18.37	17.04	21.06	**		-	
PLACE1006195	27.43	19.87	20.2	13.18	6.92	6.66	10.17	6.16	5.89	*	**	-	-
PLACE1006196	14.88	10.51	8.01	6.22	7.31	2.89	4.66	4.93	4.37		*		-
PLACE1006197	25.54	27.48	23.66	11.8	19.78	16.24	17.7	18.29	21.21	*	*	-	-
PLACE1006198	12.15	16.37	13.46	4.05	5.5	3.12	5.11	3.17	4.8	**	**	-	-
PLACE1006205	8.36	7.44	9.1	4.62	5.35	3.49	12.53	5	7.53	**		-	
PLACE1006208	10.95	10.22	9.53	5.04	9.25	5.28	4.47	4.13	4.33		**		-

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Table 481

PLACE1006211	18.15	19.46	15.85	7.8	6.56	8.15	10.56	8.16	8.98	**	**	-	-
PLACE1006219	29.22	24.03	22.82	13.99	7.2	9.8	23.91	20.19	22.03	**		-	
PLACE1006223	33.12	26.98	22.85	14.69	11.86	8.81	23.65	22.74	28.77	**		-	
PLACE1006225	9.38	7.86	6.1	4.18	4.91	3.81	6.34	5.77	7.67	*		-	
PLACE1006236	23.05	26.18	25.58	13.5	14.02	10.31	12.5	8.37	11.47	**	**	-	-
PLACE1006239	7.77	5.03	5	2.21	3.14	2.06	2.98	3.13	3.81	*		-	
PLACE1006245	11.97	10.97	10.73	4.72	5.26	4.25	5.6	4.62	4.52	**	**	-	-
PLACE1006246	14.07	10.52	9.12	4.17	12.12	4.44	10.44	8.15	11.84				
PLACE1006248	10.3	9.17	8.56	6.54	7.06	2.85	7.67	4.65	5.48		*		-
PLACE1006262	19.08	26.43	25.66	10.77	26.8	17.9	14.07	10.91	15.08		*		-
PLACE1006269	6.36	4.8	5.62	2.78	2.48	2.42	4.23	3.67	2.13	**	*	-	-
PLACE1006275	7.84	6.83	8.11	7.79	9.46	8.46	5.82	11.38	4.94				
PLACE1006277	18.16	15.2	14.15	12.95	19.65	15.77	6.69	13.62	7.81				
PLACE1006288	23.16	25	24.73	14.26	21	15.27	15.12	19.66	20.01	*	*	-	-
PLACE1006290	3.79	4.35	4.22	1.07	3.07	1.54	0.76	2.83	1.89	*	*	-	-
PLACE1006298	31.99	33.57	40.35	21.62	22.17	18.83	30.18	26.42	31.31	**		-	
PLACE1006311	24.06	25.54	26.15	17.19	20.35	18.67	6.49	6.41	12.35	**	**	-	-
PLACE1006318	23.92	22.31	22.74	9.17	11.04	10.73	16.57	17.39	15.35	**	**	-	-
PLACE1006325	10.97	6.18	13.93	5.64	5.43	6.48	6.34	4.38	3.68				
PLACE1006331	322.49	249.29	312.14	284.34	344.95	317.78	261.41	376.24	167.86				
PLACE1006335	6.01	6.97	9.42	6.43	10.77	6.27	4.79	4.63	3.75		*		-
PLACE1006357	23.6	23.65	28.41	15.45	19.92	11.71	10.11	13.97	13.07	*	**	-	-
PLACE1006360	39.03	55.89	60.83	32.56	29.33	36.42	18.81	22.42	24.3		*		-
PLACE1006364	4.49	3.79	4.52	5.2	5.32	3.04	3.31	4.72	3.85				
PLACE1006365	8.87	13.33	7.94	4.35	7.31	4.11	4.93	6.19	6.08				
PLACE1006368	7.6	5	7.22	4.35	3.51	2.72	3.12	4.28	3.68	*	*	-	-
PLACE1006371	12.84	8.89	13.13	6.85	5.51	3.89	5.93	6.19	7.36	*	*	-	-
PLACE1006373	31.88	31.57	27.89	11.44	15.9	12.05	24.23	17.9	24.85	**	*	-	-
PLACE1006382	15.81	18.11	17.64	20.83	24.97	21.9	28.68	49.67	48.66	*	*	+	+
PLACE1006385	23.74	24.67	19.54	18.57	28.47	23.59	6.72	12.92	8.24		**		-
PLACE1006391	7.09	8.24	10.32	5.76	7.9	5.35	7.26	7.31	6.16				
PLACE1006412	14.35	15.98	15.55	14.85	16.87	8.6	8.42	8.73	11.54		**		-
PLACE1006414	30.64	63.89	32.69	29.17	49.53	18.72	7.89	13.37	10.44		*		-
PLACE1006419	23.86	16.38	19.21	8.14	10.82	5.22	6.84	8.36	7.76	*	**	-	-
PLACE1006438	16.88	12.75	13.77	5.93	7.83	5.98	6.47	9.15	5.41	**	*	-	-
PLACE1006443	7.62	8.28	7.5	4.32	3.07	4.42	2.72	3.77	2.68	**	**	-	-
PLACE1006445	53.01	52.47	65.34	48.09	51.7	50.7	24.1	26.92	30.98		**		-
PLACE1006447	16.45	17.73	17.35	9.64	12.61	9.03	5.67	7.16	5.82	**	**	-	-
PLACE1006466	5.01	5.76	10.4	3.6	5.26	3.03	3.62	2.47	3.82				
PLACE1006469	9.97	6.93	12.7	4.45	5.94	2.99	6.14	5.96	3.89	*		-	
PLACE1006470	14.91	13.1	13.03	5.44	14.24	9.05	12.65	15.12	16.52				
PLACE1006472	32.56	24.9	52.53	14.86	22.47	15.58	27.13	60.66	18.13				
PLACE1006476	75.24	88.04	95	49.93	69.66	43.58	73.04	95.42	77.62	*		-	
PLACE1006482	19.52	14.87	22.77	7.46	8.75	5.8	9.29	24.88	15.09	**		-	
PLACE1006488	13.42	9.61	14.11	5.93	5.56	7.22	5.43	7.77	6	*	*	-	-
PLACE1006492	53.41	60.91	65.09	29.78	38.14	28.4	41.31	52.42	43.57	**	*	-	-
PLACE1006506	8.93	8.04	10.96	3.97	6.16	3.99	2.77	5.01	4.34	*	**	-	-
PLACE1006515	6.57	6.17	10.41	2.69	4.8	3.13	3.49	3.57	2.51	*	*	-	-
PLACE1006516	7.77	7.4	8.18	2.65	6.76	3.8	4.8	4.81	1.69		*		-
PLACE1006520	85.74	60.72	84.5	67.76	73.09	68.07	40.48	30.38	37.31		**		-
PLACE1006521	5.4	3.13	7.19	3.67	3.58	2.13	2.56	2.69	1.53				
PLACE1006529	21.37	16.93	24.45	11.55	12.23	11.32	13.1	15.15	16.91	*		-	
PLACE1006531	8.98	4.63	8.46	3.15	2.87	3.1	2.57	4.69	2.69	*		-	
PLACE1006534	11.34	12.38	19.26	6.83	8.12	7.2	8.08	5.98	8.82				
PLACE1006540	17.3	13.48	19.89	6	9.01	6.33	5.04	4.77	5.56	**	**	-	-
PLACE1006549	57.43	76.29	59.13	33.67	55.25	39.07	49.85	36.47	56.34				
PLACE1006550	27.31	23.34	17.69	10.6	24.86	11.76	7.55	11.98	6.46		*		-
PLACE1006552	41.43	35.42	38.21	18.37	17.9	12.42	28.67	34.48	34.92	**		-	
PLACE1006557	58.91	37.26	57.05	36.71	38.26	34.22	31.47	33.21	28.65		*		-
PLACE1006563	12.53	9.16	14.73	7.21	10.95	7.06	5.43	4.33	7.28		*		-
PLACE1006579	8.16	5.5	6.78	3.56	3.74	3.1	2.74	1.94	3.28	*	**	-	-
PLACE1006594	8.47	4.75	7.36	2.29	3.19	1.42	2.51	1.45	1.95	*	*	-	-
PLACE1006598	14.33	13.22	15.98	9.86	13.18	9.6	7.97	4.5	6.78		**		-
PLACE1006607	18.95	13.98	15.61	10.13	11.36	9.36	8.88	8.34	9.06	*	**	-	-

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Table 482

PLACE1006610	9.23	9.13	6.93	3.56	3.78	2.24	3.21	1.79	1.8	**	**	-	-
PLACE1006615	5.13	4.58	7.74	3.54	4.24	3.19	3.42	3.13	4.2				
PLACE1006617	10.84	9.51	10.64	5.44	6.44	4.54	8.05	7.55	8.94	**	*	-	-
PLACE1006618	16.8	17.21	17.66	12.4	9.99	12.65	9.96	9.85	12.85	**	**	-	-
PLACE1006626	9.9	9.38	11.8	4.89	3.64	3.15	3.8	3.9	3.22	**	**	-	-
PLACE1006629	97.87	77.5	62.9	75.16	89.13	71.45	50.39	46.85	45		*		-
PLACE1006637	20.62	30.53	27.31	15.03	24.3	12.77	12.77	11.41	9.09		**		-
PLACE1006640	146.09	116.55	121.62	98.73	144.79	100.95	65.85	61.12	81.72		**		-
PLACE1006644	10.36	13.76	11.01	6.08	7.62	8.85	6.47	3.27	4.59	*	**	-	-
PLACE1006657	9.47	8.7	8.11	3.37	3.88	4.59	4.46	4.41	6.15	**	**	-	-
PLACE1006673	128.37	101.12	117.47	60.38	47.28	69.57	78.35	78.65	91.83	**	*	-	-
PLACE1006678	13.14	7.54	6.57	3.78	6.24	6.14	3.95	3.22	3.7				
PLACE1006682	5.12	3.88	4.9	2.21	2.14	1.84	2.5	1.43	2.09	**	**	-	-
PLACE1006684	8.48	6.37	7.5	1.9	2.47	2.03	3.67	2.97	2.03	**	**	-	-
PLACE1006698	24.65	21.3	17.88	6.94	8.35	11.27	7.31	3.9	5.72	**	**	-	-
PLACE1006704	10.75	10.1	9.67	7.04	6.45	4.58	4.88	2.24	3.52	**	**	-	-
PLACE1006708	6.82	6.62	4.54	1.43	4.58	2.49	4.44	1.95	2.6		*		-
PLACE1006711	7.97	5.26	8.07	5.12	5.44	5.92	5.18	4.48	3.42				
PLACE1006714	19.78	16.32	14.11	6.39	7.42	10.52	4.46	5.02	4.69	*	**	-	-
PLACE1006716	21.34	19.47	16.01	5.39	7.72	5.97	12.01	9.74	13.28	**	*	-	-
PLACE1006731	8.76	6.59	9.88	4.19	4.28	3.45	3.4	4.54	3.95	*	*	-	-
PLACE1006754	12.83	10.26	11.39	6.83	5.2	6.24	8.13	4.13	6.6	**	*	-	-
PLACE1006760	17.66	24.39	15.04	22.5	23.46	11.75	21.46	9.03	14.39				
PLACE1006779	14.53	14.99	8.23	6.82	4.21	3.38	5.07	3.29	2.36	*	*	-	-
PLACE1006782	13.34	14.85	8.6	8.19	13.03	7.71	10.87	6.95	6.98				
PLACE1006783	26.1	20.43	20.94	18.8	23.33	15.04	25.48	18.52	26.77				
PLACE1006786	16.5	11.01	11.97	10.81	6.14	7.77	7.76	8.87	8.16		*		-
PLACE1006792	43	29.6	28.89	12.14	32.07	8.88	14.31	11.42	11.6		*		-
PLACE1006795	6.46	5.54	6.42	3.27	4.53	2.37	5.98	1.9	3.55	*		-	
PLACE1006800	14.69	12.26	14.82	7.42	7.86	5.36	11.02	8.63	12.6	**		-	
PLACE1006805	297.4	379.55	330.72	251.58	242.8	138.41	164.1	78.29	121.42	*	**	-	-
PLACE1006809	17.57	15.02	14.01	6.89	5.54	5.55	12.59	5.67	9	**	*	-	-
PLACE1006815	36.78	37.15	24.97	22.04	27.53	19.08	12.45	10.62	14.81		**		-
PLACE1006819	8.55	8.96	7.82	3.54	3.27	1.58	3.56	2.07	3.34	**	**	-	-
PLACE1006820	11.34	11.23	10.69	7.26	7.6	3.88	6.72	6.8	7.48	*	**	-	-
PLACE1006826	11.68	10.21	8.37	4.26	6.11	3.55	4	5.42	6.14	*	*	-	-
PLACE1006829	8.66	7.12	6.95	4.95	4.5	3.35	3.73	4.63	3.79	*	**	-	-
PLACE1006853	7.76	9.04	10.06	4.43	5.8	3.94	5.55	3.81	3.65	**	**	-	-
PLACE1006860	13.3	14.13	11.82	7.29	7.57	5.64	7.39	5.43	7.17	**	**	-	-
PLACE1006867	20.52	19.65	17.03	7.58	12.2	4.52	8.89	4.5	9.57	*	**	-	-
PLACE1006875	6.86	5.29	3.98	1.69	3.85	1.95	4.64	3.37	3.97	*		-	
PLACE1006878	5.96	7.5	9.4	3.45	4.02	4.56	4.29	5.32	7.08	*		-	
PLACE1006883	17.58	24.05	25.14	11.43	14.88	9.68	8.41	13.21	13.16	*	*	-	-
PLACE1006898	34.11	35.72	38.43	15.89	26.64	17.27	29.81	38.71	32.24	*		-	
PLACE1006901	35.59	25.34	29.52	17.57	24.59	23.14	7.06	14.35	10.26		**		-
PLACE1006904	283.91	237.86	265.1	210.53	264.05	203.01	176.62	324.88	215.9				
PLACE1006917	8.87	8.87	10.42	4.77	9.67	4.27	2.96	3.43	5.44		**		-
PLACE1006932	13.9	19.05	15.16	17.43	14.76	12.47	12.23	11.92	6.34				
PLACE1006935	5.15	5.68	5.5	4.25	5.6	3.94	4.66	3.59	4.94				
PLACE1006956	73	65.43	79.54	37.1	42.04	37.7	45.33	35.06	47.75	**	**	-	-
PLACE1006958	14.71	17.1	17.16	7.75	10.57	5.67	10.62	14.42	12.92	**		-	
PLACE1006959	6.43	6.88	7.06	3.86	5.4	3.09	3.53	7.7	6.81	*		-	
PLACE1006961	11.78	13.88	26.99	6.58	7.47	6.43	7.89	10.93	8.94				
PLACE1006962	8.5	7.71	10.43	6.5	8.54	6.61	4.94	6	6.79		*		-
PLACE1006966	30.69	63.35	44.81	30.7	31	25.61	17.51	20.36	25.7				
PLACE1006979	9.85	10.88	9.97	5.88	6.1	5.13	5.32	5.52	6.47	**	**	-	-
PLACE1006989	23.14	43.35	32.93	27.05	47.4	17.28	23.49	21.59	16.62				
PLACE1007001	14.41	12.66	17.15	10.97	5.54	6.74	6.74	7.87	8.22	*	**	-	-
PLACE1007014	9.24	9.35	10.83	6.4	6.04	5.94	4.96	6.16	5.52	**	**	-	-
PLACE1007021	56.53	38.34	63.46	20.03	40.71	38.97	20.72	29.77	27.88		*		-
PLACE1007026	65.54	56.8	77.56	57.55	60.7	57.93	57.5	56.64	67.29				
PLACE1007028	8.5	10.76	17.58	7.89	7.62	6.26	3.31	5.38	3.91		*		-
PLACE1007038	7.96	7.89	13.66	4.19	6.33	3.79	2.05	3.52	4.03		*		-
PLACE1007040	8.13	9.51	15.11	4.74	7.09	4.87	8.84	8.35	6.98				

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Table 483

PLACE1007045	15.78	21.85	22.19	13.09	30.39	13.83	9.78	12.74	10.75		*		-
PLACE1007048	19.3	14.44	24.23	9.41	10.57	11.83	9.91	12.06	15.93	*		-	
PLACE1007053	9.31	5.29	12.35	5.07	3.06	4.56	5.35	25.19	5.41				
PLACE1007068	8.67	4.77	10.34	5.02	4.28	3.54	2.63	5.02	2.74				
PLACE1007070	18.55	13.15	15.29	11.03	10.78	10.43	6.96	7.21	5.68	*	**	-	-
PLACE1007076	17.03	17.73	24.8	24.48	28.32	20.68	16.51	16.83	13.48				
PLACE1007077	7.35	10.92	12.26	4.54	5.11	3.6	6.43	5.8	5.66	*	*	-	-
PLACE1007081	41.36	35.79	51.18	37.04	46.87	29.31	28.18	20.46	26.31		*		-
PLACE1007082	14.74	14.27	12.93	7.51	10.12	5.83	13.51	10.86	10.42	*		-	
PLACE1007092	9.52	6.79	8.77	4.99	5.23	4.04	4.42	5.84	7.46	*		-	
PLACE1007096	8.7	7.04	11.33	3.9	6.35	2.61	4.31	10.62	7.33	*		-	
PLACE1007097	5.03	2.47	6.96	1.99	2.48	1.11	1.28	4.01	1.45				
PLACE1007099	14.43	9.17	8.68	4.57	6.07	4.14	4.7	5.17	7.04	*		-	
PLACE1007105	9.93	9.89	19.72	4.22	5.46	3.96	5.83	6.27	9.12				
PLACE1007108	7.87	5.2	13.72	3	3.64	1.32	1.96	5.82	6.69				
PLACE1007111	24.26	33.98	33.96	8.75	19.56	14.7	10.61	6.46	7.98	*	**	-	-
PLACE1007112	13.01	15.69	10.39	7.41	17.53	7.08	9.51	4.37	5.03		*		-
PLACE1007130	7.28	5.04	7.51	3.97	3.76	4.18	4.15	3.12	4.45	*	*	-	-
PLACE1007132	11.01	5.03	12.54	6.14	8.23	7.16	4.79	4.84	3.32				
PLACE1007140	8.1	6.86	9.35	5.74	3.15	5.4	5.1	3.71	4.08	*	*	-	-
PLACE1007143	7.85	4.78	7.3	2.76	4.42	3.52	3.05	2.29	1.7	*	*	-	-
PLACE1007169	21.25	20.42	20.37	9.68	16.47	8.01	13.15	12.99	9.63	*	**	-	-
PLACE1007178	5.69	6.23	10.18	2.7	4.22	2.51	2.33	2.04	2.65	*	*	-	-
PLACE1007190	9.72	11.86	11.22	5.23	6.85	7.11	6.69	5.59	16.1	**		-	
PLACE1007201	11.31	9.93	8.97	4.82	6.82	3.46	5.63	4.72	7.11	*	*	-	-
PLACE1007202	14.96	8.93	16.56	5.53	5.66	4.16	5.42	6.71	5.73	*	*	-	-
PLACE1007226	110.77	93.69	99.41	39.5	91.72	72.21	82.39	66.08	68.98		*		-
PLACE1007238	53.4	44.43	54.82	32.05	30.06	27.04	24.59	23.68	27.03	**	**	-	-
PLACE1007239	22.01	21.57	16.94	9.88	9.77	7.42	7.13	6.76	5.92	**	**	-	-
PLACE1007242	8.39	6.41	6.58	2.97	3.53	2.45	2.76	1.3	1.2	**	**	-	-
PLACE1007243	51.6	47.43	46.65	38.48	53.48	36.76	30.03	24.3	28.99		**		-
PLACE1007247	13.13	15.22	14.84	6.24	10.32	8.42	5.62	3.59	3.12	*	**	-	-
PLACE1007257	10	9.05	8.75	2.44	7.1	2.96	4.72	2.48	2.64	*	**	-	-
PLACE1007274	7.6	6.25	7.77	4.39	3.79	3.63	3.01	2.85	2.82	**	**	-	-
PLACE1007276	4.51	6.36	6.4	3.01	2.72	2.17	2.35	3.34	6.03	**		-	
PLACE1007282	6.97	4.05	5.61	2.64	2.11	3.56	3.82	3.22	3.39	*		-	
PLACE1007286	11.57	9.64	10.32	4.04	6.1	5.17	5.17	3.51	3.72	**	**	-	-
PLACE1007296	16.68	11.68	9.05	4.46	6.87	6.7	3.08	3.72	1.93		*		-
PLACE1007301	14.64	13.62	12.24	3.61	5.07	2.97	5.09	2.86	3.16	**	**	-	-
PLACE1007314	9.78	10.14	10.9	5.59	4.99	2.5	3.88	2.16	3.2	**	**	-	-
PLACE1007317	8.02	7.14	6.45	3.78	5.35	2.25	2.6	5.13	4.46	*	*	-	-
PLACE1007329	6.93	6.45	9.13	3.46	3.47	2.66	3.68	2.3	2.77	**	**	-	-
PLACE1007338	57.3	54.81	50.58	25.62	27.62	24.63	49.58	43.5	58.48	**		-	
PLACE1007342	41.9	26.92	32.51	26.5	30.16	25.56	24.13	20.5	25.41				
PLACE1007345	5.67	4.07	4.44	3.74	2.2	1.81	1.89	2.39	3.75	*	*	-	-
PLACE1007346	20.5	15.07	16.53	8.68	6.27	3.82	4.58	3.48	4.29	**	**	-	-
PLACE1007359	41.26	41.58	38.73	21.16	26.14	23.96	27.05	27.12	33.74	**	**	-	-
PLACE1007367	8.65	8.31	7.96	1.51	3.49	1.31	3.83	1.42	3.11	**	**	-	-
PLACE1007375	12.55	10.83	9.7	1.39	5.63	1.68	2.54	2.85	2.14	**	**	-	-
PLACE1007377	6.98	4.2	6.44	4.26	4.62	2.93	3.59	4.11	3.58				
PLACE1007386	12.07	10.56	14.15	4.68	4.55	5.21	6.12	7.62	8.27	**	*	-	-
PLACE1007392	24.21	18.68	19.13	13.92	12.02	7.51	28.83	13.55	12.42	*		-	
PLACE1007402	16.76	19.32	15.87	8.17	8.78	7.34	11.49	10.03	10.79	**	**	-	-
PLACE1007409	9.51	9.82	11.04	5.11	5.51	7.23	4.08	2.01	3.77	**	**	-	-
PLACE1007416	22.54	28.88	22.62	18.84	13.11	6.16	9.22	5.36	7.49	*	**	-	-
PLACE1007420	14.67	16.22	16.74	8.73	9.19	6.79	10.55	5.47	7.91	**	**	-	-
PLACE1007431	28.03	25.88	21.18	15.73	16.55	11.3	26.89	15.55	26.27	*		-	
PLACE1007450	6.82	6.06	4.68	4.06	4.16	1.71	5.65	4.38	4.36				
PLACE1007452	14.4	7.71	4.99	5.04	6.12	1.89	4.23	8.8	6.06				
PLACE1007454	49.36	46.08	36.43	21.1	38.54	20.65	11.86	16.68	14.49		**		-
PLACE1007460	11.52	10.93	12.45	8.16	8.35	4.82	9.8	9.12	12.38	*		-	
PLACE1007478	12.6	13.38	10.86	4.17	8.16	7.05	7.4	4.59	6.97	*	**	-	-
PLACE1007484	10.71	6.45	6.68	3.65	4	2.5	4.9	2.97	5.47	*		-	
PLACE1007488	14.59	14.99	17.16	7.24	4.48	5.55	6.08	3.67	8.77	**	**	-	-

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Table 484

PLACE1007507	16.63	14.22	12.4	6.49	10.52	5.63	19.33	11.77	17.21	*		-	
PLACE1007511	13.25	11.24	10.12	3.93	3.98	2.6	3.01	2.43	4.23	**	**	-	-
PLACE1007513	4.53	2.47	3.69	3.11	1.64	1.97	3.06	2.87	2.04				
PLACE1007524	49.4	41.73	37.58	21.38	27.05	16.04	48.44	42.69	43.18	*		-	
PLACE1007525	7.48	5.19	4.73	2.29	4.06	1.12	3.74	3.09	4.25				
PLACE1007537	8.42	7.3	9.61	4.91	5.72	3.83	6.57	5.7	5.93	*	*	-	-
PLACE1007544	5.67	4.7	5.81	1.28	3.36	2.37	4.39	1.96	2.74	*	*	-	-
PLACE1007547	16.52	13.81	13.32	8.64	13.2	6.38	11.36	9.38	8.52		*		-
PLACE1007557	22.7	26.33	16.93	8.14	13.6	7.63	24.98	15.24	20.74	*		-	
PLACE1007560	25.9	29.34	29.57	9.23	13.41	19.28	21.02	29.63	20.17	*		-	
PLACE1007565	3.88	2.26	3.15	1.89	4.77	2.57	1.98	2.22	2.43				
PLACE1007580	4.59	3.09	5.83	2.2	6.97	1.42	1.87	5.45	1.54				
PLACE1007583	3.85	2.11	3.18	1.64	4.14	4.12	2.02	2.49	2.5				
PLACE1007591	5.53	6.61	10.65	2.9	4.26	2.95	4.34	4.96	5.37				
PLACE1007598	9.38	9.28	9	2.96	15.1	3.88	2.92	7.29	5.52		*		-
PLACE1007610	3.93	7.09	11.32	4.32	11.34	3.52	4.35	8.81	6.31				
PLACE1007618	4.85	4.13	5.18	3.66	4.39	5.01	3.62	3.16	4.04		*		-
PLACE1007621	20.28	8.69	15.56	6.24	12.9	7.98	10.43	10.06	8.81				
PLACE1007626	35.43	28.05	45.42	25.74	50.46	26.54	38.37	49.51	35.74				
PLACE1007632	8.18	6.61	8.24	5.02	13.18	12.74	5.22	7.37	5.53				
PLACE1007635	17.84	21.72	22.91	16.26	21.82	12.51	7.83	15.31	12.34		*		-
PLACE1007645	29.46	44.32	50.79	23.79	28.69	29.97	18.24	19.23	26.32		*		-
PLACE1007649	5.43	7.86	6.71	4.51	9.04	3.18	4.73	2.18	2.74		*		-
PLACE1007659	23.48	33.01	29.15	18.02	23.66	14.9	25	27.47	23.31				
PLACE1007669	17.27	10.25	11.99	6.18	6.01	5.07	11.02	11.92	11.97	*		-	
PLACE1007677	15.06	16.35	15.01	8.53	7.7	12.44	11.15	10.52	8.69	*	**	-	-
PLACE1007688	30.37	21.3	31.84	9.3	9.6	6.97	5.43	7.59	4.3	**	**	-	-
PLACE1007690	15.29	14.9	13.94	8.07	9.45	10.99	5.55	6.43	7.69	**	**	-	-
PLACE1007697	7.22	8.07	8.65	7.42	10.69	12.34	4.08	7.67	5.36				
PLACE1007702	9.68	16.27	14.18	8.71	12.06	12.61	6.79	7.15	7.48		*		-
PLACE1007706	14.91	16.84	14.3	10.72	14.81	6.93	5.13	7.31	8.61		**		-
PLACE1007725	15.22	10.08	11.32	8.01	8.72	6.5	4.92	7.04	8.09		*		-
PLACE1007729	9.62	8.04	8.37	6.72	6.7	9.05	5.49	8.22	6.25				
PLACE1007730	14.54	9.51	13.82	11.08	11.03	10.92	7.95	12.03	8.17				
PLACE1007737	26.23	17.29	21.46	12.32	15.98	9.58	13.89	16.95	16.37	*		-	
PLACE1007743	15.62	16.04	17.86	8.71	10.59	7.11	6.26	11.61	4.77	**	*	-	-
PLACE1007746	42.92	48.93	37.39	28.78	37.1	35.26	16.78	10.7	15.4		**		-
PLACE1007753	14.39	18.43	15.85	13.55	30.64	24.37	6.15	10.27	7.82		**		-
PLACE1007769	10.21	11.59	12.77	11.76	15.29	7.33	6.11	7.79	6.57		**		-
PLACE1007780	5.74	2.24	6.02	2.59	3.98	3.4	2.92	4.75	4.26				
PLACE1007791	7.33	7.57	11.32	6.64	9.26	5.56	5.87	21.8	5.42				
PLACE1007807	10.4	6.68	8.59	5.19	10.28	4.84	5.47	15.67	6.17				
PLACE1007810	21.71	5.64	13.76	5.45	11.67	20.68	5.72	5.81	5.21				
PLACE1007814	23.92	18.73	27.74	15.47	17.03	13.06	6.08	14.46	7.51	*	*	-	-
PLACE1007828	9.64	11.73	14.79	8.65	13.95	8.98	3.79	6.99	9.71				
PLACE1007829	21.85	26.65	22.58	10.61	17.88	12.23	16.05	20.8	14.7	*		-	
PLACE1007841	12.3	14.26	16.38	8.52	14.37	8.97	13.64	10.06	9.74				
PLACE1007842	7.29	10.66	10.16	4.04	8.15	4.63	12.33	6.69	8.73				
PLACE1007843	8.16	7.8	8.23	4.71	8.29	4.31	4.49	6.71	2.94		*		-
PLACE1007845	14.45	11.07	14.52	8.03	11	7.42	8.69	6.18	6.07	*	*	-	-
PLACE1007846	9.52	9.87	9.08	6.82	5.35	6.86	5.9	8.42	7.28	**	*	-	-
PLACE1007848	10.96	7.82	17.21	7.21	6.58	4.31	3.05	6.37	4.05				
PLACE1007852	38.45	42.72	20.94	14.02	16.83	14.13	8.86	9.78	9.37	*	*	-	-
PLACE1007858	19.55	23.44	22.4	13.38	19.15	12.06	12.86	10.77	11.27	*	**	-	-
PLACE1007866	106.06	120.7	80.75	100.84	136.45	101.33	115.22	114.23	135.63				
PLACE1007871	46.64	38.13	36.79	13.91	18.93	11.35	19.19	30.79	21.75	**	*	-	-
PLACE1007877	11.11	8.45	11.03	7.02	8.84	8.93	6.39	7.32	5.13		*		-
PLACE1007878	37.18	35.47	41.1	20.44	30.52	24.13	17.29	22.96	22.69	*	**	-	-
PLACE1007881	7.08	8.99	9.43	6.21	6.72	5.42	3.38	3.24	2.37	*	**	-	-
PLACE1007885	13.54	9.97	15.34	8.52	12.53	23.99	7.37	7.86	5.04		*		-
PLACE1007897	9.52	10.47	10.76	6.15	8.22	8.75	3.33	3.79	2.67	*	**	-	-
PLACE1007908	27.14	31.91	21.03	11.57	16.17	12.14	8.02	9.92	9.32	*	**	-	-
PLACE1007922	13.27	17.29	11.92	8.56	15.72	12.01	8.76	6.61	6.69		*		-
PLACE1007946	8.9	7.88	9.69	3.7	5.72	2.73	4.49	7.73	5.93	**		-	

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Table 485

PLACE1007950	123	99.57	90.18	75	73.07	58.93	91.95	114.45	65.58	*		-	
PLACE1007954	8.61	7.27	7.95	5.58	7.49	5.54	3.77	4.03	2.97		**		-
PLACE1007955	17.64	15.71	13.66	11.51	9.3	9.77	6.99	7.04	4.12	*	**	-	-
PLACE1007956	11.86	9.09	7.66	6.57	9.25	6.9	4.06	4.11	3.44		*		-
PLACE1007958	9.03	7.99	9.04	2.65	4.9	3.85	2.65	3.75	2.07	**	**	-	-
PLACE1007965	15.3	16.37	14.75	7.93	11.66	10.38	7.23	6.65	5.87	*	**	-	-
PLACE1007969	24.54	27.08	14.83	16.49	16.9	27.64	8.5	10.51	6.83		*		-
PLACE1007971	14.86	11.23	10.66	4.6	5.77	4.48	5.47	4.42	6.63	**	**	-	-
PLACE1007990	13.72	7.91	11.82	6.44	6.58	7.05	6.02	6.86	7.23				
PLACE1008000	8.41	4.96	5.71	4.66	6.7	5.87	3.52	3.67	3.05				
PLACE1008002	8.38	10.22	5.77	6.22	6.73	3.91	3.28	5.34	3.3		*		-
PLACE1008037	7.47	6.35	4.25	2.21	4.95	4.35	2.35	1.88	2.58		*		-
PLACE1008044	23.79	15.95	12.5	7.05	19.86	9.73	6.75	10	6.08				
PLACE1008045	19.99	21.06	9.24	5.88	14.67	9.04	6.52	7.55	2.12				
PLACE1008080	15.75	26.6	10.27	8.38	25.41	7.91	16.05	14.95	13.99				
PLACE1008092	7.67	5.27	5.41	3.04	5.53	3.46	4.86	3.3	3.17				
PLACE1008095	16.14	13.84	10.97	4.61	15.55	7.49	3.99	9.83	5.13		*		-
PLACE1008105	10.75	13.42	9.63	5.46	13.95	7.7	10.03	7.96	6.35				
PLACE1008107	6.1	7.51	5.49	4.1	6.68	4.81	2.94	3.48	3.2		**		-
PLACE1008111	12.94	8.4	7.21	4.85	8.37	6.82	4.56	1.47	2.41		*		-
PLACE1008113	48.12	32.36	36.95	30.18	28.53	18.75	11.39	9.55	15.2		**		-
PLACE1008122	12.52	11.61	10.25	6.59	8.27	7	4.17	3.46	4.27	**	**	-	-
PLACE1008129	12.19	11.22	9.29	6.85	14.96	11.14	8.9	8.46	6.51				
PLACE1008132	21.17	14.41	14.91	9.14	12.76	11.94	8.42	8.33	8.23		*		-
PLACE1008137	10.44	6.69	4.43	4.58	5.26	3.39	2.11	5.99	2.53				
PLACE1008174	12.98	8.11	5.85	5.98	7.01	8.19	6.41	5.88	5.58				
PLACE1008177	5.92	6.91	4.83	3.39	4.55	3.28	3.39	1.53	3.61	*	*	-	-
PLACE1008181	12.18	13.31	12.04	4.81	8.68	5.04	4.65	2.16	4.62	**	**	-	-
PLACE1008195	13.39	9.3	9.62	7.44	7.76	6.35	5.1	3.44	5.91		*		-
PLACE1008198	12.57	11.23	9.83	6.75	6.36	4.49	7.75	4.45	5.55	**	*	-	-
PLACE1008201	10.88	12.64	8.33	6.13	9.66	7.65	6.3	5.05	9.18				
PLACE1008209	10.96	9.72	8.1	4.34	4.16	5.71	10.15	7.4	9.7	**		-	
PLACE1008226	27.87	17.88	18.73	12.29	14.5	8.3	21.53	17.31	27.74				
PLACE1008227	19.93	14.99	13.17	9.05	11.55	7.15	13.25	11.51	13.73	*		-	
PLACE1008231	7.21	4.7	4.12	4.59	4.49	3.26	5.49	4.08	3.39				
PLACE1008238	12.79	18.51	15.04	5.47	8.57	11.49	6.6	7.97	4.88	*	**	-	-
PLACE1008244	10.53	9.75	8.28	4.31	8.05	4.21	4.37	5.37	5.5	*	**	-	-
PLACE1008249	15.98	17.02	8.54	6.34	10.36	6.43	17.75	4.65	8.03				
PLACE1008266	102.69	124.96	102.56	88.83	113.4	78.29	73.83	64.62	80.68		*		-
PLACE1008273	14.29	12.39	14.99	6.95	10.06	11.71	9.42	8.24	5.42		*		-
PLACE1008275	5.26	4.99	6.79	3.64	10.8	3.9	3.08	3.54	1.54		*		-
PLACE1008280	6.85	6.62	6.82	4.72	8.46	4.99	3.58	6.79	2.98				
PLACE1008282	12.89	9.41	16.7	11.11	18.66	13.55	5.47	11.9	7.88				
PLACE1008297	12.14	13.11	10.26	7.3	9.97	7.71	3.51	6.91	7.44	*	*	-	-
PLACE1008303	11.47	15.79	13.39	11.12	14.28	7.92	5.84	6.87	4.96		**		-
PLACE1008309	4.41	7.26	5.38	6.98	9.29	6.05	3.56	4.2	4.65				
PLACE1008315	19.59	15.1	15.12	9.86	9.1	7.96	7.41	8.94	11.54	**	*	-	-
PLACE1008329	9.22	7.92	9.32	5.09	12.42	9.18	10.32	5.48	5.2				
PLACE1008330	11.04	9.94	11.21	6.66	7.9	5.74	7.19	13.56	9.01	**		-	
PLACE1008331	9	15.63	14.68	4.1	11.97	13.67	4.88	7.64	5.55		*		-
PLACE1008351	12.84	22	18.28	7.61	13.2	12.68	4.26	8.16	3.26		*		-
PLACE1008356	13.82	13.87	16.44	11.31	18.42	14.21	4.74	8.97	9.76		*		-
PLACE1008359	10.61	8.67	5.76	4.5	6.41	4.58	3.38	3.42	3.83		*		-
PLACE1008368	15.16	18.55	16.33	11.79	13.53	6.82	4.87	5.65	5.64		**		-
PLACE1008369	3.81	2.08	4.52	1.83	1.71	1.5	2.12	2.77	3.86				
PLACE1008392	11.15	8.41	9.64	4.52	7.73	5.42	7.63	11.47	6.48	*		-	
PLACE1008394	11.83	9.98	11.91	7.27	9.44	5.81	12.55	9.98	4.42	*		-	
PLACE1008398	23.83	19.35	38.34	11.94	10.53	17.6	18.05	34.01	14.62				
PLACE1008401	9.05	11.72	16.92	8.36	9.24	6.49	5.59	6.98	7.72				
PLACE1008402	8.61	13.91	16.2	7.29	15.86	9.77	4.08	3.77	5.17		*		-
PLACE1008405	93.35	102.54	109	58.1	65.02	51.5	64.76	63.76	63.34	**	**	-	-
PLACE1008408	9.15	10.93	10.45	7.65	10.56	6.32	5.13	6.5	6.16		**		-
PLACE1008420	4.6	3.84	4.48	2.08	3.3	3.48	3.03	3.37	1.89		*		-
PLACE1008424	8.77	7.89	8.59	4.05	4.03	4.43	4.27	11.48	5.37	**		-	

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Table 486

PLACE1008426	9.02	4.49	7.91	3	6.94	4.35	2.2	4.69	5.02				
PLACE1008429	6.72	4.48	8.18	2.61	5.16	2.94	4.14	3.81	3.51				
PLACE1008430	14.21	10.67	13.56	6.18	13.27	13.78	7.02	13.13	6.7				
PLACE1008437	10.05	12.15	13.23	7.3	7.15	7.37	5.37	12.87	6.94	**		-	
PLACE1008453	9.93	7.46	12.22	2.24	6.5	5.48	4.46	4.26	3.11		*		-
PLACE1008454	21.6	22.78	23.98	10.1	17.4	10.34	15.68	15.08	11.82	*	**	-	-
PLACE1008455	34.62	30.32	25.55	12.02	19.33	14.29	16.61	22	23.57	*	*	-	-
PLACE1008457	11.67	8.98	10.52	6.51	8.83	5.84	9.41	9.29	9.88	*		-	
PLACE1008465	7.78	1.83	9.65	2.4	6.54	3.49	3.66	7.05	5.33				
PLACE1008469	9.74	7.14	10.33	5.36	5.23	4.43	4.05	9.23	7.36	*		-	
PLACE1008488	7.69	9.06	16.27	2.87	27.47	11.79	3.3	10.09	3.95				
PLACE1008519	13.67	13.58	16.65	12.54	13.83	10.17	7.48	12.69	9.26				
PLACE1008524	16.01	17.28	16.34	7.24	7.92	7.96	6.91	6.21	5.65	**	**	-	-
PLACE1008531	10.83	9.9	10.84	3.6	7.89	4.88	5.5	5.84	4.3	*	**	-	-
PLACE1008532	31.22	27.65	29.16	13.43	17.17	10.64	20	23.65	23.08	**	**	-	-
PLACE1008533	16.83	14.02	15.02	5.15	9.56	6.45	8.04	10.1	5.87	**	**	-	-
PLACE1008542	11.05	6.89	12.38	7.62	8.01	5.5	3.52	4.43	4.89		*		-
PLACE1008549	8.08	8.32	6.56	2.76	4.31	2.64	3.19	4.98	1.09	**	*	-	-
PLACE1008560	9.22	6.82	8.11	4.41	4.7	3.86	2.93	3	1.98	**	**	-	-
PLACE1008567	12.46	12.8	11.19	3	4.87	3.76	6.88	4.77	3.6	**	**	-	-
PLACE1008568	11.23	14.36	12.98	7.02	10.07	9.2	4.7	4.88	4.71	*	**	-	-
PLACE1008569	26.76	24.83	18.12	14.19	21.2	18.33	7.27	6.81	8.32		**		-
PLACE1008584	12.08	11.9	8.94	4.22	7.86	8.69	3.89	8.17	12.55				
PLACE1008585	31.41	26.84	21.37	12.16	16.5	14.29	13.28	12.03	8.95	*	**	-	-
PLACE1008603	88.44	58.86	85.85	77.22	107.17	81.02	46.69	50.43	38.76		*		-
PLACE1008621	8.51	5.24	9.31	3.02	5.85	4.1	5.45	4.49	4.31				
PLACE1008625	5.93	4.92	6	3.54	3.65	3.16	1.59	3.39	1.97	**	**	-	-
PLACE1008626	7.17	7.14	8.41	4.47	6	4.22	1.34	2.51	2.04	*	**	-	-
PLACE1008627	16.63	17.04	15.47	5.85	10.41	6.49	6.26	6.1	3.78	**	**	-	-
PLACE1008629	17.85	11.92	13.81	7.55	20.73	20.07	19.18	21.96	10.11				
PLACE1008630	10.34	9.61	9.25	3.39	5.31	3.93	4.34	4.76	3.98	**	**	-	-
PLACE1008643	13.74	8.06	11.06	4.37	9.48	6.43	6.52	10.46	6.53				
PLACE1008650	8.08	8.41	6.76	5.59	6.65	6.55	3.49	3.07	2.46		**		-
PLACE1008657	20.07	16.69	13.65	10.15	11.39	11.63	13.41	12.65	11.83	*		-	
PLACE1008664	16.27	13.14	9.24	7.33	8.26	11.12	3.83	4.48	3.67		*		-
PLACE1008693	19.24	12.55	11.48	5.9	7.48	8.22	10.23	10.76	7.26	*		-	
PLACE1008696	15.27	18.92	13.52	8.56	14.35	6	9.09	6.63	6.3		**		-
PLACE1008715	12.07	13.35	10.97	4.79	8.42	4.36	3.79	3.86	5.13	*	**	-	-
PLACE1008716	9.95	8.16	6.63	2.27	4.4	4.51	4.19	6.11	4.54	*	*	-	-
PLACE1008722	23.06	17.9	16.82	6.63	6.45	7.4	2.92	4.69	5.05	**	**	-	-
PLACE1008738	22.32	18.29	21.17	13.47	19.87	5.51	15.63	19.57	23.28				
PLACE1008742	84.96	67.74	75.79	53.3	53.65	55.26	60.09	57.16	55.95	*	*	-	-
PLACE1008744	16.51	21.18	12.37	7.32	20.16	7.33	4.32	8.49	4.3		*		-
PLACE1008748	11.7	8.68	7.89	3.6	3.19	1.95	5.93	2.92	4.46	**	*	-	-
PLACE1008757	11.86	10.89	13.3	7.9	13.9	4.82	5.45	7.52	5.79		**		-
PLACE1008766	12.58	9.83	17.07	7.19	5.62	5.22	3.78	3.59	4.47	*	*	-	-
PLACE1008785	10.19	7.64	9.9	4.61	6.56	4.55	5.8	6.94	7.6	*		-	
PLACE1008790	13.83	10.34	7.68	5.61	9.25	7.49	3.5	9.44	5.2				
PLACE1008798	38.56	17.87	28.15	8.39	18.4	13.81	20.54	7.92	18.2				
PLACE1008807	7.39	8.08	6.82	3.5	7.56	4.57	3.41	3.26	4.62		**		-
PLACE1008808	14.69	14.79	11.52	7.99	7.57	5.08	6.28	4.51	3.87	**	**	-	-
PLACE1008813	11.75	10.29	9.69	7.89	7.9	5.45	5.57	3.03	5.81	*	**	-	-
PLACE1008836	10.67	11.89	10.55	6.13	6.4	5.79	6.93	5.51	7.49	**	**	-	-
PLACE1008851	17.38	11.13	11	56.43	9.1	6.6	16.91	8.29	14.77				
PLACE1008854	6.2	6.11	5.28	5.3	4.42	2.5	6.46	5.33	5.1				
PLACE1008864	19.27	13.51	11	10.42	10.96	6.46	14.43	10.21	14.23				
PLACE1008867	23.06	15	11.22	6.2	9.84	4.86	5.54	7.61	6.44		*		-
PLACE1008876	176.15	214.21	204.76	126.27	307.85	120.09	159.59	163.82	275.73				
PLACE1008887	10.24	8.9	12.49	4.83	6.78	7.76	5.17	4.7	6.53	*	*	-	-
PLACE1008902	13.44	7.31	7.6	4.55	6.21	3.19	5.49	3.64	7.36				
PLACE1008911	20.57	23.29	15.12	14.15	10.76	7.02	9.39	4.72	9.35	*	*	-	-
PLACE1008917	7.8	5.68	7.21	2.11	3.42	3.23	3.5	4.03	3.26	**	**	-	-
PLACE1008920	3.68	3.98	2.25	1.85	2.38	2.78	2.45	2.52	1.03				
PLACE1008925	6.03	2.49	3.19	2.51	4.89	2.3	3.22	3.16	2.76				

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Table 487

PLACE1008930	19.58	15.04	12.13	4.18	13.75	5.17	6.22	5.55	4.1		*		-
PLACE1008934	16.24	5.52	7.38	4.49	6.52	4.37	6.49	7.37	5.19				
PLACE1008941	7.73	6.12	5.84	2.96	5.21	1.59	3.04	3.68	3.45		**		-
PLACE1008947	14.65	13.48	10.43	5.14	6.75	4.89	11.51	10.32	9.84	**		-	
PLACE1008984	13.25	12.98	9.34	5.45	4.62	4.47	6.01	1.98	3.15	**	**	-	-
PLACE1008985	7.07	4.44	3.91	3.08	5.06	1.59	3.53	4.2	7.06				
PLACE1008994	3.13	3.32	2.46	1.43	1.88	1.44	1.4	0.58	1.95	**	*	-	-
PLACE1009020	10.8	10.64	11.79	9.97	10.93	10.07	6.16	7.97	6.48		**		-
PLACE1009027	3.76	1.41	3.27	1.39	2.64	1.03	1.54	3.8	0.71				
PLACE1009039	4.77	3.08	3.94	1.85	3.67	1.57	1.09	2.8	1.86		*		-
PLACE1009045	8.82	6.04	9.52	3.29	4.82	2.76	2.8	7.24	2.61	*		-	
PLACE1009048	2.06	2.51	4.63	1.04	3.38	1.38	0.62	1.42	2.18				
PLACE1009050	3.79	3.3	4.62	1.78	8.12	1.71	2.85	3.16	1.84				
PLACE1009060	19.41	22.53	16.93	15.31	14.46	12.87	9.32	9.93	14.15	*	*	-	-
PLACE1009067	9.68	7.46	10.13	4.56	10.58	6.42	9.09	6.46	12.36				
PLACE1009071	20.58	20.38	20.82	12.02	12.73	10.86	11.69	13.76	13.78	**	**	-	-
PLACE1009090	9.2	7.98	10.33	4.26	8.7	11	5.63	8.05	9.63				
PLACE1009091	83.22	75.58	81.93	64.69	72.29	69.99	50.11	57.74	52.35	*	**	-	-
PLACE1009094	10.97	9.99	9.32	7.26	14.47	8.52	5.42	12.88	9.03				
PLACE1009099	8.3	10.72	9.62	5.36	7.81	7.04	3.55	4.21	4.97	*	**	-	-
PLACE1009110	7.1	4.33	5.05	4.77	6.82	3.04	3.19	5.04	4.48				
PLACE1009111	4.96	7.16	3.67	5.5	7.31	3.03	4.35	3.44	4.4				
PLACE1009113	16.47	13.6	10.85	8.16	11.25	17.03	7.41	8	12.76				
PLACE1009130	13.26	8.46	18.05	9.61	8.47	7.77	7.71	8.47	5.51				-
PLACE1009150	9.24	9.08	10.56	5.69	8.31	5.53	5.87	7.76	4.55	*	*	-	-
PLACE1009155	15.03	18.94	19.94	9.19	13.17	10.27	14.29	28.01	20.9	*		-	
PLACE1009158	11.31	7.28	10.08	9.16	8.65	7.93	4.47	5.84	5.53		*		-
PLACE1009166	6.72	5.63	9.02	5.97	6.75	3.86	4.53	5.03	5.29				
PLACE1009172	12.12	10.58	13.44	7.25	11.43	5.16	4.32	7.13	6.22		**		-
PLACE1009174	15.11	18.12	12.65	13.74	20.86	11.26	7.87	11.41	11.21				
PLACE1009183	26.21	21.05	18.45	14.71	13.12	9.63	13.01	10.13	17.14	*		-	
PLACE1009186	16.33	12.69	14.24	9.34	9.66	8.31	3.27	14.09	4.74	**		-	
PLACE1009190	10.56	9.79	11.19	7.65	14.06	8.19	4	6.56	7.14		*		-
PLACE1009196	13.22	10.75	11.8	7.38	9.71	7.53	10.55	12.57	8.91	*		-	
PLACE1009200	19.33	23.87	22.95	10.45	11.73	10.18	10.96	16.99	17.03	**	*	-	-
PLACE1009217	14.13	24.09	16.64	11.71	10.57	10.58	3.82	4.64	6.12		*		-
PLACE1009230	27.31	26.63	32.64	10.81	26.12	18.34	16.83	20.7	24.31		*		-
PLACE1009236	9.03	10.62	12.67	7.18	9.87	8.71	6.77	9.24	7.63				
PLACE1009246	21.48	34.44	20.99	9.29	20.22	19.2	9.84	35.09	13.46				
PLACE1009265	18.86	26.11	25.51	7.08	18.04	9.4	9.34	41.89	9.73	*		-	
PLACE1009279	13.38	8.53	11.2	5.1	7.71	6.09	11.6	8.18	8.91	*		-	
PLACE1009298	49.41	26.44	34.52	26.24	34.87	27.55	30.84	25.04	29.21				
PLACE1009308	9.89	13.34	12.22	3.57	6.53	4.13	6.2	4.88	5.8	**	**	-	-
PLACE1009319	11.98	14.82	14.36	7.73	14.05	5.85	5.29	9.69	4.23		*		-
PLACE1009328	12.86	13.58	15.59	6.43	10.45	5.86	7.1	8.23	11.41	*	*	-	-
PLACE1009335	8.34	6.5	7.11	3.99	9.88	4.55	4.35	7.62	2.32				
PLACE1009338	14.56	12.99	17.79	6.9	13.74	10.92	6.69	5.83	8.27		**		-
PLACE1009344	6.92	5.13	5.98	3.02	11.98	4.73	3.18	3.89	2.88		*		-
PLACE1009355	23.17	22.99	26.45	20.27	18.4	17.42	10.13	10.79	9.83	*	**	-	-
PLACE1009368	8.63	5.09	6.32	3.35	3.66	2.95	3.35	6.92	2.66	*		-	
PLACE1009375	8.35	5.94	11.71	3.65	4.61	3.52	3.31	4.45	3.97		*		-
PLACE1009388	18.28	22.47	42.99	8.1	17.38	17.02	11.33	10.99	17.5				
PLACE1009398	16.02	15.66	15.45	5.65	12.56	7.13	6.81	5.4	4.18	*	**	-	-
PLACE1009404	17.98	10.01	28.67	4.73	28.94	16.4	9.28	9.88	5.15				
PLACE1009410	13.78	15.39	9.6	5.62	6.24	5.55	5.28	4.64	5.63	*	*	-	-
PLACE1009417	16.73	9.41	10.65	12.79	9.15	6.2	6.71	6.82	7.05				
PLACE1009424	9.71	6.5	9.08	4.75	4.94	4.28	3.44	4.18	4.16	*	*	-	-
PLACE1009434	21.73	12.22	10.01	6.12	7.87	5.95	3.69	5.83	2.87		*		-
PLACE1009443	7.33	14.79	8.94	2.98	3.24	2.54	4.85	2.06	4.82	*		-	
PLACE1009444	13.13	14.77	17.33	7.6	10.32	8.01	6.52	5.24	6.76	*	**	-	-
PLACE1009458	8.33	7.91	9.2	3.33	5.72	4.79	3.49	3.56	3.33	**	**	-	-
PLACE1009460	9.94	14.6	11.32	7.7	8.3	7.62	5.02	3.61	2.95	*	**	-	-
PLACE1009468	12.43	12.85	9.11	5.4	5.98	4.76	4.66	5.65	8.17	**	*	-	-
PLACE1009476	7.02	4.9	5.38	3	3.07	3.32	3.74	3.76	3.61	*	*	-	-

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Table 488

PLACE1009477	13.59	11.11	12.8	10.3	9.83	6.89	8.75	11.15	10.89				
PLACE1009493	5.63	4.68	4.85	3.04	3.33	2.25	3.06	2.29	1.49	**	**	-	-
PLACE1009502	11.43	9.62	8.39	5.92	5.81	5.8	4.63	7.61	3.19	*	*	-	-
PLACE1009524	7.56	7.26	7.63	1.87	3.86	2.97	2.66	3.37	2.46	**	**	-	-
PLACE1009527	18.34	12.36	9.71	6.88	11.49	9.95	6.88	5.14	3.52		*		-
PLACE1009531	25.38	45.76	31.03	26.02	25.63	22.82	19.07	17.64	15.03				
PLACE1009535	12.3	11.08	8.3	3.83	6.2	5.84	3.36	3.71	4.06	*	**	-	-
PLACE1009539	8.83	10.23	7.02	4.34	7.56	5.81	5.39	6.61	6.43				
PLACE1009540	37.43	26.63	27.99	14.5	25.74	28.63	21	11.9	8.26		*		-
PLACE1009542	12	5.45	5.7	3.62	4.51	6	3.18	3.69	2.67				
PLACE1009546	12.67	10.42	6.26	3.72	5.36	5.98	4.35	10.8	3.66				
PLACE1009556	7.91	6.37	6.72	5.1	4.62	3.16	3.16	2.46	2.95	*	**	-	-
PLACE1009569	11.99	15.44	10.67	4.76	13.77	8.59	5.94	5.33	6.24		**		-
PLACE1009571	7.82	9.37	5.59	3.8	7.13	3.69	5.84	2.83	4.48				
PLACE1009573	22.09	15.96	12.31	9.76	17.27	9.7	8.26	8.91	7.87		*		-
PLACE1009576	13.53	9.49	9.65	4.21	6.31	4.13	5.49	5.78	4.15	*	*	-	-
PLACE1009580	9.86	9.33	7.56	5.13	7.69	4.5	8.75	3.59	4.85				
PLACE1009581	12.95	12.1	8.15	7.19	5.84	4.99	3.45	2.48	3.53	*	**	-	-
PLACE1009587	13.3	7.18	8.26	7.06	6.26	5.41	3.85	4.9	4.28				
PLACE1009593	18.08	14.97	12.54	14.73	10.76	9.75	5.8	5.66	6.75		**		-
PLACE1009595	24.28	22.3	15.19	12.22	14.76	12.77	19.19	14	13.81				
PLACE1009596	8.31	5.39	3.71	3.49	5.52	2.24	4.95	2.48	3.3				
PLACE1009600	19.52	17.07	12.01	6.59	8.79	3.99	8.49	7.24	8.2	*	*	-	-
PLACE1009604	19.98	10.38	8.96	4.18	6.3	5.58	3.83	5.54	4.55				
PLACE1009607	17.2	18	14.19	8.35	9.63	7.56	19.54	17.62	14.33	**		-	
PLACE1009613	8.31	8.44	6.06	5.1	6.18	4.22	4.39	2.55	3.96		*		-
PLACE1009621	18.02	17.88	15.95	7.12	14.76	8.85	8.46	6.45	12.83	*	*	-	-
PLACE1009622	16.93	9.51	8.44	5	5.84	4.46	4.96	3.18	4.98				
PLACE1009624	23.04	19.02	15.23	8.31	9.71	5.05	7.94	5.67	7.85	*	**	-	-
PLACE1009637	8.56	7.93	7.76	3.81	7.55	4.55	3.93	3.27	4.29		**		-
PLACE1009639	14.9	6.92	3.57	7.62	5.31	8.34	6.06	5.69	7.84				
PLACE1009654	23.03	16.88	13.87	7.6	11.88	8.66	7.4	8.09	10.22	*	*	-	-
PLACE1009659	17.62	16.71	15.38	8.59	15.54	12.83	6.78	8.01	7.95		**		-
PLACE1009665	13.55	12.11	8.08	5.71	10.66	10.87	8.53	10.59	6.01				
PLACE1009669	10.91	11.58	11.44	5.71	8.38	5.23	8.32	8.02	8.98	**	**	-	-
PLACE1009670	10	4.03	5.32	3.93	4.76	8.45	5.57	4.18	5.29				
PLACE1009708	13.41	10.39	7.63	11.97	12.63	3.57	6.84	3.75	9.58				
PLACE1009721	15.79	10.82	9.31	5.16	6.52	4.42	9.11	3.24	6.91	*		-	
PLACE1009731	5.6	6.57	11.06	5.5	8.58	5.78	5.45	4.8	9.13				
PLACE1009735	9.43	10.36	12.52	8.67	8.77	6.91	8.15	10.58	12.7				
PLACE1009737	8.36	8.02	10.98	5.74	17.02	9.89	4.98	11.47	4.66				
PLACE1009741	8.67	7.59	11.34	6.59	7.8	4.16	2.63	4.89	4.5		*		-
PLACE1009752	9.51	12.78	18.39	7.46	12.57	11.15	4.36	9.17	6.85				
PLACE1009763	16.81	19.39	15.73	12.5	15.24	13.69	4.1	8.02	6.41		**		-
PLACE1009766	7.54	8.76	7.16	6.98	11.81	6.16	9.17	7.21	6.61				
PLACE1009772	12.62	18.28	13.46	16.58	26.84	15.97	7.94	11.57	13.51				
PLACE1009782	7.96	6.95	7.99	4.24	6.2	9.33	6.26	4.41	4.35		*		-
PLACE1009794	8.71	9.98	15.31	6.91	7.94	5.64	5.81	8.68	9.35				
PLACE1009798	15.7	11.58	19.23	8.55	9.28	7.81	5.76	14.83	6.68	*		-	
PLACE1009845	5.69	8.07	10.29	5.79	6.81	9.4	3.27	3.21	4.35		*		-
PLACE1009849	4.29	6.11	7.54	5.25	6.21	5.82	3.81	4.56	5.57				
PLACE1009857	5.97	7.92	9.09	4.47	4.42	3.88	4.36	2.37	3.86	*	*	-	-
PLACE1009861	21.52	19.65	20.31	10.08	12.87	8.67	13.97	16.84	16.62	**	*	-	-
PLACE1009872	225.97	496.72	352.07	405.22	548.08	335.22	583.26	839.73	801.36		*		*
PLACE1009877	93.23	95.23	121.84	37.51	29.99	31.46	33.83	34.28	50.76	**	**	-	-
PLACE1009879	8.31	6.4	8.23	4.6	3.94	4.45	5.4	6.04	6.14	**		-	
PLACE1009886	6.21	5.71	6.04	3.1	4.43	3.64	3.76	3.74	3.91	**	**	-	-
PLACE1009888	16.61	15.12	18.96	7.12	11.3	10.4	7.67	15.82	6.68	*		-	
PLACE1009908	10.69	13.22	16.94	7.9	15.1	13.2	5.89	21.59	11.16				
PLACE1009919	18.85	20.8	15.18	25.14	44.25	16.53	6.38	10.08	17.42				
PLACE1009921	12.5	11.43	13.89	6.9	11.45	10.84	6.74	7.53	6.61		**		-
PLACE1009923	37.38	53.14	35.03	28.71	69.72	45.4	23.4	36.13	28.69				
PLACE1009924	26.03	16.67	21.48	6.84	14.99	12.69	29.73	40.32	10.81				
PLACE1009925	10.23	25.64	14.3	6.85	14.35	14.82	6.32	35.83	7.94				

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PLACE1009931	29.02	24.07	26.54	12.24	15.5	14.51	9.57	9.79	10.08	**	**	-	-
PLACE1009935	8.86	7.44	9.7	2.78	11.02	5.42	14.95	3.43	6.35				
PLACE1009947	6.29	6.77	9.33	4.25	4.43	3.14	2.04	2.93	4.01	*	*	-	-
PLACE1009961	7.86	10.21	16.93	5.24	6.64	4.49	4.58	6.45	5				
PLACE1009971	7.79	7.18	10.26	3.38	7.18	3.34	3.67	4.69	3.08		*		-
PLACE1009982	20.35	18.31	15.25	6.6	11.54	11.1	7.87	5.59	13.47	*	*	-	-
PLACE1009992	12.32	8.01	11.62	6.39	8	6.72	5.24	5.76	6.38		*		-
PLACE1009995	21.27	22.11	27.33	13.99	19.4	11.61	8.12	16.7	12.66	*	*	-	-
PLACE1009997	23.76	8.03	15.66	6.79	12.9	5.63	10.63	9.44	8.19				
PLACE1010002	14.56	6.35	12.19	4.66	8.08	5.35	5.32	14.28	7.75				
PLACE1010011	15.51	14.11	17.86	6.19	7.34	6.29	9.9	6.46	10.43	**	*	-	-
PLACE1010013	6.16	5.13	12.68	2.37	2.99	1.56	3.53	4.24	2.98				
PLACE1010021	15.95	20.29	19.12	7.11	14.51	9.31	5.22	8.04	6.15	*	**	-	-
PLACE1010023	27.49	31.11	21.32	17.41	29.7	20.44	16.49	7.28	6.33		*		-
PLACE1010031	20.87	15.58	32.54	10.16	16.34	7.15	9.85	8.36	10.28				
PLACE1010039	20.5	6.62	10.22	3.99	6.51	3.25	2.91	6.23	3.6				
PLACE1010045	11.17	9.8	13.16	5.75	8.43	6.1	5.11	5.8	5.51	*	**	-	-
PLACE1010053	7.04	5.22	9.04	6.47	4.19	2.39	2.32	2.12	1.16		*		-
PLACE1010060	18.9	18.89	15.21	7.4	8.59	8.37	12.03	13.21	10.77	**	*	-	-
PLACE1010069	10.06	6.9	13.66	5.33	6.93	4.79	2.86	4.42	3.79		*		-
PLACE1010070	8.15	7.09	9.72	2.34	9.93	4.09	3.65	3.87	2.87		**		-
PLACE1010074	63.56	56.74	39.11	24.21	42.72	26.72	25.32	15.29	17.22		*		-
PLACE1010076	60.58	44.35	55.45	21.22	23.2	19.4	13.41	12.75	17.59	**	**	-	-
PLACE1010078	13.76	11.23	14.35	6.69	10.2	8.63	4.38	4.87	4.45	*	**	-	-
PLACE1010081	27.34	19.16	21.57	12.55	15.05	11.39	11.73	7.47	11.77	*	*	-	-
PLACE1010083	7.1	7.48	5.64	1.97	2.64	2.62	1.69	2.61	1.95	**	**	-	-
PLACE1010089	11.95	9.65	9.57	5.5	5.81	4.38	4.84	2.48	4.43	**	**	-	-
PLACE1010096	14.85	29.75	16.35	5.81	14.35	9.63	7.28	8.67	5.49				
PLACE1010102	22.29	34.08	23.15	9.26	16.03	13.51	7.63	9.06	7.61	*	**	-	-
PLACE1010105	18.16	20.35	15.99	6.52	12.73	7.6	4.02	4.82	4.1	*	**	-	-
PLACE1010106	19.44	22.57	15.73	8.29	8.94	12.84	10.96	10.43	10.44	*	*	-	-
PLACE1010130	6.82	6.56	4.7	3.25	3.39	2.18	3.26	3.47	3.87	*	*	-	-
PLACE1010132	20.18	25.39	20.56	20.18	19.1	12.29	12.71	11.47	12.5		**		-
PLACE1010134	10.35	11.42	9.66	6.05	6.05	5.55	6.72	4.12	2.88	**	**	-	-
PLACE1010139	74.68	88.11	79.85	37.26	51.16	43.94	15.68	26.17	18.6	**	**	-	-
PLACE1010148	10.48	7.43	9.71	13.14	7.54	4.86	3.27	4.13	7.63				
PLACE1010155	9.79	7.58	7.63	3.3	5.89	2.96	2.11	2.26	2.53	*	**	-	-
PLACE1010156	32.59	25.06	24.61	14.7	18.09	11.09	7.29	10.58	14.48	*	**	-	-
PLACE1010161	8.48	13.16	10.69	5.15	8.21	6.03	4.47	3.31	5.46		*		-
PLACE1010181	8.66	8.08	6.51	2.62	6.54	5.02	3.74	4.12	2.93		**		-
PLACE1010194	8.57	7.46	6.67	3.93	4.98	3.84	2.86	2.08	2.37	**	**	-	-
PLACE1010202	8.39	6.76	12.45	8.31	10.9	5.79	3.56	3.42	2.04		*		-
PLACE1010231	12.97	10.31	14.49	7.96	15.61	7.14	8.93	9.42	8.37		*		-
PLACE1010235	12.62	15	11.24	4.59	11.54	4.53	6.11	5.14	4.76		**		-
PLACE1010237	5.04	3.77	4.4	2.18	2.37	2.25	2.72	0.64	1.32	**	*	-	-
PLACE1010251	9.46	4.47	6.29	5.09	4.79	10.14	3.78	5.92	3.88				
PLACE1010261	8.26	6.41	4.7	3.42	2.86	2.61	4.52	5.73	4.64	*		-	
PLACE1010270	7.53	8.07	6.36	3.29	6.44	3.19	3.88	4.95	3.8		**		-
PLACE1010273	8.97	10.55	5.7	2.72	5.68	3.04	2.78	2.04	3.83		*		-
PLACE1010274	20.97	18.72	29.56	10.88	16.29	14.38	6.73	5.73	6.16		**		-
PLACE1010277	15.29	14.99	14.3	8.87	13.93	8.53	11.24	4.25	6.68		*		-
PLACE1010293	16.94	20.61	17.07	9.41	11.63	8.24	17.5	8.1	13.23	**		-	
PLACE1010297	38.08	33.94	34.95	17.91	31.69	15.63	31.8	20.1	25.32				
PLACE1010300	21.55	15.58	11.87	9.15	8.78	7.88	3.82	5.36	5.08		*		-
PLACE1010310	323.02	293.14	231.29	170.36	221.95	136.69	214.56	235.35	207.22	*		-	
PLACE1010321	10.7	10.58	7.81	4.96	7.93	6.91	5.6	6.6	6.56		*		-
PLACE1010324	6.25	5.69	6.54	2.88	4.51	2.6	4.43	3.34	2.72	*	**	-	-
PLACE1010329	14.25	11.37	11.93	5.93	10.64	4.89	9.64	9.84	9.32		*		-
PLACE1010330	12.28	14.21	10.49	11.84	10.18	7.63	12	7.94	17.86				
PLACE1010335	27.7	52.66	38.23	18.39	9.7	13.5	16.61	15.38	28.61	*		-	
PLACE1010341	6.44	4.91	4.72	2	3.7	1.35	4.14	2.93	4.21	*		-	
PLACE1010342	2.35	2.93	2.85	2.16	1.61	1.84	1.14	1.19	0.83	*	**	-	-
PLACE1010346	10.42	6.88	7.23	4.08	5.74	2.77	5.84	6.92	5.88	*		-	
PLACE1010362	13.25	8.57	9.24	6.56	7.06	3.39	11.5	13.76	14.05				

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PLACE1010364	11.29	7.43	7.22	2.26	3.51	2.16	4.95	3.65	4.16	*	*	-	-
PLACE1010368	10.78	8.61	7.03	3.98	6.56	5.19	7.58	7.15	5.73				
PLACE1010373	30.2	28.61	24.17	14.82	22.58	10.46	24.63	20.09	20.87	*		-	
PLACE1010383	18.56	18.15	16.04	10	15.54	3.52	27.13	12.41	12.03				
PLACE1010385	2.48	1.73	1.18	0.83	2.33	0.49	2.65	1.19	2.06				
PLACE1010389	8.48	7.51	8.42	3.76	4.47	5.47	3.96	4.51	2.91	**	**	-	-
PLACE1010401	3.24	0.96	4.6	2.29	2.49	1.63	2.81	2.31	1.6				
PLACE1010410	22.91	15.39	21.28	8.31	20.95	12.79	12.79	10.9	11.3		*		-
PLACE1010418	18.78	19.01	17.17	5.75	13.45	6.67	11.25	18.37	11.11	*		-	
PLACE1010425	10.58	10.75	18.36	4.2	4.88	3.19	8.87	11.17	8.75	*		-	
PLACE1010443	12.48	14.66	16.77	5.6	14.99	6.09	8.79	8.23	11.76		*		-
PLACE1010445	36.17	45.7	37.43	17.56	20.28	18.29	39.23	32.46	41.56	**		-	
PLACE1010481	60.4	46.95	65.37	22.92	26.42	21.44	27.71	30.53	27.4	**	**	-	-
PLACE1010482	127.4	82.31	84.53	104.64	120.51	109.85	62.48	50.87	49.97		*		-
PLACE1010491	71.28	72.3	73.41	43.51	47.95	35.09	68.63	86.51	74.84	**		-	
PLACE1010492	20.32	20.74	19.72	20.62	27.04	23.27	9.07	12.55	10.15		**		-
PLACE1010509	11.2	13.07	17.83	8.18	12.58	8.24	5.79	8.34	7.68		*		-
PLACE1010518	9.76	12.31	18.67	8.17	8.57	7.5	8.04	6.33	6.73				
PLACE1010522	8.32	9.35	9.63	6.71	11.42	6.63	5.37	5.88	7.65		*		-
PLACE1010529	13.09	22.15	14.64	11.31	17.05	8.58	7.61	9.45	9.29				
PLACE1010547	36.79	34.33	38.34	12.39	16.81	11.19	21.21	24.3	23.05	**	**	-	-
PLACE1010560	10.15	9.34	9.56	6.09	4.54	5.89	6.02	5.35	6.13	**	**	-	-
PLACE1010562	4.79	4.39	12.01	8.8	8.65	6.38	6.41	7.48	4.4				
PLACE1010579	74.54	67.98	59.08	46.33	48.92	48.24	56.27	84.49	60.31	*		-	
PLACE1010580	38.79	45.7	46.75	22.24	30	17.17	31.95	38.27	36.2	*		-	
PLACE1010599	29.35	25.54	32.71	12.61	15.12	14.18	19.83	24.34	23.16	**		-	
PLACE1010606	31.76	30.37	40.62	15.46	19.15	14.23	22.77	25.83	28.81	**		-	
PLACE1010616	16.39	26.11	18.04	12.86	17.78	7.33	3.49	3.67	4.92		**		-
PLACE1010622	9.08	4.75	12.08	2.52	4.26	2.63	11.54	11.12	6.28				
PLACE1010624	292.79	228.16	204.46	212.8	278.86	210.51	166.11	171.99	155.01		*		-
PLACE1010628	48.66	44.83	51.05	27.25	26.82	37.41	15.79	19.04	21	*	**	-	-
PLACE1010629	19.03	17.43	20.71	12.12	16.38	15.36	14.93	10.66	11.67	*	*	-	-
PLACE1010630	15.62	16.61	29.46	8.82	19.7	10.88	11.96	14.1	11.42				
PLACE1010631	22.99	34.46	25.54	20.07	21.82	17.69	19.23	10.89	16.98		*		-
PLACE1010651	8	10.03	11.34	5.4	9.54	5.75	4.35	5.43	5.06		**		-
PLACE1010661	13.76	16.34	32.78	7.67	13.64	27.31	6.28	10.55	7.26				
PLACE1010662	28.68	22.75	30.53	8.67	12.27	9.85	25.45	28.04	24.56	**		-	
PLACE1010668	37.33	37.7	40.55	22.62	25.66	20.72	36.78	44.21	37.46	**		-	
PLACE1010702	12.3	6.26	13.51	6.5	7.73	5.88	8.16	17.08	6.46				
PLACE1010709	70.65	75.49	68.95	55.09	47.9	57.04	50.07	52.69	55.39	**	**	-	-
PLACE1010713	80.41	68.48	77.71	36.46	48.82	48.26	28.63	32.14	23.64	**	**	-	-
PLACE1010714	14.85	12.78	15.24	4.19	7.98	4.28	3.33	8.97	5.69	**	*	-	-
PLACE1010716	10.07	15.73	17.8	4.88	22.94	9.1	5.99	13.73	3.7				
PLACE1010717	16.27	25.02	15.64	13.63	18.64	10.49	10.76	15.16	3.55				
PLACE1010720	27.49	32.65	34.2	14.65	18.34	8.25	20.45	22.85	22.74	**	*	-	-
PLACE1010739	32.05	33.62	24.71	15.33	21.42	15.16	17.5	28.68	18.95	*		-	
PLACE1010743	44.76	28.81	34.77	15.52	24.11	19.41	14.02	9.67	5.8	*	**	-	-
PLACE1010752	26.13	19.45	22.02	11.29	9.49	11.37	16.27	24.35	13.97	**		-	
PLACE1010761	15.13	12.05	32.55	15.98	9.45	8.78	11.14	13.99	12.89				
PLACE1010771	28.91	75.96	37.99	25.83	90.51	39.2	31.02	18.86	25.47				
PLACE1010784	98.45	116.91	93.11	48.56	63.14	52.26	30.32	31.37	33.38	**	**	-	-
PLACE1010786	16.19	15.53	16.87	8.23	15.52	9.85	7	6.49	9.87		**		-
PLACE1010789	46.25	33.26	40.6	14.8	19.17	10.09	44.64	47.22	35.88	**		-	
PLACE1010800	13.97	9.78	14.67	8.91	6.6	5.82	4.05	5.43	4.76	*	**	-	-
PLACE1010802	13.35	16.74	27.18	16.21	23.96	4.91	12.32	5.78	37.85				
PLACE1010811	26.9	21.58	31.28	13.09	18.01	12.69	11.33	11.86	10.25	*	**	-	-
PLACE1010813	10.21	6.96	9.67	4.84	4.38	4.87	3.92	2.83	2.64	*	**	-	-
PLACE1010827	10.79	10.81	12.05	5.43	7.46	5.87	6.65	5.02	3.76	**	**	-	-
PLACE1010833	9.18	9.98	8.82	3.14	6.94	3.42	1.97	2.07	1.97	*	**	-	-
PLACE1010839	24.14	30.08	20.18	11.7	20	12.82	16.21	11.13	15.42		*		-
PLACE1010856	15.47	10.08	17.88	6.16	6.58	4.26	11.23	8.32	12.26	*		-	
PLACE1010857	32.67	31.48	18.71	21.99	18.34	15.41	16.23	15.82	15.61				
PLACE1010870	5.83	4.92	4.28	3.87	3.55	2.92	2.91	2.04	1.94	*	**	-	-
PLACE1010877	26.07	20.6	20.89	14.13	8.42	9.71	13.42	12.71	7.25	**	*	-	-

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PLACE1010882	17.06	13.54	8.42	6.17	5.69	5.82	7.13	5.03	5.37	*		-	
PLACE1010891	27.43	30.32	21.15	13.46	14.41	7.46	15.38	15.07	24.71	*		-	
PLACE1010896	13.62	18.23	16.16	6.92	8.03	5.78	3.54	4.62	4.06	**	**	-	-
PLACE1010900	66.6	75.65	67.62	55.68	59.03	45.47	67.12	53.92	39.14	*		-	
PLACE1010916	104.52	71.53	76.5	35.13	35.16	33.1	29.84	23.73	27.17	**	**	-	-
PLACE1010917	14.21	14.67	11.27	7.82	5.59	7.41	7.69	7.06	8.76	**	**	-	-
PLACE1010924	5.86	2.7	4.5	2.89	4.47	3.08	2.47	3.1	1.31				
PLACE1010925	4.94	4.55	4.99	1.88	2.53	1.67	3.09	1.69	1.78	**	**	-	-
PLACE1010926	13.94	11.16	11.63	5.87	7.64	6.22	5.6	4.23	4.29	**	**	-	-
PLACE1010942	207.77	196.21	175.46	147.15	130.24	102.36	197.42	120.16	123.73	*		-	
PLACE1010943	31.5	26.2	22.98	12.49	22.16	9	15.12	16.22	13.62		*		-
PLACE1010944	83.2	92.75	68.43	51.82	78.63	47.87	87	58.47	73.16				
PLACE1010947	33.76	22.26	22.3	12.84	13.89	8.22	22.66	11.99	13.89	*		-	
PLACE1010954	10.33	11.3	11.05	5.3	5.81	5.51	5.34	5.12	4.22	**	**	-	-
PLACE1010960	15.62	30.44	20.31	7.94	8.28	7.04	11.37	9.05	8.5	*	*	-	-
PLACE1010965	13.17	14.34	9.79	7.54	4.78	3.78	4.15	4.73	5.18	*	**	-	-
PLACE1010968	18.41	14.95	14.27	6.84	9.6	5.59	12.62	6.34	9.37	**	*	-	-
PLACE1010978	57.65	54.74	36.05	40.68	34.09	13.7	16.85	10.36	20.32		*		-
PLACE1010982	21.44	26.06	15.9	7.42	6.54	11.09	10.66	7.85	9.32	*	*	-	-
PLACE1010990	327.98	344.55	256.15	258.07	367.78	240.66	208.45	171.08	173.44		*		-
PLACE1011017	100.16	59.4	54.99	23.72	27.4	15.8	91.94	75.46	99.74	*		-	
PLACE1011019	13.37	8.64	6.46	8.37	6.37	4.79	6.61	7.41	7.81				
PLACE1011026	17.67	16.91	13.69	8.74	11.48	8.93	15.71	13.37	15.94	*		-	
PLACE1011032	5.5	8.88	7.51	2.84	5.75	2.99	4.5	3.38	3.21		*		-
PLACE1011041	11.32	11.72	11.41	4.79	6.17	4.9	2.74	0	1.85	**	**	-	-
PLACE1011045	30.68	27.07	24.09	20.73	22.77	14.24	25.88	22.96	30.06				
PLACE1011046	10.75	10.03	9.15	3.68	6.42	4.38	4.21	3.5	2.56	**	**	-	-
PLACE1011054	23.11	26.67	18.54	13.24	17.45	11.68	27.3	21.77	27.93	*		-	
PLACE1011056	5.67	3.31	3.16	3.73	4.11	8.46	6.33	3.05	6.91				
PLACE1011057	10.04	10.53	7.99	8.15	6.14	3.72	11.95	6.55	7.6				
PLACE1011059	19.4	17.96	11.33	7.08	9.45	9.52	6.53	6.86	9.19	*	*	-	-
PLACE1011066	9.28	7.31	5.97	5.75	7.03	4.1	2.13	5.18	0.49		*		-
PLACE1011087	26.84	40.15	33.04	57.32	27.46	16.29	127.9	19.42	37.4				
PLACE1011090	10.52	7.52	6.48	3.01	5.18	3.1	6.04	4.61	6.16	*		-	
PLACE1011109	43.09	16.58	13.76	6.5	19.94	4.84	12.2	7.21	13.97				
PLACE1011114	17.98	24.04	19.89	13.12	19.15	8.13	12.09	13.25	14.96		*		-
PLACE1011116	30.03	28.53	37.37	10.98	8.87	7	8.26	10.18	5.99	**	**	-	-
PLACE1011122	5.9	6.6	5.93	4.16	4.82	3.11	3.97	4.69	2.89	*	*	-	-
PLACE1011133	6.47	4.35	6.51	3.81	3.93	3.81	2.72	5.84	2.91				
PLACE1011134	5.48	5.99	6.34	4.28	4.27	3.64	3.72	3.86	3.76	**	**	-	-
PLACE1011143	4.76	9.67	5.59	2.21	5.45	3.27	2.93	3.83	4.13				
PLACE1011146	10.48	13.56	12.48	9.3	11.11	4.11	4.38	6.69	4.48		**		-
PLACE1011160	7.71	9.99	6.71	4.98	7.77	3.25	6.45	4.47	3.78				
PLACE1011165	21.99	27.95	32.58	8.87	19.75	11.93	12.6	15.59	9.42	*	*	-	-
PLACE1011181	5.25	3.37	6	2.06	4.49	2.29	2.61	4.09	3.85				
PLACE1011185	60.3	36.78	36.17	37.68	34.15	24.31	17.32	33.87	29.05				
PLACE1011186	25.07	30.45	27.42	12.69	20.01	15.83	19.93	27.9	21.4	*		-	
PLACE1011203	10.27	18.2	13.8	9.36	12.5	6.63	8.02	13.49	10.02				
PLACE1011214	7.39	9.12	10.92	5.57	5.78	3.95	1.49	2.02	3.84	*	**	-	-
PLACE1011219	7.03	5.86	7.27	8.39	4.52	4.58	9.07	4.64	3.23				
PLACE1011221	10.63	11.42	9.42	5.44	10.51	4.92	4.92	5.52	6.28		**		-
PLACE1011229	13.76	13.72	12.78	9.23	7.48	4.86	6.43	7.1	4.99	**	**	-	-
PLACE1011231	34.58	28.7	50.02	23.03	24.8	13.83	19.12	24.97	26.97				
PLACE1011236	13.02	10.94	13.96	5.99	7.59	5.06	4.42	6.98	4.82	**	**	-	-
PLACE1011247	571.8	409.73	639.71	528.63	738.01	566.23	553.23	542.58	267.58				
PLACE1011263	4.49	7.26	9.65	4.09	5.29	4.39	2.77	4.83	3.37				
PLACE1011273	9.77	15.11	15.29	8	7.81	4.87	6.04	5.28	3.97	*	*	-	-
PLACE1011278	21.08	26.71	20.88	9.67	19.17	11.18	9.31	5.1	7.74		**		-
PLACE1011289	8.76	9.56	9.49	5.47	7.47	4.38	4.05	4.14	4.61	*	**	-	-
PLACE1011291	3.27	1.73	2.37	1.38	1.37	0.09	2.52	4.22	1.75				
PLACE1011295	15.1	14.79	20.48	7.86	6.09	7.28	12.72	18.07	15.96	**		-	
PLACE1011310	49.57	40.91	47.27	26.08	24.65	29.49	26.25	31.46	34.3	**	*	-	-
PLACE1011311	12.85	11.18	13.64	5.84	6.4	7.88	4.02	7.29	3.99	**	**	-	-
PLACE1011321	316.11	225.18	251.29	230.23	241.81	208.08	340.56	284.43	231.07				

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PLACE1011325	67.49	68.67	34.36	32.79	55.55	25.52	26.06	16.66	23.25		*		-
PLACE1011332	37.6	32.99	20.69	24.89	22.84	17.06	26.8	25.99	39.36				
PLACE1011340	6.86	4.22	8.9	7.42	3.33	10.93	4.69	3.22	3.76				
PLACE1011353	13.06	9.45	9.31	4.05	5.07	3.21	9.83	8.83	10.17	**		-	
PLACE1011360	7.09	6.29	7.09	5.01	4.64	2.08	4.25	9.92	6.13	*		-	
PLACE1011364	36.2	48	46.69	18.82	32.17	16.48	29.76	23.08	23.29	*	*	-	-
PLACE1011365	56.47	40.06	43.45	30.4	25.78	22.53	35.29	36.44	44.51	*		-	
PLACE1011371	8.03	11.85	15.3	3.37	4.12	3.15	3.67	7.88	4.18	*		-	
PLACE1011375	7.04	6.27	10.93	2.06	3.1	2.3	1.72	3.77	5.21	*		-	
PLACE1011386	164.83	196.07	182.53	143.65	164.65	123.82	185.62	179.87	160.52				
PLACE1011399	13.53	14.93	12.77	5.31	8.23	5.03	14.49	12.53	13.08	**		-	
PLACE1011406	24.35	18.36	25.14	17.24	17.93	13.01	14.05	16.63	13.24		*		-
PLACE1011407	11.96	8.15	11.8	4.39	4.52	4.88	4.7	7.06	4.99	**	*	-	-
PLACE1011419	45.6	33.74	47.01	28.72	27.55	25.25	33.12	24.14	29.66	*		-	
PLACE1011433	12.4	6.05	13.11	5.89	9.23	4.52	4.03	6.39	4.28				
PLACE1011440	22.91	21.43	16.68	17.18	6.65	6.34	4.22	2.79	3.13		**		-
PLACE1011452	21.99	27.18	21.9	7.47	5.58	8.33	1.98	2.55	3.76	**	**	-	-
PLACE1011465	8.59	10.4	8.63	4.43	3.74	3.61	3.27	3.42	2.9	**	**	-	-
PLACE1011472	12.35	11.03	8.39	5.76	5.63	4.74	4.12	4.06	4.53	*	**	-	-
PLACE1011477	6.89	4.15	8.42	3.82	3.1	2.49	5.68	5.36	7.03				
PLACE1011478	147.8	127.45	151.17	98.43	129.14	92.91	97.94	88.28	67.65		**		-
PLACE1011492	8.86	4.94	8.71	5.63	3.6	3.44	4.78	2.62	3.91				
PLACE1011498	11.86	13.27	11.87	6.42	7.11	5.44	7.49	6.76	6.34	**	**	-	-
PLACE1011501	5.51	5	4.76	1.97	2.88	1.92	1.53	1.09	0.63	**	**	-	-
PLACE1011503	8.36	7.18	8.72	3.16	3.42	2.41	3.54	1.96	1.63	**	**	-	-
PLACE1011509	6.79	8.76	6.6	2.67	3.22	3.57	3.54	1.66	2.46	**	**	-	-
PLACE1011514	39.36	42.6	35.59	29.05	24.04	21.59	28.05	21.32	28.44	**	*	-	-
PLACE1011516	2.25	2.2	3.02	1.65	1.39	0.92	2.22	1.19	1.28	*		-	
PLACE1011520	56.28	54.22	44.97	60.14	59.13	46.66	37.37	33.63	31.08		*		-
PLACE1011538	3.92	2.67	3.99	1.41	2.25	0.89	1.83	0.52	1.52	*	*	-	-
PLACE1011555	5.04	5.36	4.18	1.71	1.41	2.12	2.42	1.56	2.13	**	**	-	-
PLACE1011561	40.83	32.97	31.05	28.42	20.97	80.97	15.06	18.06	18.45		**		-
PLACE1011563	10.59	8.43	6.69	4.39	3.31	1.28	2.74	2.46	2.05	*	**	-	-
PLACE1011567	8.99	5.72	8.85	4.85	2.48	0.94	3.39	1.71	1.08	*	*	-	-
PLACE1011569	17.38	15.57	12.39	8.98	14.17	5.41	4.61	3.24	5.59		**		-
PLACE1011576	9.4	4.88	4.15	2.79	3.81	3.52	4.89	6.65	7.51				
PLACE1011586	11.29	10.02	9.62	6.88	3.58	5.49	4.18	5.75	5.57	**	**	-	-
PLACE1011635	30.93	17.84	23.55	13.98	14.55	6.78	13.1	10.06	12.62		*		-
PLACE1011641	17.21	13.31	15.5	11.83	10.3	8.13	12.16	8.31	8.02	*	*	-	-
PLACE1011642	14.04	9.07	8.81	4.73	3.8	2.98	2.08	3.09	1.68	*	**	-	-
PLACE1011643	21.88	15.91	14.62	9.69	7.73	4.5	12.37	9.92	7.66	*	*	-	-
PLACE1011646	50.88	55.98	42.92	29.54	24.58	20.05	12.83	13.88	9.31	**	**	-	-
PLACE1011649	101.51	209.33	140.08	111.98	127.38	61.19	33.86	36.5	31.67		*		-
PLACE1011650	21.23	16.3	17.27	6.34	7.58	5.35	13.14	9.77	13.14	**	*	-	-
PLACE1011661	36.54	29.6	21.98	17.54	11.85	16.02	29.9	27.07	30.09	*		-	
PLACE1011664	4693.7	3704.8	3103.3	1925.9	2495.7	2690.1	3091.7	3779.5	2474.5	*		-	
PLACE1011672	14.58	19.19	17.05	4.82	11.54	6.52	8.71	6.37	8.66	*	**	-	-
PLACE1011675	27.27	28.5	23.64	11.76	7.61	13.02	10.47	6.83	11.83	**	**	-	-
PLACE1011682	31.95	30.83	21.79	24.47	12.69	9.16	19.26	16.69	17.56		*		-
PLACE1011708	240.54	265.47	223.19	186.79	250.35	199.96	147.11	130.97	144.28		**		-
PLACE1011719	2115.1	1324.5	1826.8	1953.8	1265.9	1000.2	1428.6	860.26	1269.9				
PLACE1011725	14.63	11.44	8.67	4.74	6.3	2.04	9.22	9.94	8.53	*		-	
PLACE1011729	17.92	12.45	10.92	5.48	6.85	3.57	9.59	6.92	10.12	*		-	
PLACE1011741	19.11	16.45	8.87	6.48	6.39	4.13	6.03	4.62	6.01	*	*	-	-
PLACE1011749	198.63	245.38	186.1	98.37	139.73	93.5	146.64	106.95	169.56	*		-	
PLACE1011757	55.97	64.31	51.13	22.6	27.43	20.99	59.9	47.96	65.48	**		-	
PLACE1011762	112.55	118.61	84.99	66.65	83.7	57.21	113.37	92.71	109.2	*		-	
PLACE1011778	14.17	14.57	14.58	9.09	8.23	7.54	9.58	8.34	17.29	**		-	
PLACE1011783	34.3	38.67	23.05	14.78	12.16	17.09	15.47	21.92	20.45	*		-	
PLACE1011795	26.86	17.86	14.49	8.41	7.89	4.41	13.16	9.37	14.56	*		-	
PLACE1011810	6.46	2.52	3.35	2.53	2.07	0.8	3.19	3.06	3.38				
PLACE1011824	86.62	55.93	50.79	29.92	21.66	12.01	21.62	24.56	19.64	*	*	-	-
PLACE1011825	47.11	53.31	45.03	28.52	34.47	24.16	61.42	44.87	47	**		-	
PLACE1011835	12.82	11.42	11.32	5.55	7.84	4.84	7.39	9.98	8.67	**	*	-	-

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Table 493

PLACE1011836	18.92	14.13	10.67	5.56	9.72	5.44	13.34	9.9	14.01				
PLACE1011847	18.99	16.08	12.62	9.39	11.06	5.84	18.15	10.26	13.1	*		-	
PLACE1011855	44.57	41.99	25.3	17.11	33.33	14.76	55.6	42.68	40.57				
PLACE1011858	17.26	16.38	17.11	5.33	7.08	6.53	6.22	8.74	5.1	**	**	-	-
PLACE1011874	23.12	12.72	25.71	16.84	19.22	7.85	10.17	8.71	12.51				
PLACE1011875	10.58	9.98	11.17	5.18	10.63	6.87	7.18	6.04	4.93		**		-
PLACE1011877	4.39	5.14	4.95	3.7	5.52	3.78	2.59	4.05	4.24				
PLACE1011891	21.71	17.57	18.99	7.39	14.47	8.67	8.21	9.15	7.86	*	**	-	-
PLACE1011896	15.35	16.64	24.3	10.41	10.14	12.14	5.01	8.13	7.98		*		-
PLACE1011920	16.12	14.42	15.9	7.68	8.85	7.76	6.46	2.46	3.24	**	**	-	-
PLACE1011922	9.14	7.55	8.03	4.49	8.39	4.08	7.97	6.15	5.33				
PLACE1011923	166.86	139.43	146.9	104.2	117.42	86.95	136.93	140	124.61	*		-	
PLACE1011937	11.45	9.18	10.8	8.58	6.75	5.1	5.71	6.29	5.46	*	**	-	-
PLACE1011939	20.33	21.55	26.93	12.79	15.19	13.44	14.58	11.31	12.67	*	*	-	-
PLACE1011940	46.38	48.76	46.73	35.11	34.53	31.67	43.31	41.44	39.86	**	**	-	-
PLACE1011962	58.59	70.73	80.18	30.15	38.09	28.84	47.96	47.68	42.57	**	*	-	-
PLACE1011964	53.78	49.36	46.95	41.43	47.33	36.34	22.23	20.62	20.74		**		-
PLACE1011978	50.21	52.86	64.71	38.6	31.39	22.36	22.46	20.19	18.12	*	**	-	-
PLACE1011980	13.57	18.54	10.96	9.65	15.28	6.53	4.68	9.99	8.31				
PLACE1011981	46.23	28.89	45.44	16.98	15.61	9.98	14.66	11.01	11.18	*	**	-	-
PLACE1011982	116.69	99.4	123.56	57.42	68.6	45.01	97.45	90.55	115.07	**		-	
PLACE1011995	8.31	11.27	12.33	5	7.29	7.22	6.27	8.29	4.87	*		-	
PLACE1012023	36.36	36.13	39.16	21.46	26.03	23.3	20.6	21.06	24.79	**	**	-	-
PLACE1012026	72.96	80.46	66.75	52.71	40.29	50.42	21.72	33.87	25.71	**	**	-	-
PLACE1012031	6.69	7.34	9.86	2.73	6.11	3.89	3.41	3.11	3.97		*		-
PLACE2000003	144.75	222.75	62.64	74.47	133.88	40.79	39.01	32.21	30.64				
PLACE2000005	20.72	25.78	18.16	9.79	22.43	11.52	5.79	8.65	14.3		*		-
PLACE2000006	74.92	51.78	61.3	27.4	24.75	21.12	50.02	43.94	72.77	**		-	
PLACE2000007	11.31	11.29	12.53	6.68	7.02	5.2	5.63	10.02	7	**	*	-	-
PLACE2000011	20.07	19.36	23.84	14.92	4.58	15.77	9.39	11.52	19.43				
PLACE2000014	10.47	6.72	12.3	4.76	6.02	3.48	3.63	6.9	4.73	*		-	
PLACE2000015	63.77	83.22	43.62	34.06	43.14	43.39	19.29	26.64	36.8		*		-
PLACE2000017	64.44	66.07	78.07	40.68	48.09	29.95	59.7	61.53	44.91	*		-	
PLACE2000021	131	136.36	142.32	116.28	142.66	101.82	89.75	68.71	86.35		**		-
PLACE2000022	6.52	6.75	7.52	3.85	5.14	3.55	4.53	1.84	5.72	**		-	
PLACE2000030	277.16	275.48	252.39	182.81	167.16	156.31	125.23	96.07	135.65	**	**	-	-
PLACE2000032	8.03	6.4	8.8	4.38	5.33	2.81	4.32	15.18	4.01	*		-	
PLACE2000033	19.24	16.61	20.22	9.43	14.03	10.83	8.93	12.91	10.87	*	**	-	-
PLACE2000034	212.75	182.06	146.24	219.9	195.88	170.13	146.86	112.34	125.26				
PLACE2000039	8.9	10.84	13.51	4.94	3.89	4.8	3.72	4.38	6.52	**	*	-	-
PLACE2000043	13.64	20.44	15.11	6.28	13.12	6.04	6.05	7.64	6.22		*		-
PLACE2000044	7.28	9.48	9.44	3.48	5.71	4.79	4.48	4.25	4.59	*	**	-	-
PLACE2000047	17.41	19.39	12.83	6.83	12.83	7.05	7.81	8.54	5.78		*		-
PLACE2000050	18.34	17.87	22.05	7.34	8.98	7.31	7.51	8.31	7.94	**	**	-	-
PLACE2000061	53.75	61.97	78.23	34.92	41.03	37.86	22.68	14.04	20.77	*	**	-	-
PLACE2000062	44.19	44.8	62.08	41.54	45.17	33.58	38.88	38.06	40.24				
PLACE2000072	216.69	181.79	181.98	200.73	185.27	186.23	111.76	113.44	105.53		**		-
PLACE2000073	8.16	10.75	9.27	3.77	4.89	3.62	4.56	4.79	3.59	**	**	-	-
PLACE2000097	120.94	128.07	120.9	148.48	131.74	105.73	90.14	87.25	86.79		**		-
PLACE2000100	13.48	14.19	15.99	6.02	8.77	5.56	4.8	3.51	6.24	**	**	-	-
PLACE2000103	355.83	328.95	197.42	251.22	436.52	235.01	231.23	336.03	237.95				
PLACE2000106	32.23	23.41	23.14	14.46	6.17	13.03	9.13	10.5	5.27	*	**	-	-
PLACE2000111	152.37	157.38	125.3	88.6	105.91	83.66	90.52	44.23	69.19	*	**	-	-
PLACE2000115	27.01	16.97	16.32	19.6	21.67	16.26	13.74	11.32	11.63				
PLACE2000118	229.23	214.41	143.27	124.01	152.19	92.15	153.7	62.85	67.07				
PLACE2000124	7.33	5.71	5.57	2.12	1.78	1.55	2.01	1.56	1.09	**	**	-	-
PLACE2000132	18.07	19.01	19.11	15.64	11.16	12.49	9.7	6.52	8.48	*	**	-	-
PLACE2000136	33.6	40.68	26.33	13.95	42.68	22.54	9.98	17.8	18.28		*		-
PLACE2000137	6.87	5.34	6.91	1.61	2.95	2.09	1.24	1.8	2.36	**	**	-	-
PLACE2000140	11.37	11.51	12.2	8.07	9.45	9.49	11.48	11.25	10.8	**		-	
PLACE2000147	10.22	7.24	9.46	6.01	5.85	4.51	7.52	7.6	9.27	*		-	
PLACE2000153	17.95	21.42	13.85	5.51	9.57	6.43	4.84	5.27	2.27	*	**	-	-
PLACE2000164	8.53	12.11	9.44	3.18	4.26	4.12	4.98	3.97	2.13	**	**	-	-
PLACE2000170	38.84	46.93	33	28	28.56	22.27	30.03	23.36	30.82	*		-	

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PLACE2000172	9.55	12.02	10.86	4.88	5.87	3.32	4.01	4.8	6.2	**	**	-	-
PLACE2000173	16.63	20.86	19.04	9.66	11.13	9.7	6.74	6.23	3.14	**	**	-	-
PLACE2000174	6.73	7.76	6.4	3.37	4.73	2.4	3.08	3.26	1.62	*	**	-	-
PLACE2000176	47.07	39.92	36.01	26.8	32.78	24.97	24.68	26.79	25.41	*	**	-	-
PLACE2000187	11.49	9.44	7.22	4.28	4.58	4.45	2.47	4.64	3.94	*	*	-	-
PLACE2000216	15.24	13.28	16.1	7.83	10.53	7.67	11.12	11.23	10.67	**	*	-	-
PLACE2000219	43.32	28.21	37.3	18.17	6.67	13.94	7.68	7.79	6.4	*	**	-	-
PLACE2000221	9.58	7.64	7.46	2.22	3.99	1.24	4.08	2.43	3.07	**	**	-	-
PLACE2000223	16.67	12.34	12.95	4.95	6.75	4.32	4.43	2.01	2.87	**	**	-	-
PLACE2000231	8.48	8.65	7.01	3.78	5.92	4.27	4.19	2.32	3.59	*	**	-	-
PLACE2000235	7.02	5.03	3.66	1.54	5.33	1.9	4.43	3.57	3.78				
PLACE2000246	21.31	17.8	13.21	7.9	13.4	6.47	11.52	9.6	10.91		*		-
PLACE2000264	41.11	43.3	30.68	20.28	22.27	18.14	15.54	15.85	15.69	*	**	-	-
PLACE2000274	6.8	7.42	7.36	4.35	3.04	1.89	3.84	3.12	4.31	**	**	-	-
PLACE2000287	32.11	30.76	24.99	20.39	25.61	21.53	17.96	15.3	19.45		**		-
PLACE2000296	42.94	34.88	35.63	23.36	22.17	20.37	32.02	14.36	29.35	**		-	
PLACE2000302	252.74	304.77	237.45	265.35	267.99	217.29	124.09	112.58	108.48		**		-
PLACE2000305	21.47	23.58	17.69	16.14	17.23	16.65	22.14	18.21	22.01				
PLACE2000317	37.2	38.12	23.24	20.01	28.38	14.37	31.05	33.16	31.64				
PLACE2000324	18.44	17.84	10.35	6.13	8.75	4.98	3.24	8.74	3.2	*	*	-	-
PLACE2000334	21.38	17.6	11.43	10.36	9.7	9.37	7.54	6.15	9.1		*		-
PLACE2000335	71.59	66.59	54.82	51.15	35.99	40.86	33.77	36.69	29.67	*	**	-	-
PLACE2000340	20.62	28.95	19	17.88	23.88	12.85	16.23	14.73	16.82				
PLACE2000341	14.8	11.92	10.45	5.66	5.34	5.33	5.38	5.46	7.66	**	*	-	-
PLACE2000342	23.53	21.95	21.97	16.28	11.86	11.51	22.81	14.69	23.12	**		-	
PLACE2000347	9.57	9.26	10.05	4.16	2.94	3.3	5.78	3.54	5.48	**	**	-	-
PLACE2000357	112.17	70.59	69.73	83.45	100.62	78.25	23	68.79	48.54				
PLACE2000358	57.37	32.59	34.74	25.22	20.69	15.46	44.93	47.18	42.01				
PLACE2000359	66.39	48.68	57.2	40.91	54.54	32.45	1.96	27.1	55				
PLACE2000366	24.09	23.36	19.56	12.65	12.71	9.05	11.75	9.72	10.83	**	**	-	-
PLACE2000371	12.17	9.37	8.13	5.98	7.76	4.49	7.64	10.97	6.2				
PLACE2000373	8.3	7.58	8.83	4.52	6.25	4.81	3.89	1.17	2.44	**	**	-	-
PLACE2000374	20.82	21.57	18.21	16.3	16.71	14.02	11.71	11.44	14.19	*	**	-	-
PLACE2000379	109.97	110.55	125.02	99.68	141.5	89.14	84.64	65.75	71.64		**		-
PLACE2000386	27.43	27.19	20.99	10.83	12.4	11.22	15.3	17.99	10.26	**	*	-	-
PLACE2000388	250.97	170.84	203.4	172.85	236.63	173.11	130.31	109.84	93.57		*		-
PLACE2000392	241.74	206.31	271.34	159.33	199.67	145.83	119.57	115.9	95.8	*	**	-	-
PLACE2000394	10.9	10.42	13.61	8.59	15.25	7.68	5.68	9.12	6.51		*		-
PLACE2000398	16.83	19.82	17.04	9.21	12.98	10.99	7.5	15.14	8.57	**	*	-	-
PLACE2000399	30.6	27.17	17.03	25.83	27.41	28.06	9.08	19.74	20.17				
PLACE2000402	5.25	8.04	8.31	4.2	9.81	3.39	4.84	3.89	6.41				
PLACE2000404	24.79	49.52	29.14	49.74	21.66	25.22	16.23	19.06	8.51				
PLACE2000411	5.67	8.96	6.75	7.21	11.84	6.13	5.19	4.54	7.08				
PLACE2000418	10.3	8.94	9.67	6.1	3.09	4.67	4.68	5.3	4.11	**	**	-	-
PLACE2000419	96.71	94.48	148.23	58.48	57.97	27.06	44.37	46.85	45.47	*	*	-	-
PLACE2000425	9.83	11.3	13.49	7.49	11.26	6.24	5.84	7.49	5.62		*		-
PLACE2000427	15.21	22.92	21.67	15.7	21.56	15.92	5.61	6.9	4.76		**		-
PLACE2000433	25.58	27.32	26.12	13.97	18.4	14.15	21.62	27.64	18.08	**		-	
PLACE2000435	16.36	18.11	21.19	9.69	13.76	7.6	8.43	10.79	12.73	*	*	-	-
PLACE2000438	35.17	36.25	36.72	24.14	34.38	15.98	38.19	37.23	25.32				
PLACE2000450	24.38	41.59	23.11	16.35	37.33	18.21	23.47	16.65	30.25				
PLACE2000455	51.05	47.04	53.6	30.31	36.57	21.71	39.12	34.02	35.42	*	**	-	-
PLACE2000458	13.07	11.58	13.21	6.82	7.75	7.03	6.6	8.78	5.76	**	**	-	-
PLACE2000464	9.95	10.55	11.94	7.59	6.37	5.51	7.66	8.47	7.16	**	*	-	-
PLACE2000466	182.2	189.36	208.18	166.02	148.04	156.91	139.29	234.97	151.61	*		-	
PLACE2000473	23.66	24.51	24.43	18.65	18.15	16.44	24.18	30.07	29.1	**		-	
PLACE2000477	14.25	12.47	18.55	9.69	12.47	6.23	10.6	9.09	9.9		*		-
PLACE3000004	49.49	41.47	56.9	42.63	53.35	39.93	39.48	28.43	32.45		*		-
PLACE3000009	30.13	36.74	28.18	19.79	35.05	20.31	13.54	15.44	20.29		**		-
PLACE3000020	27.99	24.44	23.74	13.45	15.64	8.65	14.29	14.44	13.63	**	**	-	-
PLACE3000029	13.95	12.7	16.35	6.3	9.27	7.3	4.68	16.59	5.52	**		-	
PLACE3000038	6.52	4.32	7.69	5.63	3.97	4.12	2.68	6.95	6.18				
PLACE3000052	8.21	5.21	10.48	3.53	4.28	4.15	2.75	5.07	2.29				
PLACE3000059	7.39	8.1	10.8	4	5.08	2.55	2.83	4.28	4.31	*	*	-	-

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PLACE3000067	49.68	45.52	57.37	38.78	41.13	26.16	39.8	46.08	41.69				
PLACE3000069	22.6	20.15	23	9.32	14.75	10.81	1.9	9.3	14.16	**	*	-	-
PLACE3000070	28.36	29.24	22.17	14.93	25.34	18.73	8.92	18.55	16.21		*		-
PLACE3000103	7.35	7.9	9.44	5.25	4.6	6.13	2.42	4.32	5.29	*	*	-	-
PLACE3000119	35.89	28.1	30.76	15.16	14.79	15.09	26.05	30.71	30.91	**		-	
PLACE3000121	42.11	31.92	37.82	38.13	38.16	27.02	30.65	23.15	27.55				
PLACE3000124	419.8	380.05	314.65	379.74	412.05	282.09	411.56	374.59	344.25				
PLACE3000135	20.62	25.87	26.77	15.03	9.64	8.12	18.24	11.89	14.6	**	*	-	-
PLACE3000136	7.68	8.11	13.16	2.72	3.39	4.18	4.52	3.19	1.88	*	*	-	-
PLACE3000142	24.15	28.81	26.5	11.04	24.59	15.08	9.37	6.94	11.56		**		-
PLACE3000145	16.45	12.13	16.32	7.23	16.52	6.93	8.46	9.12	6.76		*		-
PLACE3000147	109.42	62.46	138.9	40.47	87.42	32.89	57.71	63.5	68.14				
PLACE3000148	66.44	59.97	67.42	62.74	65.96	38.34	37.63	26.14	36.79		**		-
PLACE3000154	10.3	11.14	12.88	7.95	8.64	6.56	7.31	6.3	7.57	*	**	-	-
PLACE3000155	54.28	50.77	22.77	23.49	28.34	24.7	10.12	11.93	8.34		*		-
PLACE3000156	9.77	6.45	8.44	2.67	5.36	4.07	2.62	2.16	2.62	*	**	-	-
PLACE3000157	38.44	50.52	36.49	23.64	29.36	25.04	21.36	24.91	20.01	*	*	-	-
PLACE3000158	10.22	9.34	10.13	4.45	4.83	3.36	2.93	2.25	3.02	**	**	-	-
PLACE3000160	19.92	29.65	15.93	8.71	11.7	10.32	5.77	7.29	4.57	*	*	-	-
PLACE3000169	4.65	6.89	7.95	4.88	4.57	2.21	2.88	2.72	3.49		*		-
PLACE3000181	12.63	9.87	13.46	6.15	6.69	4.33	5.58	7.04	5.47	**	**	-	-
PLACE3000194	1627	2636.2	1913.4	1710.4	2606.8	2399	3320.1	2826.5	2357.1				
PLACE3000197	7.18	4.55	8.38	2.14	1.71	1.66	2.79	2.24	2.57	*	*	-	-
PLACE3000199	19.46	15.17	17.17	4.98	8.73	7.24	6.33	5.56	6.07	**	**	-	-
PLACE3000205	12.53	16.93	16.84	6.91	6.83	4.67	7.28	5.87	4.15	**	**	-	-
PLACE3000207	7.97	6.69	7.83	2.48	4.45	2.85	2.71	2.19	2.08	**	**	-	-
PLACE3000208	5.49	5.5	6.02	1.68	6.49	2.8	2.64	3.52	2.46		**		-
PLACE3000213	40.02	27.48	31.62	27.29	30.91	23.89	26.59	30.58	23.2				
PLACE3000215	20.76	15.1	17.45	10.19	8.64	8.25	15.48	14.18	17.02	**		-	
PLACE3000218	13.39	10.52	10.44	6.03	3.81	4.29	4.65	4.57	4.68	**	**	-	-
PLACE3000220	61.41	56.02	42.84	39.7	37	28.53	36.15	41.5	44.54	*		-	
PLACE3000221	12.37	9.42	8.54	5.7	3.63	2.33	5.09	3.54	2.87	*	**	-	-
PLACE3000225	180.89	144.07	131.66	176.14	175.29	127.3	77.77	64.65	86.2		**		-
PLACE3000226	20.28	21.59	18.74	7.11	11.09	6.3	3.48	2.23	3.79	**	**	-	-
PLACE3000230	17.46	18.98	14.94	6.27	14.11	10.52	4.65	3.25	5.88		**		-
PLACE3000231	17.8	13.66	8.65	9.08	2.29	4.95	6.33	9.35	7.91				
PLACE3000235	9.61	7.55	8.28	4.48	5.65	4.02	5.72	2.93	4.77	**	*	-	-
PLACE3000242	58.11	27.4	48.85	17.82	13.76	17.4	11.61	10.29	11.25	*	*	-	-
PLACE3000244	18.63	13.16	20	8.5	7.54	7.64	10.16	10.96	16.61	*		-	
PLACE3000253	56.99	47.97	42.85	32.37	25.93	24.8	32.98	24.76	32.96	*	*	-	-
PLACE3000254	27.82	25.4	19.01	15.47	10.42	14.64	15.57	11.42	13.74	*	*	-	-
PLACE3000271	14.58	20.8	13.28	5.71	8.52	5.71	8.32	6.43	8.38	*	*	-	-
PLACE3000276	13.09	13.68	8.83	2.78	7.9	3.42	3.8	5.28	3.1	*	**	-	-
PLACE3000304	37.31	49.14	39.5	28.72	17.9	18.26	33.17	28.5	40.23	*		-	
PLACE3000309	12.29	9.64	9.42	6.2	5.6	4.27	5.42	4.79	6.47	**	**	-	-
PLACE3000310	51.34	49.06	45.31	11.5	35.47	14.78	19.66	9.79	16.36	*	**	-	-
PLACE3000320	24.3	28.51	23.33	14.31	20.51	12.27	15.7	15.03	15.45	*	**	-	-
PLACE3000322	43.24	35.12	33.62	31.55	31.68	23.75	27.52	20.55	23.56		*		-
PLACE3000330	28.37	27.71	24.49	12.33	15.5	11.35	20.66	17.37	21.33	**	*	-	-
PLACE3000331	6.68	8.07	7.67	6.55	5.13	3.84	2.57	2.99	0.04		**		-
PLACE3000335	393.24	473.08	270.29	359.87	515.03	396.41	470.46	662.39	717.67				
PLACE3000339	11.78	5.98	6.82	3.79	5.41	2.48	9.74	10.29	11.53				
PLACE3000341	12.2	6.88	6.99	4.2	5.65	4.02	4.35	5.75	4.94				
PLACE3000350	13.71	12.66	10.21	4.86	8.13	4.84	5.77	4.37	7.49	*	*	-	-
PLACE3000352	17.23	29.11	20.8	9.42	15.27	8.16	11.43	7.14	13.58		*		-
PLACE3000353	14.74	14.96	16.82	8.78	8.26	6.98	10.37	5.48	6.79	**	**	-	-
PLACE3000362	57.42	93.8	72.53	67.02	59.59	35.38	59.68	38.27	60.6				
PLACE3000363	9.44	8.61	10.55	4.39	5.19	4.3	7.06	4.68	6.56	**	*	-	-
PLACE3000365	5.59	7.45	4.94	1.48	2.65	3.2	4.78	2.37	2.95	*		-	
PLACE3000373	38.45	30.27	25.57	4.05	7.88	3.63	14.16	11.37	15.74	**	*	-	-
PLACE3000374	48.65	44.25	34.93	16.2	26.01	11.78	24.23	27.25	23.51	*	*	-	-
PLACE3000387	5.55	3.77	3.38	1.58	3.57	0.43	3.58	2.95	3.21				
PLACE3000388	26.03	22.21	15.9	9.86	12.79	6.37	21.94	26.7	24.22	*		-	
PLACE3000399	15.37	13.07	9.83	5.64	4.9	3.93	10.68	11.05	9.52	**		-	

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Table 496

PLACE3000400	42.78	33.52	30.29	11.43	26.51	8.47	52.76	33.47	38.46	*		-	
PLACE3000401	137.51	137.03	95.06	91.28	111.28	51.38	81.66	72.2	62.65		*		-
PLACE3000402	8.43	7.72	4.24	2.44	6.58	2.29	8.31	7.96	5.44				
PLACE3000405	7.33	4.67	7.44	2.73	3.5	5.1	3.7	5.44	3.66				
PLACE3000406	4.67	3.39	8.42	4.46	6.89	4.16	3.34	4.69	2.59				
PLACE3000413	12.33	14.38	16.34	10.31	15.31	7.77	6.83	11.34	9.07		*		-
PLACE3000416	84.6	58.17	41.71	94.16	126.08	86.52	51.61	89.65	63.01				
PLACE3000425	2.87	4.19	4.03	2.67	4.11	2.12	2.08	0.77	1.54		*		-
PLACE3000437	6.08	4.62	9.74	3.57	11.5	3	3.57	3.67	4.77				
PLACE3000455	6.66	7.45	7.23	5.48	5.38	4.19	5.5	5.74	3.82	*	*	-	-
PLACE3000475	4.99	6.71	5.08	4.69	5.48	5.91	3.2	5.35	2.87				
PLACE3000477	12.61	9.21	10.6	8.81	9.19	10.36	8.13	7.94	5.96		*		-
PLACE4000003	30	20.47	39.94	8.43	18.43	9.82	12.11	10.52	8.23	*	*	-	-
PLACE4000008	8.19	8.19	9.59	5.97	7.85	6.93	4.18	5.57	3.47		**		-
PLACE4000009	46.86	36	37.99	37.22	51.39	35.97	11.09	18.85	7.53		**		-
PLACE4000014	18.34	18.57	19.39	16.62	19.49	16.59	6.08	13.2	15.87				
PLACE4000029	5.3	5.07	5.95	2.91	4.87	2.62	3.69	3.02	2.87		**		-
PLACE4000034	10.02	8.01	6.28	5.12	7.93	4.55	5.88	5.27	5.14				
PLACE4000049	21.86	18.28	18.64	14.38	19.7	19.05	12.54	13.96	11.06		**		-
PLACE4000052	47.63	33.03	40.39	17.99	15.08	20.28	24.01	22.07	24.29	**	*	-	-
PLACE4000062	53.46	46.6	50.02	32.69	40.48	28.08	39.71	36.99	45	*	*	-	-
PLACE4000063	56.25	68.62	67.5	55.27	69.37	73.66	45.78	60.53	44.9				
PLACE4000088	10.35	13.86	13.41	10.66	10.48	9.25	5.68	5.4	5.66		**		-
PLACE4000093	15.33	18.02	19.57	10.49	13.84	10.33	17.17	14.6	14.04	*		-	
PLACE4000100	8.21	7.32	11.21	7.61	6.2	7.32	5.19	5.2	4.71		*		-
PLACE4000103	13.85	15.73	12.84	8.67	14.38	6.43	4.02	8.73	6.65		**		-
PLACE4000106	32	18.81	23.23	18.35	21.38	15.86	17.78	20.58	18.06				
PLACE4000128	22.05	18.53	23.14	8.88	10.24	9.57	11.18	17.49	11.76	**	*	-	-
PLACE4000129	266.34	156.01	188.25	120.37	95.41	112.42	146.64	98.31	136.33	*		-	
PLACE4000131	59.1	45.51	65.57	41.68	34.82	39.78	18.29	19.7	30.83	*	**	-	-
PLACE4000147	7.89	7.51	11.76	3.51	5.07	3.96	2.77	6.32	2.52	*	*	-	-
PLACE4000156	15.48	18.75	19.37	9.1	12.85	10.65	15.8	15.48	10.02	*		-	
PLACE4000175	12.45	10.41	18.08	11.94	9.67	2.46	6.38	6.69	6.89		*		-
PLACE4000190	40.84	40.93	32.85	23.06	35.22	26.66	12.42	10.73	11		**		-
PLACE4000192	35.69	24.13	23.88	16.77	21.59	17.55	17.75	19.51	19.4				
PLACE4000206	33.82	29.03	26.48	11.73	17.97	14.5	17.45	20.16	20.02	**	*	-	-
PLACE4000211	12.98	13.88	13.86	7.96	9.94	9.19	6.64	31.04	6.54	**		-.	
PLACE4000214	13.12	6.23	9.29	3.45	7.5	4.18	4.98	7.25	13.71				
PLACE4000222	35.35	30.73	34.54	24.03	24.44	20.1	20.58	28.37	25.45	**	*	-	-
PLACE4000223	14.88	14.83	15.03	7.36	10.28	5.52	4.16	7.67	5.85	**	**	-	-
PLACE4000229	12.38	12.15	12.52	4.51	6.31	4.98	4.32	4.28	3.98	**	**	-	-
PLACE4000230	9.56	8.77	9.56	4.68	7.06	5.7	4.97	9.82	3.71	**		-	
PLACE4000233	22.71	24.01	29.85	11.57	13.98	13.77	8.53	11.22	9.26	**	**	-	-
PLACE4000239	10.07	7.4	9.42	6.8	7.34	6.09	4.48	4.54	3.54		**		-
PLACE4000247	15	11.82	15.56	9.41	13.91	8.87	8.67	6.24	7.39		**		-
PLACE4000250	16.14	18.27	20.25	16.54	17.86	12.73	10.47	8.04	11.21		**		-
PLACE4000252	10.01	5.15	12.75	1.39	3.96	3.1	2.21	3.92	2.7		*		-
PLACE4000259	25.72	27.31	16.16	12.78	19.39	8.44	8.29	19.39	9.08				
PLACE4000261	23.52	25.16	22.9	11.05	14.2	9.22	13.61	14.62	13.29	**	**	-	-
PLACE4000264	176.03	156.54	119.76	135.7	191.67	147.27	105.16	95.1	89.72		*		-
PLACE4000269	71.18	49.07	62.08	23.03	41.63	24.74	71.71	82.6	52.18	*		-	
PLACE4000270	7.6	6.37	8.9	4.69	5.92	4.81	3.06	3.68	3.44	*	**	-	-
PLACE4000281	15.26	16.07	18.29	6.09	10.92	7.61	6.44	6.66	5.1	**	**	-	-
PLACE4000300	8.43	9.82	8.78	6.3	8.5	7.03	3.68	2.93	2.96		**		-
PLACE4000320	12.37	11.22	11.92	6.27	10.09	6.43	4.47	4.26	2.85	*	**	-	-
PLACE4000323	15.16	16.25	19.16	9.12	14.06	10.9	6.05	4.54	4.03	*	**	-	-
PLACE4000326	11.15	8.97	10.53	4.35	4.69	4.13	4.28	3.68	4.65	**	**	-	-
PLACE4000344	27.71	32.93	24.51	14.27	30.44	19.64	5.14	9.78	8.98		**		-
PLACE4000347	156.82	129.54	154.28	89.79	129.04	79.82	138.06	137.09	135.75				
PLACE4000354	15.47	9.46	11.43	7.01	8.32	6.55	3.28	5.96	4.83		*		-
PLACE4000367	8.63	5.47	7.82	5.38	5.39	6.72	3.84	3.95	3.64		*		-
PLACE4000369	11.27	6.37	9.31	5.27	4.5	4.05	4.11	4.32	3	*	*	-	-
PLACE4000379	6.35	6	4.77	3.22	2.93	2.33	3.1	3.32	2.21	**	**	-	-
PLACE4000387	25.99	34.88	32.06	17.28	20.68	16.67	6.75	8.86	3.97	*	**	-	-

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PLACE4000392	8.31	9.76	11.03	3.63	5.95	3.64	5.73	2.01	2.93	**	*	-	-
PLACE4000395	53.9	51.54	53.26	20.64	28.55	18.63	37.94	35.1	44.54	**	**	-	-
PLACE4000401	4.22	3.76	3.44	3.96	3.49	2.6	3.5	3.9	1.61				
PLACE4000403	8.42	5.82	6.5	4.19	7.67	4.85	3.96	3.29	3.53		*		-
PLACE4000411	20.23	15.5	15.73	8.23	11.19	9.81	14.98	10.1	11.34	*		-	
PLACE4000415	8.15	4.8	4.61	4.06	6.07	4.23	2.98	3.98	4.5				
PLACE4000416	35.43	25.11	24.69	17.72	17.34	16.23	24.55	17.6	25.73	*		-	
PLACE4000424	43.93	33.38	31.83	13.69	19.37	13.98	27.93	23.64	33	**		-	
PLACE4000431	10.44	8.78	8.78	5.88	4.85	3.5	4.69	2.33	4.08	**	**	-	-
PLACE4000443	50.64	44.47	41.43	26.49	37.08	21.33	51.22	33.11	43.74	*		-	
PLACE4000445	5.42	4.17	3.6	3.57	7.43	5.38	2.23	3.95	2.66				
PLACE4000450	9.85	6.68	6.23	4.72	6.64	4.07	3.56	7.58	3.73				
PLACE4000455	167.91	132.51	128.81	98.87	124.22	95.79	172.16	139.08	172.24				
PLACE4000465	31.84	25.74	18.83	10.79	23.42	11.27	11.29	10.8	17.69		*		-
PLACE4000466	13.01	11.54	9.57	6.56	6.92	4.59	5.76	4.65	5.6	*	**	-	-
PLACE4000472	165.28	158.69	152.44	150.34	164.09	112.33	151.06	116.56	147.01				
PLACE4000487	10.38	6.99	9.12	4.68	4.63	2.93	3.52	2.06	3.49	*	**	-	-
PLACE4000489	6.8	7.97	5.85	3.99	5.8	4.43	4.22	4.11	4.53		*		-
PLACE4000494	70.51	55.91	43.58	29.17	31.84	24.64	72.67	73.79	78.08	*		-	
PLACE4000502	204.58	180.8	176.1	156.92	166.08	118.92	216.32	165.78	200.53				
PLACE4000521	28.26	22.58	17.07	7.12	15.76	9	21.36	20.06	19.61	*		-	
PLACE4000522	18.46	20.38	16.27	10.46	14.51	9.51	16.91	13.88	17.23	*		-	
PLACE4000537	9.79	11.19	9.86	4.99	8.2	4.43	2.5	3.6	0.68	*	**	-	-
PLACE4000548	12.35	10.52	9.27	3.9	4.07	4.41	4.08	3.04	3.64	**	**	-	-
PLACE4000558	56.63	61.59	46.82	23.74	32.06	21.71	66.44	39.24	52.93	**		-	
PLACE4000581	9.34	8.43	8.7	5.21	3.71	3.17	5.23	4.69	4.75	**	**	-	-
PLACE4000590	4.28	4.39	2.54	2.29	1.9	1.58	2.69	1.47	1.72	*		-	
PLACE4000593	9.43	8.29	6.55	6.59	7.86	5.28	9.13	5.16	4.1				
PLACE4000612	50.54	44.64	46.86	32.73	32.12	18.75	8.58	0	9.68	*	**	-	-
PLACE4000638	8.47	6.12	6.11	6.07	5.18	3.4	1.44	4.91	1.37		*		-
PLACE4000650	11.71	6	6.58	1.78	5.39	2.69	5.01	3.89	2.3				
PLACE4000651	10.02	10.01	7.86	4.63	8.67	3.43	7.21	6.04	5.23		*		-
PLACE4000654	40.79	37.09	28.74	21.7	29.39	18.93	39.41	24.87	38.02				
PLACE4000670	7.33	7.03	6.77	5.23	9.34	3.97	6.41	3.63	6.87				
PLACE4000685	27.36	21.25	28.71	7.25	13.45	14.89	8.25	13.79	8.57	*	**	-	-
PLACE4000687	5.87	2.72	5.94	3.75	3.52	3.04	2.8	3.66	2.1				
PLACE5000003	13.69	15.66	16.08	8.92	15.85	13.17	6.36	9.93	8.84		**		-
PLACE5000005	17.05	13.36	13.46	14.47	17.35	13.76	5.61	8.29	7.64		**		-
PLACE5000019	9.12	11.38	11.73	6.9	5.65	5.55	3.51	3.39	6.14	**	**	-	-
PLACE5000021	28.4	29.38	31.96	18.99	19.21	16.52	23.2	21.13	21.28	**	**	-	-
PLACE5000022	44.41	59.47	62.06	68.78	41.05	40.85	49.9	41.64	44.86				
PLACE5000024	5.49	3.54	5.62	3.22	3.37	3.62	2.52	4.61	6.39				
PLACE5000036	104.88	78.2	100.83	80.5	90.12	87.43	80.46	55.18	59.66				
PLACE5000059	13.88	12.58	10.61	5.28	9.26	6.17	6.41	11.67	8.16	*		-	
PLACE5000076	102.38	115.06	146.87	71.48	155.46	121.21	73.46	149.18	129.94				
PLACE5000117	10.83	17.74	16.15	14.79	20.06	15.63	5.73	9.53	5.57		*		-
PLACE5000143	12.99	9.49	15.16	8.13	9.83	8.06	5.81	8.66	8.8				
PLACE5000152	183.88	202.8	96.28	147.85	104.4	116.95	74.92	70.73	75.92				
PLACE5000154	90.81	108.58	44.13	75.4	77.68	45.59	40.84	23.33	50.85				
PLACE5000155	33.2	24.58	26.07	16.94	31.52	23.72	16.67	17.93	27.02				
PLACE5000165	113.75	76.52	82.55	90.32	103.03	88.36	32.72	55.94	39.36		*		-
SKNMC1000004	1323.5	940.91	1083.3	665.71	1250.5	673.39	1094.9	1184.2	1060.5				
SKNMC1000011	8.28	9.06	11.81	4.48	12.47	5.45	4.79	5.44	8.03				
SKNMC1000013	14.72	15.01	20.62	10.84	11.72	12.41	4.74	6.54	6.23		**		-
SKNMC1000014	20.79	23.92	26.42	20.23	26.13	18.1	14.76	15.14	11.78		**		-
SKNMC1000018	9.56	8.87	12.44	5.32	9.73	4.54	3.81	4.41	5.25		**		-
SKNMC1000020	25.49	27.02	25.39	13.63	25.33	12.68	18.7	20.72	21.65		**		-
SKNMC1000046	24.6	15.36	17.74	13.48	22.27	16.07	12.53	14.97	15.86				
SKNMC1000050	8.51	7.09	7.49	5.47	4.73	4.3	4.47	21.02	3.74	**		-	
SKNMC1000062	26.94	17.98	24.61	14.13	15.7	9.74	23.61	36.47	28.61	*		-	
SKNMC1000075	11.6	7.44	13.24	7.34	10.78	7.51	4.21	5.3	7.09				
SKNMC1000082	22.01	16.02	26.11	8.38	13.04	9.62	12.8	21.17	16.8	*		-	
SKNMC1000091	36.26	39.39	43.7	12.98	23.22	18.68	24.3	27.26	22.42	**	**	-	-
SKNMC1000099	11.34	8.86	15.64	6.38	7.5	4.4	5.83	7.15	6.38				

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SKNMC1000104	16.76	17.55	17.05	8.52	14.24	10.52	9.72	10.59	13.24	*	**	-	-
SKNMC1000113	45.53	34.91	35.51	20.7	25.14	23.85	18.86	24.14	23.6	*	*	-	-
SKNMC1000119	17.58	14.67	21.54	10.33	12.31	8.53	8.83	13.02	8.17	*	*	-	-
SKNMC1000142	16.52	20.57	23.49	7.26	16.72	11.75	8.01	11.68	14.09		*		-
SKNMC1000170	242.49	183.41	211.38	201.28	226.18	182.82	247.45	216.7	250.73				
SKNMC1000178	15.01	12.68	14.32	6.9	9.12	6.49	4.97	7.82	9.01	**	**	-	-
SKNMC1000194	7.33	8.61	11.61	2.23	3.73	3.19	2.64	4.74	3.45	*	*	-	-
SKNMC1000198	18.76	29.87	24.52	7.87	13.1	9.06	5.41	5.23	5.02	*	**	-	-
SKNMC1000225	100.44	119.68	87.32	52.94	84.28	50.45	35.91	33.78	44.06		**		-
SKNMC1000249	23.35	22.68	30.9	13.07	19.76	17.19	12.83	14.11	14.19		*		-
SPLEN1000007	10.7	10.7	16.74	6.92	9.27	7.23	6.86	7.37	5.89		*		-
SPLEN1000012	15.31	13.75	18.53	8.26	13.65	10.56	13.22	11.71	11.02				
SPLEN1000014	74.22	59.99	63.53	32.33	49.13	32.58	29.87	29.67	37.64	*	**	-	-
SPLEN1000036	14.69	11.54	10.05	7.95	8.19	6.93	3.18	3.76	2.42	*	**	-	-
SPLEN1000059	39.71	33.5	32.87	12.1	19.81	12.24	19.97	18.35	17.18	**	**	-	-
SPLEN1000068	20.63	22.57	21.07	11.6	16.29	10.46	9.19	11.89	8.79	*	**	-	-
SPLEN1000072	19.88	16.93	14.96	6.06	9.86	7.47	5.18	4.49	6.78	**	**	-	-
SPLEN1000101	71.97	43.16	57.46	18.69	27.56	26.8	32.73	40.27	19.97	*		-	
SPLEN1000108	7.69	6.28	7.07	3.65	4.35	2.67	3.12	2.84	2.04	**	**	-	-
SPLEN1000113	11.47	6.64	12.13	7.54	8.23	7.26	5.5	6.27	7.59				
SPLEN1000114	16.01	14.75	14.36	7.29	9.65	6.3	8.14	8.22	8.73	**	**	-	-
SPLEN1000132	5.96	4.51	7.38	2.74	4.42	2.34	1.47	2.25	2.21		*		-
SPLEN1000135	10.57	8.18	9.39	3.86	4.71	4.73	4.9	2.38	2.97	**	**	-	-
SPLEN1000136	23.91	23.93	20.23	10.77	11.86	10.15	16.69	14.04	13.77	**	**	-	-
SPLEN1000141	42.88	39.73	42.83	27.16	32.91	23.4	23.31	18.41	20.57	**	**	-	-
SPLEN1000164	15.72	13.33	13.69	7.76	12.46	6.69	9.59	8.11	9.12		**		-
SPLEN1000166	12.98	9.08	11.45	4.56	6.01	5.04	6.49	5.17	6.32	**	*	-	-
SPLEN1000175	19.26	16.94	15.5	7.48	9.23	6.92	11.34	13.49	13.41	**	*	-	-
SPLEN1000182	67.34	58.35	68.22	30.69	30.43	27.88	28.16	29.1	23.7	**	**	-	-
SPLEN1000185	6.38	8.35	5.56	4.69	4.56	3.06	2.86	2.31	1.51		**		-
THYMU1000004	48.79	34.96	41.97	30.97	32.65	27.64	26.98	17.5	13.12		*		-
THYMU1000009	14.59	13.55	14.88	8.47	10.1	5	7.34	4.91	5.62	*	**	-	-
THYMU1000015	19.34	18.55	12.08	8.34	11.37	5.93	10.39	10.96	13.03	*		-	
THYMU1000016	6.78	4.3	5.54	2.79	2.51	1.91	5.14	3.5	4.34	*		-	
THYMU1000023	6.35	6.23	6.53	4.39	3.65	4.2	3.1	5.69	3.98	**		-	
THYMU1000034	390.65	392.5	375.97	306.71	379.09	270.69	454.49	361.08	369.56				
THYMU1000035	8.93	7.8	9.14	5.88	4.95	4.81	5.06	3.93	4.36	**	**	-	-
THYMU1000037	9.69	6.41	7.36	4.28	3.96	3.33	4.24	3.59	3.83	*	*	-	-
THYMU1000042	6.85	3.93	5.82	2.75	3.24	2.02	2.08	1.63	1.09	*	*	-	-
THYMU1000047	25.64	25.03	24.74	13.43	16.94	11.38	26.77	21.58	23.81	**		-	
THYMU1000080	20.17	51.54	27.22	17.42	19.98	26.99	13.06	15.8	14.07				
THYMU1000094	11.12	6.99	9.51	6.45	6.49	4.35	11.14	9.41	9.31				
THYMU1000109	228.62	201.78	195.22	195.65	173.29	154.39	235.81	205.84	221.79				
THYMU1000127	44.2	30.97	37.5	12.05	18.11	17.75	24.49	15.04	18.2	**	*	-	-
THYMU1000130	21.64	17.3	15.84	7.65	12.45	8	10.24	3.41	8.22	*	*	-	-
THYMU1000137	6.81	10.03	8.23	3.35	5.2	3.34	4.41	2.7	3.47	*	*	-	-
THYMU1000146	11.97	7.39	7.48	8.11	7.24	6.17	5.13	3.03	6.19				
THYMU1000159	10.45	10.21	8.17	6.28	6.42	3.77	4.54	3.62	4.78	*	**	-	-
THYMU1000163	8.08	8.93	9.7	5.33	5.95	3.66	7.57	4.17	4.21	**	*	-	-
THYMU1000167	67.79	51.53	54.02	27.07	31.06	17.27	75.27	48.55	70.31	**		-	
THYMU1000186	8.38	8.15	3.89	3.94	4.49	2.65	3.36	2.91	3.02				
THYRO1000017	24	17.58	11.71	8.21	11.63	5.25	6.04	5.8	4.42		*		-
THYRO1000026	10.24	8.59	6.72	5.28	7.77	4.55	4.15	3.45	6.46		*		-
THYRO1000034	39.83	32.92	35.9	29.82	39.02	28.83	26.88	25.91	22.08		*		-
THYRO1000035	34.67	27.15	24.29	22.39	30.44	22.35	22.09	19.28	23.65				
THYRO1000036	16.2	14.28	11.79	9.92	10.8	4.36	7.94	4.75	8.23		*		-
THYRO1000040	9.47	7.71	9.48	4.32	5.83	3	5.07	3.54	5.01	*	**	-	-
THYRO1000061	18.28	19.76	15.63	8.28	5.85	4.81	6.42	5.28	9.19	**	**	-	-
THYRO1000067	16.85	13.02	12.06	8.02	8.96	4.34	7.22	6.1	5.44	*	**	-	-
THYRO1000070	9.96	13.03	10.58	5.63	9.48	4.69	20.02	18.33	15.63		*		+
THYRO1000072	21.57	19.92	18.73	19.89	17.94	12.39	9.77	9.74	9.5		**		-
THYRO1000084	9.91	5.58	5.31	3.9	6.43	2.97	10.41	8.45	10.27				
THYRO1000085	29.04	36.56	22.76	13.84	17.05	13.37	10.59	14.52	10.12	*	*	-	-
THYRO1000086	13.58	10.42	8.08	7.5	9.36	4.87	6.64	6.5	4.47				

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Table 499

THYR01000087	51.14	69.3	41.47	29.99	58.4	26.89	61.05	53.08	61.77				
THYR01000092	26.07	28.19	30.84	13.75	13.51	9.94	17.56	21.51	22.34	**	*	-	-
THYR01000093	4.26	2.01	4.16	1.77	3.46	3.25	2.69	3.3	2.41				
THYR01000099	9.62	5.87	9.26	3.68	8.63	4.69	5.9	7.16	4.32				
THYR01000107	70.48	59.74	59.68	39.34	64.57	40.78	35.76	61.82	50.34				
THYR01000111	13.96	11.92	12.38	7.04	9.78	5.89	9.55	11.53	9.66	*	*	-	-
THYR01000121	31.45	32.43	38.13	15.06	18.17	17.71	26.05	28.32	34.79	**		-	
THYR01000124	54.83	35.35	48.22	37.6	35.37	31.52	34.87	27.99	31.75				
THYR01000129	8.59	9.01	8.49	5.14	9.82	6.06	8.93	8.73	10.55				
THYR01000130	12.23	8.25	10.08	6.62	6.95	6.32	6.99	9.76	9.68	*		-	
THYR01000132	7.93	8.79	12	5.35	7.15	7.04	4.12	4.66	3.86		*		-
THYR01000134	17.2	6.06	9.3	6.24	6.27	12.5	5.33	7.31	5.41				
THYR01000144	23.66	30.56	32.27	27.55	32.97	28.83	18.04	19.4	19.02		*		-
THYR01000155	35.26	37.35	35.3	18.99	24.31	20.42	31.31	40.6	29.86	**		-	
THYR01000156	37.13	43.79	38.99	24.77	34.58	23.66	18.78	36.39	21.81	*		-	
THYR01000163	56.18	53.4	58.15	23.96	28.08	23.46	11.7	14.01	16.02	**	**	-	-
THYR01000173	8.52	8.35	6.58	5.25	10.18	4.15	3.25	4.22	4.73		**		-
THYR01000186	35.39	31.09	36.48	14.41	13.8	14.41	7.62	12.05	15.91	**	**	-	-
THYR01000187	17.39	15.95	24.02	6.63	8.73	8.87	5.49	7.02	6.9	*	**	-	-
THYR01000190	7.06	7.97	10.31	6.43	5.1	6.9	4.78	5.24	5.17		*		-
THYR01000196	8.72	14.15	13.33	14.25	10.93	7.74	3.75	6.65	9.84				
THYR01000197	13.75	17.13	15.02	14.96	17.34	16.5	8.34	11.47	6.36		*		-
THYR01000199	6.8	9.71	11.38	6.6	11.32	10.32	5.5	6.51	7.17				
THYR01000206	20.09	21.74	25.04	13.14	17.5	12.03	7.45	6.8	7.63	*	**	-	-
THYR01000221	6.96	7.15	5.44	4.48	8.31	3.94	3.81	4.45	3.66		*		-
THYR01000222	56.33	56.17	63.27	37.58	40.7	31.29	35.13	33.5	43.65	**	**	-	-
THYR01000228	148.64	127.09	184.25	73.36	64.55	57.59	55.06	55.21	55.09	**	**	-	-
THYR01000241	7.79	5.72	9.15	4.42	5	4.49	2.68	4.65	4.26	*	*	-	-
THYR01000242	18.16	23.99	29.76	25.09	51.85	27.45	12.5	20.02	16.61				
THYR01000246	21.57	18.12	24.56	19.46	20.13	15.33	9.29	10.17	9.72		**		-
THYR01000253	10.77	13.3	16.4	9.6	16.01	8.45	6.71	8.04	5.73		*		-
THYR01000270	12.58	12.99	17.24	8.11	13.02	8.87	9.06	8.16	7.99		*		-
THYR01000279	15.04	13.53	16	8.28	14.2	7.73	7.71	7.11	4.92		**		-
THYR01000285	1215.2	1221.3	1148.5	961.64	1121.8	816.57	1261.8	1135.7	1518.7				
THYR01000288	24.11	22.65	22.01	13.89	25.53	14.41	22.83	21.93	20.34				
THYR01000296	40.86	36.2	38.51	33.51	37.84	29.24	32.78	49.02	40.29				
THYR01000320	12.29	9.4	14.15	6.59	7.17	6.08	5.28	11.64	9.29	*		-	
THYR01000322	37.49	34.76	35.08	17.69	26.05	19.02	19.43	23.34	20.74	**	**	-	-
THYR01000327	29.25	26.35	19.48	16.99	27.29	15.75	10.07	12.24	13.52		*		-
THYR01000343	16.65	12.58	17.82	8.18	11.42	7.21	10.1	9.05	8.44	*	*	-	-
THYR01000345	6.25	7.77	6.06	4.74	8.59	3.02	4.68	4.72	4.12		*		-
THYR01000358	13.06	10.33	11.35	6.24	8.76	7.32	8.15	6.51	9.21	*	*	-	-
THYR01000368	5.38	5.26	6.26	3.15	3.94	2.68	6.19	3.06	2.43	**		-	
THYR01000375	14.1	11.6	18.84	8.56	5.99	5.1	3.89	3.2	3.55	*	**	-	-
THYR01000381	10.31	8.3	9.78	4.37	5.3	5.96	4.17	5.35	3.59	**	**	-	-
THYR01000387	11.39	10.61	13.54	4.54	5.97	3.46	10.59	5.84	3.07	**		-	
THYR01000394	61.78	50.97	22.02	14.67	26.91	8.08	6.98	9.73	11.33		*		-
THYR01000395	29.06	37.87	27.54	18.13	24.45	14.15	25.79	23.19	25.7	*		-	
THYR01000400	10.51	10.51	9.69	3.23	12.01	5.83	3.72	3.73	3.08		**		-
THYR01000401	10.42	9.53	10.77	6.74	5.06	4.73	3.24	5.18	5.6	**	**	-	-
THYR01000407	111.95	92.99	98.17	63.29	75.05	58.17	51.33	55.33	55.02	**	**	-	-
THYR01000420	15.01	13.25	17.92	11.1	11.62	8.56	12.79	12.37	14.41	*		-	
THYR01000438	8.38	5.22	8.85	5.12	4.11	4.31	4.22	4.7	3.13		*		-
THYR01000452	15.04	12.59	12.97	5.92	10.6	6.13	2.16	3.93	4.57	*	**	-	-
THYR01000455	7.17	8.57	9.52	2.62	3.31	3.44	2.83	2.18	2.11	**	**	-	-
THYR01000471	78.16	81.99	62.01	65.6	82.48	70.86	81.77	51.28	74.06				
THYR01000481	8.9	7.89	8.46	4.91	7.54	4.12	2.78	3.16	5.02		**		-
THYR01000484	19.83	12.76	16.87	10.37	11.59	9.38	11.21	9.7	11.91	*		-	
THYR01000488	28.64	20.75	23.35	20.89	21.13	19.59	15.6	20.62	19.42				
THYR01000501	11.59	12.72	13.28	7.74	9.03	6.79	8.05	7.95	10.26	**	*	-	-
THYR01000502	55.86	52.65	49.31	44.07	46.78	38.57	44.58	40.93	38.11	*	*	-	-
THYR01000505	9.64	7.65	7.27	5.56	5.82	3.06	3.98	5.47	2.02	*	*	-	-
THYR01000535	37.32	41.34	38.41	38.72	38.24	31.02	23.49	20.01	18.32		**		-
THYR01000556	102.92	92.57	85.3	76.31	104.96	62.73	51.56	50.77	49.93		**		-

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Table 500

THYR01000558	8.54	7.17	6.38	4.15	8.61	3.01	4.26	2.04	3.45		*		-
THYR01000569	6.63	4.92	4.79	4.77	4	3.41	3.56	3.02	3.94		*		-
THYR01000570	9.09	6.95	8.33	5.27	6.38	6.54	5.25	4.89	7.09				
THYR01000572	52.16	31.52	39.78	12.92	33.15	30.73	30.68	23.84	11.23				
THYR01000573	8.96	8.49	6.82	4.33	8.49	6.35	13.45	11.85	8.38				
THYR01000577	9.73	7.83	7.69	3.93	6.26	2.6	2.58	3.82	2.74	*	**	-	-
THYR01000580	40.56	32.54	29.95	22.22	19.86	19.81	24.19	17.34	25.52	*	*	-	-
THYR01000584	39.96	36.8	31.93	19.25	25.5	16.24	26.15	21.02	19.13	*	*	-	-
THYR01000585	8.99	7.37	6.65	4.19	6.67	4.86	5.4	3.58	2.99		*		-
THYR01000596	43.85	33.14	32.61	22.94	31.65	11.59	15.52	10.88	14.47		**		-
THYR01000602	19.04	15.25	10.78	7.23	11.51	11.78	8.87	7.72	10.81				
THYR01000605	10.06	9.44	5.91	6.29	6.99	4.61	4.9	5.21	5.08				
THYR01000615	134.15	117.37	85.97	86.81	98.31	67.18	77.31	67	84.37				
THYR01000625	33.27	24.69	16.68	12.6	10.75	20.13	8.38	6.86	11.76		*		-
THYR01000636	17.91	16.49	14.48	12.48	11.49	6.7	8.72	6.17	8.59	*	**	-	-
THYR01000637	18.22	22.2	13.43	10.39	14.05	9.78	9.07	5.2	7.26		*		-
THYR01000641	7.23	5.87	6.32	4.82	10.06	3.87	8.42	4.55	2.07				
THYR01000657	10.91	9.86	8.65	6.93	7.74	7.68	9.53	8.35	10.94	*		-	
THYR01000658	14.37	9.48	5.1	6.28	6.83	5.43	4.59	4.62	4.77				
THYR01000662	10.63	9.43	8.46	6.7	6.85	6.96	7.92	7.09	10.89	*		-	
THYR01000666	30.51	33.5	45.43	12.9	20.33	13.81	14.6	13.53	16.48	*	**	-	-
THYR01000676	11.56	11.35	8.48	6.32	9.3	8.37	4.16	5.02	6.44		*		-
THYR01000678	23.44	18.73	20.73	10.13	15.99	8.49	9	7.38	9.87	*	**	-	-
THYR01000684	27.78	27.85	20.27	12.26	16.45	11.06	26.97	17.92	24.98	*		-	
THYR01000694	16.87	11.78	10.72	5.47	10.25	5.99	12.29	9.36	8.6				
THYR01000699	9.11	6.36	4.55	5.62	6.31	3.48	7.37	3.08	5.06				
THYR01000712	17.55	14.87	12.31	9.08	11.99	7.67	12.79	9.26	13				
THYR01000715	29.82	23.25	21.02	20.98	27.37	20.44	15.76	18.98	18.68				
THYR01000716	13.12	15.14	11.94	8.87	12	7.65	7.48	6.69	6.98		**		-
THYR01000717	11.89	15.21	12.45	6.9	9.22	5.08	30.93	6.96	7.18	*		-	
THYR01000723	30.36	26.4	21.78	10.82	20.63	14.48	30.94	22.3	30.26	*		-	
THYR01000734	16.61	19.91	16.12	11.94	17.61	9.39	9.31	6.61	13.3		*		-
THYR01000748	17.46	14.06	15.87	5	7.52	5.42	7.82	5.84	7.09	**	**	-	-
THYR01000755	20.17	21.24	19.88	13.28	17.61	14.04	14.7	23.04	21.01	*		-	
THYR01000756	369.81	334.57	369.63	298.51	345.41	273.28	259.37	366.07	273.4				
THYR01000776	4.97	4.99	7.55	4.25	6.18	4.82	2.58	5.02	3.55				
THYR01000777	5.42	5.63	6.34	5.34	6.01	4.03	3.82	3.75	3.21		**		-
THYR01000779	483.37	458.9	483.51	453.87	549.42	449.1	368.6	510.93	458.47				
THYR01000782	17.27	20.25	23.35	14.58	17.12	13.37	15.61	16.4	16.35				
THYR01000783	5.74	5.45	6.68	5.43	9.62	4.88	3.62	5.19	3.8		*		-
THYR01000786	25.62	30.48	26.26	16.78	13.18	14.48	32.89	30.78	26.94	**		-	
THYR01000787	50.52	37.21	54.05	28.71	18.06	26.25	20.11	24.5	22.66	*	**	-	-
THYR01000792	14.11	12.1	15.65	4.55	5.72	7.1	8.13	7.14	8.33	**	**	-	-
THYR01000793	36.92	35.83	42.61	19.08	27.16	19.55	34.91	38.74	32.64	**		-	
THYR01000795	37.33	45.29	88.32	42.19	57.36	40.15	12.57	21.17	13.38				
THYR01000796	10.25	11.83	14.01	6.19	10.21	5.98	7	11.89	11.1				
THYR01000798	9.87	14.22	12.83	9.06	8.1	7.49	5.04	7.33	5.2	*	*	-	-
THYR01000800	37.69	54.75	19.73	33.2	22.36	23.21	13.79	16.89	13.75				
THYR01000805	8.27	6.21	6.02	5.33	8.39	4.44	3.81	4.14	3.82		*		-
THYR01000815	109.41	92.13	90.62	43.51	38.14	25.61	31.76	21.16	31.98	**	**	-	-
THYR01000829	33.86	25.13	34.71	19.68	21.68	18.45	16.87	14.34	12.65	*	**	-	-
THYR01000835	9.51	9.82	10.3	6.71	6.28	4.65	5.41	5.24	6.07	**	**	-	-
THYR01000843	27.06	16.5	24.96	16.28	19.34	15.73	6.22	7.81	8.06		**		-
THYR01000846	7.86	5.91	13.48	4.53	6.28	7.74	3.89	7.02	5.26				
THYR01000852	24.69	25.37	23.66	12.87	20.2	12.5	9.33	10.39	11.62	*	**	-	-
THYR01000855	7.12	7.47	10.43	2.52	5.79	2.98	4.3	6.1	5.2	*		-	
THYR01000865	9.21	5.67	8.64	3.4	6.56	3.18	5.99	8.76	7.67				
THYR01000866	57.27	46.1	51.69	32.85	43.74	27.97	46.24	39.05	41.55	*		-	
THYR01000881	13.67	12.21	13.18	9.6	10.62	12.24	10.21	16.82	10.91				
THYR01000894	9.33	7.11	11.4	5.66	6.12	4.31	4.14	4.68	4.75	*	*	-	-
THYR01000895	8.9	5.89	10.11	3.35	4.07	4.72	4.32	4.09	3.45	*	*	-	-
THYR01000916	9.19	7.72	16.87	5.02	6.67	5.27	4.16	6.12	3.42				
THYR01000917	6.89	10.63	12.32	4.97	9.51	5.39	6.77	7.94	6.2				
THYR01000926	14.99	10.81	12.37	6.79	9.95	6.06	7.42	7.03	11.27	*		-	

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Table 501

THYR01000934	9.21	6.94	9.67	4.17	7.52	4.26	6.41	5.73	4.96		*		-
THYR01000951	21.19	13.82	17.24	10.15	10.71	6.54	7.11	11.34	11.56	*	*	-	-
THYR01000952	38.82	45.17	51.97	24.89	24.37	18.77	17.55	26.97	13.34	**	**	-	-
THYR01000956	11.42	8.41	13.85	5.27	6.34	6.15	5.07	6.61	6.85	*	*	-	-
THYR01000960	9.97	3.83	8.63	2.78	4.13	2.34	2.46	2.03	6.43				
THYR01000961	33.04	35.26	36.48	15.01	15.48	15.21	21.6	24.41	21.14	**	**	-	-
THYR01000964	14.43	12.46	17.93	3.92	6.7	5.62	5.43	7.53	4.58	**	**	-	-
THYR01000971	15.18	16.5	16.14	8.34	13.54	9	9.38	8.59	10.52	*	**	-	-
THYR01000974	7.51	5.29	9.43	2.24	6.94	1.8	3.55	5.59	3.45				
THYR01000975	7.71	4.75	6.93	3.36	5.71	4.79	3.77	4.87	3				
THYR01000983	8.4	4.14	7.44	3.86	5.03	3.36	3.1	3.21	4.03				
THYR01000984	9.35	8.4	11.52	6.49	7.32	5.22	5.08	2.55	2.65	*	**	-	-
THYR01000988	10.2	6.57	7.62	4.27	4.23	4.6	2.94	2.66	2.92	*	**	-	-
THYR01000991	12.33	10.95	12.47	5.27	7.49	7.34	5.57	6.15	6.01	**	**	-	-
THYR01000999	9.77	12.84	10.64	5.68	8.33	5.92	5.68	3.11	2.9	*	**	-	-
THYR01001003	324.55	443.5	324.63	353.93	491.59	377.12	509.02	394.65	380.17				
THYR01001015	16.58	13.37	11.66	7.36	13.81	8.4	12.04	9.04	10.47				
THYR01001016	34.7	29.76	32.31	14.48	17.7	10.51	27.97	31.88	30.58	**		-	
THYR01001022	27.6	17.2	20.61	6.98	9.39	10.85	5.35	6.58	6.8	*	**	-	-
THYR01001031	15.75	9.57	11.29	5.12	7.05	5.99	8.13	6.39	9.34	*		-	
THYR01001033	11.34	7.57	8.58	7.55	5.52	6.01	4.3	4.01	4.9		*		-
THYR01001062	12.86	12.45	12.49	4.68	5.59	4.88	3.54	3.68	2.79	**	**	-	-
THYR01001063	10.18	8.38	10.08	5.14	7.17	4.58	3.55	4.32	2.35	*	**	-	-
THYR01001071	18.49	15.5	18.23	9.12	10.91	7.86	5.73	5.41	5.84	**	**	-	-
THYR01001080	11.77	12.06	11.47	3.65	12.27	3.17	3.08	4.59	4.41		**		-
THYR01001093	12.17	9.63	9.75	5.98	4.91	5	8.58	8.31	7.24	**		-	
THYR01001100	33.06	27.59	26.02	30.29	27.98	30.28	66.02	40.22	70.38		*		†
THYR01001102	10.18	6.7	5.95	5.04	6.9	4.52	4.36	4.71	4.45				
THYR01001104	5.1	2.75	2.78	0.69	0.92	1.62	1.32	0.94	0.7	*	*	-	-
THYR01001109	19.62	18.07	14.26	10.98	10.98	9.76	8.55	11.06	8.68	*	*	-	-
THYR01001113	10.89	6.97	7.59	2.84	3.69	2.77	2.56	1.4	2.3	*	**	-	-
THYR01001120	9.27	9	8.82	3.46	4.66	2.98	4.02	3.07	2	**	**	-	-
THYR01001121	20.41	16.36	16.91	9.1	13.05	6.93	13.22	15.3	13.97	*		-	
THYR01001128	25.09	18.24	17.74	8.53	9.61	6.74	3.45	4.7	7.82	**	**	-	-
THYR01001133	7.42	6.4	5.88	4	5.05	4.23	3.88	4.14	3.81	*	**	-	-
THYR01001134	29.23	23.66	23.28	16.51	20.53	18.49	22.14	16.92	20.47	*		-	
THYR01001142	5.04	4.99	5.1	2.78	3.05	3.47	2.44	2.26	1.6	**	**	-	-
THYR01001173	31.85	26.04	28.94	20.36	18.72	13.59	18.5	15.33	18.17	*	**	-	-
THYR01001175	95.55	98.04	80.56	104.29	114.18	77.1	51.33	46.56	49.17		**		-
THYR01001177	10.9	11.18	11.71	5.13	7.17	5.9	4.63	5.82	5.02	**	**	-	-
THYR01001189	16.52	14.55	11.53	5.76	11.24	3.42	11.07	10.9	8.86				
THYR01001194	11.83	6.2	11.19	5.29	7.22	4.28	5.84	7.01	6.86				
THYR01001204	52.04	33.32	32.8	18.53	22.19	18.27	39.75	37.94	46.59	*		-	
THYR01001205	8.98	12.23	9.39	5.39	8.08	5.04	6.55	6.04	4.85	*	*	-	-
THYR01001213	41.54	37.73	35.86	23.36	25.7	20.79	37.67	32.41	38.62	**		-	
THYR01001224	10.86	11.43	10.75	5.38	8.69	6.7	7.21	4.53	6.36	*	**	-	-
THYR01001237	16.76	20.25	15.97	16.59	13.69	5.38	9.78	5.69	6.27		**		-
THYR01001242	13.1	19.03	16.06	12.27	8.61	6.73	9.21	5.95	9.02	*	*	-	-
THYR01001258	27.32	21.68	20.65	9.74	18.76	12.77	10.51	6.86	13.04	*	**	-	-
THYR01001262	8.57	4.74	4.06	3.76	5.55	4.02	4.79	3.93	5.05				
THYR01001266	25.45	17.38	17.48	9.96	11.28	8.76	13.97	15.24	19.55	*		-	
THYR01001271	27.85	25.6	17.14	13.77	18.43	9.74	22.54	18.92	23.05				
THYR01001287	126.74	172.63	126.71	56.76	169.06	71.99	103.16	93.81	120.13				
THYR01001290	11.3	8.82	9.68	4.97	7.48	6.55	3.86	5.84	8.41	*		-	
THYR01001291	13.9	16.44	13.22	8.85	8.33	3.9	6.83	3.64	6.66	*	**	-	-
THYR01001297	13.17	12.27	11.41	6.73	6.89	4.23	7.87	5.3	8.04	**	**	-	-
THYR01001302	28.98	24.47	17.01	9.99	19.11	8.25	41.39	28.42	36.98				
THYR01001313	3.4	2.28	2.86	1.62	1.97	1.71	3.09	2.85	2.3	*		-	
THYR01001320	4.85	2.3	4.45	3.81	2.95	2.21	2.67	2.22	1.94				
THYR01001321	84.54	108.43	89.51	45.59	48.9	36.67	60.61	56.13	42.33	**	*	-	-
THYR01001322	15.07	13.59	11.8	5.6	6.9	4.45	5.91	6.73	6.71	**	**	-	-
THYR01001327	61.14	62.79	47.56	27.21	36.08	29.25	40.32	44.89	30.36	**	*	-	-
THYR01001336	21.04	18.95	13.64	17.33	15.44	11.88	17.21	14.24	12.35				
THYR01001347	42.47	35.49	29.56	20.44	37.43	12.7	20.26	16.34	15.93		**		-

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THYR01001358	6.96	7.77	6.52	4.41	8.39	3.78	5.37	5.5	4.22		*		-
THYR01001363	36.77	35.26	36.97	12.86	20.63	14.65	24.19	31.52	25.12	**	*	-	-
THYR01001365	2.39	1.31	4.42	2.3	2.69	1.43	1.82	2.18	1.5				
THYR01001374	10.11	11.14	11.66	5.19	7.75	3.64	2.84	5.3	4.44	*	**	-	-
THYR01001401	11.45	8.59	8.77	5.02	5.3	5.96	5.5	8.56	6.31	*		-	
THYR01001403	3.12	3.62	7.98	1.61	2.43	2.61	3.73	1.98	3.91				
THYR01001405	84.82	60.76	92.35	68.75	78.6	50.19	53.53	29.6	47.94		*		-
THYR01001406	13.59	7.57	12.02	4.76	6.87	3.76	11.69	13.59	9.54	*		-	
THYR01001411	4.72	4.15	5.65	3.88	2.4	3.38	2.52	2.5	3.6		*		-
THYR01001420	9.34	4.82	8.71	4.7	4.71	5.55	3.24	4.39	8.81				
THYR01001426	9.26	4.52	12.27	5.65	6.22	4.37	4.27	8.59	6.13				
THYR01001430	10.74	13.91	18.18	13.99	18.28	13.49	6.82	9.48	10.77				
THYR01001434	7.66	6.66	12.91	8.64	10.68	8.13	5.38	8.91	2.99				
THYR01001456	26.49	36.99	36.96	17.02	23.99	16.92	30.71	34.81	38.85	*		-	
THYR01001457	14.33	10.91	13.26	5.72	4.54	3.33	4.05	3.22	4.83	**	**	-	-
THYR01001458	15.32	13.83	12.78	10.99	10.13	5.72	4.4	7.29	6.97	*	**	-	-
THYR01001459	5.78	4.92	7.36	2.81	3.46	4.24	3.11	4.43	5.51	*		-	
THYR01001471	13.48	10.81	13.3	5.13	9.62	6.19	6.36	8.85	9.45	*	*	-	-
THYR01001478	8.04	3.79	8.01	2.94	3.62	2.21	4.12	4.22	3.59				
THYR01001480	16.07	16.86	14.48	6.78	13.68	13.34	3.54	6.61	19.35				
THYR01001481	16.23	13.97	17.19	13.3	15.2	13.73	4.94	6.01	3.76		**		-
THYR01001487	39.34	43.94	45.87	41.49	42.62	34.09	36.78	39.23	41.44				
THYR01001495	6.21	3.33	12.71	2.18	5.51	4.67	3.43	3.46	4.85				
THYR01001498	13.82	15.45	16.61	11.32	20.15	8.37	4.81	6.08	4.31		**		-
THYR01001510	9.97	6.87	19.31	8.41	6.21	3.55	4.99	6.45	19.57				
THYR01001512	11.51	8.21	10.34	5.87	6.36	6.84	4.43	19.67	5.22	*		-	
THYR01001519	12.05	16.47	10.9	4.73	8.69	4.14	4.42	4.28	5.04	*	**	-	-
THYR01001522	10.39	6.84	12.83	6.15	7.71	8	5.13	5.33	7.56				
THYR01001523	15.14	10.51	16.01	7.01	9.2	6.38	3.77	3.19	4.5	*	**	-	-
THYR01001526	5.67	5.48	12.84	2.85	5.19	3.09	4.51	3.63	4.01				
THYR01001529	70.52	99.68	61.07	73.62	81.82	35.88	29.07	23.9	34.69		*		-
THYR01001534	10.48	7.92	11.72	6.09	7.42	11.24	6.53	6.35	3.17		*		-
THYR01001537	5.9	3.05	5.93	3.4	3.75	2.75	3.26	2.87	4.91				
THYR01001541	27.84	38.72	38.42	23.51	30.22	18.99	22.01	26.98	14.85				
THYR01001545	12.87	9.76	11.61	3.56	6.9	5.41	4.16	22.14	4.44	**		-	
THYR01001559	143.67	217.09	127.43	126.92	211.99	217.97	165.83	143.91	101.7				
THYR01001563	29.66	25.88	28.83	14.46	17.77	19.17	10.82	18.32	17.35	**	**	-	-
THYR01001570	5.85	5.24	10.72	3.21	3.79	2.31	2.47	4.03	3.05				
THYR01001573	10.58	14.52	15.67	7.66	10.98	10.26	4.93	9.17	5.76		*		-
THYR01001584	11.71	9.79	13.05	7.75	12.43	7.3	8.19	4.92	4.88		*		-
THYR01001593	119.63	87.93	122.57	37.27	54.3	33.56	100.89	84.41	119.61	**		-	
THYR01001595	9.11	9.13	10.8	7.84	8.88	6.77	4.62	12.97	7.82				
THYR01001596	6.25	3.54	8.97	3.03	4.5	2.76	3.54	3.67	4.02				
THYR01001602	7.1	6.21	7.8	6.63	4.96	5.02	4.21	4.12	2.97		**		-
THYR01001605	28.22	39.54	25.87	13.48	23.89	22.57	11.83	10.02	13.09		*		-
THYR01001608	19.26	17.94	17.77	8.3	22	8.49	8.07	8.36	11.18		**		-
THYR01001617	7.36	9.07	12.26	4.4	5.61	3.53	3.83	3.37	4.51	*	*	-	-
THYR01001634	9.8	9.15	14.08	5.65	9.76	4.62	5.62	3.69	4.86		*		-
THYR01001637	6.56	2.42	6.39	2.18	3.8	2.31	2.41	3.7	6.48				
THYR01001641	12.87	8.05	12.44	6.03	4.87	6.49	3.32	2.86	2.92	*	**	-	-
THYR01001656	20.03	12.66	30.89	7	10.07	5.22	6.32	7.53	5.64				
THYR01001658	7.58	6.85	10.14	4.65	4.77	3.94	3.38	2.8	2.5	*	**	-	-
THYR01001661	150.1	98.3	106.51	135.25	166.2	125.8	74	80.32	53.76				
THYR01001671	10.97	8.43	12.21	5	5.04	3.97	5.12	5.12	3.84	**	**	-	-
THYR01001672	12.9	11.31	11.75	5.85	6.91	5.08	3.69	2.74	2.72	**	**	-	-
THYR01001673	31.04	28.57	26.79	16.85	19.7	19.9	22.8	23.43	23.51	**	*	-	-
THYR01001677	8.63	6.86	9.97	3.55	4.9	4.2	5.4	6.55	6.85	*		-	
THYR01001683	39.34	16.85	25.87	16.11	18.7	19.17	8.36	10.76	9.09				
THYR01001700	12.31	7.03	9.15	3.61	4.23	3.04	2.79	3.63	4.8	*	*	-	-
THYR01001702	23.7	21.62	17.4	10.57	5.8	11.44	6.01	4.83	2.94	*	**	-	-
THYR01001703	7.22	4.23	5.14	2.63	3.23	1.81	2.37	2.42	2.04	*	*	-	-
THYR01001706	8.39	5.62	8.09	3.72	3.11	3.37	3.24	2.65	1.26	*	**	-	-
THYR01001721	11.69	10.42	16.73	6.09	4.98	4.46	3.92	2.33	3.87	*	**	-	-
THYR01001725	147.69	144.4	144.74	111.99	128.3	86.63	130.43	106.61	93.76	*	*	-	-

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Table 503

THYR01001730	7.74	3.57	7.41	4.48	4.19	3.07	3.64	4.09	4.72				
THYR01001738	1.57	3.03	2.24	0.97	0.17	0.58	0.7	0.99	1.64	*		-	
THYR01001743	5.12	3.48	3.39	1.67	2.12	2.94	1.98	2.6	2.48				
THYR01001745	30.25	14.84	20.6	6.81	4.65	9.25	12.7	8.09	11.05	*		-	
THYR01001746	10.78	5.89	7.69	2.83	3.1	3.64	3.64	1.32	2.13	*	*	-	-
THYR01001770	20.01	12.02	16.57	10.05	13	10.49	5.37	6.07	5.43		*		-
THYR01001772	29.2	56.08	29.11	28.47	34.34	15.95	9.21	8.24	9.37		*		-
THYR01001778	39.03	35.61	22.42	13.39	32.45	16.04	9.42	8.03	11.2		*		-
THYR01001793	9.35	3.26	5.98	4.02	4.49	3.37	4.45	4.26	5.77				
THYR01001796	66.96	62.34	52.36	31.61	31.58	30.06	74.83	63.67	78.59	**		-	
THYR01001800	25.21	17.42	21.74	19.92	16.43	13.71	8.41	10.02	11.59		**		-
THYR01001803	12.96	11.11	10.61	7.04	8.3	3.44	5.71	5.48	6.64	*	**	-	-
THYR01001809	10.44	7.96	6.8	4.59	3.72	3.71	3.62	1.76	1.34	*	**	-	-
THYR01001817	18.78	13.28	15.51	15.03	13.53	6.93	8.79	4.88	8.37		*		-
THYR01001819	14.15	14.31	9.69	5.8	6.63	6.06	6.27	4.29	5.81	*	*	-	-
THYR01001828	8.14	8.22	6.65	5.42	7.94	4.29	7.29	4.26	2.47				
THYR01001854	50.53	32.88	37.71	33.17	34.18	22.81	22.16	27.13	21.15		*		-
THYR01001895	9.86	7.83	3.92	4.41	4.53	2.55	3.7	10.54	3.46				
THYR01001907	27.03	13.41	12.49	9.48	10.54	7.02	4.92	4.41	6.47				
TRACH1000006	9.54	7.16	8.08	5.68	4.66	5.53	6.46	4.52	6.76	*		-	
TRACH1000013	9.02	5.8	8.2	2.58	4.45	3.1	3.07	2.02	4.14	*	*	-	-
TRACH1000074	13.69	9.32	8.63	4.66	5.76	4.06	6.37	3.07	3.63	*	*	-	-
TRACH1000095	11.28	8.48	10.55	5.54	3.9	3.41	3.79	4.56	3.68	**	**	-	-
TRACH1000102	26.86	26.3	20.1	15.81	18.57	15.2	32.52	24.6	27.09	*		-	
TRACH1000108	88.66	59.61	40.48	28.57	26.39	20.8	69.3	56.08	66.91				
TRACH1000126	17.36	13.19	13.78	8.07	9.6	6.46	5.91	5.75	6.51	*	**	-	-
TRACH1000146	7.25	6.83	5.07	5.29	3.75	3.17	3.49	3.25	4.97		*		-
TRACH1000160	11.76	11.24	7.7	4.05	5.59	4.95	5.32	4.22	5.87	*	*	-	-
TRACH1000184	33.51	45.86	50.29	14.82	25.81	22.15	25.29	16.88	23.76	*	*	-	-
VESEN1000004	11.35	8.9	8.13	5.46	9.59	6.32	5.53	5.44	6.01		*		-
VESEN1000007	32.64	30.13	26.81	16.7	21.99	18.54	37.52	29.73	33.89	**		-	
VESEN1000013	13.16	11.68	12.05	7.19	9.9	4.25	7.18	4.46	8.92	*	*	-	-
VESEN1000028	23.17	20.53	28.94	10.16	15.29	14.76	9.13	12.72	8.48	*	**	-	-
VESEN1000059	4.76	3.32	5.57	3.56	3.32	3.56	1.16	3.33	1.96				
VESEN1000100	8.85	5.84	8.92	5.55	6.82	5.48	3.69	5.59	3.98		*		-
VESEN1000107	158.28	125.83	134.47	126.46	135.37	133.6	74.61	79.36	82.66		**		-
VESEN1000117	3.74	4.02	10.93	3.48	5.02	4.1	2.18	2.11	2.69				
VESEN1000122	5.84	5.31	7.17	3.91	7.47	3.29	2.52	3.75	2.41		*		-
VESEN1000137	7.93	10.91	7.7	8.31	5.46	4.02	3.34	3.36	5.77		*		-
VESEN1000195	12.47	4.75	10.07	4.43	4.22	7.07	3.11	4.32	13.25				
VESEN1000215	89.55	69.15	78.83	74.46	93.71	81.06	50.08	36.95	43.24		**		-
VESEN1000279	16.42	11.12	19.97	7.86	19.23	9.52	8.84	13.86	21.33				
VESEN1000363	40.43	29.46	56.48	41.4	53.72	50.13	17.51	33.82	20.25				
VESEN1000388	4.51	6.13	9.09	5.56	8.45	6.21	3.44	6.29	2.57				
VESEN1000394	137.33	123.92	135.03	107.32	177.33	115.58	81.85	76.56	86.04		**		-
VESEN1000410	7.84	11.73	12.31	7.37	8.85	7.32	5.82	6.16	5.5		*		-
VESEN1000411	14.34	16.7	11.87	14.26	14.7	9.52	6.54	4.28	7.07		**		-
VESEN1000415	6.65	6.22	8.5	3.16	5.01	4.35	2.06	3.93	7.37	*		-	
VESEN1000440	7.1	4.56	7.48	10.06	4.69	9.04	3.62	6.97	6.76				
VESEN1000452	127.08	114.54	102.58	100.33	106.23	122.79	77.87	58.16	82.71		*		-
VESEN1000539	57.4	47.68	67.32	36.3	45.7	42.57	51.56	51.15	50.18				
VESEN1000554	7.29	12.24	14.13	6.05	4.57	6.75	3.69	3.4	3.85		*		-
VESEN1000557	4.5	6.91	10.86	5.64	5.73	4.35	3.05	2.96	4.75				
VESEN1000575	16	18.27	24.28	11.3	16.07	11.77	13.59	13.83	16.27				
VESEN1000585	14.4	14.28	13.38	9.87	13.37	6.72	4.91	4.08	5.01		**		-
VESEN1000592	28.09	20.04	22.75	8.98	11.53	7	7.53	8.48	8.84	**	**	-	-
VESEN1000658	9.27	5.98	6.99	4.92	3.93	3.11	3.31	12.18	6.06	*		-	
VESEN1000669	7.65	11.62	18.09	8.2	9.11	7.91	4.21	6.96	3.61				
VESEN1000743	27.12	25.27	28.49	19.46	23.17	19.77	12.01	15.14	12.53	*	**	-	-
VESEN1000752	23.77	18.91	24.8	11.19	11.63	9.8	14.24	19.48	18.19	**		-	
VESEN1000761	7.03	8.3	9.9	5.64	5.41	3.65	3.1	8.25	5.47	*		-	
VESEN2000039	16.58	20.4	16.46	7.12	12.23	7.45	5.23	4.66	6.91	*	**	-	-
VESEN2000102	15.76	17.97	17.55	7.45	12.52	8.13	11.35	8.16	13.31	*	*	-	-
VESEN2000164	69.66	54.85	54.07	18.32	20.39	15.6	15.69	21.51	20.97	**	**	-	-

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Table 504

VESEN2000175	7.45	6.95	7.39	3.43	6.1	3.72	4.64	8.1	4.35	*		-	
VESEN2000186	18.04	20.73	21.8	11.19	14.77	10.58	8.74	12.84	12.61	**	**	-	-
VESEN2000199	11.71	6.48	9.96	8.59	9.24	5.52	6.89	6.26	14.79				
VESEN2000200	150.21	142.83	144.63	172.94	215.31	128.05	93.38	87.48	97.05		**		-
VESEN2000204	7.05	7.07	9.65	4.56	4.24	3	2.19	4.63	3.19	*	*	-	-
VESEN2000218	16.65	12.07	17.29	7.31	8.24	6.16	8.32	5	5.15	**	**	-	-
VESEN2000230	12.09	13.48	13.57	4.57	10.45	4.08	3.93	4.19	2.98	*	**	-	-
VESEN2000272	8.95	9.01	11.14	4.32	3.66	3.22	4.36	3.53	4.22	**	**	-	-
VESEN2000299	8.61	7.23	11.81	5.04	5.83	4.25	3.6	5.71	4.76	*	*	-	-
VESEN2000323	17.3	12.74	15.22	15.36	17.47	14.24	5.84	6.35	4.65		**		-
VESEN2000327	18.5	9.19	14.45	6.81	8.17	7.45	3.2	5.07	5.85		*		-
VESEN2000328	7.53	7.78	8.38	3.45	4.17	4.12	2.35	2.19	1.81	**	**	-	-
VESEN2000330	25.07	20.15	22.73	13.34	18.45	13.16	15.63	15.15	15	*	**	-	-
VESEN2000336	7.29	9.37	11.82	5.86	9.09	5.78	3.64	3.5	5		*		-
VESEN2000354	10.99	9.78	10.4	5.27	8.22	4.93	3.58	3.58	2.59	*	**	-	-
VESEN2000378	168.58	110.88	139.59	81.44	99.69	74.23	74.17	76.59	54.75	*	*	-	-
VESEN2000379	32.08	21.47	28.34	16.72	15.12	13	22.77	26.45	21.84	*		-	
VESEN2000397	21.17	10.11	25.4	12.77	12.2	10.8	15.72	16.01	17.99				
VESEN2000416	5.92	5.21	7.48	3.5	6.28	4.01	2.87	3.94	3.48		*		-
VESEN2000420	8.47	4.35	7.18	4.04	3.81	2.46	2.31	4.27	1.92				
VESEN2000430	8.74	5.76	7.33	2.94	5.32	2.11	1.8	2.27	0.71	*	**	-	-
VESEN2000448	14.67	14.58	16.08	4.71	4.34	2.88	3.91	2.23	2.27	**	**	-	-
VESEN2000449	46.1	50.29	39.97	32.75	32.82	21.56	37.62	28.99	23.73	*	*	-	-
VESEN2000456	45.88	33.52	32.47	18.88	21.08	19.47	15.48	22.28	22.31	*	*	-	-
VESEN2000562	6.11	3.13	4.69	5.4	3.95	3.19	3.24	2.45	2.42				
VESEN2000573	26.67	20.52	18.39	14.29	11.45	8.79	8.94	7.46	12.2	*	*	-	-
VESEN2000604	9.02	7.76	4.59	4.65	4.32	4.42	1.84	4.41	1.34		*		-
VESEN2000614	9.59	7.78	6.05	4.77	5.05	4.35	3	3.94	2.87	*	*	-	-
VESEN2000638	16.75	10.83	10.74	6.38	9.46	6.26	4.67	4.46	3.5		*		-
VESEN2000641	15.71	14.29	14.25	7.95	7.6	6.71	8.94	7.41	6.6	**	**	-	-
VESEN2000645	9.28	11.51	10.66	5.27	8.01	4.95	5.42	4.96	6.81	*	**	-	-
Y79AA1000013	24.66	15.88	15.09	6.08	5.43	5.53	13.59	13.07	18.88	*		-	
Y79AA1000030	19.52	16.62	14.47	8.07	7.77	10.99	7.86	7.77	10.02	*	**	-	-
Y79AA1000033	29.91	18.65	28.38	16.37	15.72	11.59	28.15	19.64	28.85	*		-	
Y79AA1000037	4.94	2.8	4.89	5.26	3.24	0.91	1.44	1.94	2.43		*		-
Y79AA1000041	79.98	53.74	54.67	39.77	36.14	29.21	42.77	30.09	45.97	*		-	
Y79AA1000059	9.8	7.3	8.44	4.37	5.08	2.06	5.32	3.01	5.11	*	*	-	-
Y79AA1000065	116.14	101.03	106.53	93.49	124.96	111.44	68.74	63.93	65.56		**		-
Y79AA1000081	7.88	11.03	9.72	7.03	9.28	7.22	5.68	4.38	3.88		**		-
Y79AA1000127	8	5.82	6.2	3.17	4.25	2.35	5.28	6.34	4.47	*		-	
Y79AA1000130	20.16	11.01	14.68	13.04	8.43	8.05	14.41	16.35	14.16				
Y79AA1000131	17.14	8.99	11.18	6.93	10.63	6.92	6.82	8.55	6.52				
Y79AA1000134	6.34	7.52	5.68	7.86	5.61	3.09	4.16	2.2	3.07		*		-
Y79AA1000143	8.89	7.38	8.14	3.93	5.83	3.75	3.23	2.53	3.96	*	**	-	-
Y79AA1000144	11.79	8.62	9.18	5.64	6.37	5.56	3.97	3.84	3.36	*	**	-	-
Y79AA1000150	28.57	28.05	20.04	12.4	17.77	10.86	24.46	16.09	20.29	*		-	
Y79AA1000153	11.32	11.62	7.41	5.89	9.36	6.53	6.84	5.59	6.52				
Y79AA1000166	13.75	6.3	9.45	4.16	5.68	2.88	7.42	8.85	8.76				
Y79AA1000179	13.15	8.67	7.74	7.91	7.5	4.67	13.52	5.81	9.18				
Y79AA1000181	14.37	9.22	8.77	6.64	8.41	3.93	3.41	3.97	4.65		*		-
Y79AA1000202	22.9	17.78	19.17	14.55	12.31	8.36	18.27	13.59	20.94	*		-	
Y79AA1000207	52.28	63.3	44.9	24.04	38.89	23.79	15.85	13.31	14.27	*	**	-	-
Y79AA1000214	9.44	4.9	5.66	4.71	4.79	4.18	5.54	2.28	3.2				
Y79AA1000222	11.34	8.61	7.95	5.13	7.04	2.26	4.7	3.53	4.67		*		-
Y79AA1000226	27.21	25.59	19.24	12.19	15.74	11.35	24.75	16.69	21.48	*		-	
Y79AA1000227	9.07	6.57	6.62	3.66	4.45	3.9	7.4	6.45	7.51	*		-	
Y79AA1000230	32.97	25.47	29.26	12.55	10.05	6.68	4.18	3.82	4.93	**	**	-	-
Y79AA1000231	65.27	41.2	48.87	47.4	47.89	24.64	28.97	32.14	28.29		*		-
Y79AA1000239	74.35	85.68	67.35	68.07	52.75	45.41	64.49	54.97	44.91				
Y79AA1000258	8.42	5.48	5.2	4.36	4.01	3.09	3.34	2.93	4.62				
Y79AA1000268	80.53	75.19	49.36	22.18	30.03	27.42	30.39	28.87	31.5	*	*	-	-
Y79AA1000269	73.43	71.24	52.77	41.13	70.01	36.67	77.91	62.7	65.45				
Y79AA1000270	10.85	7.03	4.1	4.98	7.95	3.4	5.03	5.7	4.72				
Y79AA1000280	25.49	25.11	28.96	8.6	12.9	9.27	5.74	8.76	6.26	**	**	-	-

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Table 505

Y79AA1000285	22.27	16.31	18.63	6.85	10.3	7.36	15.47	22.31	18.9	**		-	
Y79AA1000295	4.35	2.68	5.01	1.59	3.76	2.11	2.3	2.59	2.22				
Y79AA1000307	6.82	4.93	8.12	6.39	9.3	7.36	3	5.88	4.49				
Y79AA1000313	4.28	2.34	3.94	1.66	3.1	3.25	1.93	2.47	1.62				
Y79AA1000314	1.57	1.83	4.11	1.4	1.41	0.98	0.87	0.14	1.73				
Y79AA1000328	3.78	3.39	5.43	2.09	10.7	2.68	3.27	3.33	3.32				
Y79AA1000334	9.59	9.06	7.49	5.79	6.64	3.5	5.12	3.62	4.02	*	**	-	-
Y79AA1000342	17.48	13.29	18.31	13.02	15.9	13.67	34.2	31.79	30.43		**		+
Y79AA1000346	17.08	11.48	18.69	8.72	9.82	6.74	5.35	5.97	4.15	*	**	-	-
Y79AA1000347	28.82	26.71	31.26	22.14	31.96	28.74	20.9	20.82	19.69		**		-
Y79AA1000349	15.95	20.35	20.7	17.44	19.4	18.58	5.37	7.08	5.15		**		-
Y79AA1000355	11.9	11.6	17.89	14.98	13.32	9.11	5.25	6.54	7.95		*		-
Y79AA1000368	5.31	4.56	7.88	4.89	6.47	3.77	2.77	3.21	1.95		*		-
Y79AA1000388	9.85	11.63	11.71	9.62	9.75	4.51	5.03	4.57	5.04		**		-
Y79AA1000392	13.05	13.68	11.25	7.92	12.06	6.34	12.1	13.67	13.52				
Y79AA1000405	100.68	62.31	79.28	103.67	109.59	81.35	71.19	52.24	66.44				
Y79AA1000410	8.13	6.1	10.22	6.13	5.36	5.28	4.83	4.8	5.17				
Y79AA1000420	11.1	11.77	13.46	5.41	8.52	5.43	6.77	7.21	5.64	*	**	-	-
Y79AA1000423	7.61	9.21	8.96	4.46	6.29	5.4	4.36	2.75	3.4	*	**	-	-
Y79AA1000426	5.75	6.96	10.06	4.68	5.08	3.97	3.38	2.69	2.24		*		-
Y79AA1000432	5.62	5.18	10.2	4.71	5.75	4.03	2.85	3.99	8.12				
Y79AA1000453	32.42	33.52	37.01	20.21	25.21	18.7	36.98	32.84	33.05	**		-	
Y79AA1000465	4.43	1.91	3.14	1.7	4.29	1.76	2.57	2.29	2.11				
Y79AA1000469	35.31	28.37	27.42	30.17	34.28	32.32	21.89	31.66	24.15				
Y79AA1000480	11.78	8.51	13.38	5.22	5.02	5.9	5.84	10.93	8.28	*		-	
Y79AA1000502	19.24	16.15	21.16	8.66	14	12.35	16.39	18.08	18.17	*		-	
Y79AA1000521	75.16	71.09	84.73	74.85	78.28	67.85	48.04	51.73	45.89		**		-
Y79AA1000534	13.31	15.15	20.4	13.25	14.05	10.71	13.15	11.71	11.75				
Y79AA1000538	12.36	14.67	20.45	9.58	11.27	5.96	3.97	0	4.64		**		-
Y79AA1000539	15.51	16.32	14.99	9.48	12.74	10.1	5.39	5.2	6.13	*	**	-	-
Y79AA1000540	10.2	7.44	12.08	3.41	6.65	4.35	12.15	10.44	10.32	*		-	
Y79AA1000560	180.34	128.09	149.28	162.08	194.06	150.66	118.75	125.1	108.26				
Y79AA1000574	12.15	9.72	10.83	5.66	8.8	4.53	10.59	16.21	10.56	*		-	
Y79AA1000584	40.26	35.5	37.1	23.89	28.68	25.51	26.96	34.59	37.41	**		-	
Y79AA1000589	9.65	4.15	9.45	2.79	3.53	2.1	3.54	8.38	4.6				
Y79AA1000598	34.26	29.42	37.32	17.43	15.95	16.46	24.99	27.55	21.09	**	*	-	-
Y79AA1000600	44.58	45.66	51.58	51.4	52.23	38.65	32.06	30.08	26.05		**		-
Y79AA1000609	7.91	6.61	8.76	1.95	5.66	3.3	3.74	4.36	7.05	*		-	
Y79AA1000618	20.27	20.13	21.51	6.61	13.31	6.56	19.86	14.92	16.1	**		-	
Y79AA1000627	18.35	16.53	18.66	9.09	10.58	9.21	14.78	8.21	19.69	**		-	
Y79AA1000636	5.21	2.52	7.03	3.36	4.46	4.2	2.54	3.13	1.94				
Y79AA1000649	19.51	21.35	25.26	12.58	12.75	9.69	16.99	19.63	19.13	**		-	
Y79AA1000656	7.37	5.14	7.46	2.86	2.97	2.28	2.83	3.72	2.99	**	*	-	-
Y79AA1000673	8.38	7.17	11.58	4.74	3.99	5.74	1.87	4.27	2.18	*	*	-	-
Y79AA1000674	131.64	157.11	127.73	143.89	140.32	116.2	111.11	118.96	120.08				
Y79AA1000678	22.12	27.62	25.96	12.61	21.55	13.08	21.7	19.94	19.36	*		-	
Y79AA1000682	14.62	11.86	13.44	6.55	8.13	6.38	12.74	13.35	11.29	**		-	
Y79AA1000683	37.64	24.6	33.28	19.88	16.2	12.73	33.87	33.73	36.17	*		-	
Y79AA1000697	46.01	35.33	48.41	23.15	27.46	23.15	15.24	20.88	15.95	*	**	-	-
Y79AA1000700	3.64	3.69	5.68	3.34	3.06	2.62	3.53	2.27	2.51				
Y79AA1000702	50.6	33.01	36	23.71	24.96	18.05	18.21	11.97	15.36	*	*	-	-
Y79AA1000704	93.86	71.31	88.5	110.92	93.16	106.68	74.22	61.46	46.95				
Y79AA1000705	6.23	6.74	7.37	1.82	2.22	2.09	2.28	0.26	2.39	**	**	-	-
Y79AA1000717	8.36	6.77	8.13	4.96	8.96	4.55	2.44	3.74	2.84		**		-
Y79AA1000722	10.83	11.52	10.81	4.97	5.79	3.98	6.28	5.41	5.45	**	**	-	-
Y79AA1000724	42.59	35.15	44.52	31.42	30.43	23.04	24.2	29.89	31.56	*	*	-	-
Y79AA1000726	8.78	4.43	7.31	5.15	4.77	4.25	2.41	3.94	2.09		*		-
Y79AA1000734	5.72	4.05	6.45	2.81	2.76	3.46	2.68	2.98	0.98	*	*	-	-
Y79AA1000748	7.45	7.72	6.69	2.89	2.82	2.75	2.52	2.6	2.35	**	**	-	-
Y79AA1000750	41.52	33.1	33.65	18.03	22.65	18.6	26.15	29.63	22.6	**	*	-	-
Y79AA1000752	9.11	9.26	10.14	4.75	3.47	2.23	2.34	2.01	1.29	**	**	-	-
Y79AA1000774	19.25	19.31	26.89	10.74	13.71	10.53	12.54	14.59	12.73	*	*	-	-
Y79AA1000776	12.05	9.97	9.69	5.12	6.81	2.36	10.58	10.24	7.92	*		-	
Y79AA1000777	17.61	11.59	13.15	7.32	8.15	7.21	6.02	5.12	6.68	*	*	-	-

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Table 506

Y79AA1000778	20.06	13.62	11.66	10.8	9.69	8.29	13.52	13.51	12.96				
Y79AA1000782	11.43	7.55	9.19	7.76	8.46	7.38	6.62	5.21	4.82		*		-
Y79AA1000784	13.14	10.21	12.84	4.67	6.08	6.71	10.7	9.6	9.71	**		-	
Y79AA1000794	46.19	39.88	38.82	22.35	24.71	16.75	37.28	33.24	34.17	**		-	
Y79AA1000800	7.18	3.91	5.09	0.48	0.36	0.17	2.34	0	0	**	*	-	-
Y79AA1000802	11.45	13.12	10.85	5.78	8.8	4.96	3.89	4.75	3.77	*	**	-	-
Y79AA1000805	21.22	18.33	12.77	6.7	11.14	4.1	15.87	12.52	16.72	*		-	
Y79AA1000814	27.49	21.74	19.65	16.59	17.35	12.96	22	17.22	22.17				
Y79AA1000823	14.24	7.73	9.85	4.94	4.36	5.06	6.73	6.96	8.36	*		-	
Y79AA1000824	16.24	10	9.76	8.11	9.28	6.16	6.82	5.83	8.72				
Y79AA1000827	9.71	3.82	4.6	3.63	3.22	2.56	3.51	2.06	2.83				
Y79AA1000831	7.38	5.79	7.27	4.13	3.32	2.68	4.43	0.57	1.26	**	*	-	-
Y79AA1000833	22.35	19.25	16.88	12.38	7.9	8.89	19.38	11.86	18.04	**		-	
Y79AA1000850	33.44	40.57	26.99	19.52	21.81	14.62	28.93	23.5	32.01	*		-	
Y79AA1000856	6.26	7.4	4.9	2.81	6.29	2.12	4.31	2.48	3.63		*		-
Y79AA1000862	8.84	4.04	5.05	7.04	4.31	3.07	5.61	5.34	5.05				
Y79AA1000876	21.17	10.25	11.73	7.67	6.82	6.01	5.79	7.01	6				
Y79AA1000888	32.02	25.94	21.68	17.64	17.29	12.59	18.41	20.33	23.17	*		-	
Y79AA1000902	6.26	5.68	6.17	4.27	4.4	2.72	2.73	2.97	2.19	*	**	-	-
Y79AA1000935	76.11	52.08	52.32	70.65	71.58	69.22	39.77	35.2	32.3		*		-
Y79AA1000959	48.22	40.7	37.08	25.45	33.48	19.11	26.33	21.44	21.93	*	**	-	-
Y79AA1000962	46.82	45.31	38.99	22.79	24.29	17.48	60.82	38.12	53.14	**		-	
Y79AA1000963	25.33	35.17	19.37	13.71	17.32	12.79	14.75	14.39	13.92				
Y79AA1000966	41.31	37.86	31.25	27.6	23.69	23.7	32	18.68	25.22	*		-	
Y79AA1000967	19.13	9.69	10.03	8.88	7.99	4.65	1.27	8.2	0.25				
Y79AA1000968	25.81	16.48	14.41	11.57	12.79	6.94	25.2	19.6	28.68				
Y79AA1000969	40.02	39.97	33.37	23.55	39.74	36.04	32.93	30.52	18.66				
Y79AA1000976	22.75	15.17	16.99	14.98	19.84	15.88	14.85	10.98	11.26				
Y79AA1000978	8.83	7.09	6.8	4.57	5.39	2.66	4.35	3.43	4.33	*	**	-	-
Y79AA1000985	8.02	3.9	5.83	4.32	4.39	1.76	4.37	2.17	1.99				
Y79AA1000989	295.68	243.92	218.77	78.52	138.6	77.87	70.03	46.49	61.43	**	**	-	-
Y79AA1000991	12.26	8.35	10.64	5.63	5.93	8.76	7.23	8.65	6.01				
Y79AA1001013	42.37	37.07	51.31	24.72	27.17	18.23	24.27	34.59	22.31	*	*	-	-
Y79AA1001014	16.53	17.99	19.41	12.93	20.24	14.74	13.35	18.92	15.51				
Y79AA1001019	8.07	6.21	8.29	4.14	6.05	5.04	2.84	5.3	3.51	*	*	-	-
Y79AA1001020	13.89	16.72	13.86	21.03	12.53	10.76	9.5	10.16	11.46		*		-
Y79AA1001023	7.28	6.24	9.28	4.31	8.03	5.29	3.01	3.87	2.51		*		-
Y79AA1001030	28.41	43.95	33.86	36.62	21.08	22.74	16.86	22.85	18.21		*		-
Y79AA1001035	10.6	13.73	10.93	9.68	10.73	7.69	7.26	7.72	8.91		*		-
Y79AA1001041	14.5	11.14	15.3	8.73	9.98	7.28	9.17	13.51	15.31	*		-	
Y79AA1001043	22.79	19.12	22.36	8.78	13.48	10.29	9.42	13.86	17.78	**	*	-	-
Y79AA1001048	12.86	13.5	12.88	6.65	11.19	7.59	6.44	7.55	6.3	*	**	-	-
Y79AA1001056	6.67	9.77	12.37	5.42	9.5	6.82	2.1	3.99	2.72		*		-
Y79AA1001061	11.12	17.1	15.18	5.75	10.72	7.78	8.04	10.36	12.77	*		-	
Y79AA1001062	4.7	4.96	6.24	2.95	3.71	2.56	2.92	2.19	2.28	*	**	-	-
Y79AA1001068	6.22	3.59	5.75	4.34	5.98	4.49	3.29	3.38	3.07				
Y79AA1001073	17.6	17.56	20.08	5.98	13.24	7.19	16.17	13.71	20.42	*		-	
Y79AA1001077	7.3	2.86	6.26	7.08	4.43	3.45	1.86	5.22	1.86				
Y79AA1001078	7.29	5.05	6.25	3.73	4.63	2.99	3.3	5.06	3.66	*		-	
Y79AA1001081	7.84	5.5	8.85	3.05	3.81	3.52	2.8	3.1	3.74	*	*	-	-
Y79AA1001088	36.17	40.23	42.34	24.5	22.27	19	24.36	30.94	32.13	**	*	-	-
Y79AA1001089	332.88	366.62	308.34	284.36	390.54	406.65	237.36	376.46	392				
Y79AA1001090	7.05	4.26	8.66	4.12	3.36	2.71	3.39	1.8	2.5		*		-
Y79AA1001105	22.53	22.64	23.57	8.51	14.07	9.94	17.11	15.32	15.62	**	**	-	-
Y79AA1001142	114.5	98.72	131.88	102.55	114.58	143.24	69.56	60.81	74.51		*		-
Y79AA1001145	98.33	98.57	100.63	125.36	121.38	91.71	78	59.2	74.76		**		-
Y79AA1001162	126.48	83.55	107.65	92.38	93.62	73.32	97.56	124.59	105.84				
Y79AA1001167	12.61	7.85	13.06	7.92	8.62	6.56	7.15	16.96	9.58				
Y79AA1001176	75.12	80.1	84.48	76.52	65.54	64.34	46.71	59.03	47.45		**		-
Y79AA1001177	8.46	7.48	10.23	4.06	5.51	3.51	3.45	4.68	2.96	*	**	-	-
Y79AA1001179	54.1	53.61	67.63	28.64	33.09	26.42	13.82	47.33	10.91	**		-	
Y79AA1001185	32.79	30.94	36.04	15.68	21.34	16.32	19.9	17.65	25.06	**	**	-	-
Y79AA1001201	45.08	50.33	41.06	13.71	31.35	17.81	48.16	43.78	38.95	*		-	
Y79AA1001205	18.73	12.88	21.83	8.38	8.46	6.14	7.31	11.86	11.81	*		-	

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Table 507

Y79AA1001211	21.15	21.66	22.83	13.08	12.91	10.43	0.44	20.18	19.17	**		-	
Y79AA1001212	128.68	116.33	107.84	151.9	151.84	105.91	80.87	83.57	67.14		**		-
Y79AA1001216	31.68	27.07	33.84	18.3	19.09	14.63	17.05	18.24	23.12	**	*	-	-
Y79AA1001228	7.97	5.25	12.95	3.35	3.4	3.64	3.41	10.17	4.89				
Y79AA1001233	8.26	6.53	16.79	3.45	3.77	2.51	2.28	3.79	3.13				
Y79AA1001236	8.84	5.25	11.14	5.02	5.53	3.13	4.08	4.7	2.24				
Y79AA1001239	74.22	59.48	53.54	45.62	83.11	43.05	50.35	42.44	46.18				
Y79AA1001240	70.83	49.07	64.4	30.83	35.04	20.32	48.49	59.48	54.67	*		-	
Y79AA1001255	8.89	10.29	10.55	7.47	6.78	6.42	0.72	6.35	0.76	**	*	-	-
Y79AA1001264	14.2	10.19	13.36	9.71	10.05	8.67	4.58	4.84	6.39		**		-
Y79AA1001272	15.16	12.6	13.5	3.77	6.76	5.59	8.86	7.59	6.53	**	**	-	-
Y79AA1001281	8.87	7.72	6.68	4.17	4.8	3.47	2.65	2.22	2.28	**	**	-	-
Y79AA1001299	9.39	10.08	9.6	4.21	5.3	4.49	3.28	3.68	3.29	**	**	-	-
Y79AA1001312	40.47	42.72	35.81	17.92	27.92	14.77	29.7	20.85	26.67	*	*	-	-
Y79AA1001319	31.92	23	20.23	23.19	28.4	16.96	30.43	20.02	18				
Y79AA1001323	32.99	27.82	34.32	14.07	19.03	14.31	25.9	23.32	27.9	**		-	
Y79AA1001328	28.33	16.1	28.16	14.56	12.93	12.69	4.94	7.51	4.42		*		-
Y79AA1001343	12.56	8.01	10.99	6.43	7.59	7.49	6.83	9.08	8.27				
Y79AA1001351	6.64	4.21	8.23	2.99	1.8	1.8	2.08	2.52	1.68	*	*	-	-
Y79AA1001364	8.06	5.02	6.85	3.26	2.98	2.12	4.06	2.93	1.74	*	*	-	-
Y79AA1001367	145.27	118.42	143.46	117.7	132.8	94.77	76.65	57.61	66.99		**		-
Y79AA1001384	45.86	52.17	41.89	27.43	34.83	21.42	31.33	29.86	26.76	*	**	-	-
Y79AA1001391	10.96	12.22	10.34	2.99	9.55	4.77	7.43	7.31	6.01		**		-
Y79AA1001394	24.73	14.05	14.28	9.7	6.32	9.07	6.42	10.16	9.01				
Y79AA1001402	12.42	7.77	9.12	5.62	4.8	4.67	4.74	3.87	4.52	*	*	-	-
Y79AA1001410	5.24	2.77	3.09	3.28	1.53	1.95	2.62	0.78	1.99				
Y79AA1001414	27.49	18.53	20.44	10.78	9.47	10.2	16.16	13.43	11.92	*	*	-	-
Y79AA1001426	271.77	221.23	225.78	200.19	221.07	217.77	202.63	211.55	197.64				
Y79AA1001427	15.18	10.97	10.9	6.77	10.81	5.39	6.71	6.07	6.74		*		-
Y79AA1001430	22.25	17.58	19.52	10.25	13.63	7.85	11.32	11.76	10.84	*	**	-	-
Y79AA1001438	6.75	4.58	4.31	2.6	4.23	1.25	2.94	2.35	2.98		*		-
Y79AA1001485	17.57	9.99	14.92	13.26	10.56	8.25	5.32	10.37	14.36				
Y79AA1001493	20.47	12.23	13.25	9.02	11.27	6.64	13.37	13.83	16.06				
Y79AA1001511	14.52	8.05	9.32	8.33	6.58	5.82	5.2	6	5.96				
Y79AA1001523	10.03	6.72	7.33	6.48	4.81	3.84	4.54	3.21	2.59		*		-
Y79AA1001530	11.44	7.57	8.59	6.64	8.84	5.29	6.2	7.76	5.77				
Y79AA1001532	13.55	14.73	11.04	5.35	5.16	4.93	5.08	4.52	6.49	**	**	-	-
Y79AA1001533	56.5	68.51	50.9	29.97	36.82	26.92	69.28	61.19	56.58	*		-	
Y79AA1001541	8.12	8.52	5.25	4.02	4.89	2.24	4.69	2.24	2.18		*		-
Y79AA1001548	67.38	47.55	44.48	30.61	26.42	21.92	46.07	51.22	51.86	*		-	
Y79AA1001555	14.35	9.75	8.13	8.86	4.86	4.97	8.19	7.68	10.98				
Y79AA1001562	18.44	13.73	12.82	8.99	10.6	7.19	10.2	9.39	15.75	*		-	
Y79AA1001581	24.34	18.91	17.62	9.8	12.04	10.4	15.9	9.96	16.33	*		-	
Y79AA1001585	30.32	20.83	22.83	20.22	25.12	15.45	0.69	15.13	0.14		*		-
Y79AA1001592	28.53	25.65	26.36	29.33	16.66	7.28	20.69	8.44	14.72		*		-
Y79AA1001594	23.28	21.85	24.28	14.25	15.59	10.11	22.55	14.53	20.27	**		-	
Y79AA1001603	12.47	11.04	10.84	6.8	11.48	6.78	22.63	14.33	27.5				
Y79AA1001613	25.09	18.27	18.81	23.47	16.84	13.34	20.3	16.35	18.99				
Y79AA1001630	22.94	13.91	12.22	13.14	13.53	8.02	11.73	12.98	17.67				
Y79AA1001647	33.54	24.86	22.66	23.22	25.84	16.49	26.93	21.3	26.55				
Y79AA1001664	12.2	10.56	13.13	7.78	6.05	5.54	10.34	8.1	11.69	**		-	
Y79AA1001665	11.52	9	9.75	6.87	7.31	6.13	5.92	6.12	7.69	*	*	-	-
Y79AA1001679	24.51	18.98	17.88	11.13	12.84	9.27	24.02	13.28	18.8	*		-	
Y79AA1001692	7.23	6.72	8.1	2.24	2.83	2.63	3.64	2.31	3.06	**	**	-	-
Y79AA1001696	14.23	12.31	9.21	5.29	8.48	4.61	14.27	13.28	13.01	*		-	
Y79AA1001705	12.04	11.4	8.55	9.76	11.8	6.21	4.61	5.98	4.57		**		-
Y79AA1001711	13.72	7.72	10.63	6.49	4.11	3.08	6.08	4.06	7.4	*		-	
Y79AA1001717	4.71	1.55	3.26	3.34	1.71	0.7	1.49	1.63	1.39				
Y79AA1001719	22.12	12.72	16.33	9.89	12.72	6.53	12.21	11.1	11.76				
Y79AA1001727	38.96	27.16	22.35	13.65	17.35	9.31	38.01	28.39	34.23	*		-	
Y79AA1001750	21.5	17.52	18.42	10.15	15.4	8.01	11.94	9.9	11.41	*	**	-	-
Y79AA1001760	127.24	115.03	77.78	58.26	73.6	43.62	140.25	100.84	138.73	*		-	
Y79AA1001777	6.77	6.32	6.37	2.57	5.24	2.46	5.26	4.15	4.71	*	**	-	-
Y79AA1001781	2.86	2.24	2.15	1.61	1.86	2.55	0.74	1.53	1.3		*		-

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Y79AA1001787	5.04	3.62	6.16	2.83	4.49	3.23	3.33	2.97	2.01				
Y79AA1001793	120.15	97.84	90.95	70.69	108.02	70.38	56.01	50.79	40.18		**		-
Y79AA1001795	5.66	5.4	6.21	4.2	5.9	3.1	3.91	2.49	2.28		**		-
Y79AA1001799	15.09	14.95	16.22	8.14	9.02	8.13	5.96	8.67	5.96	**	**	-	-
Y79AA1001800	25.64	16.41	26.8	14.68	31.06	13.67	17.04	13.04	14.7				
Y79AA1001801	18.54	13.81	14.73	8.69	14.72	7.61	10.02	6.35	8.81		*		-
Y79AA1001803	4.48	5.85	6.44	4.5	2.73	1.98	4.84	2.96	2.69				
Y79AA1001805	40.28	26.89	34.51	17.56	11.83	10.76	12.11	14.87	11.59	**	**	-	-
Y79AA1001807	42.38	40.49	41.45	39.87	44.56	37.42	30.19	22.76	22.12		**		-
Y79AA1001827	9.32	11.28	9.81	8.01	8.55	6.68	5.41	8.86	5.83	*	*	-	-
Y79AA1001846	22.14	19.33	18.59	11.82	17.37	13.61	12.56	15.77	9.7	*	*	-	-
Y79AA1001848	8.04	9.99	9.11	5.33	6.98	5.01	6.65	6.63	5.92	*	*	-	-
Y79AA1001853	10.87	10.1	9.06	5.77	8.29	4.56	4.63	5.75	4.91	*	**	-	-
Y79AA1001863	24.97	27.27	22.17	17.04	22	11.97	13.95	21.02	18.07		*		-
Y79AA1001866	13.46	10.72	11.93	6.28	4.52	4.93	6.56	4.65	4.51	**	**	-	-
Y79AA1001874	2.1	1.41	2.93	0.78	1.08	0.95	1.46	1.22	1.08				
Y79AA1001875	31.78	22.74	37.59	12.11	19.59	16.03	9.16	15	14.61	*	*	-	-
Y79AA1001907	517.52	778.32	567.93	750.86	875.67	821.68	479.34	605.65	529.63				
Y79AA1001908	5.27	6.69	9.96	3.58	5.35	3.25	2.93	3.09	1.48		*		-
Y79AA1001923	8.48	16.75	14.8	9.28	7.65	6.34	6.48	6.75	5.36		*		-
Y79AA1001927	18.05	21.6	19.1	12.29	16.25	12.12	14.45	14.01	14.79	*	**	-	-
Y79AA1001930	12.23	24.48	15.86	10.91	18.16	6.72	4.54	5.11	5.37		*		-
Y79AA1001932	61.74	56.58	52.19	37.44	49.06	33.54	58.52	51.29	51.59	*		-	
Y79AA1001933	9.52	6.51	10.88	6.04	6.05	6.44	4.27	11.51	4.91				
Y79AA1001942	10.76	6.66	7.93	7.97	5.94	4.4	3.29	2.7	3.99		*		-
Y79AA1001963	138.12	106.9	117.87	95.52	130.54	91.9	83.12	67.08	69.04		*		-
Y79AA1001968	147.27	91.21	62.32	82.32	49.63	76.26	20.14	2.41	10.4		*		-
Y79AA1001983	12.1	16.25	14.99	5.06	8.59	7.83	3.08	3.73	3.02	*	**	-	-
Y79AA1002000	8.87	9.86	16.46	6.28	9.55	3.45	4.66	4.84	4.51		*		-
Y79AA1002004	46.17	58.66	37.42	34.61	47	15.44	17.13	16.13	8.67		**		-
Y79AA1002008	16.52	21.1	20.83	11.85	16.14	12.02	7.95	15.74	18.89	*		-	
Y79AA1002012	13.85	12.54	10.41	5.85	6.84	6.65	8.76	11.21	9.52	**		-	
Y79AA1002017	15.21	10.94	15.42	6.73	12.23	8.22	1.29	15.64	2.06				
Y79AA1002022	42.57	32.77	37.11	21.13	22.85	16.91	21.09	21.59	19.22	**	**	-	-
Y79AA1002027	10.35	8.04	15.25	2.11	4.6	4.84	5.16	2.67	4.2	*	*	-	-
Y79AA1002050	13.21	11.11	14.39	7.26	8.9	5.9	6.9	7.16	7.33	*	**	-	-
Y79AA1002058	167.29	130.21	156.91	193.04	186.39	149.35	127.37	93.56	137.15				
Y79AA1002060	54.35	76.53	61.68	36.08	41.21	29.16	24.43	9.99	5.28	*	**	-	-
Y79AA1002062	49.46	32.53	50.05	16.65	20.72	17.6	35.11	28.1	35.48	*		-	
Y79AA1002065	113.45	69.34	64.62	65.01	102.96	72.96	82.29	90.04	44.91				
Y79AA1002067	33.46	37.19	43.9	21.85	20.1	22.68	15.4	10.55	10.37	**	**	-	-
Y79AA1002069	5.33	3.94	7.12	3.04	1.49	2.47	3.1	3.24	2.29	*		-	
Y79AA1002070	67.39	142.78	83.33	77.38	149.87	86.41	153.3	88.92	78.17				
Y79AA1002074	1225	1102	498.16	721.59	1162.7	771.32	764.45	491.49	312.45				
Y79AA1002076	8.24	11.39	15.58	4.01	6.13	3.99	13	9.01	11.16	*		-	
Y79AA1002083	11.94	6.94	9.48	4.49	4.53	3.15	4.48	1.37	1.78	*	*	-	-
Y79AA1002084	20.05	13.84	17.88	7.41	8.36	6.24	10.42	8.8	8.13	**	*	-	-
Y79AA1002086	15.57	8.01	9.58	4.16	3.65	3.41	3.6	4.3	3.59	*	*	-	-
Y79AA1002087	265.36	258.38	345.6	296.44	355.85	246.9	347.62	322.78	317.34				
Y79AA1002089	15.8	12.04	15.08	6.67	9.17	6.14	12.29	9.32	9.91	**		-	
Y79AA1002093	13.66	12.64	9.33	5.35	6.21	4.47	3.01	2.8	2.57	**	**	-	-
Y79AA1002101	6.58	7.04	8.08	3.07	2.77	1.96	3.3	4.71	1.2	**	*	-	-
Y79AA1002103	11.98	11.79	10.9	4.11	5.96	4.92	4.54	2.99	2.4	**	**	-	-
Y79AA1002115	15.51	18.46	14.58	9.3	11.82	8.45	4.13	9.04	5.86	*	**	-	-
Y79AA1002121	6.93	5.28	6.92	6.7	3.27	4.36	3.68	3.01	3.29		**		-
Y79AA1002125	40.85	21.04	26.11	14.22	18.4	17.66	12.21	8.56	11.75		*		-
Y79AA1002129	7.76	7.25	11.87	4.36	3.94	3.2	3.76	3.8	4.37	*	*	-	-
Y79AA1002131	5.89	3.57	4.65	1.58	2.79	2.27	3.32	1.61	2.75	*		-	
Y79AA1002139	8.48	7.22	6.23	4.06	4.42	2.47	3.44	3.86	2.67	*	**	-	-
Y79AA1002144	53.23	47.33	47.13	32.96	42.65	28.86	30.69	36.28	25.23	*	**	-	-
Y79AA1002177	14.09	13.17	13.65	5.87	6.08	5.05	5.82	4.1	4.34	**	**	-	-
Y79AA1002183	76.21	99.47	69.64	24.87	40.12	25.67	26.7	15.32	11.38	**	**	-	-
Y79AA1002202	29.69	18.4	18.04	8.22	10.65	9.82	13.41	13.22	16.71	*		-	
Y79AA1002204	4.17	2.23	3.23	5.04	1.05	2.68	3.28	2.4	2.69				

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Table 509

Y79AA1002206	7.86	6.79	4.86	2.41	3.6	5.74	5.49	1.51	2.8			
Y79AA1002208	21.91	17.64	15.14	5.6	4.07	5.57	6.81	5.17	2.55	**	**	- -
Y79AA1002209	14.82	11.28	11.86	6.23	4.7	2.82	4.71	1.33	3.18	**	**	- -
Y79AA1002210	13.64	7.39	7.59	9.08	4.62	5.18	20.5	2.05	6.37			
Y79AA1002211	11.76	19.59	13.47	10.43	6.65	6.52	12.32	8.42	11.25			
Y79AA1002213	40.78	31.99	22.96	18.41	26.57	14.98	45.88	32.4	41.97			
Y79AA1002215	54.92	41.69	39.55	24.88	24.36	11.26	37.49	23.6	35.98	*		-
Y79AA1002220	17.03	11.5	20.58	7.13	5.68	5.31	4.57	4.8	6.51	*	*	- -
Y79AA1002226	48.55	31.27	31.34	7.35	12.72	13.65	9.19	6.65	11.13	*	**	- -
Y79AA1002229	7.88	6.84	5.37	6.02	4.67	2.85	3.67	2.52	3.73		*	-
Y79AA1002234	20.83	13.27	12.39	9.34	6.36	3.6	6.9	3.36	5.84	*	*	- -
Y79AA1002235	28.03	23.84	21.24	15.07	14.87	9.39	10.75	8.42	13.64	*	**	- -
Y79AA1002246	9.72	14.9	10.35	5.25	6.99	4.12	8.31	3.82	6.69	*		-
Y79AA1002258	12.35	12.02	7.88	7.82	11.57	8.55	9.77	4.5	4.81			
Y79AA1002279	51.52	49.19	41.11	5.28	2.78	2.07	15.99	20.03	22.13	**	**	- -
Y79AA1002292	13.64	7.58	4.14	5.73	4.43	2.94	6.45	6.01	8.36			
Y79AA1002298	9.43	8.29	4.77	3.29	5.48	4.2	4.42	4.85	3.79			
Y79AA1002307	9.31	8.07	6.62	3.9	4.4	2.44	5.17	1.76	2.58	*	*	- -
Y79AA1002309	8.88	7.96	8.79	3.32	4.26	2.83	4.23	2.88	3.97	**	**	- -
Y79AA1002311	16.51	9.27	11.76	6.9	6.2	3.45	7.45	3.09	6.4	*		-
Y79AA1002334	13.05	8.36	7.7	5.13	4.89	3.36	5.91	4.32	5.92	*		-
Y79AA1002351	13.61	12.49	9.42	7.1	4.15	6.19	7.95	4.93	5.8	*	*	- -
Y79AA1002355	31.74	30.6	21.85	12.21	15.81	9.74	20.54	18.29	18.48	*	*	- -
Y79AA1002361	23.42	15.4	18.02	12.53	10.73	6.85	25.86	17.1	25.5	*		-
Y79AA1002365	12.42	6.37	7.19	3.15	4.11	3.03	4.29	4.74	4.01			
Y79AA1002373	8.95	6.89	5.46	5.13	4.81	3.4	9.6	4.57	7.84			
Y79AA1002376	1550.5	2569.2	1680.8	462.62	827.86	616.71	1477.6	1040.3	1062.1	*		-
Y79AA1002378	20.24	17.32	13.54	5.14	9.41	4.23	19.28	11.07	16.88	*		-
Y79AA1002381	116.11	128.86	74.48	110.66	141.78	92.68	155.95	123.08	170.94			
Y79AA1002388	33.4	33.3	27.31	13.85	26.75	11.62	21.29	16.32	21.24		*	-
Y79AA1002399	11.13	8.22	7.72	4.28	5.54	4.87	7.56	5.9	6.25	*		-
Y79AA1002407	12.66	14.43	18.13	7.72	14.18	6.84	5.83	9.78	4.59		*	-
Y79AA1002413	16.98	12.77	14.95	6.14	9.13	4.62	8.44	10.73	7.99	*	*	- -
Y79AA1002416	7.52	8.19	8.76	5.47	10.72	5.8	8.2	6.05	6.59			
Y79AA1002429	17.73	18.61	8.81	5.82	10.24	4.73	3.65	6.89	5.66		*	-
Y79AA1002431	3.38	3.05	6.2	3.01	5.89	1.6	2.81	2.79	1.69			
Y79AA1002433	9.94	11.67	9.29	5.11	5.57	3.18	3.49	4.6	3.87	**	**	- -
Y79AA1002445	33.47	25.62	23.49	15.99	10.67	7.02	18.92	25.26	13.87	*		-
Y79AA1002461	7.94	6.22	7.84	3.36	7.35	4.7	3.49	2.25	3.85		**	-
Y79AA1002466	778.44	339.4	681.02	542.56	499.15	369	592.67	971	768.71			
Y79AA1002471	11.38	8.13	15.35	12.81	13.4	11.43	4.94	6.06	4.47		*	-
Y79AA1002472	31.22	33.06	31.17	18.15	21.85	9.34	16.29	20.14	20.03	*	**	- -
Y79AA1002474	10.68	12.29	10.71	6.77	7.3	7.75	3.17	7.37	4.86	**	*	- -
Y79AA1002482	30.09	33.68	36.63	19.02	23.45	17.38	21.9	25.81	23.08	**	*	- -
Y79AA1002487	8.33	8.29	7.43	7.28	8.45	6.44	5.34	3.78	3.86		**	-
Y79AA1002490	143.18	106.89	117.63	56.22	71.49	57.31	59.76	51.39	52.37	**	**	- -
Y79AA1002493	44.75	41.56	40.36	20.64	28.52	19.33	38.02	46.19	46.7	**		-
ZRV6C1006278	5.26	7	5.52	3.16	2.97	2.19	2.99	2.6	2.72	**	**	- -

EXAMPLE 16

Selection of novel cDNA clones from cDNA libraries prepared by oligo-capping method

[0246] The following 54 clones were newly selected from cDNA libraries prepared by oligo-capping method, based on the criterion that the 5'-end sequence of a cDNA clone contained a coding region which was initiated with ATG codon and which encoded 50 amino acids or more:

HEMBA1000497, HEMBA1001750, HEMBA1003854, HEMBA1004193, HEMBA1004860, HEMBA1005572, HEMBA1006038, HEMBA1006092, HEMBA1006406, HEMBA1006650, HEMBA1006812, HEMBB1000672, HEMBB1001197, HEMBB1001871, MAMMA1001252, MAMMA1002094, NT2RM4000634, NT2RM4000657,

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NT2RM4000783, NT2RM4000857, NT2RM4001178, NT2RM4002420, NT2RP2000198, NT2RP2000551, NT2RP2000660,
NT2RP2001214, NT2RP2001460, NT2RP2001756, NT2RP2002056, NT2RP2002677, NT2RP2002755, NT2RP2002843, NT2RP2003101, NT2RP2003799, NT2RP2004095, NT2RP2004732, NT2RP2004920, NT2RP2005454, NT2RP2005776, NT2RP2005806, NT2RP2005882, NT2RP3001282, NT2RP3001723, NT2RP3002099, NT2RP3003155, NT2RP3004028, OVARC1000008, OVARC1000724, OVARC1000751, OVARC1001029, PLACE1000814, PLACE1003030, PLACE1005549, PLACE1007218.

Among them, the following 23 clones was predicted to contain a coding region encoding 100 amino acids or more: HEMBA1000497, HEMBA1003854, HEMBA1004193, HEMBA1006812, HEMBB1001871, NT2RM4000657, NT2RM4001178, NT2RP2001756, NT2RP2002677, NT2RP2002755, NT2RP2002843, NT2RP2004095, NT2RP2004920, NT2RP2005806, NT2RP3001282, NT2RP3002099, NT2RP3003155, OVARC1000724, OVARC1001029, PLACE1000814, PLACE1003030, PLACE1005549, PLACE1007218. This indicates that the clones encode proteins.

[0247] Table 510 shows maximal ATGprl value determined for each clone. Since the respective maximal ATGprl values for HEMBA1006812, HEMBB1001871 and NT2RRP3001282 are higher than 0.3, the clones would be full-length. Other clones indicated below have maximal ATGprl values of 0.3 or less. and this means that the fullness ratios of the clones are low.

However, the sequences can still be full-length:HEMBA1000497, HEMBA1001750, HEMBA1003854, HEMBA1004193, HEMBA1004860, HEMBA1005572, HEMBA1006038, HEMBA1006092, HEMBA1006406, HEMBA1006650, HEMBB1000672, HEMBB1001197, MAMMA1001252, MAMMA1002094, NT2RM4000634, NT2RM4000657, NT2RM4000783, NT2RM4000857, NT2RM4001178, NT2RM4002420, NT2RP2000198, NT2RP2000551, NT2RP2000660, NT2RP2001214, NT2RP2001460, NT2RP2001756, NT2RP2002056, NT2RP2002677, NT2RP2002755, NT2RP2002843, NT2RP2003101, NT2RP2003799, NT2RP2004095, NT2RP2004732, NT2RP2004920, NT2RP2005454, NT2RP2005776, NT2RP2005806, NT2RP2005882, NT2RP3001723, NT2RP3002099, NT2RP3003155, NT2RP3004028, OVARC1000008, OVARC1000724, OVARC1000751, OVARC1001029, PLACE1000814, PLACE1003030, PLACE1005549, PLACE1007218

[0248] Table 511 (same as Table 2) shows SEQ ID NOs of the nucleotide sequences located at the 5'-end and 3'-end of each of the 54 clones and the corresponding plasmid clone, which was obtained herein, containing a polynucleotide as an insert. SEQ ID NO for a 5'-end sequence is indicated on the right side of the corresponding Sequence name of 5'-end sequence, and SEQ ID NO for a 3'-end sequence is indicated on the right side of the corresponding Sequence name of 3'-end sequence.

[0249] Swiss-Prot was searched for data homologous to the 5' -end sequences of the selected 54 clones, and GenBank and UniGene were searched for data homologous to the 5' -end and 3'-end sequences of the same clones. The search results are indicated as Homology search results 1-7 in the last part of this SPECIFICATION.

[0250] Based on the matching data obtained by the search, 7 clones presumably encode proteins belonging to any of the categories of secretory or membrane proteins, glycoproteins, signal transduction-associated proteins, transcription-associated proteins, disease-associated proteins, and protein synthesis- and/or protein transport-associated proteins. These were clones exhibiting relatively low homology to any of known proteins belonging to said categories. Here. the term "relatively low homology" means that a nucleotide sequence does not satisfy the conditions under which the nucleotide sequence exhibits "relatively high homology" (which means that, when the nucleotide sequence is compared with the known sequences in Swiss-Prot database, the sequence identity is 60% or higher and the P value is 10^{-10} or less) and that, when the nucleotide sequence is compared with the known sequences in Swiss-Prot database, the sequence to be compared contains 55 nucleotides or more, the sequence identity is 25% or higher, and the P value is 10^{-6} or less.

[0251] Among the 7 clones, clones presumably encoding proteins belonging to the category of secretory or membrane proteins are the two clones, HEMBB1001871 and NT2RM4000857 (which also belong to other categories); clones presumably encoding proteins belonging to the category of glycoproteins are the two clones, HEMBB1001871 and NT2RM4000857 (which also belong to other categories);- a clone presumably encoding a protein belonging to the category of signal transduction-associated proteins is PLACE1005549; clones presumably encoding proteins belonging to the category of transcription-associated proteins are the three clones, HEMBA1005572, NT2RP2001756, and NT2RP2005776; a clone presumably encoding a protein belonging to the category of disease-associated proteins is NT2RM4000857 (which also belong to other categories); a clone presumably encoding a protein belonging to the category of protein synthesis- and/or protein transport-associated proteins is HEMBA1001750 (see Examples 12).

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Table 510

The maximal ATGprl value of each clone selected in Example 16

clone name	name of sequence	maximal ATGprl score
HEMBA1000497	F-HEMBA1000497	0.25
HEMBA1001750	F-HEMBA1001750	0.08
HEMBA1003854	F-HEMBA1003854	0.23
HEMBA1004193	F-HEMBA1004193	0.22
HEMBA1004860	F-HEMBA1004860	0.29
HEMBA1005572	F-HEMBA1005572	0.24
HEMBA1006038	F-HEMBA1006038	0.29
HEMBA1006092	F-HEMBA1006092	0.28
HEMBA1006406	F-HEMBA1006406	0.26
HEMBA1006650	F-HEMBA1006650	0.22
HEMBA1006812	F-HEMBA1006812	0.71
HEMBB1000672	F-HEMBB1000672	0.24
HEMBB1001197	F-HEMBB1001197	0.22
HEMBB1001871	F-HEMBB1001871	0.94
MAMMA1001252	F-MAMMA1001252	0.29
MAMMA1002094	F-MAMMA1002094	0.28
NT2RM4000634	F-NT2RM4000634	0.07
NT2RM4000657	F-NT2RM4000657	0.24
NT2RM4000783	F-NT2RM4000783	0.22
NT2RM4000857	F-NT2RM4000857	0.12
NT2RM4001178	F-NT2RM4001178	0.27
NT2RM4002420	F-NT2RM4002420	0.06
NT2RP2000198	F-NT2RP2000198	0.15
NT2RP2000551	F-NT2RP2000551	0.07
NT2RP2000660	F-NT2RP2000660	0.22
NT2RP2001214	F-NT2RP2001214	0.26
NT2RP2001460	F-NT2RP2001460	0.07
NT2RP2001756	F-NT2RP2001756	0.17

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NT2RP2002056	F-NT2RP2002056	0.12
NT2RP2002677	F-NT2RP2002677	0.14
NT2RP2002755	F-NT2RP2002755	0.12
NT2RP2002843	F-NT2RP2002843	0.11
NT2RP2003101	F-NT2RP2003101	0.13
NT2RP2003799	F-NT2RP2003799	0.24
NT2RP2004095	F-NT2RP2004095	0.16
NT2RP2004732	F-NT2RP2004732	0.18
NT2RP2004920	F-NT2RP2004920	0.15
NT2RP2005454	F-NT2RP2005454	0.09
NT2RP2005776	F-NT2RP2005776	0.19
NT2RP2005806	F-NT2RP2005806	0.27
NT2RP2005882	F-NT2RP2005882	0.11
NT2RP3001282	F-NT2RP3001282	0.39
NT2RP3001723	F-NT2RP3001723	0.22
NT2RP3002099	F-NT2RP3002099	0.20
NT2RP3003155	F-NT2RP3003155	0.29
NT2RP3004028	F-NT2RP3004028	0.13
OVARC1000008	F-OVARC1000008	0.23
OVARC1000724	F-OVARC1000724	0.27
OVARC1000751	F-OVARC1000751	0.28
OVARC1001029	F-OVARC1001029	0.25
PLACE1000814	F-PLACE1000814	0.21
PLACE1003030	F-PLACE1003030	0.26
PLACE1005549	F-PLACE1005549	0.16
PLACE1007218	F-PLACE1007218	0.30

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Table 511

clone name	name of the 5'-end sequence	SEQ ID NO of the 5'-end sequence	name of the 3'-end sequence	SEQ ID NO of the 3'-end sequence
HEMBA1000497	F-HEMBA1000497	16111	R-HEMBA1000497	16165
HEMBA1001750	F-HEMBA1001750	16112	R-HEMBA1001750	16166
HEMBA1003854	F-HEMBA1003854	16113	R-HEMBA1003854	16167
HEMBA1004193	F-HEMBA1004193	16114	R-HEMBA1004193	16168
HEMBA1004860	F-HEMBA1004860	16115	R-HEMBA1004860	16169
HEMBA1005572	F-HEMBA1005572	16116	R-HEMBA1005572	16170
HEMBA1006038	F-HEMBA1006038	16117	R-HEMBA1006038	16171
HEMBA1006092	F-HEMBA1006092	16118	R-HEMBA1006092	16172
HEMBA1006406	F-HEMBA1006406	16119	R-HEMBA1006406	16173
HEMBA1006650	F-HEMBA1006650	16120	R-HEMBA1006650	16174
HEMBA1006812	F-HEMBA1006812	16121	R-HEMBA1006812	16175

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HEMBB1000672	F-HEMBB1000672	16122	R-HEMBB1000672	16176
HEMBB1001197	F-HEMBB1001197	16123	R-HEMBB1001197	16177
HEMBB1001871	F-HEMBB1001871	16124	R-HEMBB1001871	16178
MAMMA1001252	F-MAMMA1001252	16125	R-MAMMA1001252	16179
MAMMA1002094	F-MAMMA1002094	16126	R-MAMMA1002094	16180
NT2RM4000634	F-NT2RM4000634	16127	R-NT2RM4000634	16181
NT2RM4000657	F-NT2RM4000657	16128	R-NT2RM4000657	16182
NT2RM4000783	F-NT2RM4000783	16129	R-NT2RM4000783	16183
NT2RM4000857	F-NT2RM4000857	16130	R-NT2RM4000857	16184
NT2RM4001178	F-NT2RM4001178	16131	R-NT2RM4001178	16185
NT2RM4002420	F-NT2RM4002420	16132	R-NT2RM4002420	16186
NT2RP2000198	F-NT2RP2000198	16133	R-NT2RP2000198	16187
NT2RP2000551	F-NT2RP2000551	16134	R-NT2RP2000551	16188
NT2RP2000660	F-NT2RP2000660	16135	R-NT2RP2000660	16189
NT2RP2001214	F-NT2RP2001214	16136	R-NT2RP2001214	16190
NT2RP2001460	F-NT2RP2001460	16137	R-NT2RP2001460	16191
NT2RP2001756	F-NT2RP2001756	16138	R-NT2RP2001756	16192
NT2RP2002056	F-NT2RP2002056	16139	R-NT2RP2002056	16193
NT2RP2002677	F-NT2RP2002677	16140	R-NT2RP2002677	16194
NT2RP2002755	F-NT2RP2002755	16141	R-NT2RP2002755	16195
NT2RP2002843	F-NT2RP2002843	16142	R-NT2RP2002843	16196
NT2RP2003101	F-NT2RP2003101	16143	R-NT2RP2003101	16197
NT2RP2003799	F-NT2RP2003799	16144	R-NT2RP2003799	16198
NT2RP2004095	F-NT2RP2004095	16145	R-NT2RP2004095	16199
NT2RP2004732	F-NT2RP2004732	16146	R-NT2RP2004732	16200
NT2RP2004920	F-NT2RP2004920	16147	R-NT2RP2004920	16201
NT2RP2005454	F-NT2RP2005454	16148	R-NT2RP2005454	16202
NT2RP2005776	F-NT2RP2005776	16149	R-NT2RP2005776	16203
NT2RP2005806	F-NT2RP2005806	16150	R-NT2RP2005806	16204
NT2RP2005882	F-NT2RP2005882	16151	R-NT2RP2005882	16205
NT2RP3001282	F-NT2RP3001282	16152	R-NT2RP3001282	16206
NT2RP3001723	F-NT2RP3001723	16153	R-NT2RP3001723	16207
NT2RP3002099	F-NT2RP3002099	16154	R-NT2RP3002099	16208
NT2RP3003155	F-NT2RP3003155	16155	R-NT2RP3003155	16209
NT2RP3004028	F-NT2RP3004028	16156	R-NT2RP3004028	16210
OVARC1000008	F-OVARC1000008	16157	R-OVARC1000008	16211
OVARC1000724	F-OVARC1000724	16158	R-OVARC1000724	16212
OVARC1000751	F-OVARC1000751	16159	R-OVARC1000751	16213
OVARC1001029	F-OVARC1001029	16160	R-OVARC1001029	16214
PLACE1000814	F-PLACE1000814	16161	R-PLACE1000814	16215
PLACE1003030	F-PLACE1003030	16162	R-PLACE1003030	16216
PLACE1005549	F-PLACE1005549	16163	R-PLACE1005549	16217
PLACE1007218	F-PLACE1007218	16164	R-PLACE1007218	16218

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EXAMPLE 17

Search for a signal sequence, transmembrane region and functional domain in deduced amino acid sequences

[0252] The deduced amino acid sequences from the full-length nucleotide sequences were examined to predict the presence of a signal sequence in their amino-termini as well as the presence of a transmembrane region. The amino acid sequences were also searched for a protein functional domain (motif). The examinations for a signal sequence in the amino-terminus, for a transmembrane region and for a functional domain were performed by using PSORT [K. Nakai & M. Kanehisa, Genomics, 14:897-911 (1992)], SOSUI [T. Hirokawa et al., Bioinformatics, 14:378-379 (1998)] (Mitsui Knowledge Industry Co., Ltd.) and Pfam (http://www.sanger.ac.uk/Software/Pfam/index.shtml), respectively. When the presence of a signal sequence or a transmembrane region in the amino-terminus was predicted in the amino acid sequence by PSORT or SOSUI, the protein was predicted to be a secretory protein or a membrane protein. When the amino acid sequence matched a functional domain in the Pfam search for a functional domain, the function of the protein is predictable based on the matching data, for example, by referring to the functional categories in PROSITE (http://www.expasy.ch/cgi-bin/prosite-list.pl). The functional domain search can be performed by using PROSITE instead of Pfam.

[0253] Search results obtained by using the respective software programs are indicated below.

[0254] Clones whose deduced amino acid sequences were predicted to have signal sequences by PSORT search are as follows:

HEMBA1001052, HEMBA1001407, HEMBA1002486, HEMBA1002661, HEMBA1002818, HEMBA1002876, HEMBA1003086, HEMBA1003711, HEMBA1004752, HEMBA1005991, HEMBA1006067, HEMBA1006173, HEMBA1006198, HEMBA1006789, HEMBA1006921, HEMBB1000054, HEMBB1000175, HEMBB1002692, MAMMA1000798, MAMMA1002427, MAMMA1002881, MAMMA1003035, NT2RM1000035, NT2RM1000742, NT2RM1000811, NT2RM1000905, NT2RM1001008, NT2RM2000287, NT2RM2000609, NT2RM2001613, NT2RM4000634, NT2RM4000778, NT2RM4002339, NT2RM4002460, NT2RP1000782, NT2RP1000856, NT2RP1001247, NT2RP1001546, NT2RP1001569, NT2RP2001597, NT2RP2002537, NT2RP2004142, NT2RP2005752, NT2RP2005812, NT2RP3001084, NT2RP3001589, NT2RP3002163, NT2RP3002650, NT2RP3003145, NT2RP3003242, NT2RP3003621, NT2RP3004282, NT2RP3004503, NT2RP4000051, NT2RP4000151, NT2RP4000243, NT2RP4000259, NT2RP4000323, NT2RP4000417, NT2RP4001064, NT2RP4001117, NT2RP4001730, NT2RP4001739, NT2RP4002075, NT2RP5003500, OVARC1001154, PLACE1000611, PLACE1003030, PLACE1003044, PLACE1003369, PLACE1003596, PLACE1004258, PLACE1005086, PLACE1006239, PLACE1006754, PLACE1006829, PLACE1007954, PLACE1008424, PLACE1008533, PLACE1008693, PLACE1010622, PLACE1010942, PLACE2000176, PLACE2000341, PLACE2000379, PLACE2000427, PLACE2000477, PLACE4000431, PLACE4000593, THYRO1000156, THYRO1001134, THYRO1001287, Y79AA1000258, Y79AA1001874, Y79AA1002399 HEMBB1001871, HEMBB1001925, MAMMA1000778, MAMMA1000897, MAMMA1001080, NT2RP2004300, NT2RP3002985, NT2RP3003059, OVARC1000689, OVARC1000890, PLACE1005162, PLACE3000399, PLACE3000455, PLACE4000247, PLACE4000259, PLACE4000494

[0255] Clones whose deduced amino acid sequences were predicted to have transmembrane regions by SOSUI search are as follows:

HEMBA1000005, HEMBA1000356, HEMBA1000518, HEMBA1000531, HEMBA1000637, HEMBA1000719, HEMBA1000817, HEMBA1000822, HEMBA1000870, HEMBA1000991, HEMBA1001052, HEMBA1001085, HEMBA1001286, HEMBA1001351, HEMBA1001407, HEMBA1001446, HEMBA1001510, HEMBA1001515, HEMBA1001557, HEMBA1001746, HEMBA1002092, HEMBA1002125, HEMBA1002150, HEMBA1002166, HEMBA1002462, HEMBA1002477, HEMBA1002486, HEMBA1002609, HEMBA1002659, HEMBA1002661, HEMBA1002780, HEMBA1002818, HEMBA1002876, HEMBA1002921, HEMBA1003077, HEMBA1003079, HEMBA1003086, HEMBA1003096, HEMBA1003281, HEMBA1003286, HEMBA1003711, HEMBA1003742, HEMBA1003803, HEMBA1004143, HEMBA1004146, HEMBA1004341, HEMBA1004461, HEMBA1004577, HEMBA1004637, HEMBA1004752, HEMBA1004756, HEMBA1004850, HEMBA1004889, HEMBA1004923, HEMBA1004930, HEMBA1005029, HEMBA1005035, HEMBA1005050, HEMBA1005552, HEMBA1005588, HEMBA1005616, HEMBA1005991, HEMBA1006036, HEMBA1006067, HEMBA1006293, HEMBA1006492, HEMBA1006502, HEMBA1006659, HEMBA1006758, HEMBA1006789, HEMBA1006921, HEMBA1006926, HEMBA1007203, HEMBB1000050, HEMBB1000054, HEMBB1000556, HEMBB1000593, HEMBB1000631, HEMBB1000763, HEMBB1000827, HEMBB1000915, HEMBB1000975, HEMBB1001112, HEMBB1001177, HEMBB1001302, HEMBB1001348, HEMBB1001962, HEMBB1002142, HEMBB1002190, HEMBB1002247, HEMBB1002387, HEMBB1002550, HEMBB1002600, HEMBB1002692, MAMMA1000129, MAMMA1000133, MAMMA1000277, MAMMA1000278, MAMMA1000410, MAMMA1000416, MAMMA1000472, MAMMA1000714, MAMMA1000731, MAMMA1000734, MAMMA1000798, MAMMA1000842, MAMMA1000956, MAMMA1001008,

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[0256] Names of clones whose deduced amino acid sequences were predicted to have functional domains by Pfam search, and names of the matched functional domains are shown below.
When multiple functional domains matched a clone, each domain name was indicated, separated by a double-slash mark, //.

HEMBA1000005//DnaJ, prokaryotic heat shock protein
HEMBA1000020//Tubulin
HEMBA1000129//Helicases conserved C-terminal domain
HEMBA1000156//RNA recognition motif. (aka RRM, RBD, or RNP domain)
HEMBA1000158//Fork head domain, eukaryotic transcription factors //Zinc finger, C2H2 type
HEMBA1000303//Src homology domain 3 //Zinc finger, C3HC4 type (RING finger)
HEMBA1000411//Ank repeat
HEMBA1000491//Ras family (contains ATP/GTP binding P-loop)
HEMBA1000531//Heat shock hsp70 proteins
HEMBA1000561//Zinc finger, C2H2 type
HEMBA1000608//Src homology domain 3
HEMBA1000919//WD domain, G-beta repeats
HEMBA1001043//Ank repeat
HEMBA1001088//LIM domain containing proteins
HEMBA1001137//Zinc finger, C2H2 type
HEMBA1001174//ADP-ribosylation factors (Arf family) (contains ATP/GTP binding P-loop)
HEMBA1001247//WW/rsp5/WWP domain containing proteins
HEMBA1001286//Sushi domain
HEMBA1001510//Basic region plus leucine zipper transcription factors
HEMBA1001515//Reverse transcriptase (RNA-dependent DNA polymerase)
HEMBA1001661//Cadherin
HEMBA1001723//WD domain, G-beta repeats
HEMBA1001744//Eukaryotic protein kinase domain
HEMBA1001804//Zinc finger, C2H2 type
HEMBA1001819//Zinc finger, C2H2 type
HEMBA1001847//Zinc finger, C2H2 type
HEMBA1002035//Bromodomain
HEMBA1002102//Ank repeat
HEMBA1002161//Myosin head (motor domain) (contains ATP/GTP binding P-loop)

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HEMBA1002177//GATA family of transcription factors //Zinc finger, C2H2 type
HEMBA1002212//Eukaryotic protein kinase domain
HEMBA1002215//LIM domain containing proteins
HEMBA1002419//RNA recognition motif. (aka RRM, RBD, or RNP domain)
HEMBA1002547//Kazal-type serine protease inhibitor domain //Laminin EGF-like (Domains III and V)
HEMBA1002768//Src homology domain 3
HEMBA1002810//WW/rsp5/WWP domain containing proteins
HEMBA1002818//EGF-like domain
HEMBA1002935//Zinc finger, C2H2 type
HEMBA1002939//Ank repeat
HEMBA1002973//3'5'-cyclic nucleotide phosphodiesterases
HEMBA1003077//Fibronectin type III domain
HEMBA1003250//Eukaryotic protein kinase domain
HEMBA1003257//Zinc finger, C2H2 type
HEMBA1003281//IG superfamily
HEMBA1003291//Eukaryotic protein kinase domain
HEMBA1003433//Forkhead-associated (FHA) domain
HEMBA1003545//Homeobox domain //LIM domain containing proteins
HEMBA1003591//RNA recognition motif. (aka RRM, RBD, or RNP domain)
HEMBA1003684//Zinc finger, C2H2 type
HEMBA1003953//Zinc finger, C2H2 type
HEMBA1004202//Ras family (contains ATP/GTP binding P-loop)
HEMBA1004227//Protein phosphatase 2C
HEMBA1004321//Zinc finger, C2H2 type
HEMBA1004356//RNA recognition motif. (aka RRM, RBD, or RNP domain)
HEMBA1004408//Peptidyl-prolyl cis-trans isomerases
HEMBA1004596//RNA recognition motif. (aka RRM, RBD, or RNP domain)
HEMBA1004734//Ubiquitin-conjugating enzymes
HEMBA1004973//Fibronectin type III domain
HEMBA1005009//Actins
HEMBA1005101//RNA recognition motif. (aka RRM, RBD, or RNP domain)
HEMBA1005581//EGF-like domain //Laminin G domain
HEMBA1005732//Polyprenyl synthetases
HEMBA1005737//EF hand
HEMBA1006248//Zinc finger, C2H2 type
HEMBA1006284//Ubiquitin family
HEMBA1006293//IG superfamily
HEMBA1006344//Band 4.1 family
HEMBA1006445//Ras family (contains ATP/GTP binding P-loop)
HEMBA1006492//Ank repeat
HEMBA1006559//Zinc finger, C3HC4 type (RING finger)
HEMBA1006708//WD domain, G-beta repeats
HEMBA1006737//Ank repeat
HEMBA1006758//Cadherin
HEMBA1006941//Thioredoxins
HEMBA1007243//Purine/pyrimidine phosphoribosyl transferases
HEMBA1007300//3'5'-cyclic nucleotide phosphodiesterases
HEMBB1000083//IG superfamily
HEMBB1000317//EGF-like domain //Thrombospondin type 1 domain
HEMBB1000556//Actinin-type actin-binding domain containing proteins //LIM domain containing proteins
HEMBB1000725//Ras family (contains ATP/GTP binding P-loop)
HEMBB1000781//Eukaryotic protein kinase domain
HEMBB1000915//Thrombospondin type 1 domain
HEMBB1000927//EF hand
HEMBB1000947//Double-stranded RNA binding motif
HEMBB1001112//eubacterial secY protein
HEMBB1001175//Ank repeat
HEMBB1001234//WW/rsp5/WWP domain containing proteins

BNSDOCID: <EP___1074617A2_I_>

HEMBB1001282//Ank repeat
HEMBB1001294//Ras family (contains ATP/GTP binding P-loop)
HEMBB1001339//Forkhead-associated (FHA) domain
HEMBB1001673//Forkhead-associated (FHA) domain //Zinc finger, C3HC4 type (RING finger)
HEMBB1001802//Intermediate filament proteins
HEMBB1001839//Zinc finger, C2H2 type
HEMBB1002217//Zinc finger, C2H2 type
HEMBB1002342//Thioredoxins
HEMBB1002600//4 transmembrane segments integral membrane proteins
MAMMA1000173//Src homology domain 3
MAMMA1000388//Zinc finger, C2H2 type
MAMMA1000402//Reverse transcriptase (RNA-dependent DNA polymerase)
MAMMA1000612//WD domain, G-beta repeats
MAMMA1000672//Serine carboxypeptidases
MAMMA1000731//SNF2 and others N-terminal domain
MAMMA1001008//Eukaryotic aspartyl proteases
MAMMA1001041//Actinin-type actin-binding domain containing proteins
MAMMA1001059//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
MAMMA1001105//Zinc finger, C2H2 type
MAMMA1001260//Zinc finger, C3HC4 type (RING finger)
MAMMA1001576//Tubulin
MAMMA1001735//Tubulin
MAMMA1001768//ATPases associated with various cellular activities (AAA)
MAMMA1001837//Zinc finger, C2H2 type
MAMMA1002170//Ribosomal protein S5
MAMMA1002385//RNA recognition motif. (aka RRM, RBD, or RNP domain)
MAMMA1002619//Ubiquitin carboxyl-terminal hydrolases family 2
MAMMA1002637//Kinesin light chain repeat
MAMMA1002650//Zinc finger, C2H2 type
MAMMA1002671//AMP-binding enzymes
MAMMA1002869//LIM domain containing proteins
MAMMA1002881//SCP-like extracellular Proteins
MAMMA1002937//Zinc finger, C2H2 type
MAMMA1002938//Multicopper oxidases
MAMMA1003011//Core histones H2A, H2B, H3 and H4
MAMMA1003057//WD domain, G-beta repeats
MAMMA1003127//Myosin head (motor domain) (contains ATP/GTP binding P-loop)
NT2RM1000086//Zinc finger, C3HC4 type (RING finger)
NT2RM1000199//CUB domain //Sushi domain
NT2RM1000256//Glutamine amidotransferases class-II
NT2RM1000499//Ank repeat
NT2RM1000555//'Cold-shock' DNA-binding domain containing proteins
NT2RM1000666//'Cold-shock' DNA-binding domain containing proteins //Zinc finger, CCHC class
NT2RM1000772//WD domain, G-beta repeats
NT2RM1000826//'Cold-shock' DNA-binding domain containing proteins
NT2RM1000850//Ank repeat //Eukaryotic protein kinase domain
NT2RM1000852//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
NT2RM1000882//Heme-binding domain in cytochrome b5 and oxidoreductases
NT2RM1000885//Zinc finger, C3HC4 type (RING finger)
NT2RM1001059//RNA recognition motif. (aka RRM, RBD, or RNP domain)
NT2RM1001072//C2 domain //Phosphatidylinositol-specific phospholipase C, X domain //Phosphatidylinositol-specific phospholipase C, Y domain
NT2RM2000092//Ubiquitin carboxyl-terminal hydrolases family 2
NT2RM2000101//Zinc finger, C3HC4 type (RING finger)
NT2RM2000191//3'5'-cyclic nucleotide phosphodiesterases
NT2RM2000422//Sodium:neurotransmitter symporter family
NT2RM2000490//C2 domain
NT2RM2000566//Integrins alpha chain

BNSDOCID: <EP___1074617A2_I_>

NT2RM2000577//tRNA synthetases class I
NT2RM2000594//C-5 cytosine-specific DNA methylases
NT2RM2000691//Actins
NT2RM2000735//Zinc finger, C2H2 type
NT2RM2000740//Helicases conserved C-terminal domain
NT2RM2000951//FGGY family of carbohydrate kinases
NT2RM2001324//LIM domain containing proteins
NT2RM2001499//Amino acid permeases
NT2RM2001547//DnaJ, prokaryotic heat shock protein //Thioredoxins
NT2RM2001613//eubacterial secY protein
NT2RM2001670//Zinc finger, C2H2 type
NT2RM2001700//Acyl-CoA dehydrogenases
NT2RM2001730//Ubiquitin carboxyl-terminal hydrolases family 2
NT2RM2001813//WD domain, G-beta repeats
NT2RM2001823//Helicases conserved C-terminal domain //SNF2 and others N-terminal domain
NT2RM2001896//Cytochrome C oxidase subunit II
NT2RM2001989//RNA recognition motif. (aka RRM, RBD, or RNP domain)
NT2RM2001997//Thioredoxins
NT2RM2002088//KH domain family of RNA binding proteins
NT2RM2002100//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
NT2RM2002109//IG superfamily
NT2RM4000046//Zinc finger, C3HC4 type (RING finger)
NT2RM4000104//Zinc finger, C2H2 type
NT2RM4000167//Kinesin motor domain
NT2RM4000191//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
NT2RM4000202//Zinc finger, C2H2 type
NT2RM4000229//PH (pleckstrin homology) domain
NT2RM4000344//ATPases associated with various cellular activities (AAA)
NT2RM4000356//Ras family (contains ATP/GTP binding P-loop)
NT2RM4000471//Aminotransferases class-V
NT2RM4000496//ATPases associated with various cellular activities (AAA)
NT2RM4000611//WD domain, G-beta repeats
NT2RM4000657//C2 domain //Phosphatidylinositol-specific phospholipase C, Y domain
NT2RM4000712//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
NT2RM4000733//Forkhead-associated (FHA) domain
NT2RM4000734//Zinc finger, C2H2 type
NT2RM4000751//Zinc finger, C2H2 type
NT2RM4000795//Carboxylesterases
NT2RM4000996//Zinc finger, C2H2 type
NT2RM4001054//eubacterial secY protein
NT2RM4001140//Homeobox domain
NT2RM4001178//DEAD and DEAH box helicases
NT2RM4001200//Zinc finger, C2H2 type
NT2RM4001313//Phosphatidylinositol 3- and 4-kinases
NT2RM4001316//Acyl-CoA dehydrogenases
NT2RM4001320//Src homology domain 3
NT2RM4001411//PH (pleckstrin homology) domain //Src homology domain 2
NT2RM4001454//PH (pleckstrin homology) domain
NT2RM4001483//Zinc finger, C2H2 type
NT2RM4001629//Src homology domain 3
NT2RM4001758//Eukaryotic protein kinase domain
NT2RM4001810//Zinc finger, C2H2 type
NT2RM4001813//Lectin C-type domain short and long forms
NT2RM4001823//Zinc finger, C2H2 type
NT2RM4001828//Zinc finger, C2H2 type
NT2RM4001979//Zinc finger, C2H2 type
NT2RM4001987//IG superfamily
NT2RM4002013//WD domain, G-beta repeats

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NT2RM4002073//AMP-binding enzymes
NT2RM4002093//RNA recognition motif. (aka RRM, RBD, or RNP domain)
NT2RM4002145//IG superfamily
NT2RM4002287//Fibronectin type III domain
NT2RM4002527//WD domain, G-beta repeats
NT2RM4002623//tRNA synthetases class II
NT2RP1000101//Zinc finger, C2H2 type
NT2RP1000202//Ank repeat
NT2RP1000272//RNA recognition motif. (aka RRM, RBD, or RNP domain)
NT2RP1000363//PH (pleckstrin homology) domain
NT2RP1000376//Ank repeat
NT2RP1000470//DEAD and DEAH box helicases
NT2RP1000478//Tubulin
NT2RP1000522//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
NT2RP1000677//Kazal-type serine protease inhibitor domain
NT2RP1000701//WD domain, G-beta repeats
NT2RP1000733//Elongation factor Tu family (contains ATP/GTP binding P-loop)
NT2RP1000782//4 transmembrane segments integral membrane proteins
NT2RP1000833//3'5'-cyclic nucleotide phosphodiesterases
NT2RP1000856//4 transmembrane segments integral membrane proteins
NT2RP1000947//Ubiquitin-conjugating enzymes
NT2RP1000959//60s Acidic ribosomal protein
NT2RP1000966//RNA recognition motif. (aka RRM, RBD, or RNP domain)
NT2RP1001033//Tubulin
NT2RP1001080//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
NT2RP1001177//Core histones H2A, H2B, H3 and H4
NT2RP1001247//Transforming growth factor beta like domain
NT2RP1001294//WD domain, G-beta repeats
NT2RP1001302//WD domain, G-beta repeats
NT2RP1001313//Heme-binding domain in cytochrome b5 and oxidoreductases
NT2RP1001457//WD domain, G-beta repeats
NT2RP1001546//4 transmembrane segments integral membrane proteins
NT2RP2000008//Zinc finger, C2H2 type
NT2RP2000040//C2 domain
NT2RP2000045//DnaJ, prokaryotic heat shock protein
NT2RP2000054//Zinc finger, C3HC4 type (RING finger)
NT2RP2000070//Cadherin
NT2RP2000126//Helicases conserved C-terminal domain //SNF2 and others N-terminal domain
NT2RP2000153//RNA recognition motif. (aka RRM, RBD, or RNP domain)
NT2RP2000224//PH (pleckstrin, homology) domain
NT2RP2000257//Mitochondrial carrier proteins
NT2RP2000329//Adenylate kinases
NT2RP2000414//RNA recognition motif. (aka RRM, RBD, or RNP domain)
NT2RP2000448//PH (pleckstrin homology) domain
NT2RP2000660//ATPases associated with various cellular activities (AAA)
NT2RP2000668//Eukaryotic protein kinase domain
NT2RP2000710//tRNA synthetases class II
NT2RP2000764//Aminotransferases class-V
NT2RP2000842//7 transmembrane receptor (rhodopsin family)
NT2RP2000880//Elongation factor Tu family (contains ATP/GTP binding P-loop)
NT2RP2000931//RNA recognition motif. (aka RRM, RBD, or RNP domain)
NT2RP2000932//Ank repeat
NT2RP2001081//C2 domain
NT2RP2001174//Zinc finger, C2H2 type
NT2RP2001397//Cyclins
NT2RP2001520//Mitochondrial carrier proteins
NT2RP2001597//Zinc finger, C3HC4 type (RING finger)
NT2RP2001740//Ubiquitin carboxyl-terminal hydrolases family 2

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NT2RP2001748//Polyprenyl synthetases
NT2RP2001756//Zinc finger, C2H2 type
NT2RP2001839//Eukaryotic protein kinase domain
NT2RP2001900//Actins
NT2RP2001991//Sodium:neurotransmitter symporter family
NT2RP2002058//WD domain, G-beta repeats
NT2RP2002124//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
NT2RP2002185//Ubiquitin family
NT2RP2002208//Zinc finger, C3HC4 type (RING finger)
NT2RP2002256//Cytochrome P450
NT2RP2002479//ABC transporters
NT2RP2002503//Zinc finger, C2H2 type
NT2RP2002520//Ank repeat
NT2RP2002591//Zinc finger, C2H2 type
NT2RP2002741//Src homology domain 3
NT2RP2002929//WD domain, G-beta repeats
NT2RP2002939//Zinc finger, C2H2 type
NT2RP2002959//Ubiquitin-conjugating enzymes
NT2RP2002980//Ribosomal protein S10
NT2RP2003137//Ubiquitin family
NT2RP2003164//Eukaryotic protein kinase domain
NT2RP2003228//MCM2/3/5 family
NT2RP2003243//Fibronectin type III domain
NT2RP2003272//Ubiquitin family
NT2RP2003307//Kinesin light chain repeat
NT2RP2003401//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases, family 2
NT2RP2003433//eubacterial secY protein
NT2RP2003480//Zinc finger, C2H2 type
NT2RP2003713//Ubiquitin carboxyl-terminal hydrolases family 2
NT2RP2003737//Ubiquitin-conjugating enzymes
NT2RP2003777//Zinc finger, C3HC4 type (RING finger)
NT2RP2003840//Ubiquitin-conjugating enzymes
NT2RP2003857//Ank repeat
NT2RP2003981//Zinc finger, C3HC4 type (RING finger)
NT2RP2004170//WD domain, G-beta repeats
NT2RP2004187//Zinc finger, C2H2 type
NT2RP2004232//Phorbol esters / diacylglycerol binding domain //PH (pleckstrin homology) domain //Eukaryotic protein kinase domain
NT2RP2004389//Ribosomal protein S9
NT2RP2004538//PH (pleckstrin homology) domain
NT2RP2004568//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
NT2RP2004710//WW/rsp5/WWP domain containing proteins
NT2RP2004768//Eukaryotic protein kinase domain
NT2RP2004933//Eukaryotic protein kinase domain
NT2RP2004961//Zinc finger, C2H2 type
NT2RP2005003//Zinc finger, C3HC4 type (RING finger)
NT2RP2005012//DnaJ, prokaryotic heat shock protein
NT2RP2005126//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
NT2RP2005139//Ank repeat
NT2RP2005140//PH (pleckstrin homology) domain
NT2RP2005239//Aminotransferases class-V
NT2RP2005288//Regulator of chromosome condensation (RCC1)
NT2RP2005293//PH (pleckstrin homology) domain
NT2RP2005325//Homeobox domain //LIM domain containing proteins
NT2RP2005344//E1-E2 ATPases
NT2RP2005465//Mitochondrial carrier proteins
NT2RP2005525//Forkhead-associated (FHA) domain
NT2RP2005531//Band 4.1 family

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NT2RP2005557//Bacterial mutT protein
NT2RP2005654//DnaJ, prokaryotic heat shock protein
NT2RP2005701//Zinc finger, C3HC4 type (RING finger)
NT2RP2005722//Zinc finger, C2H2 type
NT2RP2005752//TNFR/NGFR cysteine-rich region
NT2RP2005763//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
NT2RP2005767//HMG (high mobility group) box
NT2RP2006312//HMG (high mobility group) box
NT2RP2006464//HMG (high mobility group) box
NT2RP2006571//Cytochrome P450
NT2RP3000050//Zinc finger, C2H2 type
NT2RP3000068//PH (pleckstrin homology) domain
NT2RP3000085//Biotin-requiring enzymes //Carbamoyl-phosphate synthase (CPSase)
NT2RP3000299//Src homology domain 3
NT2RP3000359//Adenylate kinases
NT2RP3000366//Ras family (contains ATP/GTP binding P-loop)
NT2RP3000403//WW/rsp5/WWP domain containing proteins
NT2RP3000487//WW/rsp5/WWP domain containing proteins
NT2RP3000512//Homeobox domain
NT2RP3000527//Zinc finger, C2H2 type
NT2RP3000531//IG superfamily
NT2RP3000590//Zinc finger, C3HC4 type (RING finger)
NT2RP3000603//Helix-loop-helix DNA-binding domain
NT2RP3000605//Zinc finger, C2H2 type
NT2RP3000632//Zinc finger, C2H2 type
NT2RP3000742//Phosphatidylinositol-specific phospholipase C, X domain //Phosphatidylinositol-specific phospholipase C, Y domain
NT2RP3000759//ADP-ribosylation factors (Arf family) (contains ATP/GTP binding P-loop)
NT2RP3000825//EGF-like domain
NT2RP3000869//ATPases associated with various cellular activities (AAA)
NT2RP3000994//Double-stranded RNA binding motif
NT2RP3001057//Zinc finger, C2H2 type
NT2RP3001084//PH (pleckstrin homology) domain
NT2RP3001120//Zinc finger, C2H2 type
NT2RP3001140//Thrombospondin type 1 domain
NT2RP3001150//Forkhead-associated (FHA) domain
NT2RP3001155//HMG (high mobility group) box
NT2RP3001214//Zinc finger, C2H2 type
NT2RP3001268//Zinc finger, C2H2 type
NT2RP3001338//Zinc finger, C2H2 type
NT2RP3001355//Mitochondrial carrier proteins
NT2RP3001398//Zinc finger, C2H2 type
NT2RP3001426//DnaJ, prokaryotic heat shock protein
NT2RP3001453//ABC transporters
NT2RP3001457//PH (pleckstrin homology) domain
NT2RP3001472//HMG (high mobility group) box
NT2RP3001495//Alcohol/other dehydrogenases, short chain type //WW/rsp5/WWP domain containing proteins
NT2RP3001497//Zinc finger, C3HC4 type (RING finger)
NT2RP3001724//Helicases conserved C-terminal domain
NT2RP3001792//RNA recognition motif. (aka RRM, RBD, or RNP domain)
NT2RP3001943//Zinc finger, C3HC4 type (RING finger)
NT2RP3001944//Zinc finger, C3HC4 type (RING finger)
NT2RP3002007//ATPases associated with various cellular activities (AAA)
NT2RP3002054//Low-density lipoprotein receptor domain class A
NT2RP3002151//Elongation factor Tu family (contains ATP/GTP binding P-loop)
NT2RP3002399//MCM2/3/5 family
NT2RP3002501//Serine/threonine dehydratases
NT2RP3002602//Thioredoxins

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NT2RP3002628//DnaJ, prokaryotic heat shock protein //Thioredoxins
NT2RP3002663//PH (pleckstrin homology) domain
NT2RP3002909//Ank repeat
NT2RP3002953//Cadherin
NT2RP3002969//AMP-binding enzymes
NT2RP3003061//Ank repeat
NT2RP3003145//Zinc carboxypeptidases
NT2RP3003230//WD domain, G-beta repeats
NT2RP3003251//Zinc finger, C3HC4 type (RING finger)
NT2RP3003278//Ank repeat //Zinc finger, C2H2 type
NT2RP3003282//PH (pleckstrin homology) domain
NT2RP3003311//PH (pleckstrin homology) domain
NT2RP3003385//Ank repeat //Chaperonins clpA/B
NT2RP3003589//Ras family (contains ATP/GTP binding P-loop)
NT2RP3003621//CUB domain //Kringle domain
NT2RP3003701//Thrombospondin type 1 domain
NT2RP3003716//Fibronectin type III domain
NT2RP3003809//ATPases associated with various cellular activities (AAA)
NT2RP3004016//Zinc finger, C3HC4 type (RING finger)
NT2RP3004207//CUB domain //Sushi domain
NT2RP3004209//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
NT2RP3004242//PH (pleckstrin homology) domain
NT2RP3004262//DnaJ, prokaryotic heat shock protein
NT2RP3004566//Zinc finger, C2H2 type
NT2RP3004569//Ank repeat
NT2RP3004594//HMG (high mobility group) box
NT2RP3004617//Zinc finger, C3HC4 type (RING finger)
NT2RP4000259//Glutathione peroxidases
NT2RP4000370//Prokaryotic-type class I peptide chain release factors
NT2RP4000376//WD domain, G-beta repeats
NT2RP4000398//Zinc finger, C2H2 type
NT2RP4000455//Forkhead-associated (FHA) domain //Zinc finger, C3HC4 type (RING finger)
NT2RP4000457//Ubiquitin carboxyl-terminal hydrolases family 2
NT2RP4000518//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
NT2RP4000588//Actinin-type actin-binding domain containing proteins
NT2RP4000614//RNA recognition motif. (aka RRM, RBD, or RNP domain)
NT2RP4000648//Forkhead-associated (FHA) domain //Zinc finger, C3HC4 type (RING finger)
NT2RP4000837//Zinc finger, C2H2 type
NT2RP4000839//WD domain, G-beta repeats
NT2RP4000865//Zinc finger, C2H2 type
NT2RP4000907//Fibronectin type III domain //IG superfamily
NT2RP4000925//Fibronectin type III domain
NT2RP4000927//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
NT2RP4000973//DnaJ, prokaryotic heat shock protein //Thioredoxins
NT2RP4001079//E1-E2 ATPases
NT2RP4001080//RNA recognition motif. (aka RRM, RBD, or RNP domain)
NT2RP4001117//eubacterial secY protein
NT2RP4001150//Fibronectin type III domain
NT2RP4001213//Zinc finger, C2H2 type
NT2RP4001219//Thioredoxins
NT2RP4001235//Zinc finger, CCHC class
NT2RP4001433//Zinc finger, C2H2 type
NT2RP4001498//Ank repeat
NT2RP4001568//Ank repeat
NT2RP4001644//Eukaryotic protein kinase domain
NT2RP4001725//WD domain, G-beta repeats
NT2RP4001753//Zinc finger, C2H2 type
NT2RP4001790//Zinc finger, C2H2 type

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NT2RP4001822//4 transmembrane segments integral membrane proteins
NT2RP4001823//Fibrinogen beta and gamma chains, C-terminal globular domain
NT2RP4001893//Ank repeat
NT2RP4001896//WD domain, G-beta repeats
NT2RP4001927//WD domain, G-beta repeats
NT2RP4001938//Zinc finger, C2H2 type
NT2RP4002047//Elongation factor Tu family (contains ATP/GTP binding P-loop)
NT2RP4002078//Zinc finger, C2H2 type
NT2RP4002408//Eukaryotic protein kinase domain
NT2RP4002905//Cyclins
NT2RP5003477//WD domain, G-beta repeats
OVARC1000006//Core histones H2A, H2B, H3 and H4
OVARC1000085//Proteasome A-type and B-type
OVARC1000148//RNA recognition motif. (aka RRM, RBD, or RNP domain)
OVARC1000556//Eukaryotic protein kinase domain
OVARC1000649//PH (pleckstrin homology) domain //Src homology domain 2
OVARC1000746//Double-stranded RNA binding motif
OVARC1000885//Alcohol/other dehydrogenases, short chain type
OVARC1000937//Cyclins
OVARC1000999//Ank repeat
OVARC1001154//Granulins
OVARC1001180//Ubiquitin family
OVARC1001306//Helix-loop-helix DNA-binding domain
OVARC1001577//RNA recognition motif. (aka RRM, RBD, or RNP domain)
OVARC1001731//Tropomyosins
OVARC1001943//Zinc finger, C2H2 type
OVARC1002050//Spectrin alpha chain, repeated domain
OVARC1002112//Core histones H2A, H2B, H3 and H4
OVARC1002138//ATPases associated with various cellular activities (AAA)
OVARC1002182//WD domain, G-beta repeats
PLACE1000014//Zinc finger, C3HC4 type (RING finger)
PLACE1000040//Ras family (contains ATP/GTP binding P-loop)
PLACE1000050//Zinc finger, C2H2 type
PLACE1000081//PH (pleckstrin homology) domain
PLACE1000142//Enoyl-CoA hydratase/isomerase
PLACE1000401//IG superfamily
PLACE1000406//RNA recognition motif. (aka RRM, RBD, or RNP domain)
PLACE1000420//Bacterial mutT protein
PLACE1000706//Bromodomain
PLACE1000769//KH domain family of RNA binding proteins
PLACE1000786//PH (pleckstrin homology) domain
PLACE1000863//Ribosomal protein S4
PLACE1000909//Ank repeat
PLACE1000972//Src homology domain 3
PLACE1000979//Zinc finger, C2H2 type
PLACE1001304//Zinc finger, C2H2 type
PLACE1001387//Src homology domain 3
PLACE1001632//Zinc finger, C2H2 type
PLACE1001672//Aminotransferases class-III pyridoxal-phosphate
PLACE1001716//Zinc finger, CCHC class
PLACE1001739//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
PLACE1001781//Phosphoglucomutase and phosphomannomutase phosphoserine
PLACE1001869//FGGY family of carbohydrate kinases
PLACE1002438//Zinc finger, C2H2 type
PLACE1002450//Zinc finger, C2H2 type
PLACE1002474//EGF-like domain //von Willebrand factor type A domain
PLACE1002499//Zinc finger, C3HC4 type (RING finger)
PLACE1002532//Homeobox domain

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PLACE1002571//Actins
PLACE1002685//Src homology domain 2
PLACE1002722//7 transmembrane receptor (rhodopsin family)
PLACE1002775//Bromodomain
PLACE1002834//Zinc finger, C2H2 type
PLACE1003100//Alcohol/other dehydrogenases, short chain type
PLACE1003174//Ubiquitin-conjugating enzymes
PLACE1003238//7 transmembrane receptor (rhodopsin family)
PLACE1003302//Zinc finger, C2H2 type
PLACE1003334//RNA recognition motif. (aka RRM, RBD, or RNP domain)
PLACE1003366//C2 domain
PLACE1003394//Ras family (contains ATP/GTP binding P-loop)
PLACE1003420//Mitochondrial carrier proteins
PLACE1003493//C1q domain
PLACE1003519//KH domain family of RNA binding-proteins
PLACE1003723//Src homology domain 2
PLACE1003738//Zinc finger, C2H2 type
PLACE1003888//C2 domain //Phosphatidylinositol-specific phospholipase C, X domain //Phosphatidylinositol-specific phospholipase C, Y domain
PLACE1004128//WD domain, G-beta repeats
PLACE1004358//PH (pleckstrin homology) domain
PLACE1004428//Acyl-CoA dehydrogenases
PLACE1004437//Isocitrate and isopropylmalate dehydrogenases
PLACE1004506//LIM domain containing proteins
PLACE1004674//EF hand
PLACE1004918//L-lactate dehydrogenases
PLACE1005243//Eukaryotic protein kinase domain
PLACE1005305//Adenylate kinases
PLACE1005327//Src homology domain 3
PLACE1005530//Zinc finger, C3HC4 type (RING finger)
PLACE1005646//Helicases conserved C-terminal domain
PLACE1005656//Ribonucleotide reductases
PLACE1005966//WD domain, G-beta repeats
PLACE1006157//Sushi domain
PLACE1006196//DEAH and DEAR box helicases //Helicases conserved C-terminal domain
PLACE1006438//Zinc finger, C2H2 type
PLACE1006626//Double-stranded RNA binding motif
PLACE1006754//IG superfamily
PLACE1006829//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
PLACE1006917//RNA recognition motif. (aka RRM, RBD, or RNP domain)
PLACE1006956//ABC transporters
PLACE1006958//Heat shock hsp70 proteins
PLACE1007375//C2 domain
PLACE1007488//PH (pleckstrin homology) domain
PLACE1007511//Intermediate filament proteins
PLACE1007537//Ank repeat
PLACE1007544//Zinc finger, C2H2 type
PLACE1007547//Zinc finger, C3HC4 type (RING finger)
PLACE1007598//Zinc finger, C2H2 type
PLACE1007697//ABC transporters
PLACE1007958//3'5'-cyclic nucleotide phosphodiesterases
PLACE1007969//RNA recognition motif. (aka RRM, RBD, or RNP domain)
PLACE1008201//Zinc finger, C2H2 type
PLACE1008429//Ank repeat
PLACE1008465//Zinc finger, C2H2 type
PLACE1008650//WD domain, G-beta repeats
PLACE1009020//Aminotransferases class-V
PLACE1009094//von Willebrand factor type C domain

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PLACE1009099//Zinc finger, C2H2 type
PLACE1009246//LIM domain containing proteins
PLACE1009468//WD domain, G-beta repeats
PLACE1009476//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
PLACE1009524//PH (pleckstrin homology) domain
PLACE1009596//WD domain, G-beta repeats
PLACE1009622//Double-stranded RNA binding motif
PLACE1009861//Cysteine proteases
PLACE1009925//Helicases conserved C-terminal domain
PLACE1009992//CUB domain //EGF-like domain //Sushi domain //Trypsin
PLACE1010053//Double-stranded RNA binding motif
PLACE1010089//Ubiquitin carboxyl-terminal hydrolases family 2
PLACE1010702//Zinc finger, C2H2 type
PLACE1010833//EF hand
PLACE1010926//Src homology domain 3
PLACE1010960//Actins
PLACE1011041//Src homology domain 3
PLACE1011046//C2 domain //Phosphatidylinositol-specific phospholipase C, X domain //Phosphatidylinositol-specific phospholipase C, Y domain
PLACE1011114//Helicases conserved C-terminal domain
PLACE1011160//Zinc finger, C3HC4 type (RING finger)
PLACE1011263//Ank repeat
PLACE1011433//Zinc finger, C2H2 type
PLACE1011576//Zinc finger, C2H2 type
PLACE1011923//Eukaryotic protein kinase domain
PLACE2000034//Fibronectin type III domain //IG superfamily
PLACE2000072//Zinc finger, C2H2 type
PLACE2000111//IG superfamily
PLACE2000164//WD domain, G-beta repeats
PLACE2000216//PH (pleckstrin homology) domain
PLACE2000341//Sodium:solute symporter family
PLACE2000371//Src homology domain 2
PLACE2000373//Thrombospondin type 1 domain
PLACE2000398//IG superfamily
PLACE2000427//Helicases conserved C-terminal domain
PLACE2000458//Cadherin
PLACE3000020//Guanylate cyclases
PLACE3000169//Zinc finger, C2H2 type
PLACE4000014//Helicases conserved C-terminal domain
PLACE4000052//ABC transporters
PLACE4000192//Zinc finger, C2H2 type
PLACE4000211//Bromodomain
PLACE4000431//Helicases conserved C-terminal domain
PLACE4000522//Ank repeat
PLACE4000581//EGF-like domain //Sushi domain
PLACE4000654//Ubiquitin-conjugating enzymes
THYRO1000072//IG superfamily
THYRO1000242//Zinc finger, C2H2 type
THYRO1000288//Zinc-binding metalloprotease domain
THYRO1000488//Zinc finger, C3HC4 type (RING finger)
THYRO1000501//Zinc finger, C3HC4 type (RING finger)
THYRO1000666//Kinesin motor domain
THYRO1000748//Src homology domain 3
THYRO1000926//3' 5'-cyclic nucleotide phosphodiesterases
THYRO1001661//RNA recognition motif. (aka RRM, RBD, or RNP domain)
THYRO1001671//Ubiquitin family
Y79AA1000037//Zinc finger, C3HC4 type (RING finger)
Y79AA1000214//Core histones H2A, H2B, H3 and H4

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Y79AA1000342//Zinc finger, C2H2 type
Y79AA1000349//Double-stranded RNA binding motif
Y79AA1000627//Zinc finger, C2H2 type
Y79AA1000705//Helicases conserved C-terminal domain
Y79AA1000752//KH domain family of RNA binding proteins
Y79AA1000833//Tubulin
Y79AA1001048//Acyl-CoA dehydrogenases
Y79AA1001391//Homeobox domain
Y79AA1001394//ATPases associated with various cellular activities (AAA)
Y79AA1001493//Ubiquitin-conjugating enzymes
Y79AA1001613//Zinc finger, C2H2 type
Y79AA1001874//TNFR/NGFR cysteine-rich region
Y79AA1002027//Ubiquitin-conjugating enzymes
Y79AA1002139//DnaJ, prokaryotic heat shock protein
Y79AA1002208//Ank repeat
Y79AA1002246//C2 domain
Y79AA1002307//Fibronectin type III domain
Y79AA1002472//Zinc finger, C2H2 type
HEMBA1003538//CUB domain HEMBA1003645//WD domain, G-beta repeats //Src homology domain 3 HEMBA1005206//Glutathione S-transferases.
HEMBA1006521//Alcohol/other dehydrogenases, short chain type
HEMBB1001482//Zinc finger, C2H2 type HEMBB1001915//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2 HEMBB1002044//Cadherin MAMMA1000183//Zinc finger, C2H2 type MAMMA1000897//von Willebrand factor type A domain MAMMA1001080//IG superfamily MAMMA1002498//IG superfamily MAMMA1002573//KH domain family of RNA binding proteins MAMMA1002617//Zinc finger, C2H2 type NT2RM1000833//eubacterial secY protein NT2RM2001797//Zinc finger, C2H2 type
NT2RP1001013//Zinc finger, C2H2 type NT2RP2001233//Zinc finger, C2H2 type
NT2RP2001440//14-3-3 proteins NT2RP2002105//7 transmembrane receptor (rhodopsin family) NT2RP3001723//Laminin G domain NT2RP3001938//Eukaryotic protein kinase domain NT2RP3002330//Elongation factor Tu family (contains ATP/GTP binding P-loop) NT2RP3003133//Zinc finger, C2H2 type
NT2RP3003500//Eukaryotic protein kinase domain NT2RP3003799//C2 domain
NT2RP3003800//Eukaryotic protein kinase domain NT2RP3004013//Double-stranded RNA binding motif NT2RP3004125//Zinc finger, C2H2 type
OVARC1001244//Bromodomain OVARC1001496//D-isomer specific 2-hydroxyacid dehydrogenases PLACE1000007//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2 PLACE1001118//Zinc finger, C2H2 type PLACE1010310//Zinc finger, C2H2 type PLACE1011896//wnt family of developmental signaling proteins PLACE3000124//Src homology domain 2
PLACE4000100//D-isomer specific 2-hydroxyacid dehydrogenases
PLACE4000259//Helicases conserved C-terminal domain PLACE4000261//Bromodomain SKNMC1000013//ABC transporters SKNMC1000091//Basic region plus leucine zipper transcription factors THYRO1000343//Src homology domain 3 THYRO1000569//Zinc finger, C2H2 type THYRO1001189//Zinc finger, C2H2 type Y79AA1002103//Zinc finger, C2H2 type PLACE3000350//Eukaryotic protein kinase domain
PLACE4000156//Zinc finger, C2H2 type

EXAMPLE 18

Classification of cDNA clones into functional categories based on the full-length nucleotide sequences

[0257] Prediction of functions of proteins encoded by the clones and the categorization thereof were performed based on the results of homology search (see Homology search results 6, 12, 13 and 14) of the databases, GenBank, Swiss-Prot and UniGene, for the full-length nucleotide sequences of 4997 clones and based on the results of domain search (see Example 17) of the deduced amino acid sequences encoded by the full-length nucleotide sequences. The target 4997 clones are listed below:

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[0258] Among the 4997 clones, there are 2189 clones that presumably encode proteins belonging to any of the categories of secretory or membrane proteins, glycoprotein-associated proteins, signal transduction-associated proteins, transcription-associated proteins, disease-associated proteins, enzymes and/or metabolism-associated proteins, ATP- and/or GTP-binding proteins, nuclear proteins, DNA- and/or RNA-binding proteins, RNA synthesis-associated proteins, protein synthesis- and/or protein transport-associated proteins, cytoskeleton-associated proteins, cell division- and/or cell proliferation-associated proteins, embryogenesis- and/or development-associated proteins, or cellular defense-associated proteins.

[0259] The clones that presumably encode proteins belonging to the category of secretory or membrane proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "growth factor", "cytokine", "hormone", "signal", "transmembrane", "membrane", "extracellular matrix", "receptor", "G-protein coupled receptor", "ionic channel", "voltage-gated channel", "calcium channel" , "cell adhesion" , "collagen", or "connective tissue"; those which matched the data, suggesting that the proteins are secretory or membrane proteins; or those which matched the full-length sequences of GenBank or UniGene database with similar description; and, further, those predicted to have an N-terminal signal sequence or a transmembrane region as a result of domain search for the amino acid sequences deduced from the full-length nucleotide sequences.

[0260] The clones that presumably encode proteins belonging to the category of glycoprotein-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "glycoprotein"; those which matched the data, suggesting that the proteins are glycoprotein; or those which matched the full-length sequences of GenBank or UniGene database with similar description.

[0261] The clones that presumably encode proteins belonging to the category of signal transduction-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "serine/threonine-protein kinase", "tyrosine-protein kinase", or "SH3 domain"; those which matched the data, suggesting that the proteins are signal transduction-associated proteins (for example, "ADP-ribosylation factor"); or those which matched the full-length sequences of GenBank or UniGene database with similar description.

[0262] The clones that presumably encode proteins belonging to the category of transcription-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "transcription regulation", "zinc finger", or "homeobox"; those which matched the data, suggesting that the proteins are transcription-associated proteins; or those which matched the full-length sequences of GenBank or UniGene database with similar description.

[0263] The clones that presumably encode proteins belonging to the category of disease-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "disease mutation" or "syndrome"; those which matched the data, suggesting that the proteins are disease-associated proteins; or those which matched the full-length sequences of Swiss-Prot database and GenBank or UniGene database where the matched sequences of genes or proteins which had been registered in the database of Online Mendelian Inheritance in Man (OMIM) (http://www.ncbi.nlm.nih.gov/Omim/), which is a database of human genes and diseases.

[0264] The clones that presumably encode proteins belonging to the category of enzymes and/or metabolism-associated proteins are those which showed the terms " metabolism", "oxidoreductase", or "E.C. No. (Enzyme commission number)" in the matching data.

[0265] The clones that presumably encode proteins belonging to the category of ATP- and/or GTP-binding proteins are those which matched the data with the terms "ATP-binding" or "GTP-binding".

[0266] The clones that presumably encode proteins belonging to the category of nuclear proteins are those which matched the data with the terms "nuclear protein".

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[0267] The clones that presumably encode proteins belonging to the category of DNA- and/or RNA-binding proteins are those which matched the data with the terms "DNA-binding" or "RNA-binding".

[0268] The clones that presumably encode proteins belonging to the category of RNA synthesis-associated proteins are those which matched the data with the terms "RNA splicing", "RNA processing", "RNA helicase", or "polyadenylation".

[0269] The clones that presumably encode proteins belonging to the category of protein synthesis- and/or protein transport-associated proteins are those which matched the data with the terms "translation regulation", "protein biosynthesis", "amino-acid biosynthesis", "ribosomal protein", "protein transport", or "signal recognition particle".

[0270] The clones that presumably encode proteins belonging to the category of cytoskeleton-associated proteins are those which matched the data with the terms "structural protein", "cytoskeleton", "actin-binding", or "microtubules".

[0271] The clones that presumably encode proteins belonging to the category of cell division- and/or cell proliferation-associated proteins are those which matched the data with the terms "cell division", "cell cycle", "mitosis", "chromosomal protein", "cell growth", or "apoptosis" .

[0272] The clones that presumably encode proteins belonging to the category of embryogenesis- and/or development-associated proteins are those which matched the data with the terms "developmental protein".

[0273] The clones that presumably encode proteins belonging to the category of cellular defense-associated proteins are those which matched the data with the terms "heat shock", "DNA repair", or "DNA damage".

[0274] When a clone belonged to the above-mentioned multiple functional categories, the clone was classified into the multiple categories. However, the functions of the protein encoded by the clone are not limited to the functions of the categories into which the clone was classified, and therefore, additional functions can be found for the protein by further analyses.

[0275] The following 796 clones are categorized into secretory or membrane proteins.

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[0276] The following 141 clones are categorized into glycoproteins-associated proteins.

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[0277] The following 129 clones are categorized into signal transduction-associated proteins.

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[0278] The following 309 clones are categorized into transcription -associated proteins.

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[0279] The following 392 clones are categorized into disease-associated proteins.

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[0280] Among them, Swiss-Prot database search and GenBank or UniGene database search revealed that the following 380 clones matched the data of genes or proteins which had been registered in the database of Online Mendelian Inheritance in Man (OMIM) (http://www.ncbi.nlm.nih.gov/Omim/), which is a database of human genes and diseases. (The corresponding OMIM numbers are parenthetically indicated following the clone names.)

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Y79AA1001874(600315), Y79AA1002204(605033), Y79AA1002210(191161), Y79AA1002472(603971), Y79AA1002482(603971),

[0281] The following 425 clones presumably belong to enzymes and/or metabolism-associated proteins.

HEMBA1000012, HEMBA1000129, HEMBA1000141, HEMBA1000150, HEMBA1000542, HEMBA1000852, HEMBA1001019, HEMBA1001257, HEMBA1001526, HEMBA1001620, HEMBA1001866, HEMBA1001896, HEMBA1002212, HEMBA1002513, HEMBA1002746, HEMBA1002973, HEMBA1003046, HEMBA1003136, HEMBA1003179, HEMBA1003250, HEMBA1003291, HEMBA1003408, HEMBA1003538, HEMBA1003679, HEMBA1003680, HEMBA1004199, HEMBA1004227, HEMBA1004408, HEMBA1004509, HEMBA1004734, HEMBA1004768, HEMBA1005394, HEMBA1005513, HEMBA1005737, HEMBA1005815, HEMBA1006031, HEMBA1006272, HEMBA1006278, HEMBA1006291, HEMBA1006309, HEMBA1006347, HEMBA1006485, HEMBA1006521, HEMBA1006624, HEMBA1006885, HEMBA1006976, HEMBA1007121, HEMBA1007224, HEMBA1007243, HEMBA1007300, HEMBB1000083, HEMBB1000217, HEMBB1000915, HEMBB1000947, HEMBB1001137, HEMBB1001346, HEMBB1001429, HEMBB1001443, HEMBB1001915, HEMBB1001950, HEMBB1002042, MAMMA1000020, MAMMA1000085, MAMMA1000672, MAMMA1000713, MAMMA1000841, MAMMA1000897, MAMMA1001008, MAMMA1001038, MAMMA1001059, MAMMA1001476, MAMMA1001501, MAMMA1002268, MAMMA1002470, MAMMA1002530, MAMMA1002573, MAMMA1002619, MAMMA1002655, MAMMA1002671, MAMMA1003013, MAMMA1003035, NT2RM1000039, NT2RM1000132, NT2RM1000153, NT2RM1000256, NT2RM1000280, NT2RM1000377, NT2RM1000553, NT2RM1000648, NT2RM1000702, NT2RM1000894, NT2RM1001072, NT2RM1001115, NT2RM2000013, NT2RM2000092, NT2RM2000322, NT2RM2000368, NT2RM2000371, NT2RM2000469, NT2RM2000504, NT2RM2000577, NT2RM2000594, NT2RM2000951, NT2RM2001238, NT2RM2001547, NT2RM2001632, NT2RM2001664, NT2RM2001698, NT2RM2001700, NT2RM2001730, NT2RM2001782, NT2RM2001803, NT2RM2001886, NT2RM2001935, NT2RM2001997, NT2RM2002030, NT2RM2002128, NT2RM4000024, NT2RM4000155, NT2RM4000344, NT2RM4000471, NT2RM4000616, NT2RM4000657, NT2RM4000712, NT2RM4000820, NT2RM4001313, NT2RM4001316, NT2RM4001444, NT2RM4001592, NT2RM4001758, NT2RM4001819, NT2RM4001880, NT2RM4002062, NT2RM4002063, NT2RM4002189, NT2RM4002213, NT2RM4002251, NT2RM4002409, NT2RM4002532, NT2RM4002623, NT2RP1000376, NT2RP1000443, NT2RP1000522, NT2RP1000834, NT2RP1000947, NT2RP1001079, NT2RP1001185, NT2RP1001253, NT2RP1001361, NT2RP1001543, NT2RP2000056, NT2RP2000114, NT2RP2000183, NT2RP2000248, NT2RP2000329, NT2RP2000422, NT2RP2000448, NT2RP2000668, NT2RP2000710, NT2RP2000816, NT2RP2001070, NT2RP2001392, NT2RP2001601, NT2RP2001663, NT2RP2001740, NT2RP2001748, NT2RP2001898, NT2RP2002124, NT2RP2002256, NT2RP2002609, NT2RP2002618, NT2RP2002959, NT2RP2002993, NT2RP2003230, NT2RP2003286, NT2RP2003401, NT2RP2003506, NT2RP2003543, NT2RP2003643, NT2RP2003702, NT2RP2003704, NT2RP2003713, NT2RP2003737, NT2RP2003840, NT2RP2003912, NT2RP2003952, NT2RP2004098, NT2RP2004239, NT2RP2004245, NT2RP2004768, NT2RP2004791, NT2RP2004799, NT2RP2004933, NT2RP2005038, NT2RP2005139, NT2RP2005162, NT2RP2005204, NT2RP2005239, NT2RP2005276, NT2RP2005344, NT2RP2005360, NT2RP2005457, NT2RP2005498, NT2RP2005549, NT2RP2005557, NT2RP2005605, NT2RP2005635, NT2RP2005723, NT2RP2005773, NT2RP2005775, NT2RP2005776, NT2RP2005784, NT2RP2005835, NT2RP2005942, NT2RP2006534, NT2RP2006571, NT2RP2006573, NT2RP3000031, NT2RP3000085, NT2RP3000207, NT2RP3000359, NT2RP3000578, NT2RP3000742, NT2RP3000845, NT2RP3000875, NT2RP3000917, NT2RP3001055, NT2RP3001221, NT2RP3001495, NT2RP3001898, NT2RP3001938, NT2RP3002303, NT2RP3002351, NT2RP3002501, NT2RP3002602, NT2RP3002628, NT2RP3002663, NT2RP3003301, NT2RP3003385, NT2RP3003490, NT2RP3003659, NT2RP3003825, NT2RP3003831, NT2RP3003846, NT2RP3003914, NT2RP3004148, NT2RP3004209, NT2RP3004378, NT2RP3004669, NT2RP3004670, NT2RP4000259, NT2RP4000312, NT2RP4000367, NT2RP4000417, NT2RP4000457, NT2RP4000657, NT2RP4000817, NT2RP4000855, NT2RP4000879, NT2RP4000927, NT2RP4000973, NT2RP4000997, NT2RP4001041, NT2RP4001079, NT2RP4001095, NT2RP4001143, NT2RP4001219, NT2RP4001375, NT2RP4001389, NT2RP4001483, NT2RP4001555, NT2RP4001592, NT2RP4001644, NT2RP4001730, NT2RP4001946, NT2RP4002408, NT2RP5003500, NT2RP5003522, OVARC1000013, OVARC1000060, OVARC1000139, OVARC1000288, OVARC1000309, OVARC1000473, OVARC1000556, OVARC1000682, OVARC1000722, OVARC1000751, OVARC1000885, OVARC1000915, OVARC1001107, OVARC1001713, OVARC1001762, OVARC1001809, OVARC1001942, OVARC1002156, OVARC1002165, PLACE1000007, PLACE1000142, PLACE1000185, PLACE1000213, PLACE1000383, PLACE1000420, PLACE1000547, PLACE1000653, PLACE1000755, PLACE1001054, PLACE1001062, PLACE1001672, PLACE1001692, PLACE1001748, PLACE1001781, PLACE1001817, PLACE1001869, PLACE1001989, PLACE1002073, PLACE1002598, PLACE1002908, PLACE1002991, PLACE1003174, PLACE1003176, PLACE1003709, PLACE1003885, PLACE1003888, PLACE1003903, PLACE1003915, PLACE1004270, PLACE1004428, PLACE1004437, PLACE1004751,

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PLACE1004804, PLACE1004918, PLACE1005243, PLACE1005305, PLACE1005373, PLACE1005656, PLACE1005763, PLACE1005804, PLACE1005953, PLACE1005955, PLACE1006011, PLACE1006469, PLACE1006534, PLACE1006626, PLACE1006731, PLACE1006819, PLACE1006829, PLACE1006878, PLACE1007226, PLACE1007416, PLACE1007649, PLACE1007706, PLACE1007729, PLACE1007954, PLACE1007958, PLACE1008111, PLACE1008275, PLACE1008330, PLACE1008643, PLACE1009094, PLACE1009130, PLACE1009444, PLACE1009763, PLACE1009861, PLACE1009992, PLACE1009997, PLACE1010096, PLACE1010362, PLACE1010481, PLACE1010662, PLACE1011046, PLACE1011219, PLACE1011229, PLACE1011332, PLACE1011635, PLACE1011923, PLACE2000021, PLACE2000034, PLACE2000398, PLACE2000404, PLACE2000438, PLACE3000009, PLACE3000020, PLACE3000059, PLACE3000147, PLACE3000339, PLACE3000350, PLACE4000063, PLACE4000100, PLACE4000401, PLACE4000548, PLACE4000654, SKNMC1000050, THYRO1000072, THYRO1000197, THYRO1000288, THYRO1000605, THYRO1000662, THYRO1000756, THYRO1000852, THYRO1000926, THYRO 1000934, THYRO1000951, THYRO 1000983, THYRO1001003, THYRO1001287, THYRO1001374, THYRO1001406, THYRO1001617, THYRO1001671, THYRO1001738, Y79AA1000782, Y79AA1001048, Y79AA1001233, Y79AA1001394, Y79AA1001493, Y79AA1001548, Y79AA1001581, Y79AA1001603, Y79AA1001827, Y79AA1002027, Y79AA1002209, Y79AA1002211, Y79AA1002361, Y79AA1002416.

[0282] The following 217 clones presumably belong to a group of cDNAs encoding ATP- and/or GTP-binding proteins.

HEMBA1000012, HEMBA1000129, HEMBA1000185, HEMBA1000491, HEMBA1000531, HEMBA1001019, HEMBA1001174, HEMBA1001387, HEMBA1001595, HEMBA1001723, HEMBA1001913, HEMBA1002161, HEMBA1002212, HEMBA1002876, HEMBA1002997, HEMBA1003250, HEMBA1003291, HEMBA1003369, HEMBA1003555, HEMBA1003560, HEMBA1004131, HEMBA1004199, HEMBA1004202, HEMBA1004354, HEMBA1004697, HEMBA1005047, HEMBA1005595, HEMBA1007018, HEMBA1007151, HEMBB1000083, HEMBB1000226, HEMBB1000264, HEMBB1000632, HEMBB1000725, HEMBB1001294, HEMBB1002193, MAMMA1000085, MAMMA1000612, MAMMA1000731, MAMMA1000738, MAMMA1001038, MAMMA1001735, MAMMA1001768, MAMMA1003127, NT2RM1000187, NT2RM1000388, NT2RM1000702, NT2RM1000772, NT2RM1000924, NT2RM2000469, NT2RM2000577, NT2RM2000740, NT2RM2001100, NT2RM2001201, NT2RM2001345, NT2RM2001823, NT2RM2002128, NT2RM4000155, NT2RM4000191, NT2RM4000356, NT2RM4000496, NT2RM4000611, NT2RM4000733, NT2RM4000820, NT2RM4001084, NT2RM4001178, NT2RM4001344, NT2RM4001444, NT2RM4001592, NT2RM4001714, NT2RM4001758, NT2RM4001880, NT2RM4002062, NT2RM4002174, NT2RM4002205, NT2RM4002527, NT2RM4002594, NT2RM4002623, NT2RP1000470, NT2RP1000478, NT2RP1000915, NT2RP1000958, NT2RP1001080, NT2RP1001410, NT2RP1001569, NT2RP2000126, NT2RP2000258, NT2RP2000329, NT2RP2000660, NT2RP2000668, NT2RP2000710, NT2RP2000812, NT2RP2000880, NT2RP2001245, NT2RP2001392, NT2RP2002606, NT2RP2003277, NT2RP2003912, NT2RP2004538, NT2RP2004568, NT2RP2004689, NT2RP2004768, NT2RP2004791, NT2RP2004920, NT2RP2005344, NT2RP2005393, NT2RP2005763, NT2RP2006534, NT2RP3000046, NT2RP3000252, NT2RP3000350, NT2RP3000359, NT2RP3000366, NT2RP3000397, NT2RP3000759, NT2RP3000845, NT2RP3000875, NT2RP3001150, NT2RP3001427, NT2RP3001453, NT2RP3001529, NT2RP3001730, NT2RP3001799, NT2RP3001857, NT2RP3001938, NT2RP3002007, NT2RP3002151, NT2RP3002330, NT2RP3002399, NT2RP3002671, NT2RP3003301, NT2RP3003353, NT2RP3003589, NT2RP3003809, NT2RP3003876, NT2RP3004189, NT2RP3004428, NT2RP3004578, NT2RP4000290, NT2RP4000481, NT2RP4000518, NT2RP4000781, NT2RP4000839, NT2RP4000929, NT2RP4001041, NT2RP4001079, NT2RP4001375, NT2RP4001414, NT2RP4001592, NT2RP4001634, NT2RP4001644, NT2RP4001656, NT2RP4001896, NT2RP4002047, NT2RP4002058, NT2RP4002408, NT2RP5003477, OVARC1000013, OVARC1000304, OVARC1000556, OVARC1000771, OVARC1000800, OVARC1001068, OVARC1002138, PLACE1000040, PLACE1000588, PLACE1001104, PLACE1001739, PLACE1002433, PLACE1002437, PLACE1002714, PLACE1003394, PLACE1003521, PLACE1003915, PLACE1004902, PLACE1005243, PLACE1005305; PLACE1005549, PLACE1005739, PLACE1005921, PLACE1006119, PLACE1006196, PLACE1006552, PLACE1006956, PLACE1007409, PLACE1007697, PLACE1007946, PLACE1008244, PLACE1009404, PLACE1009476, PLACE1009596, PLACE1009908, PLACE1010134, PLACE1010720, PLACE1010896, PLACE1011109, PLACE1011114, PLACE1011310, PLACE1011922, PLACE2000014, PLACE2000039, PLACE2000274, PLACE2000404, PLACE2000427, PLACE3000350, PLACE4000009, PLACE4000014, PLACE4000326, SKNMC1000013, THYRO1000072, THYRO1001458, Y79AA1000833, Y79AA1000962, Y79AA1001394, Y79AA1001875, Y79AA1001963, Y79AA1002209,

[0283] The following 320 clones presumably belong to nuclear proteins.

HEMBA1000005, HEMBA1000158, HEMBA1000216, HEMBA1000561, HEMBA1000591, HEMBA1001088, HEMBA1001137, HEMBA1001405, HEMBA1001510, HEMBA1001579, HEMBA1001809, HEMBA1001819, HEMBA1001824, HEMBA1001847, HEMBA1001869, HEMBA1002177, HEMBA1002241, HEMBA1002495,

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HEMBA1002569, HEMBA1002935, HEMBA1002951, HEMBA1002999, HEMBA1003408, HEMBA1003545, HEMBA1003662, HEMBA1003684, HEMBA1003690, HEMBA1003760, HEMBA1004203, HEMBA1004321, HEMBA1004353, HEMBA1004479, HEMBA1004973, HEMBA1005219, HEMBA1005359, HEMBA1005558, HEMBA1005931, HEMBA1006278, HEMBA1006283, HEMBA1006359, HEMBA1006485, HEMBA1007087, HEMBB1000226, HEMBB1000789, HEMBB1001011, HEMBB1001056, HEMBB1001242, HEMBB1001482, HEMBB1001915, HEMBB1002134, HEMBB1002217, MAMMA1000183, MAMMA1000731, MAMMA1001105, MAMMA1001222, MAMMA1001260, MAMMA1001633, MAMMA1001743, MAMMA1001837, MAMMA1002617, MAMMA1002869, MAMMA1002937, MAMMA1003011, NT2RM1000086, NT2RM1000187, NT2RM1000666, NT2RM1000885, NT2RM1000894, NT2RM1001059, NT2RM1001092, NT2RM2000013, NT2RM2000588, NT2RM2000624, NT2RM2000735, NT2RM2000740, NT2RM2001105, NT2RM2001635, NT2RM2001670, NT2RM2001771, NT2RM2001823, NT2RM2001936, NT2RM2001989, NT2RM2002004, NT2RM2002088, NT2RM2002091, NT2RM4000024, NT2RM4000046, NT2RM4000104, NT2RM4000202, NT2RM4000215, NT2RM4000290, NT2RM4000531, NT2RM4000751, NT2RM4000996, NT2RM4001092, NT2RM4001140, NT2RM4001200, NT2RM4001483, NT2RM4001566, NT2RM4001592, NT2RM4001597, NT2RM4001783, NT2RM4001823, NT2RM4001828, NT2RM4001858, NT2RM4001979, NT2RP1000035, NT2RP1000111, NT2RP1000493, NT2RP1000574, NT2RP1000630, NT2RP1000902, NT2RP1000915, NT2RP1000958, NT2RP1000966, NT2RP1001013, NT2RP1001177, NT2RP2000008, NT2RP2000076, NT2RP2000126, NT2RP2000153, NT2RP2000161, NT2RP2000248, NT2RP2000258, NT2RP2000297, NT2RP2000420, NT2RP2000931, NT2RP2001233, NT2RP2001420, NT2RP2001756, NT2RP2001869, NT2RP2002079, NT2RP2002270, NT2RP2002503, NT2RP2002591, NT2RP2002880, NT2RP2002939, NT2RP2002993, NT2RP2003137, NT2RP2003157, NT2RP2003277, NT2RP2003286, NT2RP2003308, NT2RP2003347, NT2RP2003714, NT2RP2003912, NT2RP2004013, NT2RP2004187, NT2RP2004689, NT2RP2004920, NT2RP2005393, NT2RP2005436, NT2RP2005496, NT2RP2005539, NT2RP2005701, NT2RP2005767, NT2RP2005776, NT2RP2005933, NT2RP2005942, NT2RP2006043, NT2RP2006436, NT2RP3000031, NT2RP3000050, NT2RP3000397, NT2RP3000512, NT2RP3000527, NT2RP3000590, NT2RP3000603, NT2RP3000632, NT2RP3000917, NT2RP3001057, NT2RP3001107, NT2RP3001120, NT2RP3001253, NT2RP3001338, NT2RP3001384, NT2RP3001398, NT2RP3001427, NT2RP3001428, NT2RP3001472, NT2RP3001646, NT2RP3001671, NT2RP3001792, NT2RP3001855, NT2RP3002056, NT2RP3002165, NT2RP3002399, NT2RP3002876, NT2RP3003193, NT2RP3003212, NT2RP3003555, NT2RP3004016, NT2RP3004206, NT2RP3004424, NT2RP3004428, NT2RP3004566, NT2RP3004617, NT2RP4000078, NT2RP4000111, NT2RP4000210, NT2RP4000398, NT2RP4000481, NT2RP4000518, NT2RP4000997, NT2RP4001148, NT2RP4001206, NT2RP4001213, NT2RP4001433, NT2RP4001568, NT2RP4001638, NT2RP4001696, NT2RP4001753, NT2RP4001938, NT2RP4002058, NT2RP4002078, NT2RP4002081, NT2RP4002791, OVARC1000006, OVARC1000087, OVARC1000091, OVARC1000241, OVARC1000326, OVARC1000556, OVARC1000846, OVARC1001038, OVARC1001180, OVARC1001232, OVARC1001271, OVARC1001306, OVARC1001436, OVARC1002112, PLACE1000133, PLACE1000184, PLACE1000406, PLACE1000583, PLACE1000596, PLACE1000979, PLACE1001118, PLACE1001383, PLACE1001632, PLACE1002171, PLACE1002433, PLACE1002438, PLACE1002532, PLACE1002775, PLACE1002816, PLACE1002834, PLACE1003100, PLACE1003190, PLACE1003302, PLACE1003519, PLACE1003521, PLACE1003605, PLACE1003704, PLACE1003738, PLACE1003885, PLACE1003923, PLACE1004302, PLACE1004471, PLACE1004564, PLACE1004814, PLACE1004902, PLACE1005287, PLACE1005876, PLACE1005966, PLACE1006167, PLACE1006438, PLACE1006482, PLACE1006829, PLACE1006878, PLACE1006917, PLACE1007014, PLACE1007547, PLACE1007598, PLACE1007688, PLACE1007969, PLACE1008044, PLACE1008132, PLACE1008603, PLACE1009099, PLACE1009130, PLACE1009308, PLACE1009398, PLACE1010134, PLACE1010194, PLACE1010702, PLACE1010720, PLACE1010870, PLACE1011056, PLACE1011433, PLACE1011664, PLACE2000014, PLACE2000427, PLACE3000009, PLACE3000169, PLACE4000014, PLACE4000156, PLACE4000192, PLACE4000261, PLACE4000326, PLACE4000489, SKNMC1000011, THYRO1000085, THYRO1000242, THYRO1000585, THYRO1001100, THYRO1001189, THYRO1001809, Y79AA1000037, Y79AA1000214, Y79AA1000231, Y79AA1000589, Y79AA1000752, Y79AA1001391, Y79AA1001613, Y79AA1001705, Y79AA1001963, Y79AA1002431, Y79AA1002472, Y79AA1002482

[0284] The following 292 clones presumably belong to DNA- and/or RNA-binding proteins.

HEMBA1000158, HEMBA1000216, HEMBA1000561, HEMBA1000591, HEMBA1000851, HEMBA1001088, HEMBA1001137, HEMBA1001405, HEMBA1001510, HEMBA1001804, HEMBA1001809, HEMBA1001819, HEMBA1001847, HEMBA1001869, HEMBA1002177, HEMBA1002935, HEMBA1003408, HEMBA1003545, HEMBA1003568, HEMBA1003591, HEMBA1003662, HEMBA1003684, HEMBA1003760, HEMBA1003783, HEMBA1003805, HEMBA1003953, HEMBA1004321, HEMBA1004354, HEMBA1004389, HEMBA1004479, HEMBA1004669, HEMBA1004847, HEMBA1004973, HEMBA1005202, HEMBA1005359, HEMBA1005931,

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HEMBA1006248, HEMBA1006278, HEMBA1006283, HEMBA1006359, HEMBA1006652, HEMBA1007087, HEMBA1007194, HEMBB1000264, HEMBB1000789, HEMBB1001011, HEMBB1001482, HEMBB1001736, HEMBB1001749, HEMBB1001839, HEMBB1002217, MAMMA1000183, MAMMA1000284, MAMMA1000731, MAMMA1001105, MAMMA1001222, MAMMA1001260, MAMMA1001743, MAMMA1001837, MAMMA1002385, MAMMA1002617, MAMMA1002869, MAMMA1002937, MAMMA1003011, NT2RM1000086, NT2RM1000539, NT2RM1000555, NT2RM1000666, NT2RM1000691, NT2RM1000826, NT2RM1000885, NT2RM1001059, NT2RM1001092, NT2RM2000371, NT2RM2000624, NT2RM2000735, NT2RM2001105, NT2RM2001424, NT2RM2001575, NT2RM2001605, NT2RM2001670, NT2RM2001771, NT2RM2001823, NT2RM2001989, NT2RM2002004, NT2RM2002014, NT2RM2002088, NT2RM2002091, NT2RM4000046, NT2RM4000104, NT2RM4000167, NT2RM4000191, NT2RM4000202, NT2RM4000531, NT2RM4000595, NT2RM4000733, NT2RM4000751, NT2RM4000996, NT2RM4001092, NT2RM4001140, NT2RM4001178, NT2RM4001200, NT2RM4001483, NT2RM4001592, NT2RM4001783, NT2RM4001823, NT2RM4001828, NT2RM4001858, NT2RM4001880, NT2RM4001979, NT2RM4002093, NT2RM4002109, NT2RP1000470, NT2RP1000493, NT2RP1000574, NT2RP1000902, NT2RP1000966, NT2RP1001013, NT2RP1001073, NT2RP1001080, NT2RP2000008, NT2RP2000153, NT2RP2000258, NT2RP2000297, NT2RP2001127, NT2RP2001174, NT2RP2001233, NT2RP2001511, NT2RP2001756, NT2RP2001869, NT2RP2002079, NT2RP2002099, NT2RP2002503, NT2RP2002591, NT2RP2002939, NT2RP2003157, NT2RP2003329, NT2RP2003347, NT2RP2003480, NT2RP2003522, NT2RP2003564, NT2RP2003714, NT2RP2004187, NT2RP2004568, NT2RP2004920, NT2RP2005003, NT2RP2005139, NT2RP2005168, NT2RP2005436, NT2RP2005496, NT2RP2005701, NT2RP2005763, NT2RP2005776, NT2RP2005942, NT2RP2006043, NT2RP2006436, NT2RP2006464, NT2RP3000050, NT2RP3000512, NT2RP3000527, NT2RP3000562, NT2RP3000590, NT2RP3000603, NT2RP3000624, NT2RP3000632, NT2RP3000994, NT2RP3001057, NT2RP3001107, NT2RP3001120, NT2RP3001150, NT2RP3001155, NT2RP3001338, NT2RP3001398, NT2RP3001472, NT2RP3001672, NT2RP3001688, NT2RP3001724, NT2RP3001792, NT2RP3001855, NT2RP3002165, NT2RP3002399, NT2RP3002876, NT2RP3003138, NT2RP3003193, NT2RP3003251, NT2RP3003327, NT2RP3003555, NT2RP3004013, NT2RP3004078, NT2RP3004428, NT2RP3004490, NT2RP3004566, NT2RP3004594, NT2RP3004617, NT2RP3004618, NT2RP4000111, NT2RP4000398, NT2RP4000455, NT2RP4000518, NT2RP4000648, NT2RP4000865, NT2RP4000929, NT2RP4001080, NT2RP4001095, NT2RP4001213, NT2RP4001433, NT2RP4001568, NT2RP4001696, NT2RP4001753, NT2RP4001838, NT2RP4001938, NT2RP4002078, OVARC1000006, OVARC1000087, OVARC1000241, OVARC1000746, OVARC1000846, OVARC1001232, OVARC1001271, OVARC1001306, OVARC1001987, OVARC1002112, PLACE1000406, PLACE1000583, PLACE1000979, PLACE1001118, PLACE1001632, PLACE1001739, PLACE1002438, PLACE1002532, PLACE1002775, PLACE1002834, PLACE1003302, PLACE1003519, PLACE1003605, PLACE1003704, PLACE1003738, PLACE1003885, PLACE1004471, PLACE1004564, PLACE1004814, PLACE1005584, PLACE1005876, PLACE1005951, PLACE1006196, PLACE1006482, PLACE1006488, PLACE1006531, PLACE1006917, PLACE1007346, PLACE1007547, PLACE1007598, PLACE1007688, PLACE1007969, PLACE1008132, PLACE1009099, PLACE1009246, PLACE1009398, PLACE1009476, PLACE1009622, PLACE1010053, PLACE1010194, PLACE1010702, PLACE1010870, PLACE1011056, PLACE1011114, PLACE1011433, PLACE2000427, PLACE3000009, PLACE3000169, PLACE4000014, PLACE4000156, PLACE4000192, PLACE4000261, PLACE4000489, SKNMC1000091, THYRO1000085, THYRO1000242, THYRO1000501, THYRO1001100, THYRO1001189, THYRO1001809, Y79AA1000037, Y79AA1000349, Y79AA1000752, Y79AA1001211, Y79AA1001312, Y79AA1001391, Y79AA1001613, Y79AA1002103, Y79AA1002472, Y79AA1002482,

[0285] The following 66 clones presumably belong to the category of RNA synthesis-associated proteins.

HEMBA1000591, HEMBA1001579, HEMBA1003179, HEMBA1003591, HEMBA1006278, HEMBB1000226, NT2RM1000187, NT2RM1000852, NT2RM2000624, NT2RM2001989, NT2RM2002100, NT2RM4000191, NT2RM4001178, NT2RM4002093, NT2RP1000035, NT2RP1000272, NT2RP1000470, NT2RP1001080, NT2RP2000153, NT2RP2002928, NT2RP2003157, NT2RP2004568, NT2RP2005126, NT2RP2005436, NT2RP2005539, NT2RP2005605, NT2RP2005776, NT2RP2005942, NT2RP2006043, NT2RP2006238, NT2RP3000361, NT2RP3000397, NT2RP3001671, NT2RP3004504, NT2RP4000078, NT2RP4000111, NT2RP4000481, NT2RP4000518, NT2RP4000614, NT2RP4000929, NT2RP4001696, NT2RP4002058, OVARC1001232, OVARC1001577, PLACE1000406, PLACE1000596, PLACE1000755, PLACE1001739, PLACE1003704, PLACE1003885, PLACE1004564, PLACE1004814, PLACE1004902, PLACE1005373, PLACE1005646, PLACE1005876, PLACE1006196, PLACE1006626, PLACE1006878, PLACE1006917, PLACE1009476, PLACE1009925, PLACE1010194, PLACE1011114, THYRO1000121, Y79AA1001963,

[0286] The following 183 clones presumably belong to protein synthesis-associated and/or protein transport-associated proteins.

HEMBA1000012, HEMBA1000141, HEMBA1000592, HEMBA1003617, HEMBA1003773, HEMBA1004202,

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HEMBA1004276, HEMBA1004734, HEMBA1004847, HEMBA1004929, HEMBA1004930, HEMBA1005047, HEMBA1005202, HEMBA1006031, HEMBA1006272, HEMBA1006474, HEMBA1006652, HEMBA1006914, HEMBA1006973, HEMBA1007224, HEMBB1000915, HEMBB1001112, HEMBB1001137, HEMBB1001736, HEMBB1001831, HEMBB1001915, MAMMA1000085, MAMMA1000734, MAMMA1001008, MAMMA1002170, MAMMA1002219, MAMMA1002236, MAMMA1002619, NT2RM1000661, NT2RM1000833, NT2RM2000092, NT2RM2000504, NT2RM2000577, NT2RM2000821, NT2RM2001201, NT2RM2001592, NT2RM2001613, NT2RM2001648, NT2RM2001730, NT2RM2001760, NT2RM2002055, NT2RM4000155, NT2RM4000169, NT2RM4000344, NT2RM4000356, NT2RM4000421, NT2RM4000712, NT2RM4001054, NT2RM4001203, NT2RM4001382, NT2RM4001444, NT2RM4002062, NT2RM4002205, NT2RM4002623, NT2RP1000326, NT2RP1000522, NT2RP1000547, NT2RP1000746, NT2RP1000947, NT2RP1001569, NT2RP2000147, NT2RP2000710, NT2RP2000880, NT2RP2000943, NT2RP2001290, NT2RP2001392, NT2RP2001601, NT2RP2001613, NT2RP2001660, NT2RP2001740, NT2RP2002124, NT2RP2002606, NT2RP2002862, NT2RP2002959, NT2RP2002980, NT2RP2003137, NT2RP2003158, NT2RP2003391, NT2RP2003394, NT2RP2003401, NT2RP2003433, NT2RP2003704, NT2RP2003713, NT2RP2003737, NT2RP2003760, NT2RP2003981, NT2RP2004366, NT2RP2004389, NT2RP2004791, NT2RP2005012, NT2RP2005116, NT2RP2005360, NT2RP2005763, NT2RP2005784, NT2RP3000366, NT2RP3000759, NT2RP3000968, NT2RP3001113, NT2RP3001690, NT2RP3002045, NT2RP3002151, NT2RP3002529, NT2RP3002671, NT2RP3003301, NT2RP3003846, NT2RP3003876, NT2RP3004209, NT2RP4000370, NT2RP4000457, NT2RP4000879, NT2RP4000927, NT2RP4001041, NT2RP4001117, NT2RP4001313, NT2RP4001315, NT2RP4001574, NT2RP4001592, OVARC1000013, OVARC1000071, OVARC1000085, OVARC1000465, OVARC1000564, OVARC1000771, OVARC1000862, OVARC1001171, OVARC1001180, OVARC1001342, PLACE1000007, PLACE1000061, PLACE1000081, PLACE1000492, PLACE1000863, PLACE1001092, PLACE1001748, PLACE1002090, PLACE1003174, PLACE1003915, PLACE1004104, PLACE1004270, PLACE1004743, PLACE1005557, PLACE1005813, PLACE1006170, PLACE1006488, PLACE1006829, PLACE1007706, PLACE1007729, PLACE1008273, PLACE1008402, PLACE1008790, PLACE1008813, PLACE1009094, PLACE1009130, PLACE1009477, PLACE1009721, PLACE1009845, PLACE1010074, PLACE1010547, PLACE1011109, PLACE1011229, PLACE1011477, PLACE1012031, PLACE2000404, PLACE3000059, PLACE3000121, PLACE4000269, PLACE4000654, SKNMC1000011, THYRO1000983, THYRO1001003, THYRO1001313, Y79AA1000560, Y79AA1000784, Y79AA1000968, Y79AA1001493, Y79AA1001875, Y79AA1002027, Y79AA1002209,

[0287] The following 130 clones presumably belong to cytoskeletal-associated proteins.

HEMBA1000156, HEMBA1000168, HEMBA1000411, HEMBA1000588, HEMBA1001043, HEMBA1001651, HEMBA1001661, HEMBA1002102, HEMBA1002161, HEMBA1002939, HEMBA1003235, HEMBA1003581, HEMBA1004499, HEMBA1004534, HEMBA1004697, HEMBA1004929, HEMBA1004972, HEMBA1005582, HEMBA1005595, HEMBA1006344, HEMBA1006737, HEMBB1001175, HEMBB1001282, HEMBB1001562, HEMBB1001802, MAMMA1000824, MAMMA1001041, MAMMA1001576, MAMMA1001679, MAMMA1001735, MAMMA1002297, MAMMA1002351, MAMMA1002622, MAMMA1002637, MAMMA1003127, NT2RM1000850, NT2RM1000898, NT2RM2000030, NT2RM2000260, NT2RM2000691, NT2RM2001324, NT2RM4000169, NT2RM4000229, NT2RM4000515, NT2RM4001217, NT2RP1000202, NT2RP1000348, NT2RP1000460, NT2RP1000478, NT2RP1001033, NT2RP1001294, NT2RP1001302, NT2RP2000070, NT2RP2000812, NT2RP2000814, NT2RP2001168, NT2RP2001245, NT2RP2001634, NT2RP2001900, NT2RP2003307, NT2RP2003394, NT2RP2004041, NT2RP2004242, NT2RP2004538, NT2RP2004587, NT2RP2004681, NT2RP2004732, NT2RP2004978, NT2RP2005491, NT2RP2005531, NT2RP2005712, NT2RP2006275, NT2RP3000753, NT2RP3001113, NT2RP3001216, NT2RP3001239, NT2RP3001272, NT2RP3001554, NT2RP3001690, NT2RP3001799, NT2RP3002688, NT2RP3003061, NT2RP3003185, NT2RP3003230, NT2RP3004569, NT2RP3004578, NT2RP4001004, NT2RP4001086, NT2RP4001256, NT2RP4001567, NT2RP4001927, OVARC1000001, OVARC1000106, OVARC1000437, OVARC1000520, OVARC1000679, OVARC1001731, OVARC1002050, PLACE1001104, PLACE1002571, PLACE1002591, PLACE1002655, PLACE1002714, PLACE1003625, PLACE1005287, PLACE1006552, PLACE1007946, PLACE1008426, PLACE1010148, PLACE1010547, PLACE1010743, PLACE1010896, PLACE1010960, PLACE1011310, PLACE1011922, PLACE2000216, PLACE2000274, PLACE2000371, PLACE2000458, PLACE3000145, PLACE3000416, PLACE4000009, THYRO1000132, THYRO1001405, THYRO1001458, Y79AA1000368, Y79AA1000794, Y79AA1000833, Y79AA1000962, Y79AA1002208,

[0288] The following 54 clones presumably belong to cell division-associated and/or cell proliferation-associated proteins.

HEMBA1001019, HEMBA1001595, HEMBA1002363, HEMBA1002997, HEMBA1003136, HEMBA1003369, HEMBA1004131, HEMBA1004354, HEMBA1005621, HEMBB1000037, HEMBB1000264, MAMMA1001768, MAMMA1002769, NT2RM1000354, NT2RM1000430, NT2RM1000874, NT2RM2001256, NT2RM2001743,

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NT2RM2001896, NT2RM2002145, NT2RM4000215, NT2RM4001714, NT2RP1000163, NT2RP1000333, NT2RP1000439, NT2RP2000346, NT2RP2001397, NT2RP2002595, NT2RP2003177, NT2RP2003596, NT2RP2003912, NT2RP2004396, NT2RP2005037, NT2RP2005520, NT2RP2005669, NT2RP2005835, NT2RP3001730, NT2RP3002081, NT2RP4000210, NT2RP4000415, NT2RP4001414, NT2RP4001634, OVARC1000013, OVARC1000937, PLACE1001383, PLACE1002433, PLACE1004316, PLACE1005287, PLACE1008808, PLACE1010720, PLACE1010833, Y79AA1000748, Y79AA1001236, Y79AA1001394,

[0289] The following 36 clones presumably belong to the category of embryogenesis- and/or development-associated proteins.

HEMBA1000518, HEMBA1001847, HEMBA1001869, HEMBA1003545, HEMBA1004973, HEMBB1002442, MAMMA1001837, NT2RM2001670, NT2RM4000046, NT2RM4000531, NT2RM4001140, NT2RM4001858, NT2RP2002078, NT2RP2004187, NT2RP2006436, NT2RP3000603, NT2RP3000994, NT2RP3001580, NT2RP3001708, NT2RP3003071, NT2RP3004472, NT2RP3004617, NT2RP4000246, NT2RP4001567, OVARC1000304, OVARC1000746, PLACE1000793, PLACE1002532, PLACE1003258, PLACE1003625, PLACE1004460, PLACE1009622, PLACE4000558, THYRO1000085, Y79AA1001391, Y79AA1001692,

[0290] The following 30 clones presumably belong to cellular defense-associated proteins.

HEMBA1000005, HEMBA1000531, HEMBA1003417, HEMBA1006253, NT2RM4000354, NT2RM4001880, NT2RP1000333, NT2RP1000493, NT2RP2000006, NT2RP2000045, NT2RP2000809, NT2RP2001536, NT2RP2002464, NT2RP2004920, NT2RP2005037, NT2RP3000590, NT2RP3001426, NT2RP3002062, NT2RP3002785, NT2RP3004262, NT2RP4001555, NT2RP4001638, PLACE1006958, PLACE1008275, PLACE1009113, PLACE1011858, PLACE4000014, THYRO1000684, Y79AA1002139, Y79AA1002229,

[0291] Although it is unclear whether or not 261 clones out of clones other than the above-mentioned clones belong to any of the above-described categories, these clones are predicted to have some functions, based on the homology search using the full-length sequences thereof. The clone names and the gene definitions found in the result of homology search are shown below, separated with a double-slash mark, //.

HEMBA1000030//Homo sapiens ARF GTPase-activating protein GIT1 mRNA, complete cds.

HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1

HEMBA1000333//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.
HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).
HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.
HEMBA1001197//Homo sapiens rap2 interacting protein x mRNA, complete cds.
HEMBA1001302//Homo sapiens calcium binding protein precursor, mRNA, complete cds.
HEMBA1001455//Mus musculus transposon-derived Buster2 transposase-like protein gene, partial cds.
HEMBA1001675//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.
HEMBA1001714//Homo sapiens mRNA for ATPase inhibitor precursor, complete cds.
HEMBA1001744//SCY1 PROTEIN.
HEMBA1001967//Homo sapiens NY-REN-57 antigen mRNA, partial cds.
HEMBA1002151//Rattus norvegicus p34 mRNA, complete cds.
HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].
HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.
HEMBA1002777//Fugu rubripes BAW (BAW) mRNA, complete cds.
HEMBA1003098//Homo sapiens NY-REN-6 antigen mRNA, partial cds.
HEMBA1003199//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.
HEMBA1003615//Homo sapiens ART-4 mRNA, complete cds.
HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).
HEMBA1004295//Homo sapiens NY-REN-25 antigen mRNA, partial cds.
HEMBA1004573//Homo sapiens mRNA for HELG protein.
HEMBA1004604//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.
HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).
HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.
HEMBA1005201//Homo sapiens CGI-07 protein mRNA, complete cds.
HEMBA1005206//Drosophila simulans anon73B1 gene and Su(P) gene.
HEMBA1005530//Homo sapiens anaphase-promoting complex subunit 7 (APC7) mRNA, complete cds.
HEMBA1005666//Homo sapiens mRNA for DIPB protein.
HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.
HEMBA1006268//Homo sapiens HQOO24c mRNA, complete cds.

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HEMBA1006398//Human L1 element L1.6 putative p150 gene, complete cds.
HEMBA1006445//Homo sapiens putative tumor supressor NOEY2 mRNA, complete cds.
HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds.
HEMBA1007251//Homo sapiens F-box protein FBX29 (FBX29) mRNA, partial cds. HEMBB1000036//Homo sapiens CGI-51 protein mRNA, complete cds.
HEMBB1000144//GUANYLATE CYCLASE ACTIVATING PROTEIN 2 (GCAP 2) (RETINAL GUANYLYL CYCLASE ACTIVATOR PROTEIN P24).
HEMBB1000973//Mus musculus schlafen3 (Slfn3) mRNA, complete cds.
HEMBB1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds
HEMBB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).
HEMBB1001288//COPPER HOMEOSTASIS PROTEIN CUTC.
HEMBB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.
HEMBB1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.
HEMBB1002266//NEURONAL PROTEIN.
HEMBB1002510//GYP7 PROTEIN.
HEMBB1002705//Homo sapiens CGI-27 protein mRNA, complete cds.
MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TEST)].
MAMMA1000625//GYP7 PROTEIN.
MAMMA1001075//Homo sapiens CGI-72 protein mRNA, complete cds.
MAMMA1001181//ABC1 PROTEIN HOMOLOG PRECURSOR.
MAMMA1001259//Mus musculus F-box protein FBX18 mRNA, partial cds.
MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.
MAMMA1002143//Homo sapiens Cdc42 effector protein 4 mRNA, complete cds.
MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.
MAMMA1002972//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27.
MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.
NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).
NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).
NT2RM1000244//Homo sapiens TRAF4 associated factor 1 mRNA, partial cds.
NT2RM1000421//RIBONUCLEASE INHIBITOR.
NT2RM1000499//Caenorhabditis elegans mRNA for centaurin gamma 1A.
NT2RM1000623//RIBONUCLEASE INHIBITOR.
NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.
NT2RM2000502//Rattus norvegicus W3O7 mRNA, complete cds.
NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.
NT2RM2000718//Homo sapiens endocrine regulator mRNA, complete cds.
NT2RM2001065//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.
NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).
NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.
NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.
NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.
NT2RM4000030//LAS1 PROTEIN.
NT2RM4000139//R.norvegicus trg mRNA.
NT2RM4000156//H. sapiens HPBRII-7 gene.
NT2RM4000386//Mus musculus ODZ3 (Odz3) mRNA, partial cds.
NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).
NT2RM4001047//MO25 PROTEIN.
NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN.
NT2RM4001256//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.
NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds.
NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).
NT2RM4001347//Homo sapiens NY-REN-25 antigen mRNA, partial cds.
NT2RM4001371//Homo sapiens IDN3 mRNA, partial cds.
NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.
NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).

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NT2RM4001731//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.
NT2RM4001969//R.norvegicus mRNA for IP63 protein.
NT2RM4002034//Homo sapiens hiwi mRNA, partial cds.
NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).
NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.
NT2RP1000040//Mus musculus donson protein (Donson) mRNA, partial cds.
NT2RP1000363//R.norvegicus LL5 mRNA.
NT2RP1000481//Homo sapiens antigen NY-CO-3 (NY-CO-3) mRNA, partial cds.
NT2RP1000513//Human NifU-like protein (hNifU) mRNA, partial cds.
NT2RP1000733//Human mRNA for GSPT1-TK protein,complete cds.
NT2RP1000860//Homo sapiens KLO4P mRNA, complete cds.
NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).
NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds.
NT2RP1001395//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.
NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).
NT2RP1001494//MALE STERILITY PROTEIN 2.
NT2RP2000054//Homo sapiens putative ring zinc finger protein NY-REN-43 antigen mRNA, complete cds.
NT2RP2000067//Mus musculus ODZ3 (Odz3) mRNA, partial cds.
NT2RP2000133//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.
NT2RP2000157//MLO2 PROTEIN.
NT2RP2000764//NIFS PROTEIN.
NT2RP2000965//Homo sapiens mRNA for fls353, complete cds.
NT2RP2001839//SCY1 PROTEIN.
NT2RP2001883//Homo sapiens CGI-01 protein mRNA, complete cds.
NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA, complete cds.
NT2RP2001985//Homo sapiens high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha mRNA, complete cds.
NT2RP2002185//Homo sapiens ubiquilin mRNA, complete cds.
NT2RP2002442//HESA PROTEIN.
NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.
NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.
NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds.
NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.
NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.
NT2RP2003272//Homo sapiens ubiquilin mRNA, complete cds.
NT2RP2003857//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).
NT2RP2003871//Homo sapiens transposon-derived Buster1 transposase-like protein gene, complete cds.
NT2RP2004425//Mus musculus axotrophin mRNA, complete cds.
NT2RP2004476//Homo sapiens cyclin L ania-6a mRNA, complete cds.
NT2RP2004710//Mus musculus formin binding protein 30 mRNA, complete cds.
NT2RP2004816//H58 PROTEIN.
NT2RP2005441//Homo sapiens hypothalamus protein HT002 mRNA, complete cds.
NT2RP2005490//Mus musculus D3Mm3e (D3Mm3e) mRNA, complete cds.
NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.
NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).
NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.
NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.
NT2RP2005841//Homo sapiens mRNA for ALEX3, complete cds.
NT2RP2006598//Homo sapiens retinoid x receptor interacting protein mRNA, complete cds.
NT2RP3000047//NPL4 PROTEIN.
NT2RP3000233//RING CANAL PROTEIN (KELCH PROTEIN).
NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.
NT2RP3000869//Drosophila melanogaster AAA family protein Bor (bor) mRNA, complete cds.
NT2RP3001399//SSU72 PROTEIN.
NT2RP3001407//SCY1 PROTEIN.
NT2RP3001457//Drosophila melanogaster Melted (melt) mRNA, partial cds.
NT2RP3001587//Human anthracycline-associated resistance ARX mRNA, complete cds.

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NT2RP3001712//Homo sapiens HP1-BP74 protein mRNA, complete cds.
NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN).
NT2RP3001854//Homo sapiens novel retinal pigment epithelial cell protein (NORPEG) mRNA, complete cds.
NT2RP3001931//Rattus norvegicus clone C48 CDK5 activator-binding protein mRNA, complete cds.
NT2RP3002273//SCD6 PROTEIN.
NT2RP3002631//Homo sapiens Ran binding protein 11 mRNA, complete cds.
NT2RP3002682//Homo sapiens CGI-145 protein mRNA, complete cds.
NT2RP3002770//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.
NT2RP3002818//INSERTION ELEMENT IS2A HYPOTHETICAL 48.2 KD PROTEIN.
NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).
NT2RP3002972//Halocynthia roretzi mRNA for HrPET-1, complete cds.
NT2RP3003032//Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds.
NT2RP3003290//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.
NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.
NT2RP3003491//Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.
NT2RP3003500//SCY1 PROTEIN.
NT2RP3003726//Homo sapiens spermatogenesis associated PD1 mRNA, complete cds.
NT2RP3004348//R. norvegicus mRNA for cytosolic resiniferatoxin-binding protein.
NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).
NT2RP4000129//Xenopus laevis F-box protein 28 (Fbx28) mRNA, partial cds.
NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).
NT2RP4000528//NPL4 PROTEIN.
NT2RP4000737//Mus musculus F-box protein FBL10 mRNA, partial cds.
NT2RP4000979//Homo sapiens putative HIV-1 infection related protein mRNA, partial cds.
NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds.
NT2RP4001207//Homo sapiens Ran binding protein 11 mRNA, complete cds.
NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).
NT2RP4001260//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.
NT2RP4001339//Homo sapiens mRNA for AMMERC1 protein.
NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.
NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.
NT2RP4001966//Mus musculus ODZ3 (Odz3) mRNA, partial cds.
NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).
OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.
OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).
OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.
OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857O7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).
OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds.
OVARC1001555//NGG1-INTERACTING FACTOR 3.
OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).
OVARG1001943//Mus musculus DEBT-91 mRNA, complete cds.
PLACE1000004//Homo sapiens IDN3-B mRNA, complete cds.
PLACE1000066//SSU72 PROTEIN.
PLACE1000610//MSN5 PROTEIN.
PLACE1000636//MALE STERILITY PROTEIN 2.
PLACE1000769//Homo sapiens CGI-18 protein mRNA, complete cds.
PLACE1000987//Rattus norvegicus late gestation lung 2 protein (Lgl2) mRNA, complete cds.
PLACE1001036//Homo sapiens mRNA for alpha integrin binding protein 63, partial.
PLACE1001845//Mus musculus cyclin ania-6a mRNA, complete cds.
PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.
PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.
PLACE1003602//Homo sapiens mRNA expressed in placenta.
PLACE1003611//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.
PLACE1004256//Mus musculus short coiled coil protein SCOCO (Scoc) mRNA, complete cds.
PLACE1004550//Homo sapiens CGI-20 protein mRNA, complete cds.

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PLACE1004868//MALE STERILITY PROTEIN 2.
PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds
PLACE1005052//Homo sapiens CGI-16 protein mRNA, complete cds.
PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).
PLACE1005176//Homo sapiens hypothalamus protein HT001 mRNA, complete cds.
PLACE1005187//APAG PROTEIN.
PLACE1005331//Homo sapiens 7h3 protein mRNA, partial cds.
PLACE1005727//Homo sapiens STRIN protein (STRIN) mRNA, complete cds.
PLACE1006003//Homo sapiens CGI-94 protein mRNA, complete cds.
PLACE1006335//Homo sapiens NY-REN-50 antigen mRNA, partial cds.
PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.
PLACE1006506//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.
PLACE1007105//Homo sapiens muskelin (MKLN1) mRNA, complete cds.
PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds.
PLACE1007705//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.
PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds.
PLACE1007897//Homo sapiens FLASH mRNA, complete cds.
PLACE1008080//Homo sapiens mRNA for HEXIM1 protein, complete cds.
PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).
PLACE1008398//GENE 33 POLYPEPTIDE.
PLACE1008465//Homo sapiens mRNA for rapa-1 (rapa gene).
PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.
PLACE1009020//NIFS PROTEIN.
PLACE1009060//BRO1 PROTEIN.
PLACE1009186//Homo sapiens small zinc finger-like protein (TIM9b) mRNA, complete cds.
PLACE1009443//Mus musculus F-box protein FBL8 mRNA, complete cds.
PLACE1009571//Homo sapiens PTD002 mRNA, complete cds.
PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.
PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).
PLACE1010261//SEGREGATION DISTORTER PROTEIN.
PLACE1010310//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).
PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induced by progesterone), complete cds.
PLACE1010579//Homo sapiens CED-6 protein (CED-6) mRNA, complete cds.
PLACE1010628//Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds.
PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS13.
PLACE1010761//Homo sapiens mRNA for cisplatin resistance-associated overexpressed protein, complete cds.
PLACE1011185//INSERTION ELEMENT IS1 PROTEIN INSB.
PLACE1011340//Homo sapiens IDN3-B mRNA, complete cds.
PLACE1011586//Rattus norvegicus clone C53 CDK5 activator-binding protein mRNA, complete cds.
PLACE2000246//RING CANAL PROTEIN (KELCH PROTEIN).
PLACE2000411//Homo sapiens epsin 2b mRNA, complete cds.
PLACE3000477//Homo sapiens phosphoprotein pp75 mRNA, partial cds.
THYRO1000173//Homo sapiens AP-mu chain family member mu1B (HSMU1B) mRNA, complete cds.
THYRO1000401//Human TcD37 homolog (HTcD37) mRNA, partial cds.
THYRO1000666//Mus musculus mRNA for kinesin like protein 9.
THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.
THYRO1001347//Homo sapiens RAN binding protein 16 mRNA, complete cds.
THYRO1001656//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.
THYRO1001703//NIFR3-LIKE PROTEIN.
THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).
Y79AA1000059//Homo sapiens aryl-hydrocarbon interacting protein-like 1 (AIPL1) gene, complete cds.
Y79AA1000181//Homo sapiens CGI-01 protein mRNA, complete cds.
Y79AA1000268//Mus musculus Nip2l mRNA, complete cds.
Y79AA1000313//CALPHOTIN.
Y79AA1000540//CELL POLARITY PROTEIN TEA1.
Y79AA1000966//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.
Y79AA1000985//Human centrosomal protein kendrin mRNA, complete cds.

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Y79AA1001323//Mus musculus mRNA for GSG1, complete cds.
Y79AA1001402//Homo sapiens paraneoplastic cancer-testis-brain antigen (MA4) mRNA, partial cds.
Y79AA1001679//Homo sapiens lambda-crystallin mRNA, complete cds.
Y79AA1001923//Homo sapiens F-box protein Fbx22 (FBX22) gene, partial cds. Y79AA1002083//H. sapiens mRNA for MUF1 protein.
Y79AA1002307//Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds.
Y79AA1002311//R. norvegicus mRNA for cytosolic resiniferatoxin-binding protein.
Y79AA1002487//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.

[0292] Among the clones other than the above-mentioned, there were 36 clones that were similarly classified into the functional categories based on the results of functional domain search using the Pfam program. These clones were categorized as follows.

[0293] Clones presumably belonging to the category of secretory or membrane proteins are two clones, MAMMA1002498 and NT2RM4002287; a clone presumably belonging to the category of glycoproteins-associated proteins is a clone MAMMA1002498; clones presumably belonging to the category of signal transduction-associated proteins are 11 clones, HEMBA1001247, NT2RM2001813, NT2RM4001454, NT2RP2005140, NT2RP2005293, NT2RP3000487, NT2RP3003311, PLACE1000972, PLACE1003723, PLACE1005327, and PLACE3000124; clones presumably belonging to the category of transcription-associated proteins are 12 clones, HEMBA1003257, NT2RM2000101, NT2RM2001797, NT2RP1000101, NT2RP2002208, NT2RP3001214, NT2RP3003278, NT2RP4001235, PLACE1000050, PLACE1001716, PLACE1002499, and PLACE1007544; clones presumably belonging to the category of enzymes and/or metabolism-associated proteins are 2 clones, HEMBA1005732 and MAMMA1000402; clones presumably belonging to the category of DNA- and/or RNA-binding proteins are 4 clones, HEMBA1004596, OVARC1000148, PLACE1003334, and THYRO1001661; a clone presumably belonging to the category of protein synthesis- and/or protein transport-associated proteins is a clone, HEMBA1006284.

[0294] So far, useful information for presuming the functions is unavailable for the remaining 2511 clones. Their functions will possibly be revealed by further analyses. Names of the clones are listed below.

[0295] So far, useful information for presuming the functions are unavailable for the remaining 2511 clones. Their functions will possibly be revealed by further analyses. Names of the clones are listed below.

HEMBA1000042, HEMBA1000046, HEMBA1000050, HEMBA1000076, HEMBA1000193, HEMBA1000213,
HEMBA1000227, HEMBA1000231, HEMBA1000243, HEMBA1000244, HEMBA1000251, HEMBA1000264,
HEMBA1000280, HEMBA1000282, HEMBA1000288, HEMBA1000290, HEMBA1000302, HEMBA1000327,
HEMBA1000338, HEMBA1000351, HEMBA1000357, HEMBA1000376, HEMBA1000387, HEMBA1000392,
HEMBA1000396, HEMBA1000428, HEMBA1000442, HEMBA1000456, HEMBA1000459, HEMBA1000460,
HEMBA1000469, HEMBA1000497, HEMBA1000501, HEMBA1000504, HEMBA1000505, HEMBA1000508,
HEMBA1000519, HEMBA1000520, HEMBA1000534, HEMBA1000545, HEMBA1000557, HEMBA1000568,
HEMBA1000575, HEMBA1000594, HEMBA1000604, HEMBA1000622, HEMBA1000636, HEMBA1000655,
HEMBA1000673, HEMBA1000682, HEMBA1000686, HEMBA1000702, HEMBA1000722, HEMBA1000726,
HEMBA1000727, HEMBA1000749, HEMBA1000752, HEMBA1000769, HEMBA1000773, HEMBA1000774,
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Homology Search Result Data 1.

[0296] The result of the homology search of the SwissProt using the 5'-end sequence.

[0297] Data include

the name of clone,
definition of the top hit data,
the P-value: the length of the compared sequence: identity (%), and
the organism and the Accession No. of the top hit data, as in the order separated by //.

[0298] Data are not shown for the clones in which the P-value was higher than 1.

[0299] The P-value is a score obtained statistically by taking into account the possible similarity between two sequences. In general, the smaller P-value reflects the higher similarity. (Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410; Gish. W. &

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States, D.J. (1993) "Identification of protein coding regions by database similarity search." Nature Genet. 3:266-272).

F-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.8e-85:244:75//MUS MUSCULUS (MOUSE).//Q61712

F-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINETRNA LIGASE) (LEURS).//7.6e-57:231:53//CAENORHABDITIS ELEGANS.//Q09996

F-HEMBA1000020//TUBULIN BETA CHAIN.//1.0e-92:143:80//AJELLOMYCES CAPSULATA (HISTOPLASMA CAPSULATUM).//P41742

F-HEMBA1000030//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//0.021:136:33//PLASMODIUM KNOWLESI (STRAIN NURI).//P04922

F-HEMBA1000042//METALLOTHIONEIN 10-II (MT-10-II).//0.71:64:32//MYTILUS EDULIS (BLUE MUSSEL).//P80247

F-HEMBA1000046//PROTEIN Q300.//0.92:40:37//MUS MUSCULUS (MOUSE).//Q02722

F-HEMBA1000050//COMPETENCE PROTEIN S.//0.50:28:35//BACILLUS SUBTILIS.//P80355

F-HEMBA1000076//ATP SYNTHASE E CHAIN, MITOCHONDRIAL (EC 3.6.1.34).//0.86:41:41//HOMO SAPIENS (HUMAN).//P56385

F-HEMBA1000111

F-HEMBA1000129//UVSW PROTEIN (DAR PROTEIN).//0.023:68:33//BACTERIOPHAGE T4.//P20703

F-HEMBA1000141//YSY6 PROTEIN.//0.90:29:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38374

F-HEMBA1000150//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//8.4e-16:47:70//HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1000156//IMMEDIATE-EARLY PROTEIN.//8.1e-07:143:28//HERPESVIRUS SAIMIRI (STRAIN 11).//Q01042

F-HEMBA1000158//HYPOTHETICAL PROTEIN KIAA0192 (FRAGMENT).//7.9e-11:129:40//HOMO SAPIENS (HUMAN).//Q93074

F-HEMBA1000168//INSULIN RECEPTOR SUBSTRATE-2 (IRS-2) (4PS).//0.00055:86:36//MUS MUSCULUS (MOUSE).//P81122

F-HEMBA1000180//VPU PROTEIN (U ORF PROTEIN).//0.22:73:28//CHIMPANZEE IMMUNODEFICIENCY VIRUS (SIV(CPZ)) (CIV).//P17286

F-HEMBA1000185//RAS-1 PROTEIN.//5.1e-10:121:29//NEUROSPORA CRASSA.//P22126

F-HEMBA1000193//PROLINE-RICH PEPTIDE P-B.//0.00078:56:41//HOMO SAPIENS (HUMAN).//P02814

F-HEMBA1000201//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.00061:49:42//MUS MUSCULUS (MOUSE).//P05142

F-HEMBA1000213

F-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//1.6e-59:115:53//MUS MUSCULUS (MOUSE).//Q61221

F-HEMBA1000227//SUPPRESSOR PROTEIN SRP40.//0.00059:135:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583

F-HEMBA1000231//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME I.//0.024:60:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10264

F-HEMBA1000243//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.0038:125:34//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1000244//HYPOTHETICAL 123.6 KD PROTEIN IN POR2-COX5B INTERGENIC REGION.//3.1e-17:149:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40480

F-HEMBA1000251

F-HEMBA1000264//PROBABLE E5 PROTEIN.//1.0:49:36//HUMAN PAPILLOMAVIRUS TYPE 58.//P26552

F-HEMBA1000280//SHORT NEUROTOXIN 1 (TOXIN C-6).//0.98:58:31//NAJA NAJA KAOUTHIA (MONOCLED COBRA) (NAJA NAJA SIAMENSIS).//P14613

F-HEMBA1000282//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.14:26:65//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1000288

F-HEMBA1000290//HYPOTHETICAL 14 KD PROTEIN IN TVRI-6 REPETITIVE REGION.//3.8e-06:98:39//HOMO SAPIENS (HUMAN).//P10516

F-HEMBA1000302

F-HEMBA1000303//HYPOTHETICAL 104.4 KD PROTEIN F54G8.4 IN CHROMOSOME III.//1.3e-05:69:42//CAENORHABDITIS ELEGANS.//Q03601

F-HEMBA1000304//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//0.021:18:83//HOMO SAPIENS (HUMAN).//

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P39194
F-HEMBA1000307//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//7.1e-06:235:25//HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS).//P39922
F-HEMBA1000327
F-HEMBA1000333//SRP1 PROTEIN.//1.0:159:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10193
F-HEMBA1000338//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//8.8e-26:36:83//HOMO SAPIENS (HUMAN).//P39193
F-HEMBA1000351
F-HEMBA1000355//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.99:22:50//HOMO SAPIENS (HUMAN).//P02811
F-HEMBA1000356//IMMEDIATE-EARLY PROTEIN IE180.//0.11:82:36//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675
F-HEMBA1000357//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//2.1e-35:105:74//HOMO SAPIENS (HUMAN).//P39192
F-HEMBA1000366//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR AF1627.//1.0:28:42//ARCHAEOGLOBUS FULGIDUS.//O28646
F-HEMBA1000369//PRESYNAPTIC DENSITY PROTEIN 95 (PSD-95).//0.013:140:26//HOMO SAPIENS (HUMAN).//P78352
F-HEMBA1000376//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//6.8e-08:66:42//MUS MUSCULUS (MOUSE).//P11369
F-HEMBA1000387//HYPOTHETICAL 63.2 KD PROTEIN C1F3.09 IN CHROMOSOME I.//1.5e-15:177:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10414
F-HEMBA1000390//PARATHYMOSIN.//0.0071:61:29//HOMO SAPIENS (HUMAN).//P20962
F-HEMBA1000392//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.1e-30:92:69//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1000396/LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.9e-23:64:57//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1000411
F-HEMBA1000418
F-HEMBA1000422//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//8.3e-10:90:53//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1000428//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.1e-12:72:55//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1000434
F-HEMBA1000442//GENE 11 PROTEIN.//1.0:28:46//SPIROPLASMA VIRUS SPV1-R8A2 B.//P15902
F-HEMBA1000456//26S PROTEASOME REGULATORY SUBUNIT MTS4 (19S REGULATORY CAP REGION OF 26S PROTEASE SUBUNIT 2).//0.077:118:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87048
F-HEMBA1000459//HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-) (HRI).//4.8e-62:102:78//ORYCTOLAGUS CUNICULUS (RABBIT).//P33279
F-HEMBA1000460//LYSIS PROTEIN (E PROTEIN) (GPE).//1.0:24:50//BACTERIOPHAGE ALPHA-3.//P31280
F-HEMBA1000464
F-HEMBA1000469//PILI PROTEIN.//1.0:27:44//PSEUDOMONAS AERUGINOSA.//P43502
F-HEMBA1000488//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//1.1e-07:90:38//HOMO SAPIENS (HUMAN).//Q13105
F-HEMBA1000490//PLECTIN.//0.74:254:25//RATTUS NORVEGICUS (RAT).//P30427
F-HEMBA1000491//RAS-RELATED PROTEIN M-RAS.//3.0e-14:100:36//RATTUS NORVEGICUS (RAT).//P97538
F-HEMBA1000501//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.5e-20:81:54//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1000504
F-HEMBA1000505//NEURON-SPECIFIC X11 PROTEIN (FRAGMENT).//0.00028:128:32//HOMO SAPIENS (HUMAN).//Q02410
F-HEMBA1000508//CHITIN SYNTHASE 3 (EC 2.4.1.16) (CHITIN-UDP ACETYL-GLUCOSAMINYL TRANSFERASE 3).//0.61:132:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P29465
F-HEMBA1000518
F-HEMBA1000519//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//1.8e-37:68:75//HOMO SAPIENS (HUMAN).//P39189

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F-HEMBA1000520//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//5.2e-09:75:49//HOMO SAPIENS (HUMAN).// P39192
F-HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.//1.5e-35:257:36//MUS MUSCULUS (MOUSE).// Q01755
F-HEMBA1000531//HEAT SHOCK PROTEIN 70 B2.//1.6e-14:72:44//ANOPHELES ALBIMANUS (NEW WORLD MALARIA MOSQUITO).//P41827
F-HEMBA1000534//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//9.7e-32:96:78//HOMO SAPIENS (HUMAN).// P39193
F-HEMBA1000540//LANTIBIOTIC LACTICIN 481 PRECURSOR (LACTOCOCCIN DR).//1.0:12:75//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).//P36499
F-HEMBA1000542//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.0089:79:31//MUS MUSCULUS (MOUSE).//P15265
F-HEMBA1000545//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.0e-83:256:66//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1000555//TRANSLATION INITIATION FACTOR IF-2.//3.6e-06:252:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39730
F-HEMBA1000557
F-HEMBA1000561//ZINC FINGER PROTEIN 81 (FRAGMENT).//9.1 e-18:200:28//HOMO SAPIENS (HUMAN).// P51508
F-HEMBA1000563
F-HEMBA1000568
F-HEMBA1000569//GPI-ANCHORED PROTEIN P137.//1.0e-40:137:54//HOMO SAPIENS (HUMAN).//Q14444
F-HEMBA1000575
F-HEMBA1000588
F-HEMBA1000591//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.1e-17:41:92//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1000592//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//0.18:128:23//HOMO SAPIENS (HUMAN).//Q02224
F-HEMBA1000594//HYPOTHETICAL 29.3 KD PROTEIN B0280.6 IN CHROMOSOME III.//0.93:24:54// CAENORHABDITIS ELEGANS.//P41997
F-HEMBA1000604//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.00010:49:55//HOMO SAPIENS (HUMAN).// P39188
F-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8e-55:179:61//HOMO SAPIENS (HUMAN).//O43295
F-HEMBA1000622//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.1e-21:94:62//HOMO SAPIENS (HUMAN).// P39188
F-HEMBA1000636//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.34:73:36//VOLVOX CARTERI.// P21997
F-HEMBA1000637//BASIC PROLINE-RICH PEPTIDE IB-1.//0.0057:76:38//HOMO SAPIENS (HUMAN).//P04281
F-HEMBA1000655
F-HEMBA1000657//ZINC FINGER PROTEIN GCS1.//1.5e-07:66:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35197
F-HEMBA1000662//METALLOTHIONEIN-II (MT-II).//0.79:33:39//CRICETULUS GRISEUS (CHINESE HAMSTER).//P02799
F-HEMBA1000673//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//3.1e-17:86:59//HOMO SAPIENS (HUMAN).// P39193
F-HEMBA1000682//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//3.0e-13:45:44//MUS MUSCULUS (MOUSE).//P11369
F-HEMBA1000686//HYPOTHETICAL 48.0 KD PROTEIN C1B3.08 IN CHROMOSOME I.//4.5e-07:79:34// SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13873
F-HEMBA1000702
F-HEMBA1000705//PROTEIN Q300.//0.80:25:44//MUS MUSCULUS (MOUSE).//Q02722
F-HEMBA1000719//MYOSIN IC HEAVY CHAIN.//0.0026:115:44//ACANTHAMOEBA CASTELLANII (AMOEBA).// P10569
F-HEMBA1000722
F-HEMBA1000726//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//7.4e-32:83:77//HOMO SAPIENS (HUMAN).//P39191
F-HEMBA1000727//ZINC FINGER PROTEIN CTH2 (YTIS11 PROTEIN).//0.73:26:46//SACCHAROMYCES CER-

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EVISIAE (BAKER'S YEAST).//P47977
F-HEMBA1000747
F-HEMBA1000749//HYPOTHETICAL PROTEIN HI1484.//1.0:42:35//HAEMOPHILUS INFLUENZAE.//P44211
F-HEMBA1000752//RETROVIRUS-RELATED ENV POLYPROTEIN.//1.0e-08:84:39//HOMO SAPIENS (HUMAN).//P10267
F-HEMBA1000769
F-HEMBA1000773//PAIRED BOX PROTEIN PAX-4.//1.0:107:33//HOMO SAPIENS (HUMAN).//O43316
F-HEMBA1000774//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.3e-23:92:63//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1000791
F-HEMBA1000817//PROLACTIN RECEPTOR PRECURSOR (PRL-R).//0.079:87:29//CERVUS ELAPHUS (RED DEER).//Q28235
F-HEMBA1000822
F-HEMBA1000827//HYPOTHETICAL 8.4 KD PROTEIN.//0.98:48:39//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20546
F-HEMBA1000843//HYPOTHETICAL 7.3 KD PROTEIN D1044.5 IN CHROMOSOME III.//0.92:46:34//CAENORHABDITIS ELEGANS.//P41953
F-HEMBA1000851//HOMEOBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEOBOX PROTEIN 2).//0.048:39:51//HOMO SAPIENS (HUMAN).//P52951
F-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD).//4.0e-24:29:100//HOMO SAPIENS (HUMAN).//P51689
F-HEMBA1000867
F-HEMBA1000869//PROBABLE E5 PROTEIN.//0.99:70:27//HUMAN PAPILLOMAVIRUS TYPE 18.//P06792
F-HEMBA1000870//MYOTOXIN 3 PRECURSOR (CROTAMINE 3).//0.79:43:32//CROTALUS DURISSUS TERRIFICUS (SOUTH AMERICAN RATTLESNAKE).//P24333
F-HEMBA1000872//GAR2 PROTEIN.//0.89:70:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891
F-HEMBA1000876//DEFENSIN.//0.89:34:38//ALLOMYRINA DICHOTOMA.//Q10745
F-HEMBA1000908//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.69:43:37//HOMO SAPIENS (HUMAN).//P30808
F-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B3 (MAGE-B3 ANTIGEN).//5.1e-08:44:38//HOMO SAPIENS (HUMAN).//O15480
F-HEMBA1000918//60S RIBOSOMAL PROTEIN L37-A (YL35) (FRAGMENT).//1.0:19:52//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P22667
F-HEMBA1000919//69 KD PARAFLAGELLAR ROD PROTEIN (69 KD PFR PROTEIN) (PFR-A/PFR-B).//0.29:116:30//TRYPANOSOMA BRUCEI BRUCEI.//P22225
F-HEMBA1000934
F-HEMBA1000942//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.85:27:59//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1000943
F-HEMBA1000946//STO-2 PROTEIN.//0.82:82:30//CAENORHABDITIS ELEGANS.//Q19958
F-HEMBA1000960//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//0.0097:29:72//HOMO SAPIENS (HUMAN).//P39192
F-HEMBA1000968//METALLOTHIONEIN 20-III ISOFORMS A AND B (MT-20-IIIA AND MT-20-IIIB).//0.047:45:37//MYTILUS EDULIS (BLUE MUSSEL).//P80253
F-HEMBA1000971//HYPOTHETICAL BHLF1 PROTEIN.//0.038:172:31//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
F-HEMBA1000972
F-HEMBA1000974//HYPOTHETICAL PROTEIN MG441.//0.98:66:28//MYCOPLASMA GENITALIUM.//P47679
F-HEMBA1000975//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT).//0.028:57:36//HOMO SAPIENS (HUMAN).//P25067
F-HEMBA1000985
F-HEMBA1000986//SUBMANDIBULAR GLAND SECRETORY GLX-RICH PROTEIN CB PRECURSOR (GRP-CB) (CONTIGUOUS REPEAT POLYPEPTIDE) (CRP).//0.13:91:34//RATTUS NORVEGICUS (RAT).//P08462
F-HEMBA1000991//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II.//5.6e-05:37:45//CAENORHABDITIS ELEGANS.//Q18964
F-HEMBA1001007//HYPOTHETICAL PROTEIN KIAA0179.//0.27:72:41//HOMO SAPIENS (HUMAN).//Q14684
F-HEMBA1001008//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.4e-25:61:70//HOMO SAPIENS (HU-

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MAN).//P39194
F-HEMBA1001009//CUTICLE COLLAGEN 34.//0.044:214:29//CAENORHABDITIS ELEGANS.//P34687
F-HEMBA1001017//SYNDECAN-3 PRECURSOR (N-SYNDECAN) (NEUROGLYCAN).//5.0e-85:191:84//RATTUS NORVEGICUS (RAT).//P33671
F-HEMBA1001019
F-HEMBA1001020//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//6.7e-24:49:73//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1001022
F-HEMBA1001024//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.0e-11:61:59//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1001026//HYPOTHETICAL PROTEIN BB0073.//0.94:63:34//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//O51100
F-HEMBA1001043//INVOLUCRIN.//0.0036:238:25//SAGUINUS OEDIPUS (COTTON-TOP TAMARIN).//P24712
F-HEMBA1001051//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//3.3e-32:95:75//HOMO SAPIENS (HUMAN).//P39189
F-HEMBA1001052//CURROMYCIN RESISTANCE PROTEIN.//1.0:31:38//STREPTOMYCES HYGROSCOPICUS.//P16961
F-HEMBA1001059//N-ACETYLGALACTOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.4) (N- ACETYLGALACTOSAMINE-6-SULFATE SULFATASE) (GALACTOSE-6-SULFATE SULFATASE) (GALNAC6S SULFATASE) (CHONDROITINSULFATASE) (CHONDROITINASE).//3.2e-132:249:94//HOMO SAPIENS (HUMAN).//P34059
F-HEMBA1001060
F-HEMBA1001071//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//8.3e-23:51:96//HOMO SAPIENS (HUMAN).//P02461
F-HEMBA1001077//AUTOIMMUNE REGULATOR (APECED PROTEIN).//3.4e-06:37:56//HOMO SAPIENS (HUMAN).//O43918
F-HEMBA1001080//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP34.5).//0.0012:70:38//HERPES SIMPLEX VIRUS (TYPE 1 / STRAW MGH-10).//P37319
F-HEMBA1001085//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PPS) (PROTEIN PHOSPHATASE T) (PPT) (FRAGMENT).//0.00018:76:32//MUS MUSCULUS (MOUSE).//Q60676
F-HEMBA1001088//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//3.5e-50:176:57//HOMO SAPIENS (HUMAN).//P48059
F-HEMBA1001094
F-HEMBA1001099//LIGHT-HARVESTING PROTEIN B800/850/890, ALPHA-2 CHAIN (EHA-ALPHA-2) (ANTENNA PIGMENT PROTEIN, ALPHA-2 CHAIN) (FRAGMENT).//1.0:15:60//ECTOTHIORHODOSPIRA HALOPHILA.//P80101
F-HEMBA1001109//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//6.7e-37:102:82//HOMO SAPIENS (HUMAN).//P39189
F-HEMBA1001121//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.036:49:46//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1001122
F-HEMBA1001123
F-HEMBA1001133//HYPOTHETICAL 9.4 KD PROTEIN (ORF2).//0.86:29:41//FELINE IMMUNODEFICIENCY VIRUS (ISOLATE SAN DIEGO) (FIV), AND FELINE IMMUNODEFICIENCY VIRUS (ISOLATE PETALUMA) (FIV).//P19033
F-HEMBA1001137//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.0e-22:103:52//HOMO SAPIENS (HUMAN).//P51523
F-HEMBA1001140//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.//0.032:94:36//HOMO SAPIENS (HUMAN).//P53420
F-HEMBA1001172
F-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//2.9e-78:179:79//RATTUS NORVEGICUS (RAT).//P51646
F-HEMBA1001197//MAJOR PRION PROTEIN PRECURSOR (PRP) (PRP27-30) (PRP33-35C) (FRAGMENT).//0.051:96:32//CERCOCEBUS ATERRIMUS, AND MACACA SYLVANUS (BARBARY APE).//Q95145
F-HEMBA1001208
F-HEMBA1001213
F-HEMBA1001226//PROTEASOME COMPONENT C8 (EC 3.4.99.46) (MACROPAIN SUBUNIT C8) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8).//1.5e-08:24:91//HOMO SAPIENS (HUMAN).//P25788
F-HEMBA1001235//FIBRONECTIN (FN) (FRAGMENT).//0.76:50:38//ORYCTOLAGUS CUNICULUS (RABBIT).//

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Q28749
F-HEMBA1001247//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.00052:16:81//VOLVOX CARTERI.//P21997
F-HEMBA1001257//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-).//1.6e-68:178:77//RATTUS NORVEGICUS (RAT).//P70473
F-HEMBA1001265//MANNAN ENDO-1,4-BETA-MANNOSIDASE A PRECURSOR (EC 3.2.1.78) (BETA- MANNANASE A) (1,4-BETA-D-MANNAN MANNANOHYDROLASE A).//0.67:23:60//PIROMYCES SP.//P55296
F-HEMBA1001281//HYPOTHETICAL 8.9 KD PROTEIN YCF34 (ORF76).//0.83:48:35//PORPHYRA PURPUREA.//P51229
F-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//1.3e-07:185:29//CAVIA PORCELLUS (GUINEA PIG).//Q60401
F-HEMBA1001289//METABOTROPIC GLUTAMATE RECEPTOR 3 PRECURSOR.//0.00018:159:30//RATTUS NORVEGICUS (RAT).//P31422
F-HEMBA1001294
F-HEMBA1001299//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//5.3e-07:27:77//HOMO SAPIENS (HUMAN).//P39195
F-HEMBA1001302//45 KD CALCIUM-BINDING PROTEIN PRECURSOR (STROMAL CELL-DERIVED FACTOR 4) (SDF-4).//3.3e-61:150:76//MUS MUSCULUS (MOUSE).//Q61112
F-HEMBA1001303
F-HEMBA1001310//HYPOTHETICAL PROTEIN KIAA0161.//2.7e-10:170:27//HOMO SAPIENS (HUMAN).//P50876
F-HEMBA1001319
F-HEMBA1001323
F-HEMBA1001326//HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION.//1.1e-39:144:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43601
F-HEMBA1001327
F-HEMBA1001330
F-HEMBA1001351//VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPTOBREVIN BINDING PROTEIN (VAP-33).//1.9e-37:155:46//APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).//Q16943
F-HEMBA1001361//RUBREDOXIN (RD).//0.95:44:29//ALCALIGENES EUTROPHUS.//P31912
F-HEMBA1001375//AEROLYSIN REGULATORY PROTEIN.//0.013:45:33//AEROMONAS SOBRIA.//P09165
F-HEMBA1001377//SPERM PROTAMINE P1.//1.0:22:40//PLANIGALE MACULATA SINUALIS (COMMON PLANIGALE).//O18746
F-HEMBA1001383//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.60:37:29//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z2/CDC-Z34 ISOLATE) (HIV-1).//P12506
F-HEMBA1001387//GTP-BINDING PROTEIN TC10.//6.6e-43:83:92//HOMO SAPIENS (HUMAN).//P17081
F-HEMBA1001388//HYPOTHETICAL PROTEIN KIAA0136 (FRAGMENT).//0.00088:46:45//HOMO SAPIENS (HUMAN).//Q14149
F-HEMBA1001391
F-HEMBA1001398//CLOACIN (EC 3.1.-.-) (RIBONUCLEASE).//1.0:59:37//ESCHERICHIA COLI.//P00645
F-HEMBA1001405//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.25:41:34//HOMO SAPIENS (HUMAN).//P22531
F-HEMBA1001407//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.0e-09:129:40//HOMO SAPIENS (HUMAN).//P04280
F-HEMBA1001411//HYPOTHETICAL 34.9 KD PROTEIN IN CYSJ-ENO INTERGENIC REGION (O313).//0.95:88:31//ESCHERICHIA COLI.//P55140
F-HEMBA1001413//SOX-12 PROTEIN (FRAGMENT).//0.95:46:32//MUS MUSCULUS (MOUSE).//Q04890
F-HEMBA1001415//HISTONE H5.//0.43:95:29//GALLUS GALLUS (CHICKEN).//P02259
F-HEMBA1001432//LANTIBIOTIC NISIN A PRECURSOR.//0.77:46:32//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).//P13068
F-HEMBA1001433//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.8e-09:132:31//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
F-HEMBA1001435//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//1.2e-31:84:77//HOMO SAPIENS (HUMAN).//P39189
F-HEMBA1001442
F-HEMBA1001446//ANTIFREEZE PEPTIDE 4 PRECURSOR.//0.71:41:39//PSEUDOPLEURONECTA AMERICANUS (WINTER FLOUNDER).//P02734
F-HEMBA1001450//PROLINE-RICH PROTEIN LAS17.//0.13:127:27//SACCHAROMYCES CEREVISIAE (BAK-

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ER'S YEAST).//Q12446
F-HEMBA1001454//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.57:38:47//HANSENULA WINGEI (YEAST).//P48882
F-HEMBA1001455//CHEMOTAXIS PROTEIN CHEA (EC 2.7.3.-).//0.98:124:25//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//Q44737
F-HEMBA1001463//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.8e-32:62:67//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1001476//NUCLEOPORIN NUP159 (NUCLEAR PORE PROTEIN NUP159).//6.8e-09:252:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40477
F-HEMBA1001478
F-HEMBA1001497//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.2e-33:105:72//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1001510//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//8.3e-37:54:81//HOMO SAPIENS (HUMAN).//P39189
F-HEMBA1001515//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.0e-63:223:57//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1001517
F-HEMBA1001522//TROPOMYOSIN ALPHA CHAIN, SMOOTH MUSCLE.//0.78:150:22//COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).//P49437
F-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//1.6e-06:130:29//CLOSTRIDIUM PASTEURIANUM.//P29166
F-HEMBA1001533//PROBABLE E5A PROTEIN.//0.73:35:37//HUMAN PAPILLOMAVIRUS TYPE 6A.//Q84296
F-HEMBA1001557//HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION.//1.5e-07:99:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38898
F-HEMBA1001566//HYPOTHETICAL PROTEIN BB0692.//0.91:27:44//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//O51635
F-HEMBA1001569//SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2).//2.2e-50:110:95//HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE).//P19065
F-HEMBA1001570//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//3.3e-33:107:72//HOMO SAPIENS (HUMAN).//P39195
F-HEMBA1001579//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-14:111:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
F-HEMBA1001581
F-HEMBA1001585
F-HEMBA1001589//PROBABLE DNA-BINDING PROTEIN (AGNOPROTEIN).//0.98:51:33//HUMAN ADENOVIRUS TYPE 2.//P03263
F-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//3.0e-124:274:85//HOMO SAPIENS (HUMAN).//Q14141
F-HEMBA1001608//RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER).//0.99:28:39//ORYCTOLAGUS CUNICULUS (RABBIT).//Q28615
F-HEMBA1001620//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//4.3e-45:222:46//SPIRODELA POLYRRHIZA.//P42803
F-HEMBA1001635//FIBRILLARIN.//0.10:72:38//CAENORHABDITIS ELEGANS.//Q22053
F-HEMBA1001636//PAIRED BOX PROTEIN PAX-8, ISOFORMS 8C/8D.//0.75:38:47//HOMO SAPIENS (HUMAN).//Q09155
F-HEMBA1001640//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!/14.7e-06:80:41//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1001647//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.075:165:32//HOMO SAPIENS (HUMAN).//O00268
F-HEMBA1001651//GOLGIN-95.//6.8e-05:141:24//HOMO-SAPIENS (HUMAN).//Q08379
F-HEMBA1001655//PROLINE-RICH PROTEIN LAS17.//0.19:97:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12446
F-HEMBA1001658//TETRAHYDROMETHANOPTERIN S-METHYLTRANSFERASE 12 KD SUBUNIT (EC 2.1.1.86) (N5-METHYLTETRAHYDROMETHANOPTERIN-COENZYME M METHYLTRANSFERASE 12 KD SUBUNIT).//1.0:29:44//METHANOBACTERIUM THERMOAUTOTROPHICUM (STRAIN MARBURG / DSM 2133).//Q50773
F-HEMBA1001661//CELLULOSE COMPLEMENTING PROTEIN.//0.35:87:33//ACETOBACTER XYLINUM (ACETOBACTER PASTEURIANUS).//P37697

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F-HEMBA1001672//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//2.7e-10:216:35//PLASMODIUM CYNOMOLGI (STRAIN BEROK).//P08672
F-HEMBA1001675//NODULIN 20 PRECURSOR (N-20).//0.98:36:44//GLYCINE MAX (SOYBEAN).//P08960
F-HEMBA1001678//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//8.2e-13:62:64//HOMO SAPIENS (HUMAN).// P39195
F-HEMBA1001681//HYPOTHETICAL 41.5 KD PROTEIN IN P6.5-VP48 INTERGENIC REGION (P40) (ORF3) (ORF102).//1.0:51:39//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).// P24653
F-HEMBA1001702//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.017:54:37//TRYPANOSOMA BRUCEI BRUCEI.//P24499
F-HEMBA1001709//HYPOTHETICAL 21.2 KD PROTEIN IN TOR2-MNN4 INTERGENIC REGION.//0.59:109:35// SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36042
F-HEMBA1001711
F-HEMBA1001712//HYPOTHETICAL 6.9 KD PROTEIN IN 100 KD PROTEIN REGION.//0.54:44:34//HUMAN ADENOVIRUS TYPE 41.//P23690
F-HEMBA1001714//ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR.//1.2e-19:60:75//RATTUS NORVEGICUS (RAT).//Q03344
F-HEMBA1001718//HYPOTHETICAL PROTEIN UL63.//1.0:54:37//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16820
F-HEMBA1001723//HYPOTHETICAL 34.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION.//5.1e-26:90:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41318
F-HEMBA1001731//HYPOTHETICAL 16.6 KD PROTEIN.//0.71:49:32//AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN 52/70) (IBDV).//P25221
F-HEMBA1001734
F-HEMBA1001744//SCY1 PROTEIN.//2.1e-11:182:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).// P53009
F-HEMBA1001745//HYPOTHETICAL 11.6 KD PROTEIN IN NUT1-ARO2 INTERGENIC REGION PRECURSOR.//1.0:36:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53116
F-HEMBA1001746//PROTEIN-EXPORT MEMBRANE PROTEIN SECG HOMOLOG.//0.94:48:35//MYCOBACTERIUM LEPRAE.//P38388
F-HEMBA1001761
F-HEMBA1001781//ZINC FINGER PROTEIN 19 (ZINC FINGER PROTEIN KOX12) (FRAGMENT).//0.028:47:40// HOMO SAPIENS (HUMAN).//P17023
F-HEMBA1001784//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X.//0.00068:32:46// CAENORHABDITIS ELEGANS .//Q11116
F-HEMBA1001791//METALLOTHIONEIN (MT).//1.0:34:35//PLEURONECTES PLATESSA (PLAICE).//P07216
F-HEMBA1001800//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//1.5e-14:60:48//MUS MUSCULUS (MOUSE).//P16372
F-HEMBA1001803
F-HEMBA1001804//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1 PRECURSOR.//9.3e-17:56:57// ORYZA SATIVA (RICE).//P25074
F-HEMBA1001808//PARANEOPLASTIC ENCEPHALOMYELITIS ANTIGEN HUD HOMOLOG (HU-ANTIGEN D).//0.75:97:31//RATTUS NORVEGICUS (RAT).//O09032
F-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//4.5e-11:206:36//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675
F-HEMBA1001815//60S RIBOSOMAL PROTEIN L37-B (YL27) (FRAGMENT).//0.34:30:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P05733
F-HEMBA1001819//ZINC FINGER PROTEIN 135.//2.6e-102:262:66//HOMO SAPIENS (HUMAN).//P52742
F-HEMBA1001820
F-HEMBA1001822//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15).//1.2e-18:251:33//MUS MUSCULUS (MOUSE).//P42567
F-HEMBA1001824//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//4.7e-11:124:37// OVIS ARIES (SHEEP).//P26372
F-HEMBA1001835
F-HEMBA1001844//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//4.3e-14:36:63//HOMO SAPIENS (HUMAN).// P39195
F-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//2.7e-36:135:51//MUS MUSCULUS (MOUSE).// Q07230

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F-HEMBA1001861
F-HEMBA1001864//HEAT-STABLE ENTEROTOXIN A3/A4 PRECURSOR (STA3/STA4) (ST-IB) (ST-H).//1.0:31:38//ESCHERICHIA COLI.//P07965
F-HEMBA1001866//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//9.7e-42:234:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q09332
F-HEMBA1001869//HYPOTHETICAL 94.9 KD PROTEIN C22E12.11C IN CHROMOSOME I.//5.3e-13:65.47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10362
F-HEMBA1001888//HYPOTHETICAL 11.4 KD PROTEIN (ORF1).//0.85:62:37//STREPTOMYCES FRADIAE.//P26800
F-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (ME2GLYDH).//9.8e-20:250:29//RATTUS NORVEGICUS (RAT).//Q63342
F-HEMBA1001910//EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-4F 25 KD SUBUNIT).//0.94:44:38//CAENORHABDITIS ELEGANS.//O61955
F-HEMBA1001912//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//8.7e-07:53:62//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1001913//GCN20 PROTEIN.//1.8e-21:68:60//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43535
F-HEMBA1001915//KLEE PROTEIN (KCRB3 PROTEIN).//0.94:64:21//ESCHERICHIA COLI.//Q52280
F-HEMBA1001918
F-HEMBA1001921
F-HEMBA1001939//CHLOROPLAST 50S RIBOSOMAL PROTEIN L24.//1.0:47:31//ODONTELLA SINENSIS.//P49560
F-HEMBA1001940//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.0017:31:77//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1001942//HIBERNATION-ASSOCIATED PLASMA PROTEIN HP-27 PRECURSOR (HIBERNATOR-SPECIFIC BLOOD COMPLEX, 27 KD SUBUNIT).//1.0:77:28//TAMIAS ASIATICUS (CHIPMUNK).//Q06577
F-HEMBA1001945//HYPOTHETICAL 4.6 KD PROTEIN IN GP47-AGT INTERGENIC REGION (ORF E).//1.0:35:37//BACTERIOPHAGE T4.//P32269
F-HEMBA1001950//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.43:18:44//DROSOPHILA YAKUBA (FRUIT FLY).//P03933
F-HEMBA1001960//HOMEOBOX PROTEIN HOX-C5 (HOX-3D) (CP11).//0.17:12:66//HOMO SAPIENS (HUMAN).//Q00444
F-HEMBA1001962//HYPOTHETICAL 9.0 KD PROTEIN IN ADH4 5'REGION.//1.0:30:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53056
F-HEMBA1001964
F-HEMBA1001967//HYPOTHETICAL PROTEIN UL61.//0.027:111:36//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818
F-HEMBA1001979
F-HEMBA1001987//HYPOTHETICAL 11.2 KD PROTEIN (ORF117).//1.0:83:32//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10356
F-HEMBA1001991//NEUROTOXIN 1 (TOXIN ATX-I).//0.99:31:45//ANEMONIA SULCATA (SNAKE-LOCKS SEA ANEMONE).//P01533
F-HEMBA1002003//GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, TESTIS-SPECIFIC (EC 1.2.1.12) (GAPDH).//5.5e-07:109:32//MUS MUSCULUS (MOUSE).//Q64467
F-HEMBA1002008
F-HEMBA1002018//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.83:66:33//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q42377
F-HEMBA1002022//INSULIN.//1.0:59:32//SQUALUS ACANTHIAS (SPINY DOGFISH).//P12704
F-HEMBA1002035//MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN.//8.3e-15:64:40//HOMO SAPIENS (HUMAN).//Q92794
F-HEMBA1002039//HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269.//0.0070:70:40//HOMO SAPIENS (HUMAN).//Q92558
F-HEMBA1002049//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.5e-07:37:75//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1002084
F-HEMBA1002092//SPT23 PROTEIN.//0.12:208:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35210
F-HEMBA1002100

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F-HEMBA1002102//ANKYRIN.//1.4e-12:106:35//MUS MUSCULUS (MOUSE).//Q02357
F-HEMBA1002113//EARLY NODULIN 20 PRECURSOR (N-20).//0.073:155:32//MEDICAGO TRUNCATULA (BARREL MEDIC).//P93329
F-HEMBA1002119//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.85:22:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
F-HEMBA1002125//GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30].//0.35:111:33//FELINE SARCOMA VIRUS (STRAIN SNYDER-THEILEN).//P03338
F-HEMBA1002139//HYPOTHETICAL 12.4 KD PROTEIN IN SEC17-QCR1 INTERGENIC REGION.//0.88:72:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38192
F-HEMBA1002144
F-HEMBA1002150//THROMBOMODULIN (FETOMODULIN) (TM) (FRAGMENT).//4.8e-10:65:46//BOS TAURUS (BOVINE).//P06579
F-HEMBA1002151//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.24:146:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
F-HEMBA1002153//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.93:58:25//APIS MELLIFERA (HONEYBEE).//P34859
F-HEMBA1002160//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//5.1e-21:94:65//HOMO SAPIENS (HUMAN).//P39193
F-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.4e-51:180:56//SUS SCROFA (PIG).//P79293
F-HEMBA1002162//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//4.1e-40:102:75//HOMO SAPIENS (HUMAN).//P39193
F-HEMBA1002166//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.8e-13:133:45//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1002177//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//0.0014:153:26//HOMO SAPIENS (HUMAN).//P52746
F-HEMBA1002185
F-HEMBA1002189//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//0.86:46:45//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1002191//MALE SPECIFIC SPERM PROTEIN MST84DC.//0.037:14:57//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01644
F-HEMBA1002199
F-HEMBA1002204
F-HEMBA1002212//DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE DSOR1 (EC 2.7.1.-) (DOWNSTREAM OF RAF) (MAPKK).//3.2e-13:201:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24324
F-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//1.1e-62:147:84//MUS MUSCULUS (MOUSE).//P47226
F-HEMBA1002226//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.6e-26:168:44//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1002229//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!//6.8e-18:68:72//HOMO SAPIENS (HUMAN).//P39190
F-HEMBA1002237//EAMZP30-47 PROTEIN (FRAGMENT).//0.96:21:61//EIMERIA ACERVULINA.//P21959
F-HEMBA1002241//METALLOTHIONEIN (MT).//0.95:25:48//PARACENTROTUS LIVIDUS (COMMON SEA URCHIN).//P80367
F-HEMBA1002253//METALLOTHIONEIN-II (MT-II).//0.97:27:48//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//P17808
F-HEMBA1002257
F-HEMBA1002265//MALE SPECIFIC SPERM PROTEIN MST84DC.//0.95:24:50//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01644
F-HEMBA1002267//NEURONAL PROTEIN 3.1 (P311 PROTEIN).//0.94:33:33//GALLUS GALLUS (CHICKEN).//Q90667
F-HEMBA1002270
F-HEMBA1002321//HYPOTHETICAL IMMUNITY REGION PROTEIN 14.//0.99:22:40//BACTERIOPHAGE PHI-105.//P10437
F-HEMBA1002328
F-HEMBA1002337
F-HEMBA1002341//P53-BINDING PROTEIN 53BP2 (FRAGMENT).//3.7e-55:109:96//MUS MUSCULUS

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(MOUSE).//Q62415
F-HEMBA1002348//PROBABLE E5 PROTEIN.//0.43:30:50//HUMAN PAPILLOMAVIRUS TYPE 35.//P27226
F-HEMBA1002349
F-HEMBA1002363//CHROMOSOME ASSEMBLY PROTEIN XCAP-E.//5.7e-105:278:71//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P50533
F-HEMBA1002381//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.3e-24:69:73//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1002389//EARLY NODULIN 20 PRECURSOR (N-20).//0.16:110:31//MEDICAGO TRUNCATULA (BARREL MEDIC).//P93329
F-HEMBA1002417//TIGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1).//2.6e-51:187:56//MUS MUSCULUS (MOUSE).//P39447
F-HEMBA1002419//PROLINE-RICH PEPTIDE P-B.//1.0:18:61//HOMO SAPIENS (HUMAN).//P02814
F-HEMBA1002430//HYPOTHETICAL 12.3 KD PROTEIN IN GAP1-NAP1 INTERGENIC REGION.//0.042:41:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36140
F-HEMBA1002439//CHLOROPLAST 50S RIBOSOMAL PROTEIN L27 (FRAGMENT).//0.99:47:29//CALYPTROSPHAERA SPHAEROIDEA.//P41548
F-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.//4.1e-24:109:55//HOMO SAPIENS (HUMAN).//Q00994
F-HEMBA1002460
F-HEMBA1002462//SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).//0.00025:80:30//HOMO SAPIENS (HUMAN).//P81489
F-HEMBA1002469//PUTATIVE TUMOR SUPPRESSOR LUCA15.//0.0012:110:33//HOMO SAPIENS (HUMAN).//P52756
F-HEMBA1002475//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.37:106:33//MUS MUSCULUS (MOUSE).//P05143
F-HEMBA1002477//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.3e-34:96:71//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1002486
F-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1.//2.9e-31:110:39//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P48732
F-HEMBA1002498//SFT2 PROTEIN.//1.0:54:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38166
F-HEMBA1002503//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.0e-06:49:63//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1002508//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.6e-22:169:44//HOMO SAPIENS (HUMAN).//P39195
F-HEMBA1002513//HYPOTHETICAL 89.8 KD PROTEIN F41H10.6 IN CHROMOSOME IV.//0.00017:79:35//CAENORHABDITIS ELEGANS.//Q20296
F-HEMBA1002515
F-HEMBA1002538//ATP SYNTHASE E CHAIN, MITOCHONDRIAL (EC 3.6.1.34).//1.0:53:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P81449
F-HEMBA1002542//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//5.7e-32:96:75//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1002547//AGRIN PRECURSOR.//2.5e-100:218:80//RATTUS NORVEGICUS (RAT).//P25304
F-HEMBA1002552//HEP27 PROTEIN (PROTEIN D).//9.5e-12:29:82//HOMO SAPIENS (HUMAN).//Q13268
F-HEMBA1002555//COLLAGEN ALPHA 1(III) CHAIN.//2.4e-15:207:36//BOS TAURUS (BOVINE).//P04258
F-HEMBA1002558//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.0:34:50//HOMO SAPIENS (HUMAN).//P39193
F-HEMBA1002561//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-05:49:46//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
F-HEMBA1002569//SINGLE-STRANDED DNA-BINDING PROTEIN P12.//0.97:60:33//BACTERIOPHAGE PRD1.//P17637
F-HEMBA1002583
F-HEMBA1002590//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//5.6e-15:54:55//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1002592//HISTIDINE-RICH PROTEIN.//0.99:39:28//PLASMODIUM FALCIPARUM (ISOLATE FCM17 / SENEGAL).//P14586
F-HEMBA1002609//SSM4 PROTEIN.//1.9e-12:135:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//

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P40318
F-HEMBA1002621//CYTOCHROME B6-F COMPLEX 3.5 KD SUBUNIT (CYTOCHROME B6-F COMPLEX SUBUNIT 6).//1.0:20:55//ZEA MAYS (MAIZE).//P19445
F-HEMBA1002624//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.0035:124:33//NICOTIANA TABACUM (COMMON TOBACCO).//P13983
F-HEMBA1002628
F-HEMBA1002629//IMMEDIATE-EARLY PROTEIN IE180.//0.84:80:36//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479
F-HEMBA1002645//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.8e-16:57:68//HOMO SAPIENS (HUMAN).//P39193
F-HEMBA1002651
F-HEMBA1002659//CUTICLE COLLAGEN 2.//0.0077:77:38//CAENORHABDITIS ELEGANS.//P17656
F-HEMBA1002661//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.3e-89:116:72//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1002666//BETA CRYSTALLIN A4.//0.18:58:44//GALLUS GALLUS (CHICKEN).//P49152
F-HEMBA1002678
F-HEMBA1002679//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//5.7e-06:219:27//PLASMODIUM FALCIPARUM (ISOLATE FC27 / PAPUA NEW GUINEA).//P13816
F-HEMBA1002688//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//1.1e-07:198:32//NEPHILA CLAVIPES (ORB SPIDER).//P46804
F-HEMBA1002696//COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN).//0.16:158:33//HOMO SAPIENS (HUMAN).//Q02388
F-HEMBA1002703//HYPOTHETICAL BHLF1 PROTEIN.//0.78:147:29//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
F-HEMBA1002712//11.2 KD PROTEIN (ORF 103).//0.029:75:34//BACTERIOPHAGE PF1.//P25133
F-HEMBA1002716//50S RIBOSOMAL PROTEIN L28.//1.0:44:27//BACILLUS SUBTILIS.//P37807
F-HEMBA1002728//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//5.4e-18:56:75//HOMO SAPIENS (HUMAN).//P39195
F-HEMBA1002730//HYPOTHETICAL PROTEIN MJ0316.//0.097:84:35//METHANOCOCCUS JANNASCHII.//Q57764
F-HEMBA1002742//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII).//0.97:26:50//SUS SCROFA (PIG).//P27917
F-HEMBA1002746//CALPHOTIN.//0.35:65:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q02910
F-HEMBA1002748//PLATELET GLYCOPROTEIN IB BETA CHAIN PRECURSOR (GP-IB BETA) (GPIBB).//1.0:74:32//MUS MUSCULUS (MOUSE).//P56400
F-HEMBA1002750//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//7.0e-15:49:75//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1002768//HYPOTHETICAL 72.2 KD PROTEIN C12C2.05C IN CHROMOSOME II.//0.00036:197:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09746
F-HEMBA1002770//UTEROGLOBIN PRECURSOR (BLASTOKININ).//023:88:27//ORYCTOLAGUS CUNICULUS (RABBIT).//P02779
F-HEMBA1002777//HOMEOBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3).//0.00018:67:43//MUS MUSCULUS (MOUSE).//P06798
F-HEMBA1002779//HYPOTHETICAL 17.6 KD PROTEIN IN NPR1-RPS3 INTERGENIC REGION.//0.70:30:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53880
F-HEMBA1002780//OLFACTORY RECEPTOR 3 (K10) (FRAGMENT).//1.0:31:45//MUS MUSCULUS (MOUSE).//Q60879
F-HEMBA1002794//HMG-Y RELATED PROTEIN B (SB16B PROTEIN) (FRAGMENT).//0.0044:66:37//GLYCINE MAX (SOYBEAN).//Q10370
F-HEMBA1002801
F-HEMBA1002810//HYPOTHETICAL 25.9 KD PROTEIN AH6.3 IN CHROMOSOME II.//0.0033:116:31//CAENORHABDITIS ELEGANS.//Q09202
F-HEMBA1002816//HYPOTHETICAL 47.1 KD PROTEIN C9G1.13C IN CHROMOSOME I.//1.0e-17:68:48//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14308
F-HEMBA1002818//FIBULIN-2 PRECURSOR.//2.1e-27:92:44//MUS MUSCULUS (MOUSE).//P37889
F-HEMBA1002826//DNA-BINDING PROTEIN 65 (PROTEIN GP65).//0.28:46:34//BACTERIOPHAGE T4.//P16012
F-HEMBA1002833

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F-HEMBA1002850//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:27:37//METRIDIUM SENILE (BROWN SEA ANEMONE) (FRILLED SEA ANEMONE).//O47493
F-HEMBA1002863//PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV (PHOTOSYSTEM I 8.1 KD PROTEIN) (P30 PROTEIN) (PSI-E).//0.84:37:43//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P12975
F-HEMBA1002876//OCTAPEPTIDE-REPEAT PROTEIN T2.//0.74:58:34//MUS MUSCULUS (MOUSE).//Q06666
F-HEMBA1002886
F-HEMBA1002896//HOMEOBOX PROTEIN HOX-B3 (HOX-2G) (HOX-2.7).//4.7e-05:84:35//HOMO SAPIENS (HUMAN).//P14651
F-HEMBA1002921//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.21:42:42//HUMAN IMUNODEFICIENCY VIRUS TYPE 1 (RF/HAT ISOLATE) (HIV-1).//P05908
F-HEMBA1002924//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.85:75:22//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q42377
F-HEMBA1002934//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.4e-31:92:72//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1002935//GASTRULA ZINC FINGER PROTEIN XLCGF58.1 (FRAGMENT).//7.7e-06:187:29//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18730
F-HEMBA1002937//SUPPRESSOR PROTEIN SRP40.//0.00031:150:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
F-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//5.2e-25:225:33//HOMO SAPIENS (HUMAN).//P16157
F-HEMBA1002944
F-HEMBA1002951//TRICHOHYALIN.//0.0011:220:24//HOMO SAPIENS (HUMAN).//Q07283
F-HEMBA1002954//PROBABLE E8 PROTEIN.//0.98:49:32//BOVINE PAPILLOMAVIRUS TYPE 4.//P08352
F-HEMBA1002968//ACCESSORY GLAND PEPTIDE PRECURSOR (PARAGONIAL PEPTIDE B).//0.93:41:34//DROSOPHILA SECHELLIA (FRUIT FLY).//O18417
F-HEMBA1002970//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//0.00010:35:62//HOMO SAPIENS (HUMAN).//P39193
F-HEMBA1002971//INSULIN.//1.0:31:35//HYDROLAGUS COLLIEI (SPOTTED RATFISH) (PACIFIC RATFISH), AND CHIMAERA MONSTROSA (RABBIT FISH).//P09536 F-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17) (DPDE4).//3.0e-29:63:100//RATTUS NORVEGICUS (RAT).//P14646
F-HEMBA1002997//HYPOTHETICAL 106.5 KD PROTEIN IN CTT1-PRP31 INTERGENIC REGION.//1.0e-08:211:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53253
F-HEMBA1002999//SUPPRESSOR PROTEIN SRP40.//0.026:175:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
F-HEMBA1003021//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.3e-36:102:70//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1003033//HYPOTHETICAL 23.1 KD PROTEIN CY277.20C.//0.029:75:29//MYCOBACTERIUM TUBERCULOSIS.//P71779
F-HEMBA1003034//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//6.3e-23:144:46//HOMO SAPIENS (HUMAN).//P39192
F-HEMBA1003035//HYPOTHETICAL 13.3 KD PROTEIN IN AROD-COMER INTERGENIC REGION.//0.99:55:30//BACILLUS SUBTILIS.//P54457
F-HEMBA1003037//DNA-BINDING PROTEIN INHIBITOR ID-4.//0.17:42:40//HOMO SAPIENS (HUMAN).//P47928
F-HEMBA1003041//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.69:28:46//HOMO SAPIENS (HUMAN).//P30808
F-HEMBA1003046//MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT PRECURSOR (EC 3.4.24.64) (BETA-MPP) (P-52).//7.9e-124:253:96//HOMO SAPIENS (HUMAN).//O75439
F-HEMBA1003064//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3).//0.25:263:22//TRYPANOSOMA BRUCEI BRUCEI.//P04540
F-HEMBA1003067//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//4.1e-05:189:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214
F-HEMBA1003071//CUTICLE COLLAGEN 40.//6.0e-07:126:38//CAENORHABDITIS ELEGANS.//P34804
F-HEMBA1003077//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//2.4e-12:139:34//HOMO SAPIENS (HUMAN).//Q06828
F-HEMBA1003078//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//7.2e-05:60:40//MUS MUSCULUS (MOUSE).//P11369

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F-HEMBA1003079//PROTEIN Q300.//0.0012:16:87//MUS MUSCULUS (MOUSE).//Q02722
F-HEMBA1003083//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//3.3e-32:95:75//HOMO SAPIENS (HUMAN).//P39189
F-HEMBA1003086
F-HEMBA1003096//PROTAMINE IA (IRIDINE IA).//0.36:20:40//SALMO IRIDEUS (RAINBOW TROUT).//P02328
F-HEMBA1003098//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.4e-09:43:72//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1003117//PUTATIVE CUTICLE COLLAGEN C09G5.5.//1.0:88:38//CAENORHABDITIS ELEGANS.//Q09456
F-HEMBA1003129//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.61:63:25//APIS MELLIFERA (HONEYBEE).//P34859
F-HEMBA1003133//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT).//0.48:79:37//HOMO SAPIENS (HUMAN).//P25067
F-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//3.6e-25:190:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41940
F-HEMBA1003142
F-HEMBA1003148//HYPOTHETICAL 56.4 KD PROTEIN IN RPL30-CWH41 INTERGENIC REGION PRECURSOR.//0.068:171:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53189
F-HEMBA1003166//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//1.8e-13:54:66//HOMO SAPIENS (HUMAN).//P39192
F-HEMBA1003175//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.015:147:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214
F-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE (EC 2.1.1.61).//2.6e-51:164:47//BACILLUS SUBTILIS.//O35020
F-HEMBA1003197
F-HEMBA1003199//HOMEOBOX PROTEIN HOX-A4 (HOX-1D) (HOX-1.4).//0.00049:83:38//HOMO SAPIENS (HUMAN).//Q00056
F-HEMBA1003202//SPERM PROTAMINE P1.//0.98:53:28//PLANIGALE GILESI (FLAT-SKULLED MARSUPIAL MOUSE).//O18747
F-HEMBA1003204//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//5.2e-22:42:80//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1003212//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.6e-18:74:71//HOMO SAPIENS (HUMAN).//P39193
F-HEMBA1003220//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.3e-18:56:78//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1003222//HYPOTHETICAL 37.5 KD PROTEIN IN GNTR-HTPG INTERGENIC REGION.//0.0018:159:27//BACILLUS SUBTILIS.//P46327
F-HEMBA1003229//DIHYDRODIPICOLINATE SYNTHASE 1 PRECURSOR (EC 4.2.1.52) (DHDPS).//1.0:85:28//TRITICUM AESTIVUM (WHEAT).//P24846
F-HEMBA1003235//TROPOMYOSIN://8.3e-07:109:33//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q02088
F-HEMBA1003250
F-HEMBA1003257//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//1.5e-07:27:74//OWENIA FUSIFORMIS.//P21260
F-HEMBA1003273
F-HEMBA1003276
F-HEMBA1003278
F-HEMBA1003281//HOMEOBOX PROTEIN HOX-A4 (CHOX-1.4).//0.0053:116:36//GALLUS GALLUS (CHICKEN).//P17277
F-HEMBA1003286//DNA-DIRECTED RNA POLYMERASE SUBUNIT N (EC 2.7.7.6).//0.96:37:35//SULFOLOBUS ACIDOCALDARIUS.//P39472
F-HEMBA1003291//5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-2 CHAIN (EC 2.7.1.-) (AMPK ALPHA-2 CHAIN) (FRAGMENT).//3.3e-15:68:39//SUS SCROFA (PIG).//Q28948
F-HEMBA1003296//PULMONARY SURFACTANT-ASSOCIATED PROTEIN B (SP-B) (6 KD PROTEIN) (PULMONARY SURFACTANT-ASSOCIATED PROTEOLIPID SPL(PHE)).//0.98:49:28//BOS TAURUS (BOVINE).//P15781
F-HEMBA1003304//MITOCHONDRIAL RIBOSOMAL PROTEIN S19.//0.99:36:30//PROTOTHECA WICKERHAMII.//P46750

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F-HEMBA1003309//HYPOTHETICAL 7.9 KD PROTEIN.//0.69:54:37//VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPENHAGEN).//P04306
F-HEMBA1003314//MIXED LINEAGE KINASE 2 (EC 2.7.1.-) (FRAGMENT).//2.3e-06:143:22//HOMO SAPIENS (HUMAN).//Q02779
F-HEMBA1003322//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.5e-30:53:77//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1003327
F-HEMBA1003328//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).//0.53:21:42//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1).//P04612
F-HEMBA1003330//LONG NEUROTOXIN 3 (TOXIN VN2).//1.0:26:34//DENDROASPIS POLYLEPIS POLYLEPIS (BLACK MAMBA).//P25667
F-HEMBA1003348//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//6.5e-09:56:66//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1003369//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.//0.0042:97:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P40602
F-HEMBA1003370//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//7.0e-18:99:53//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1003373
F-HEMBA1003376//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//4.7e-16:60:75//HOMO SAPIENS (HUMAN).//P39189
F-HEMBA1003380//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.8e-10:50:68//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1003384
F-HEMBA1003395//PROBABLE E5 PROTEIN.//0.62:64:29//HUMAN PAPILLOMAVIRUS TYPE 16.//P06927
F-HEMBA1003402//HYPOTHETICAL 12.0 KD PROTEIN IN TUB1-CPR3 INTERGENIC REGION PRECURSOR.//0.89:74:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04521
F-HEMBA1003403//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.0010:69:33//RATTUS NORVEGICUS (RAT).//P10164
F-HEMBA1003408//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//4.8e-06:93:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38968
F-HEMBA1003417//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].//0.0021:140:34//MUS MUSCULUS (MOUSE).//P28481
F-HEMBA1003418//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.7e-14:188:33//HOMO SAPIENS (HUMAN).//Q08170
F-HEMBA1003433//DNA REPAIR PROTEIN XRS2.//1.0:88:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33301
F-HEMBA1003447//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.0061:69:33//RATTUS NORVEGICUS (RAT).//P10164
F-HEMBA1003461//SPIDROIN 1 (DRAGLINE SILK FIBROIN 1) (FRAGMENT).//2.3e-09:239:33//NEPHILA CLAVIPES (ORB SPIDER).//P19837
F-HEMBA1003463//METALLOTHIONEIN-A (MTA) (FRAGMENT).//1.0:40:35//SPHAERECHINUS GRANULARIS (PURPLE SEA URCHIN).//Q26497
F-HEMBA1003480//FUSARIC ACID RESISTANCE PROTEIN FUSB.//0.0043:96:32//BURKHOLDERIA CEPACIA (PSEUDOMONAS CEPACIA).//P24127.
F-HEMBA1003528//36.4 KD PROLINE-RICH PROTEIN.//6.4e-15:167:33//LYCOPERSICON ESCULENTUM (TOMATO).//Q00451
F-HEMBA1003531//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//1.2e-18:56:78//HOMO SAPIENS (HUMAN).//P39189
F-HEMBA1003538//COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41).//2.5e-28:136:47//HOMO SAPIENS (HUMAN).//P00736
F-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (ISLET-2).//9.2e-105:217:85//RATTUS NORVEGICUS (RAT).//P50480
F-HEMBA1003548
F-HEMBA1003555//HYPOTHETICAL 31.9 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION.//8.7e-57:180:55//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40558
F-HEMBA1003556//HYPOTHETICAL 19.2 KD PROTEIN IN COX-REP INTERGENIC REGION (ORF5) (ORF21).//0.53:97:25//BACTERIOPHAGE HP1.//P51706
F-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAM-

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MA-I).//1.8e-32:71:100//BOS TAURUS (BOVINE).//P16874
F-HEMBA1003568//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//4.1e-19:126:31//HOMO SAPIENS (HUMAN).//P14373
F-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1.//3.9e-83:143:74//HOMO SAPIENS (HUMAN).//Q13330
F-HEMBA1003571//HYPOTHETICAL 8.7 KD PROTEIN (READING FRAME D).//1.0:64:25//STAPHYLOCOCCUS AUREUS.//P03860
F-HEMBA1003579//CYTOTOXIN 1 (CYTOTOXIN V-II-1) (TOXIN V(II)1).//1.0:41:29//NAJA MELANOLEUCA (FOREST COBRA) (BLACK-LIPPED COBRA).//P01448
F-HEMBA1003581//TALIN.//3.7e-36:52:98//MUS MUSCULUS (MOUSE).//P26039
F-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP).//1.6e-05:91:31//NICOTIANA SYLVESTRIS (WOOD TOBACCO).//P19682
F-HEMBA1003595//HYPOTHETICAL 12.0 KD PROTEIN IN DST1-HEM2 INTERGENIC REGION.//1.0:55:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53182
F-HEMBA1003597
F-HEMBA1003598//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11)//4.9e-10:85:41//ORYCTOLAGUS CUNICULUS (RABBIT).//P06333
F-HEMBA1003615//PUTATIVE MINOR COAT PROTEIN (ORF43).//0.086:10:70//BACTERIOPHAGE PHI-LF.//Q07482
F-HEMBA1003617//HYPOTHETICAL 36.8 KD PROTEIN C26A3.16 IN CHROMOSOME I.//4.4e-13:58:48//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10169
F-HEMBA1003621//LONG NEUROTOXIN 1 (NEUROTOXIN A).//0.096:40:37//OPHIOPHAGUS HANNAH (KING COBRA) (NAJA HANNAH).//P01387
F-HEMBA1003622
F-HEMBA1003630
F-HEMBA1003637//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.4e-13:47:74//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1003640//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//0.87:25:64//HOMO SAPIENS (HUMAN).//P39193
F-HEMBA1003645//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHROMOSOME III.//1.8e-10:157:26//CAENORHABDITIS ELEGANS.//Q17963
F-HEMBA1003646//SERINE-ARGININE PROTEIN 55 (SRP55) (ENHANCER OF DEFORMED) (52-KD BRACKETING PROTEIN) (B52 PROTEIN).//4.9e-05:207:27//DROSOPHILA MELANOGASTER (FRUIT FLY).//P26686
F-HEMBA1003656
F-HEMBA1003662//PROLINE-RICH PEPTIDE P-B.//0.57:17:52//HOMO SAPIENS (HUMAN).//P02814
F-HEMBA1003667//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//6.0e-16:43:72//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1003679
F-HEMBA1003680//PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-).//3.9e-08:137:27//CAENORHABDITIS ELEGANS.//P34629
F-HEMBA1003684//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).//2.1e-20:127:40//MUS MUSCULUS (MOUSE).//Q60821
F-HEMBA1003690//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//3.0e-85:201:78//HOMO SAPIENS (HUMAN).//P56524
F-HEMBA1003692//CELL DIVISION CONTROL PROTEIN 1.//0.13:69:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40986
F-HEMBA1003711//CARCINOEMBRYONIC ANTIGEN PRECURSOR (CEA) (MECONIUM ANTIGEN 100) (CD66E ANTIGEN).//0.021:153:26//HOMO SAPIENS (HUMAN).//P06731
F-HEMBA1003714//ABAECIN.//0.99:34:32//BOMBUS PASCUORUM.//P81463
F-HEMBA1003715
F-HEMBA1003720//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.4e-34:155:56//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1003725//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.3e-27:181:41//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1003729//PTB-ASSOCIATED SPLICING FACTOR (PSF).//0.0037:103:33//HOMO SAPIENS (HUMAN).//P23246
F-HEMBA1003733//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.0e-54:210:58//HOMO SAPIENS (HUMAN).//P08547

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F-HEMBA1003742//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.066:72:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
F-HEMBA1003758
F-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//1.5e-51:220:52//MUS MUSCULUS (MOUSE).//Q61221
F-HEMBA1003773
F-HEMBA1003783
F-HEMBA1003784
F-HEMBA1003799//SHORT NEUROTOXIN 1 (TOXIN AA C).//0.95:27:37//ACANTHOPHIS ANTARCTICUS (COMMON DEATH ADDER).//P01434
F-HEMBA1003803//GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30].//0.46:96:34//FELINE SARCOMA VIRUS (STRAIN SNYDER-THEILEN).//P03338
F-HEMBA1003804//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.019:30:50//HOMO SAPIENS (HUMAN).//P30808
F-HEMBA1003805//HYPOTHETICAL 75.0 KD PROTEIN B0280.11 IN CHROMOSOME III.//1.8e-20:109:47//CAENORHABDITIS ELEGANS.//P42083
F-HEMBA1003807
F-HEMBA1003827//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//2.1e-09:23:78//OWENIA FUSIFORMIS.//P21260
F-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).//2.0e-31:134:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40484
F-HEMBA1003838//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//3.9e-22:39:76//HOMO SAPIENS (HUMAN).//P39192
F-HEMBA1003856
F-HEMBA1003864//HYPOTHETICAL 39.4 KD PROTEIN IN MET1-SIS2 INTERGENIC REGION.//1.5e-15:194:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36151
F-HEMBA1003866//PROTEIN A39.//0.0027:72:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P21062
F-HEMBA1003879//80 KD NUCLEAR CAP BINDING PROTEIN (NCBP 80 KD SUBUNIT) (CBP80).//2.9e-16:22:100//HOMO SAPIENS (HUMAN).//Q09161
F-HEMBA1003880//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:39:38//FELIS SILVESTRIS CATUS (CAT).//P48896
F-HEMBA1003885//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//3.5e-28:47:76//HOMO SAPIENS (HUMAN).//P39193
F-HEMBA1003893//HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//1.7e-57:215:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53215
F-HEMBA1003902
F-HEMBA1003908
F-HEMBA1003926//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.3e-10:60:63//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1003937//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//8.1e-29:68:64//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1003939//PROTEIN Q300.//0.0025:24:62//MUS MUSCULUS (MOUSE).//Q02722
F-HEMBA1003942//EXCITATORY INSECT TOXIN BJXTR-IT PRECURSOR (BJ-XTRIT).//0.084:67:31//BUTHOTUS JUDAICUS (SCORPION) (HOTTENTOTTA JUDAICA).//P56637
F-HEMBA1003950//HYPOTHETICAL 8.1 KD PROTEIN IN SPEA-METK INTERGENIC REGION (O71).//0.95:26:34//ESCHERICHIA COLI.//P46878
F-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//2.5e-17:89:46//MUS MUSCULUS (MOUSE).//P16372
F-HEMBA1003958//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.2e-23:43:76//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1003959
F-HEMBA1003976//HYPOTHETICAL PROTEIN KIAA0076 (HA0936).//0.99:88:28//HOMO SAPIENS (HUMAN).//Q14999
F-HEMBA1003978//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.98:19:57//HOMO SAPIENS (HUMAN).//P22531
F-HEMBA1003985//LYSYL-TRNA SYNTHETASE (EC 6.1.1.6) (LYSINE--TRNA LIGASE) (LYSRS) (FRAGMENT).//1.0:40:32//MYCOBACTERIUM LEPRAE.//P46861
F-HEMBA1003987//HYPOTHETICAL PROTEIN UL66.//0.27:65:33//HUMAN CYTOMEGALOVIRUS (STRAIN

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AD169).//P16822
F-HEMBA1003989//MALE SPECIFIC SPERM PROTEIN MST84DB.//5.2e-05:64:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
F-HEMBA1004000//PROTEIN Q300.//0.00042:17:82//MUS MUSCULUS (MOUSE).//Q02722
F-HEMBA1004011//ALPHA-TYPE CALCITONIN GENE-RELATED PEPTIDE PRECURSOR (CGRP-1).//0.47:106:32//HOMO SAPIENS (HUMAN).//P06881
F-HEMBA1004012//ATP SYNTHASE PROTEIN 9, MITOCHONDRIAL (EC 3.6.1.34) (LIPID-BINDING PROTEIN).//0.96:36:33//PARAMECIUM TETRAURELIA.//P16001
F-HEMBA1004015//HYPOTHETICAL 29.3 KD PROTEIN B0280.6 IN CHROMOSOME III.//0.00018:90:34//CAENORHABDITIS ELEGANS.//P41997
F-HEMBA1004024//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//5.1e-34:75:80//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1004038
F-HEMBA1004042
F-HEMBA1004045//40S RIBOSOMAL PROTEIN S27A.//1.0:20:55//ASPARAGUS OFFICINALIS (GARDEN ASPARAGUS).//P31753
F-HEMBA1004048//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.3e-06:158:35//MUS MUSCULUS (MOUSE).//P05143
F-HEMBA1004049//32 KD HEAT SHOCK PROTEIN (4-1 PROTEIN).//0.098:106:32//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P54658
F-HEMBA1004055//HYPOTHETICAL PROTEIN HI0258/259.//0.87:133:23//HAEMOPHILUS INFLUENZAE.//P43974
F-HEMBA1004056//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//3.3e-25:39:64//HOMO SAPIENS (HUMAN).//P39191
F-HEMBA1004074//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//9.9e-08:35:68//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1004086
F-HEMBA1004097//IMMEDIATE-EARLY PROTEIN IE4 (IE68) (FRAGMENT)//0.71:95:35//HERPES SIMPLEX VIRUS (TYPE 2).//P14379
F-HEMBA1004111//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.7e-26:84:64//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT).//2.8e-34:108:63//HOMO SAPIENS (HUMAN).//Q14141
F-HEMBA1004132//HYPOTHETICAL PROTEIN HI1736.//1.0:44:34//HAEMOPHILUS INFLUENZAE.//P44300
F-HEMBA1004133//HYPOTHETICAL 8.5 KD PROTEIN CY274.40C.//0.89:21:57//MYCOBACTERIUM TUBERCULOSIS.//Q10826
F-HEMBA1004138//EARLY NODULIN 75 (N-75) (NGM-75) (FRAGMENT).//0.016:39:41//MEDICAGO SATIVA (ALFALFA).//P11728
F-HEMBA1004143//CYTOCHROME C OXIDASE POLYPEPTIDE VIII PRECURSOR (EC 1.9.3.1).//0.93:34:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P04039
F-HEMBA1004146//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.63:52:36//HOMO SAPIENS (HUMAN).//P02811
F-HEMBA1004150//METALLOTHIONEIN-II (MT-II).//1.0:20:45//MUS MUSCULUS (MOUSE).//P02798
F-HEMBA1004164//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//3.0e-13:57:71//HOMO SAPIENS (HUMAN).//P39195
F-HEMBA1004168//V-TYPE SODIUM ATP SYNTHASE SUBUNIT F (EC 3.6.1.34) (NA(+)-TRANSLOCATING ATPASE SUBUNIT F).//0.00035:90:34//ENTEROCOCCUS HIRAE.//P43437
F-HEMBA1004199//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//5.1e-14:115:31//CAENORHABDITIS ELEGANS.//P34529
F-HEMBA1004200
F-HEMBA1004202//YPT1-RELATED PROTEIN 1.//2.5e-24:96:52//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P11620
F-HEMBA1004203//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//2.2e-09:48:64//HOMO SAPIENS (HUMAN).//P39193
F-HEMBA1004207//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70).//0.98:51:33//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779
F-HEMBA1004225//METALLOTHIONEIN-II.//1.0:30:33//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA).//P15114

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F-HEMBA1004227//PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015).//5.9e-06:109:33//HOMO SAPIENS (HUMAN).//P49593
F-HEMBA1004238//VERY HYPOTHETICAL XYLU PROTEIN.//0.98:39:38//ESCHERICHIA COLI.//P05056
F-HEMBA1004241//SOX-13 PROTEIN (FRAGMENT).//0.66:36:38//MUS MUSCULUS (MOUSE).//Q04891
F-HEMBA1004246
F-HEMBA1004248//INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 (IMMEDIATE-EARLY PROTEIN CL-6).//1.0e-43:98:84//RATTUS NORVEGICUS (RAT).//Q08755
F-HEMBA1004264//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//0.014:160:28//NEPHILA CLAVIPES (ORB SPIDER).//P46804
F-HEMBA1004267//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//1.8e-52:56:83//HOMO SAPIENS (HUMAN).//P39189
F-HEMBA1004272
F-HEMBA1004274//HYPOTHETICAL 13.0 KD PROTEIN F59B2.10 IN CHROMOSOME III.//0.00084:33:54//CAENORHABDITIS ELEGANS.//P34485
F-HEMBA1004275//HYPOTHETICAL 56.5 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION)/9.3e-06:125:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40034
F-HEMBA1004276//BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A).//3.7e-30:239:32//HOMO SAPIENS (HUMAN).//Q10567
F-HEMBA1004286//CUTICLE COLLAGEN 34.//0.0027:71:38//CAENORHABDITIS ELEGANS.//P34687
F-HEMBA1004289//PTR3 PROTEIN (SSY3 PROTEIN).//1.0:76:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43606
F-HEMBA1004295//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.075:58:39//HOMO SAPIENS (HUMAN).//P30808
F-HEMBA1004306//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.020:132:30//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341
F-HEMBA1004312//EARLY PROTEIN I73R.//0.99:65:32//AFRICAN SWINE FEVER VIRUS (STRAIN BA71V) (ASFV).//P27946
F-HEMBA1004321//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).//4.3e-43:133:44//MUS MUSCULUS (MOUSE).//Q61967
F-HEMBA1004323
F-HEMBA1004327//SMALL PROLINE-RICH PROTEIN 2-1.//0.027:48:43//HOMO SAPIENS (HUMAN).//P35326
F-HEMBA1004330//HOMEOBOX PROTEIN ENGRAILED-1 (HU-EN-1).//0.46:70:34//HOMO SAPIENS (HUMAN).//Q05925
F-HEMBA1004334//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.7e-05:83:34//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1004335//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.0e-24:41:80//HOMO SAPIENS (HUMAN).//P39195
F-HEMBA1004341//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//2.8e-06:148:35//MUS MUSCULUS (MOUSE).//P05143
F-HEMBA1004353//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.2e-29:57:80//HOMO SAPIENS (HUMAN).//P39195
F-HEMBA1004354//CHL1 PROTEIN.//0.017:40:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P22516
F-HEMBA1004356
F-HEMBA1004366//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.00045:49:46//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1004372//VERY HYPOTHETICAL 20.6 KD PROTEIN C56F8.15 IN CHROMOSOME I.//1.0:125:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10263
F-HEMBA1004389//HYPOTHETICAL 113.1 KD PROTEIN IN PRE5-FET4 INTERGENIC REGION.//0.76:170:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04893
F-HEMBA1004394
F-HEMBA1004396//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.2e-10:72:51//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1004405
F-HEMBA1004408//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN-10).//2.7e-29:146:48//CAENORHABDITIS ELEGANS.//P52017
F-HEMBA1004429//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//0.0019:47:59//HOMO SAPIENS (HU-

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MAN).//P39191
F-HEMBA1004433//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//1.1e-20:47:68//HOMO SAPIENS (HUMAN).//P39192
F-HEMBA1004460//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//6.2e-64:134:69//HOMO SAPIENS (HUMAN).//P39193
F-HEMBA1004461//METALLOTHIONEIN-LIKE PROTEIN 1.//1.0:39:35//PISUM SATIVUM (GARDEN PEA).//P20830
F-HEMBA1004479//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//9.7e-43:101:48//MUS MUSCULUS (MOUSE).//Q61221
F-HEMBA1004482//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34).//1.0:41:36//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA).//P05040
F-HEMBA1004499//TUBULIN BETA CHAIN.//0.00021:55:36//CAENORHABDITIS ELEGANS.//P52275
F-HEMBA1004502
F-HEMBA1004506//HYPOTHETICAL PROTEIN ORF-1137.//5.3-11:119:35//MUS MUSCULUS (MOUSE).//P11260
F-HEMBA1004507//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.00072:90:37//HOMO SAPIENS (HUMAN).//Q15428
F-HEMBA1004509//HYPOTHETICAL 52.2 KD PROTEIN IN MPR1-GCN20 INTERGENIC REGION.//6.3e-28:169:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43589
F-HEMBA1004534//ENDOTHELIAL ACTIN-BINDING PROTEIN (ABP-280) (NONMUSCLE FILAMIN) (FILAMIN 1).//1.3e-80:226:66//HOMO SAPIENS (HUMAN).//P21333
F-HEMBA1004538//HYPOTHETICAL PROTEIN MJ0764.//0.96:28:35//METHANOCOCCUS JANNASCHII.//Q58174
F-HEMBA1004542//METALLOTHIONEIN (MT).//0.78:36:41//GADUS MORHUA (ATLANTIC COD).//P51902
F-HEMBA1004554
F-HEMBA1004560//HYPOTHETICAL PROTEIN KIAA0281 (HA6725).//4.2e-15:56:69//HOMO SAPIENS (HUMAN).//Q92556
F-HEMBA1004573//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//0.65:31:58//PLASMODIUM BERGHEI.//P06915
F-HEMBA1004577//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//3.9e-08:35:80//HOMO SAPIENS (HUMAN).//P39195
F-HEMBA1004586//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//6.6e-08:64:54//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1004596//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN C (HNRNP C) (HNRNP CORE PROTEIN C) (FRAGMENT).//0.00057:88:31//RATTUS NORVEGICUS (RAT).//P17132
F-HEMBA1004604//COLLAGEN ALPHA 2(XI) CHAIN PRECURSOR (FRAGMENT).//0.045:37:45//MUS MUSCULUS (MOUSE).//Q64739
F-HEMBA1004610//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.3e-11:73:54//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1004617
F-HEMBA1004629
F-HEMBA1004631//HYPOTHETICAL 7.8 KD PROTEIN IN WAPA-LICT INTERGENIC REGION.//1.0:36:38//BACILLUS SUBTILIS.//P42303
F-HEMBA1004632//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING 8.0 KD POLYPEPTIDE).//0.86:48:35//SYNECHOCOCCUS ELONGATUS NAEGELI.//P20453
F-HEMBA1004637//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III.//1.7e-32:159:42//CAENORHABDITIS ELEGANS.//P34535
F-HEMBA1004638//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//2.8e-06:50:46//OWENIA FUSIFORMIS.//P21260
F-HEMBA1004666//TOXIN S6C4.//1.0:36:30//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S MAMBA).//P25682
F-HEMBA1004669//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.6e-12:105:42//HOMO SAPIENS (HUMAN).//Q08170
F-HEMBA1004670//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//2.5e-06:62:45//HOMO SAPIENS (HUMAN).//P02452
F-HEMBA1004672//HYPOTHETICAL PROTEIN MJ0437.//0.95:37:29//METHANOCOCCUS JANNASCHII.//Q57879
F-HEMBA1004693//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN,

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TYPE B) (NMMHC-B).//0.00035:217:23//HOMO SAPIENS (HUMAN).//P35580
F-HEMBA1004697//IMMUNOGLOBULIN G BINDING PROTEIN H PRECURSOR (PROTEIN H).//0.058:118:30//STREPTOCOCCUS PYOGENES.//P50470
F-HEMBA1004705//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//6.8e-09:43:72//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1004709//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//8.8e-18:50:84//HOMO SAPIENS (HUMAN).//P39189
F-HEMBA1004711//ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2).//0.0027:148:30//HOMO SAPIENS (HUMAN).//000321
F-HEMBA1004725//CUTICLE COLLAGEN 2.//0.0051:41:41//CAENORHABDITIS ELEGANS.//P17656
F-HEMBA1004730//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.4e-22:210:37//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1004733//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.7e-07:50:62//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.9e-39:143:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P42743
F-HEMBA1004736//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.1e-60:210:61//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1004748
F-HEMBA1004751//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.8e-20:88:63//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1004752//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.0043:126:34//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437
F-HEMBA1004753//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//7.8e-28:47:78//HOMO SAPIENS (HUMAN).//P39193
F-HEMBA1004756//HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.//0.22:77:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39981
F-HEMBA1004758
F-HEMBA1004763//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//1.1e-06:58:43//OWENIA FUSIFORMIS.//P21260
F-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.7e-65:298:53//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1004770
F-HEMBA1004771
F-HEMBA1004776//GRANULIN 1.//0.78:28:42//CYPRINUS CARPIO (COMMON CARP).//P81013
F-HEMBA1004778
F-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).//6.9e-20:74:63//HOMO SAPIENS (HUMAN).//P50851
F-HEMBA1004803//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.4e-22:58:86//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1004806//HYPOTHETICAL 24.3 KD PROTEIN IN PSBH-RPL11 INTERGENIC REGION (ORF182).//0.72:75:33//CYANOPHORA PARADOXA.//P48324
F-HEMBA1004807
F-HEMBA1004816
F-HEMBA1004820//HEMOLYMPH TRYPSIN INHIBITOR A (BPI-TYPE) (FRAGMENT).//1.0:50:38//MANDUCA SEXTA (TOBACCO HAWKMOTH) (TOBACCO HORNWORM).//P26226
F-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//3.0e-76:171:91//CANIS FAMILIARIS (DOG).//Q00004
F-HEMBA1004850//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//3.0e-05:64:43//BOS TAURUS (BOVINE).//P25508
F-HEMBA1004863//TOXIN C13S1C1 PRECURSOR.//0.38:52:30//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P18329
F-HEMBA1004864//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).//0.89:24:50//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1).//P04612
F-HEMBA1004865
F-HEMBA1004880
F-HEMBA1004889//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.66:23:47//HOMO SAPIENS (HUMAN).//P22532

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F-HEMBA1004900
F-HEMBA1004909
F-HEMBA1004918//CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 (FRAGMENT).//0.56:37:32//SPINACIA OLERACEA (SPINACH).//P09597
F-HEMBA1004923//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.5e-24:44:68//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1004929//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.97:39:38//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).//P15997
F-HEMBA1004930//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.6e-15:64:59//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1004933//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.34:58:41//HOMO SAPIENS (HUMAN).//P50552
F-HEMBA1004934
F-HEMBA1004944
F-HEMBA1004954//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).//0.58:78:30//PARAMECIUM TETRAURELIA.//P15579
F-HEMBA1004956//HYPOTHETICAL 18.8 KD PROTEIN (ORF4).//0.98:57:31//PARAMECIUM TETRAURELIA.//P15605
F-HEMBA1004960//HYPOTHETICAL 12.6 KD PROTEIN-(ORFJ) (RETRON EC67).//1.0:58:27//ESCHERICHIA COLI.//P21324
F-HEMBA1004972
F-HEMBA1004973//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.90:55:30//HOMO SAPIENS (HUMAN).//P22531
F-HEMBA1004977
F-HEMBA1004978
F-HEMBA1004980//MOTILIN PRECURSOR.//0.088:79:31//MACACA MULATTA (RHESUS MACAQUE).//018811
F-HEMBA1004983//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES).//0.87:51:31//BUCHNERA APHIDICOLA.//Q59176
F-HEMBA1004995//MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE FACTOR-LIKE PROTEIN 2) (XMEF2) (RSRFR2).//0.17:52:40//HOMO SAPIENS (HUMAN).//Q02080
F-HEMBA1005008//METALLOTHIONEIN (MT).//1.0:52:32//CRASSOSTREA VIRGINICA (EASTERN OYSTER).//P23038
F-HEMBA1005009//ACTIN.//3.5e-27:171:38//CANDIDA ALBICANS (YEAST).//P14235
F-HEMBA1005019//HYPOTHETICAL PROTEIN HI1222.//0.13:58:31//HAEMOPHILUS INFLUENZAE.//P44129
F-HEMBA1005029//P2Y PURINOCEPTOR 5 (P2Y5) (PURINERGIC RECEPTOR 5) (6H1).//0.76:72:31//GALLUS GALLUS (CHICKEN).//P32250
F-HEMBA1005035//HOMEOBOX PROTEIN HB9.//0.0086:60:40//HOMO SAPIENS (HUMAN).//P50219
F-HEMBA1005039//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.47:49:32//HOMO SAPIENS (HUMAN).//P22532
F-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16).//1.5e-19:39:100//MUS MUSCULUS (MOUSE).//P35290
F-HEMBA1005050//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.074:34:44//BOS TAURUS (BOVINE).//P25508
F-HEMBA1005062
F-HEMBA1005066//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.1e-44:126:65//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1005075//SUPPRESSOR PROTEIN SRP40.//0.35:96:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
F-HEMBA1005079//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//3.6e-20:75:64//HOMO SAPIENS (HUMAN).//P39191
F-HEMBA1005083//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.00015:72:34//BOS TAURUS (BOVINE).//P25508
F-HEMBA1005101//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP 48) (HRP48.1).//4.8e-10:176:25//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48809
F-HEMBA1005113
F-HEMBA1005123//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.6e-24:99:60//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1005133//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION.//0.11:22:54//

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SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40490
F-HEMBA1005149//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.7e-16:59:71//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1005152//GENOME POLYPROTEIN 2 [CONTAINS: HELPER COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); 70 KD PROTEIN].//1.0:77:27//BARLEY YELLOW MOSAIC VIRUS (JAPANESE STRAIN II-1) (BAYMV).//Q01207
F-HEMBA1005159//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.40:53:33//APIS MELLIFERA (HONEYBEE).//P34859
F-HEMBA1005185//MYOSIN IB HEAVY CHAIN.//0.011:58:48//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34092
F-HEMBA1005201//HYPOTHETICAL 56.6 KD PROTEIN C16C9.03 IN CHROMOSOME I.//3.9e-67:241:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09817
F-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//3.8e-124:257:95//CANIS FAMILIARIS (DOG).//Q00004
F-HEMBA1005206//CUTICLE COLLAGEN 1.//0.010:118:33//CAENORHABDITIS ELEGANS.//P08124
F-HEMBA1005219//PTB-ASSOCIATED SPLICING FACTOR (PSF).//0.99:85:40//HOMO SAPIENS (HUMAN).//P23246
F-HEMBA1005223//HYPOTHETICAL GENE 1.05 PROTEIN.//0.31:75:28//BACTERIOPHAGE T3.//P07715
F-HEMBA1005232//HYPOTHETICAL 7.8 KD PROTEIN.//0.99:48:29//VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPENHAGEN).//P20544
F-HEMBA1005241//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.4e-28:138:55//HOMO SAPIENS (HUMAN).//P39193
F-HEMBA1005244//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.014:39:41//HOMO SAPIENS (HUMAN).//P22531
F-HEMBA1005251//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.55:15:46//DICENTRARCHUS LABRAX (EUROPEAN SEA BASS).//Q36362
F-HEMBA1005252//EC PROTEIN HOMOLOG (ZINC-METALLOTHIONEIN CLASS II).//0.088:33:42//ZEA MAYS (MAIZE).//P43401
F-HEMBA1005274
F-HEMBA1005275//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.96:42:45//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1005293//PROBABLE COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP).//0.55:98:30//CAENORHABDITIS ELEGANS.//Q20168
F-HEMBA1005296//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//0.095:75:34//HOMO SAPIENS (HUMAN).//Q02817
F-HEMBA1005304//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//5.4e-33:103:74//HOMO SAPIENS (HUMAN).//P39189
F-HEMBA1005311//PERIOD CLOCK PROTEIN (FRAGMENT).//0.99:45:31//DROSOPHILA SALTANS (FRUIT FLY).//Q04536
F-HEMBA1005314//HYPOTHETICAL 6.3 KD PROTEIN T19C3.3 IN CHROMOSOME III.//0.98:30:30//CAENORHABDITIS ELEGANS.//Q10009
F-HEMBA1005315//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.1e-05:35:51//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1005318//OLFACTORY RECEPTOR-LIKE PROTEIN COR8 (FRAGMENT).//0.57:44:38//GALLUS GALLUS (CHICKEN).//Q98913
F-HEMBA1005331//IMMEDIATE-EARLY PROTEIN IE180.//0.57:106:33//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675
F-HEMBA1005338//CARTIAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).//1.8e-55:199:59//GALLUS GALLUS (CHICKEN).//P05099
F-HEMBA1005353//CHLOROPLAST 30S RIBOSOMAL PROTEIN S17.//0.88:33:36//PORPHYRA PURPUREA.//P51305
F-HEMBA1005359//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.1e-68:255:48//HOMO SAPIENS (HUMAN).//P51522
F-HEMBA1005367//ALPHA-AMYLASE INHIBITOR AAI.//1.0:25:40//AMARANTHUS HYPOCHONDRIACUS (PRINCE'S FEATHER).//P80403
F-HEMBA1005372
F-HEMBA1005374//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.0e-34:92:75//HOMO SAPIENS (HUMAN).//P39194

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F-HEMBA1005382//APOLIPOPROTEIN C-II (APO-CII).//0.99:39:33//BOS TAURUS (BOVINE).//P19034
F-HEMBA1005389//HYPOTHETICAL 70.0 KD PROTEIN IN DNAK 3'REGION (ORF4).//0.82:164:31//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).//P42377
F-HEMBA1005394//HYPOTHETICAL 8.9 KD PROTEIN IN IE0-IE1 INTERGENIC REGION.//0.98:44:38// AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41703
F-HEMBA1005403//SPERM HISTONE P2 PRECURSOR (PROTAMINE MP2).//0.066:64:29//MUS MUSCULUS (MOUSE).//P07978
F-HEMBA1005408//50S RIBOSOMAL PROTEIN L33.//0.77:32:25//BACILLUS SUBTILIS.//Q06798
F-HEMBA1005410//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//0.0065:38:52//MUS MUSCULUS (MOUSE).//P11369
F-HEMBA1005411//TOXIN S4C8.//0.16:46:28//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S MAMBA).//P25683
F-HEMBA1005423//CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT KINASE 4 INHIBITOR C) (P18-INK4C).//4.3e-09:29:96//HOMO SAPIENS (HUMAN).//P42773
F-HEMBA1005426//TOXIN C10S2C2.//0.99:49:34//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P25684
F-HEMBA1005443//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.9e-16:78:60//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1005447//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:57:31//DASYPUS NOVEMCINCTUS (NINE-BANDED ARMADILLO).//O21329
F-HEMBA1005468//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRAGMENTS).//0.68:41:31//ARTEMIA SALINA (BRINE SHRIMP).//P19040
F-HEMBA1005469
F-HEMBA1005472//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-39:142:70//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1005474//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//5.8e-10:44:68//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1005475//U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD (U1 SNRNP 70 KD) (SNRP70).//9.2e-14:179:33//HOMO SAPIENS (HUMAN).//P08621
F-HEMBA1005497
F-HEMBA1005500//60S RIBOSOMAL PROTEIN L37.//0.11:53:33//SCHISTOSOMA MANSONI (BLOOD FLUKE).//044125
F-HEMBA1005506
F-HEMBA1005508
F-HEMBA1005511//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.5e-30:92:73//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//2.0e-39:95:61//DROSOPHILA MELANOGASTER (FRUIT FLY).//O02193
F-HEMBA1005517//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//2.1e-06:56:44//MUS MUSCULUS (MOUSE).//P05142
F-HEMBA1005518//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//5.8e-05:192:33//BOS TAURUS (BOVINE).//P02453
F-HEMBA1005520//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!/2.0e-18:87:57//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1005526//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!/5.1e-22:77:54//HOMO SAPIENS (HUMAN).//P39191
F-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.2e-81:157:98//MUS MUSCULUS (MOUSE).//Q60809
F-HEMBA1005530//POLLEN ALLERGEN AMB P 5-A PRECURSOR (AMB P V-A).//0.98:19:47//AMBROSIA PSILOSTACHYA (WESTERN RAGWEED).//P43174
F-HEMBA1005548//TRANSCRIPTION FACTOR MAF1.//1.4e-72:137:97//RATTUS NORVEGICUS (RAT).//P54842
F-HEMBA1005552//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.7e-29:47:78//HOMO SAPIENS (HUMAN).//P39193
F-HEMBA1005558//HYPOTHETICAL 25.6 KD PROTEIN IN ABF2-CHL12 INTERGENIC REGION.//1.6e-20:202:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04272
F-HEMBA1005568
F-HEMBA1005570//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6 (EC 1.6.5.3).//1.0:80:31//

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CAENORHABDITIS ELEGANS.//P24885
F-HEMBA1005576//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//8.5e-58:152:75//HOMO SAPIENS (HUMAN).//P51805
F-HEMBA1005577//KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A.//0.98:57:36//OVIS ARIES (SHEEP).//P02438
F-HEMBA1005581//SLIT PROTEIN PRECURSOR.//1.1e-62:254:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//P24014
F-HEMBA1005582//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP-150) (DAP-150) (P150-GLUED).//0.0091:189:29//RATTUS NORVEGICUS (RAT).//P28023
F-HEMBA1005583//HYPOTHETICAL 41.2 KD PROTEIN IN CPS REGION (ORF7).//0.83:119:23//KLEBSIELLA PNEUMONIAE.//Q48453
F-HEMBA1005588//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.9e-17:108:53//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1005593//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.23:24:54//HOMO SAPIENS (HUMAN).//P22532
F-HEMBA1005595//DYNEIN HEAVY CHAIN, CYTOSOUC (DYHC).//2.7e-39:257:39//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34036
F-HEMBA1005606
F-HEMBA1005609//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//3.2e-20:27:96//HOMO SAPIENS (HUMAN).//P39192
F-HEMBA1005616//LATE CONTROL GENE B PROTEIN (GPB).//0.48:51:33//BACTERIOPHAGE 186.//P08711
F-HEMBA1005621//MITOTIC MAD2 PROTEIN.//1.2e-06:137:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40958
F-HEMBA1005627//HYPOTHETICAL 17.1 KD PROTEIN IN PUBS 3'REGION.//0.18:100:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38898
F-HEMBA1005631
F-HEMBA1005632//HYPOTHETICAL 7.4 KD PROTEIN.//0.32:59:32//VACCINIA VIRUS (STRAIN WR).//P04309
F-HEMBA1005634//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.6e-14:93:58//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1005666//HYPOTHETICAL PROTEIN KIAA0129.//2.1e-05:126:25//HOMO SAPIENS (HUMAN).//Q14142
F-HEMBA1005670
F-HEMBA1005679//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.2e-08:40:72//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1005680//SMALL PROLINE-RICH PROTEIN 2-1.//0.015:19:47//HOMO SAPIENS (HUMAN).//P35326
F-HEMBA1005685
F-HEMBA1005699//EPHRIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 8) (LERK-8) (EPH-RELATED RECEPTOR TRANSMEMBRANE LIGAND ELK-L3).//4.2e-38:98:81//HOMO SAPIENS (HUMAN).//Q15768
F-HEMBA1005705//PROTEIN Q300.//0.11:23:56//MUS MUSCULUS (MOUSE).//Q02722
F-HEMBA1005717
F-HEMBA1005732//BACTENECIN 7 PRECURSOR (BAC7).//0.22:55:41//OVIS ARIES (SHEEP).//P50415
F-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT).//4.5e-18:167:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25296
F-HEMBA1005746
F-HEMBA1005755//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.4e-30:69:65//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1005765//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.8e-19:60:63//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1005780//METALLOTHIONEIN-I (MT-1).//1.0:31:38//COLUMBA LIVIA (DOMESTIC PIGEON).//P15786
F-HEMBA1005813
F-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU/M-TYPE).//1.0e-23:200:31//GALLUS GALLUS (CHICKEN).//P00789
F-HEMBA1005822//PROTEIN Q300.//0.0016:21:80//MUS MUSCULUS (MOUSE).//Q02722 F-HEMBA1005829//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//9.6e-33:96:73//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1005834//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.6e-22:103:46//NYCTICEBUS COU-

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CANG (SLOW LORIS).//P08548
F-HEMBA1005852//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//8.8e-06:95:35//MUS MUSCULUS (MOUSE).//P05143
F-HEMBA1005853//HYPOTHETICAL PROTEIN
MJ0647.//0.39:28:39//METHANOCOCCUS JANNASCHII.//Q58063
F-HEMBA1005884
F-HEMBA1005891//HYPOTHETICAL PROTEIN MTH137.//0.95:51:27//METHANOBACTERIUM THERMOAUTOTROPHICUM.//O26240
F-HEMBA1005894//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.6e-29:81:71//HOMO SAPIENS (HUMAN).//P39195
F-HEMBA1005909//HYPOTHETICAL 8.2 KD PROTEIN B0353.1 IN CHROMOSOME III.//0.98:19:52//CAENORHABDITIS ELEGANS.//Q10958
F-HEMBA1005911//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.9e-27:86:70//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1005921//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.3e-38:99:81//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1005931//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//2.3e-17:76:51//HOMO SAPIENS (HUMAN).//P51522
F-HEMBA1005934//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//0.024:54:40//HOMO SAPIENS (HUMAN).//P39189
F-HEMBA1005962
F-HEMBA1005963//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.7e-32:89:79//BOS TAURUS (BOVINE).//P53620
F-HEMBA1005990//HYPOTHETICAL BHLF1 PROTEIN.//3.0e-09:180:36//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
F-HEMBA1005991//HYPOTHETICAL PROTEIN KIAA0032.//3.0e-17:107:43//HOMO SAPIENS (HUMAN).//Q15034
F-HEMBA1005999
F-HEMBA1006002
F-HEMBA1006005//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).//0.0017:45:44//MUS MUSCULUS (MOUSE).//Q62267
F-HEMBA1006031//BASIC PROLINE-RICH PEPTIDE IB-1.//0.00016:84:39//HOMO SAPIENS (HUMAN).//P04281
F-HEMBA1006035//DNAK PROTEIN 1 (HEAT SHOCK PROTEIN 70) (HSP70).//0.43:100:27//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q55154
F-HEMBA1006036//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//6.2e-64:150:74//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1006042
F-HEMBA1006067//METALLOTHICNEIN A (MT-A).//0.86:34:41//THERMARCES CERBERUS.//P52721
F-HEMBA1006081
F-HEMBA1006090//SODIUM/GLUCOSE COTRANSPORTER 3 (NA(+)/GLUCOSE COTRANSPORTER 3) (LOW AFFINITY SODIUM-GLUCOSE COTRANSPORTER).//0.87:35:54//SUS SCROFA (PIG).//P31636
F-HEMBA1006091//EARLY NODULIN 20 PRECURSOR (N-20).//0.027:87:32//MEDICAGO TRUNCATULA (BARREL MEDIC).//P93329
F-HEMBA1006100//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//8.1e-09:58:60//HOMO SAPIENS (HUMAN).//P39195
F-HEMBA1006108//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//5.6e-16:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867
F-HEMBA1006121//HOMEOBOX PROTEIN CDX-1 (CAUDAL-TYPE HOMEOBOX PROTEIN 1).//3.4e-05:106:37//HOMO SAPIENS (HUMAN).//P47902
F-HEMBA1006124//50S RIBOSOMAL PROTEIN L33.//1.0:12:83//BACILLUS STEAROTHERMOPHILUS.//P23375
F-HEMBA1006130//SEL-10 PROTEIN.//7.7e-05:129:28//CAENORHABDITIS ELEGANS.//Q93794
F-HEMBA1006138//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//7.8e-13:41:73//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1006142//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//2.3e-39:101:77//HOMO SAPIENS (HUMAN).//P39192
F-HEMBA1006155//GENE 33 POLYPEPTIDE.//0.21:70:31//RATTUS NORVEGICUS (RAT).//P05432

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F-HEMBA1006158
F-HEMBA1006173//PROTEIN-TYROSINE PHOSPHATASE STRIATUM-ENRICHED (EC 3.1.3.48) (STEP) (NEURAL-SPECIFIC PROTEIN-TYROSINE PHOSPHATASE) (FRAGMENT).//0.017:20:95//HOMO SAPIENS (HUMAN).//P54829
F-HEMBA1006182//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.37:31:61//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1006198//HOMEOBOX PROTEIN HOX-B3 (HOX-2.7) (MH-23).//0.85:61:29//MUS MUSCULUS (MOUSE).//P09026
F-HEMBA1006235//50S RIBOSOMAL PROTEIN L33.//1.0:26:38//AQUIFEX AEOLICUS.//O67756
F-HEMBA1006248//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.0041:64:37//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
F-HEMBA1006252//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR DE-3.//1.0:22:40//DOLICHOS AXILLARIS (MACROTYLOMA AXILLARE).//P01057
F-HEMBA1006253//DISINTEGRIN ERISTICOPHIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).//0.95:19:47//ERISTOCOPHIS MACMAHONI (LEAF-NOSED VIPER).//P22826
F-HEMBA1006259
F-HEMBA1006268//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//7.0e-05:32:65//HOMO SAPIENS (HUMAN).//P39192
F-HEMBA1006272//RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 2).//4.8e-112:248:78//HOMO SAPIENS (HUMAN).//P10264
F-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE) (FRAGMENT).//2.5e-71:164:75//HOMO SAPIENS (HUMAN).//P51003
F-HEMBA1006283//50S RIBOSOMAL PROTEIN L32.//0.81:27:44//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P80339
F-HEMBA1006284//CUTICLE COLLAGEN 2.//0.36:42:40//CAENORHABDITIS ELEGANS.//P17656
F-HEMBA1006291//HYPOTHETICAL 43.3 KD PROTEIN IN EVGS-GLK INTERGENIC REGION.//2.4e-37:143:31//ESCHERICHIA COLI.//P76518
F-HEMBA1006293//MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR.//0.20:134:29//RATTUS NORVEGICUS (RAT).//Q63345 F-HEMBA1006309//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION.//2.1e-43:187:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38821
F-HEMBA1006310//SIGNAL TRANSDUCER CD24 PRECURSOR (HEAT STABLE ANTIGEN) (HSA) (NECTADRIN).//0.71:46:39//RATTUS NORVEGICUS (RAT).//Q07490
F-HEMBA1006328//RNA POLYMERASE ALPHA SUBUNIT (EC 2.7.7.48) (NUCLEOCAPSID PHOSPHOPROTEIN).//0.44:141:24//HUMAN PARAINFLUENZA 1 VIRUS (STRAIN CI-5/73).//P32531
F-HEMBA1006334//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR AF1627.//0.98:26:46//ARCHAEOGLOBUS FULGIDUS.//028646
F-HEMBA1006344//EZRIN (P81) (CYTOVILLIN) (VILLIN-2).//8.8e-08:91:36//MUS MUSCULUS (MOUSE).//P26040
F-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//9.1e-48:149:50//DROSOPHILA MELANOGASTER (FRUIT FLY).//O2193
F-HEMBA1006349//METALLOTHIONEIN-LIKE PROTEIN 1.//0.015:59:33//CASUARINA GLAUCA (SWAMP OAK).//Q39511
F-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//6.8e-96:261:66//HOMO SAPIENS (HUMAN).//P28160
F-HEMBA1006364//PUTATIVE ENDONUCLEASE C1F12.06C (EC 3.1.-.-).//0.97:60:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10348
F-HEMBA1006377//EARLY NODULIN 20 PRECURSOR (N-20).//0.00023:110:35//MEDICAGO TRUNCATULA (BARREL MEDIC).//P93329
F-HEMBA1006380
F-HEMBA1006381//METALLOTHIONEIN-II.//1.0:26:38//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA).//P15114
F-HEMBA1006398//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.3e-26:123:52//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1006416
F-HEMBA1006419//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//1.2e-24:102:50//HOMO SAPIENS (HUMAN).//P39189
F-HEMBA1006421//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.1e-21:101:57//HOMO SAPIENS (HUMAN).//P39188

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F-HEMBA1006424//HYPOTHETICAL PROTEIN IORF1.//0.85:55:30//BOVINE CORONAVIRUS (STRAIN MEBUS), AND BOVINE CORONAVIRUS (STRAIN QUEBEC).//P22053
F-HEMBA1006426//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.8e-36:78:74//HOMO SAPIENS (HUMAN).//P39195
F-HEMBA1006438//HYPOTHETICAL 8.1 KD PROTEIN (ORF65).//1.0:38:36//GUILLARDIA THETA (CRYPTOMONAS PHI).//O78421
F-HEMBA1006445//RAS-LIKE PROTEIN 3.//1.9e-06:40:47//RHIZOMUCOR RACEMOSUS (MUCOR CIRCINELLOIDES F. LUSITANICUS).//P22280
F-HEMBA1006446
F-HEMBA1006461//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//4.1e-18:68:67//HOMO SAPIENS (HUMAN).//P39192
F-HEMBA1006467
F-HEMBA1006471
F-HEMBA1006474//40 KD PROTEIN.//1.1e-37:231:38//BORNA DISEASE VIRUS (BDV).//Q01552
F-HEMBA1006483//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//6.1e-38:77:74//HOMO SAPIENS (HUMAN).//P39192
F-HEMBA1006485//HYPOTHETICAL 9.3 KD PROTEIN IN NAD3-NAD7 INTERGENIC REGION (ORF 79).//0.91:30:40//MARCHANTIA POLYMORPHA (LIVERWORT).//P38465
F-HEMBA1006486//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.1e-12:78:51//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1006489//FUN34 PROTEIN.//0.94:58:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32907
F-HEMBA1006492//NADH-UBIQUINONE OXIDOREDUCTASE MWFE SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-MWFE) (CI-MWFE).//0.87:44:36//HOMO SAPIENS (HUMAN).//O15239
F-HEMBA1006494//FERREDOXIN-LIKE PROTEIN IN NIF REGION.//0.11:46:26//RHIZOBIUM LEGUMINOSARUM (BIOVAR TRIFOLII).//P42711
F-HEMBA1006497
F-HEMBA1006502//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.15:26:73//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1006507//DIAPHANOUS PROTEIN.//0.0055:129:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48608
F-HEMBA1006521//3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE).//1.1e-32:177:41//ESCHERICHIA COLI.//P25716
F-HEMBA1006530//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.052:84:26//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//P15583
F-HEMBA1006535//INHIBITOR OF APOPTOSIS PROTEIN 1 (MIAP1) (MIAP-1).//6.6e-05:53:39//MUS MUSCULUS (MOUSE).//O08863
F-HEMBA1006540//PRESYNAPTIC PROTEIN SAP97 (SYNAPSE-ASSOCIATED PROTEIN 97) (DISCS, LARGE HOMOLOG 1).//2.1e-07:206:23//RATTUS NORVEGICUS (RAT).//Q62696
F-HEMBA1006546//PROBABLE E5 PROTEIN.//0.11:70:32//HUMAN PAPILLOMAVIRUS TYPE 51.//P26553
F-HEMBA1006559//SUPPRESSOR PROTEIN SRP40.//0.015:221:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
F-HEMBA1006562//SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S).//1.5e-07:122:33//HOMO SAPIENS (HUMAN).//P10163
F-HEMBA1006566//CELL DIVISION PROTEIN KINASE 2 (EC 2.7.1.-) (CDC2 HOMOLOG EG1 PROTEIN KINASE).//0.63:53:37//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P23437
F-HEMBA1006569//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//4.4e-06:88:39//BOS TAURUS (BOVINE).//P02465
F-HEMBA1006579
F-HEMBA1006583//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.011:61:40//MUS MUSCULUS (MOUSE).//P05142
F-HEMBA1006595//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//5.6e-34:93:77//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1006597//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.9e-26:75:74//HOMO SAPIENS (HUMAN).//P39195
F-HEMBA1006612//SUPPRESSOR PROTEIN SRP40.//0.026:221:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
F-HEMBA1006617//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//6.6e-20:73:63//HOMO SAPIENS (HUMAN).//

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P39188
F-HEMBA1006624//HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION.//2.6e-31:209:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40506
F-HEMBA1006631//HYPOTHETICAL 62.8 KD PROTEIN IN TAF145-YOR1 INTERGENIC REGION.//1.5e-15:131:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53331
F-HEMBA1006635
F-HEMBA1006639//POLYADENYLATE-BINDING PROTEIN 1 (POLY(A) BINDING PROTEIN 1) (PABP 1).//2.2e-11:48:75//MUS MUSCULUS (MOUSE).//P29341
F-HEMBA1006643//LONG NEUROTOXIN CR1 PRECURSOR (KAPPA NEUROTOXIN).//0.28:48:27//BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT).//P15817
F-HEMBA1006648//ZINC FINGER PROTEIN 12 (ZINC FINGER PROTEIN KOX3) (FRAGMENT).//0.26:17:47//HOMO SAPIENS (HUMAN).//P17014
F-HEMBA1006652//60S RIBOSOMAL PROTEIN L7.//2.4e-44:206:47//MUS MUSCULUS (MOUSE).//P14148
F-HEMBA1006653
F-HEMBA1006659
F-HEMBA1006665//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.018:43:58//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1006674//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//2.9e-05:154:33//HOMO SAPIENS (HUMAN).//O00268
F-HEMBA1006676//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//3.6e-09:52:51//OWENIA FUSIFORMIS.//P21260
F-HEMBA1006682
F-HEMBA1006695//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.1e-06:35:65//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1006696
F-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMC1-TFG2 INTERGENIC REGION.//3.4e-19:104:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53196
F-HEMBA1006709//RETINOIC ACID RECEPTOR RXR-BETA.//0.24:111:36//HOMO SAPIENS (HUMAN).//P28702
F-HEMBA1006717
F-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//5.8e-09:111:40//HOMO SAPIENS (HUMAN).//Q01485
F-HEMBA1006744//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//1.8e-32:84:78//HOMO SAPIENS (HUMAN).//P39191
F-HEMBA1006754//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.3e-75:220:62//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1006758//VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VECADHERIN) (CADHERIN-5) (7B4 ANTIGEN) (CD144 ANTIGEN).//0.024:110:29//HOMO SAPIENS (HUMAN).//P33151
F-HEMBA1006767
F-HEMBA1006779//MITOCHONDRIAL RIBOSOMAL PROTEIN S12.//0.67:19:42//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//Q34940
F-HEMBA1006780
F-HEMBA1006789//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.056:98:30//MUS MUSCULUS (MOUSE).//P05143
F-HEMBA1006795//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.9e-11:143:30//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
F-HEMBA1006796//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).//0.16:38:42//MUS MUSCULUS (MOUSE).//P70315
F-HEMBA1006807//HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMOSOME III.//4.4e-75:184:77//CAENORHABDITIS ELEGANS.//P34568
F-HEMBA1006821//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//0.011:20:85//HOMO SAPIENS (HUMAN).//P39194
F-HEMBA1006824//PROTEIN B11.//0.44:27:44//VACCINIA VIRUS (STRAIN WR).//Q01229
F-HEMBA1006832//HYPOTHETICAL 34.6 KD PROTEIN C13G5.2 IN CHROMOSOME III.//1.0:46:36//CAENORHABDITIS ELEGANS.//P34327
F-HEMBA1006849
F-HEMBA1006865//ACROSIN INHIBITORS IIA AND IIB (BUSI-II).//1.0:41:31//BOS TAURUS (BOVINE).//P01001
F-HEMBA1006877//OXYSTEROL-BINDING PROTEIN.//3.7e-26:239:36//ORYCTOLAGUS CUNICULUS (RAB-

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BIT).//P16258
F-HEMBA1006885//HYPOTHETICAL 27.2 KD PROTEIN F09E5.8 IN CHROMOSOME II.//4.5e-38:185:43//CAENORHABDITIS ELEGANS.//P52057
F-HEMBA1006900
F-HEMBA1006914//UBIQUITIN-ACTIVATING ENZYME E1-LIKE (POLYMERASE-INTERACTING PROTEIN 2).//5.2e-27:269:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P52488
F-HEMBA1006921//CYTOTOXIN 3 (COMPONENT 3.20).//0.99:32:37//NAJA MELANOLEUCA (FOREST COBRA) (BLACK-LIPPED COBRA).//P01473
F-HEMBA1006926//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//0.0024:148:33//RATTUS NORVEGICUS (RAT).//P54258
F-HEMBA1006929//HYPOTHETICAL PROTEIN MJ0525.//0.95:35:20//METHANOCOCCUS JANNASCHII.//Q57945
F-HEMBA1006936//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1 / PRP-3) (PRP-2/ PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C) [CONTAINS: PEPTIDE P-C].//0.074:116:31//HOMO SAPIENS (HUMAN).//P02810
F-HEMBA1006938
F-HEMBA1006941//THIOREDOXIN H-TYPE 1 (TRX-H1).//2.1e-13:90:33//NICOTIANA TABACUM (COMMON TOBACCO).//P29449
F-HEMBA1006949
F-HEMBA1006973//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.75:29:55//BOS TAURUS (BOVINE).//P25508
F-HEMBA1006976//CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (EC 2.4.99.-) (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALIII) (ALPHA 2,3-ST) (GAL-NAC6S) (STZ) (SIAT4-C) (SAT-3) (ST-4).//3.9c-108:117:95//HOMO SAPIENS (HUMAN).//Q11206
F-HEMBA1006993
F-HEMBA1006996//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70).//0.12:51:33//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779
F-HEMBA1007002//PLATELET GLYCOPROTEIN IX PRECURSOR (GPIX) (CD42A).//0.00096:60:33//HOMO SAPIENS (HUMAN).//P14770
F-HEMBA1007017//HYPOTHETICAL 7.2 KD PROTEIN IN CYAY-DAPF INTERGENIC REGION.//1.0:25:56//ESCHERICHIA COLI.//P39166
F-HEMBA1007018//DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (LIC57/59) (DYNEIN LIGHT CHAIN A) (DLC-A).//8.5e-120:278:80//GALLUS GALLUS (CHICKEN).//Q90828
F-HEMBA1007045//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//2.1e-12:158:29//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437
F-HEMBA1007051
F-HEMBA1007052//60S RIBOSOMAL PROTEIN L37-B (L35) (YP55).//0.94:37:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P51402
F-HEMBA1007062//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.93:55:29//RHINOCEROS UNICORNIS (GREATER INDIAN RHINOCEROS).//Q96063
F-HEMBA1007066//ECLOSION HORMONE PRECURSOR (ECDYSIS ACTIVATOR) (EH).//0.58:49:38//BOMBYX MORI (SILK MOTH).//P25331
F-HEMBA1007073//PUTATTVE SMALL MEMBRANE PROTEIN (ORF 4).//0.86:46:34//CANINE ENTERIC CORONAVIRUS (STRAIN INSAVC-1) (CCV).//P36696
F-HEMBA1007078//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//8.6e-29:56:67//HOMO SAPIENS (HUMAN).//P39193
F-HEMBA1007080//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.028:122:30//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437
F-HEMBA1007085//RTOA PROTEIN (RATIO-A).//7.4e-11:221:31//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P54681
F-HEMBA1007087//HYPOTHETICAL PROTEIN MJ0162.//3.3e-29:173:36//METHANOCOCCUS JANNASCHII.//Q57626
F-HEMBA1007112
F-HEMBA1007113
F-HEMBA1007121//INOSITOL POLYPHOSPHATE 1-PHOSPHATASE (EC 3.1.3.57) (IPP).//5.4e-07:90:28//HOMO SAPIENS (HUMAN).//P49441
F-HEMBA1007129//HIRUSTASIN.//0.88:37:32//HIRUDO MEDICINALIS (MEDICINAL LEECH) //P80302
F-HEMBA1007147//HYPOTHETICAL 12.0 KD PROTEIN IN DST1-HEM2 INTERGENIC REGION.//0.92:23:34//

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SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53182
F-HEMBA1007149//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//0.0078:17:70//ESCHERICHIA COLI.//P05834
F-HEMBA1007151//WDNM1 PROTEIN PRECURSOR.//0.25:45:37//MUS MUSCULUS (MOUSE).//Q62477
F-HEMBA1007174//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REGION.//6.9e-18:97:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160
F-HEMBA1007178//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!/9.8e-06:38:65//HOMO SAPIENS (HUMAN).//P39195
F-HEMBA1007194//GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM PRECURSOR (EC 1.1.1.49) (G6PD).//1.0:80:32//NICOTIANA TABACUM (COMMON TOBACCO).//Q43793
F-HEMBA1007203//PROTEIN A22.//1.0:115:26//VARIOLA VIRUS.//P33845
F-HEMBA1007206
F-HEMBA1007224//HYPOTHETICAL 35.7 KD PROTEIN C41C4.6 IN CHROMOSOME II.//2.4e-05:92:30//CAENORHABDITIS ELEGANS.//Q09275
F-HEMBA1007243//HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) (HGPRT) (HGPRTASE) (HPRT B).//3.1e-74:205:67//MUS MUSCULUS (MOUSE).//P00493
F-HEMBA1007251//VITELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN TU-4) (PROTEIN SV23).//0.52:108:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13238
F-HEMBA1007256
F-HEMBA1007267//CALICIN (FRAGMENT).//0.060:88:31//HOMO SAPIENS (HUMAN).//Q13939
F-HEMBA1007273//HYPOTHETICAL 8.1 KD PROTEIN (ORF65).//0.95:40:37//GUILLARDIA THETA (CRYPTOMONAS PHI).//O78421
F-HEMBA1007279//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.6e-24:98:64//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1007281
F-HEMBA1007288//HYPOTHETICAL 13.5 KD PROTEIN IN ZMS1-MNS1 INTERGENIC REGION.//0.88:11:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47162
F-HEMBA1007300//CGMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE (EC 3.1.4.17) (CGB-PDE).//2.7e-43:220:41//BOS TAURUS (BOVINE).//Q28156
F-HEMBA1007301//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//3.3e-22:115:33//HOMO SAPIENS (HUMAN).//P02461
F-HEMBA1007319
F-HEMBA1007320//HYPOTHETICAL 28.0 KD PROTEIN IN GLOB-RNHA INTERGENIC REGION.//1.0:48:37//ESCHERICHIA COLI.//P75672
F-HEMBA1007322//THREONINE DEHYDRATASE OPERON ACTIVATOR PROTEIN.//1.0:59:33//ESCHERICHIA COLI.//P11866
F-HEMBA1007327
F-HEMBA1007341//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//9.1e-12:37:62//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1007342//PROBABLE E5 PROTEIN.//0.89:96:29//PYGMY CHIMPANZEE PAPILLOMAVIRUS TYPE 1.//Q02268
F-HEMBA1007347//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2).//0.92:62:43//OVIS ARIES (SHEEP).//Q29400
F-HEMBB1000005//WEAK NEUROTOXIN 5.//0.98:30:33//NAJA NAJA (INDIAN COBRA).//P29179
F-HEMBB1000008//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.7e-35:73:84//HOMO SAPIENS (HUMAN).//P39195
F-HEMBB1000018//HYPOTHETICAL BHLF1 PROTEIN.//0.39:90:37//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
F-HEMBB1000024//VIRE LOCUS 9 KD VIRULENCE PROTEIN.//0.66:36:41//AGROBACTERIUM TUMEFACIENS.//P08061
F-HEMBB1000025//MUSCARINIC TOXIN ALPHA (MT-ALPHA).//0.46:32:40//DENDROASPIS POLYLEPIS POLYLEPIS (BLACK MAMBA).//P80494
F-HEMBB1000030//SUPPRESSOR PROTEIN SRP40.//6.7e-07:50:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
F-HEMBB1000036//HYPOTHETICAL 43.2 KD PROTEIN C34E10.1 IN CHROMOSOME III.//2.5e-07:120:29//CAENORHABDITIS ELEGANS.//P46576
F-HEMBB1000037//HYPOTHETICAL 59.9 KD PROTEIN-IN SGA1-KTR7 INTERGENIC REGION.//1.7e-05:71:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40492

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F-HEMBB1000039//VERY HYPOTHETICAL 11.9 KD PROTEIN C4H3.12C IN CHROMOSOME I.//1.0:61:21//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10219
F-HEMBB1000044
F-HEMBB1000048//HYPOTHETICAL 15.7 KD PROTEIN IN IDH-DEOR INTERGENIC REGION.//1.0:63:31//BACILLUS SUBTILIS.//P54942
F-HEMBB1000050//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//9.0e-14:34:79//HOMO SAPIENS (HUMAN).//P39194
F-HEMBB1000054//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//5.9e-31:45:73//HOMO SAPIENS (HUMAN).//P39193
F-HEMBB1000055//MUSCARINIC TOXIN ALPHA (MT-ALPHA).//1.0:14:57//DENDROASPIS POLYLEPIS POLYLEPIS (BLACK MAMBA).//P80494
F-HEMBB1000059//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.0e-21:82:59//HOMO SAPIENS (HUMAN).//P39195
F-HEMBB1000083//CHROMOGRANIN A PRECURSOR (CGA) [CONTAINS: PANCREASTATIN; BETA-GRANIN; WE-14].//0.87:172:28//RATTUS NORVEGICUS (RAT).//P10354
F-HEMBB1000089//HYPOTHETICAL 9.5 KD PROTEIN IN SPEA-METK INTERGENIC REGION (F83).//1.0:42:33//ESCHERICHIA COLI.//P46879
F-HEMBB1000099//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//7.7e-08:31:87//HOMO SAPIENS (HUMAN).//P39189
F-HEMBB1000103/LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.4e-38:136:58//HOMO SAPIENS (HUMAN).//P08547
F-HEMBB1000113//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.9e-13:57:64//HOMO SAPIENS (HUMAN).//P39188
F-HEMBB1000119//MAF PROTEIN.//3.6e-32:195:43//BACILLUS SUBTILIS.//Q02169
F-HEMBB1000136//HYPOTHETICAL 12.7 KD PROTEIN IN PCS60-ABD1 INTERGENIC REGION.//0.65:71:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38327
F-HEMBB1000141//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.00014:34:64//HOMO SAPIENS (HUMAN).//P20931
F-HEMBB1000144//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//2.0e-26:81:69//HOMO SAPIENS (HUMAN).//P39191
F-HEMBB1000173//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//9.2e-29:91:71//HOMO SAPIENS (HUMAN).//P39188
F-HEMBB1000175//ANTIMICROBIAL PEPTIDE ENAP-1 (FRAGMENT).//0.97:41:36//EQUUS CABALLUS (HORSE).//P80930
F-HEMBB1000198//HYPOTHETICAL 7.7 KD PROTEIN YCF33 (ORF67).//0.91:21:52//PORPHYRA PURPUREA.//P51329
F-HEMBB1000215//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//3.4e-08:39:76//HOMO SAPIENS (HUMAN).//P39192
F-HEMBB1000217//DNA DAMAGE TOLERANCE PROTEIN RHC31 (RAD31 HOMOLOG).//2.9e-32:174:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06624
F-HEMBB1000218//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.73:31:38//MICROTUS PENNSYLVANICUS (MEADOW VOLE).//P24949
F-HEMBB1000226//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//6.5e-26:191:34//CAENORHABDITIS ELEGANS.//Q09217
F-HEMBB1000240
F-HEMBB1000244//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.9e-05:44:61//HOMO SAPIENS (HUMAN).//P39188
F-HEMBB1000250
F-HEMBB1000258
F-HEMBB1000264//CUTICLE COLLAGEN SQT-1.//0.15:89:33//CAENORHABDITIS ELEGANS.//P12114
F-HEMBB1000266//TRANSLATION INITIATION FACTOR IF-2.//2.7e-06:167:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39730
F-HEMBB1000272//CYTOCHROME C OXIDASE POLYPEPTIDE VIB (EC 1.9.3.1) (AED).//0.75:30:43//BOS TAURUS (BOVINE).//P00429
F-HEMBB1000274//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).//1.0:38:36//SUS SCROFA (PIG).//P35323
F-HEMBB1000284//CALTRIN (CALCIUM TRANSPORT INHIBITOR).//1.0:56:30//MUS MUSCULUS (MOUSE).//Q09098

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F-HEMBB1000307
F-HEMBB1000312
F-HEMBB1000317//THROMBOSPONDIN 1 PRECURSOR.//3.2e-32:135:43//HOMO SAPIENS (HUMAN).//P07996
F-HEMBB1000318//PUTATIVE SMALL MEMBRANE PROTEIN (NONSTRUCTURAL PROTEIN NS3) (NONSTRUCTURAL 9.5 KD PROTEIN).//0.41:51:31//HUMAN CORONAVIRUS (STRAIN OC43).//Q04854
F-HEMBB1000335//ZINC FINGER PROTEIN 13 (ZFP-13) (KROX-8 PROTEIN) (FRAGMENT).//0.82:33:45//MUS MUSCULUS (MOUSE).//P10754
F-HEMBB1000336//ALDEHYDE OXIDASE (EC 1.2.3.1) (FRAGMENTS).//0.80:44:40//ORYCTOLAGUS CUNICULUS (RABBIT).//P80456
F-HEMBB1000337//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//0.94:118:22//HOMO SAPIENS (HUMAN).//Q08170
F-HEMBB1000338//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.042:33:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01642
F-HEMBB1000339//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.2e-14:54:55//HOMO SAPIENS (HUMAN).//P39188
F-HEMBB1000341//GENE 74 PROTEIN (GP74).//1.0:39:33//MYCOBACTERIOPHAGE L5.//Q05289
F-HEMBB1000343
F-HEMBB1000354//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.1e-15:83:56//HOMO SAPIENS (HUMAN).//P39188
F-HEMBB1000369//PROTEIN Q300.//0.99:27:40//MUS MUSCULUS (MOUSE).//Q02722
F-HEMBB1000374//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//4.7e-34:56:78//HOMO SAPIENS (HUMAN).//P39189
F-HEMBB1000376
F-HEMBB1000391//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.0013:79:35//BOS TAURUS (BOVINE).//P25508
F-HEMBB1000399//CHECKPOINT PROTEIN RAD17.//2.8e-15:187:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P50531
F-HEMBB1000402//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.027:60:38//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//P15583
F-HEMBB1000404//CYANELLE 50S RIBOSOMAL PROTEIN L28.//0.94:29:27//CYANOPHORA PARADOXA.//P48129
F-HEMBB1000420//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//0.023:97:35//HOMO SAPIENS (HUMAN).//Q15427
F-HEMBB1000434//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//4.8e-20:111:54//HOMO SAPIENS (HUMAN).//P39194
F-HEMBB1000438//HYPOTHETICAL 7.9 KD PROTEIN IN GP55-NRDG INTERGENIC REGION.//0.93:24:50//BACTERIOPHAGE T4.//P07076
F-HEMBB1000441//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.4e-23:85:70//HOMO SAPIENS (HUMAN).//P39188
F-HEMBB1000449//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.88:27:51//HOMO SAPIENS (HUMAN).//P39195
F-HEMBB1000455
F-HEMBB1000472
F-HEMBB1000480//PROTEIN STBC.//1.0:52:30//ESCHERICHIA COLI.//P11905
F-HEMBB1000487//SHORT NEUROTOXIN 1 (NEUROTOXIN ALPHA) (NEUROTOXIN II).//0.93:29:34//NAJA OXIANA (CENTRAL ASIAN COBRA) (OXUS COBRA).//P01427
F-HEMBB1000490//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.3e-16:50:80//HOMO SAPIENS (HUMAN).//P39195
F-HEMBB1000491
F-HEMBB1000493//3A PROTEIN.//1.0:51:35//AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN BEAUDETTE) (IBV).//P30237
F-HEMBB1000510//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.7e-27:132:45//HOMO SAPIENS (HUMAN).//P08547
F-HEMBB1000518//CYTOCHROME C OXIDASE POLYPEPTIDE III (EC 1.9.3.1).//0.021:47:40//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//P14546
F-HEMBB1000523
F-HEMBB1000530//COLLAGEN ALPHA 1(XIV) CHAIN PRECURSOR (UNDULIN).//9.8e-14:43:83//GALLUS

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GALLUS (CHICKEN).//P32018
F-HEMBB1000550//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3).//0.19:97:30//TRYPANOSOMA BRUCEI BRUCEI.//P04540
F-HEMBB1000554//MATERNAL B9.10 PROTEIN (P30 B9.10).//0.94:82:25//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P40744
F-HEMBB1000556//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.043:201:29//HOMO SAPIENS (HUMAN).//000268
F-HEMBB1000564//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:5:2:34//METRIDIUM SENILE (BROWN SEA ANEMONE) (FRILLED SEA ANEMONE).//O47493
F-HEMBB1000573//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//2.3e-10:52:73//HOMO SAPIENS (HUMAN).//P39191
F-HEMBB1000575//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//1.8e-26:76:76//HOMO SAPIENS (HUMAN).//P39192
F-HEMBB1000586//NADH-UBIQUINONE OXIDOREDUCTASE MLRQ SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-MLRQ) (CI-MLRQ).//0.74:23:52//HOMO SAPIENS (HUMAN).//O00483
F-HEMBB1000589//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//2.9e-25:61:75//HOMO SAPIENS (HUMAN).//P39193
F-HEMBB1000591//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:34:35//PETROMYZON MARINUS (SEA LAMPREY).//Q35537
F-HEMBB1000592//SMALL PROLINE-RICH PROTEIN 2-1.//0.0016:49:42//HOMO SAPIENS (HUMAN).//P35326
F-HEMBB1000593//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENTS).//0.0070:189:32//GALLUS GALLUS (CHICKEN).//P12105
F-HEMBB1000598//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.7e-10:110:41//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
F-HEMBB1000623//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III.//0.0022:98:28//CAENORHABDITIS ELEGANS.//P34284
F-HEMBB1000630
F-HEMBB1000631//ALPHA-2C-1 ADRENERGIC RECEPTOR (ALPHA-2C-1 ADRENOCEPTOR) (SUBTYPE C4).//8.8e-06:59:40//HOMO SAPIENS (HUMAN).//P18825
F-HEMBB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//7.3e-13:173:28//MUS MUSCULUS (MOUSE).//P27671
F-HEMBB1000637//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//4.6e-41:94:82//HOMO SAPIENS (HUMAN).//P39193
F-HEMBB1000638//INVOLUCRIN.//1.9e-06:144:29//HOMO SAPIENS (HUMAN).//P07476
F-HEMBB1000643//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//8.3e-30:77:76//HOMO SAPIENS (HUMAN).//P39195
F-HEMBB1000649//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//2.5e-37:58:81//HOMO SAPIENS (HUMAN).//P39189
F-HEMBB1000652//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//2.2e-37:61:77//HOMO SAPIENS (HUMAN).//P39193
F-HEMBB1000665//HYPOTHETICAL PROTEIN BBD24.//0.83:38:36//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//P70845
F-HEMBB1000671//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.8e-51:74:71//HOMO SAPIENS (HUMAN).//P08547
F-HEMBB1000673//HEAT-STABLE ENTEROTOXIN A3/A4 PRECURSOR (STA3/STA4) (ST-IB) (ST-H).//0.012:37:37//ESCHERICHIA COLI.//P07965
F-HEMBB1000684//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//3.1e-21:66:72//HOMO SAPIENS (HUMAN).//P39193
F-HEMBB1000693//HUNTINGTIN ASSOCIATED PROTEIN 1 (HAP1).//5.2e-26:121:49//RATTUS NORVEGICUS (RAT).//P54256
F-HEMBB1000705
F-HEMBB1000706
F-HEMBB1000709//HYPOTHETICAL 5.8 KD PROTEIN.//1.0:29:44//CLOVER YELLOW MOSAIC VIRUS (CYMV).//P16485
F-HEMBB1000725//RAS-RELATED PROTEIN RAB-8B.//7.4e-105:205:98//RATTUS NORVEGICUS (RAT).//P70550
F-HEMBB1000726//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.4e-25:85:70//HOMO SAPIENS (HUMAN).//P39194

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F-HEMBB1000738//50S RIBOSOMAL PROTEIN L33.//1.0:41:31//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P35871
F-HEMBB1000749//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.3e-29:42:85//HOMO SAPIENS (HUMAN).//P39194
F-HEMBB1000763//NIFU PROTEIN.//0.089:63:36//FRANKIA ALNI.//P46045
F-HEMBB1000770//CALTRIN-LIKE PROTEIN II.//0.98:13:69//CAVIA PORCELLUS (GUINEA PIG).//P22075
F-HEMBB1000774//HIGH MOBILITY GROUP PROTEIN HMG-Y.//0.029:53:32//MUS MUSCULUS (MOUSE).//P17095
F-HEMBB1000781//MAPK/ERK KINASE KINASE 2 (EC 2.7.1.-) (MEK KINASE 2) (MEKK 2).//3.5e-75:144:98//MUS MUSCULUS (MOUSE).//Q61083
F-HEMBB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//2.6e-49:232:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39956
F-HEMBB1000790//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.9e-16:93:51//HOMO SAPIENS (HUMAN).//P39188
F-HEMBB1000794
F-HEMBB1000807//MUSCARINIC ACETYLCHOLINE RECEPTOR M3.//0.54:111:27//GALLUS GALLUS (CHICKEN).//P49578
F-HEMBB1000810
F-HEMBB1000821
F-HEMBB1000822//HYPOTHETICAL 10 KD PROTEIN (ORF 6).//0.10:50:34//NARCISSUS MOSAIC VIRUS (NMV).//P15099
F-HEMBB1000826//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.00025:73:39//HOMO SAPIENS (HUMAN).//P20931
F-HEMBB1000827//HYPOTHETICAL 7.4 KD PROTEIN.//0.89:23:52//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19302
F-HEMBB1000831//MALE SPECIFIC SPERM PROTEIN MST87F.//0.98:35:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175
F-HEMBB1000835//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.8e-31:96:46//HOMO SAPIENS (HUMAN).//P08547
F-HEMBB1000840//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.00012:102:36//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
F-HEMBB1000848//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.3e-97:239:70//HOMO SAPIENS (HUMAN).//P08547
F-HEMBB1000852
F-HEMBB1000870
F-HEMBB1000876//METALLOTHIONEIN (MT).//0.99:14:64//PERCA FLUVIATILIS (PERCH).//P52725
F-HEMBB1000883//HYPOTHETICAL 7.8 KD PROTEIN (ORF62).//0.34:60:33//GUILLARDIA THETA (CRYPTOMONAS PHI).//O78459
F-HEMBB1000887//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//1.0:26:42//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//Q48251
F-HEMBB1000888
F-HEMBB1000890
F-HEMBB1000893
F-HEMBB1000908//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.0074:45:51//HOMO SAPIENS (HUMAN).//P39188
F-HEMBB1000910//PROBABLE E5 PROTEIN.//1.0:49:36//HUMAN PAPILLOMAVIRUS TYPE 58.//P26552
F-HEMBB1000913//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.29:56:46//HOMO SAPIENS (HUMAN).//P39195
F-HEMBB1000915//CYTOCHROME B (EC 1.10.2.2).//2.5e-24:62:90//HOMO SAPIENS (HUMAN).//P00156
F-HEMBB1000917//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//5.9e-26:53:66//HOMO SAPIENS (HUMAN).//P39193
F-HEMBB1000927//NEURONAL CALCIUM SENSOR 1 (NCS-1) (FREQUENIN).//3.9e-44:182:45//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q91614
F-HEMBB1000947//SMALL PROLINE-RICH PROTEIN 2-1.//0.24:69:27//HOMO SAPIENS (HUMAN).//P35326
F-HEMBB1000959//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//3.0e-31:89:68//HOMO SAPIENS (HUMAN).//P39195
F-HEMBB1000973//CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.//0.96:66:36//BOS TAURUS (BOVINE).//018739

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F-HEMBB1000975//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR (HISTIDINE-PROLINE RICH GLYCOPROTEIN) (HPRG).//0.00042:77:41//HOMO SAPIENS (HUMAN).//P04196
F-HEMBB1000981
F-HEMBB1000985//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//1.0e-18:178:30//MUS MUSCULUS (MOUSE).//P28575
F-HEMBB1000991
F-HEMBB1000996//HYPOTHETICAL 10.1 KD PROTEIN IN RHSD-GCL INTERGENIC REGION (ORFD3).//0.58:34:35//ESCHERICHIA COLI.//P33669
F-HEMBB1001004//PROBABLE E4 PROTEIN.//0.24:110:35//HUMAN PAPILLOMAVIRUS TYPE 5B.//P26550
F-HEMBB1001008
F-HEMBB1001011//ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4) (ZINC FINGER PROTEIN HF.16).//3.2e-17:104:47//HOMO SAPIENS (HUMAN).//P17097
F-HEMBB1001014//EOTAXIN PRECURSOR (EOSINOPHIL CHEMOTACTIC PROTEIN).//1.0:58:39//RATTUS NORVEGICUS (RAT).//P97545
F-HEMBB1001020//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//1.4e-07:36:75//HOMO SAPIENS (HUMAN).//P39189
F-HEMBB1001024
F-HEMBB1001037//FERREDOXIN.//1.0:52:25//MOORELLA THERMOACETICA (CLOSTRIDIUM THERMOACETICUM).//P00203
F-HEMBB1001047
F-HEMBB1001051//PROTEIN FAN (FACTOR ASSOCIATED WITH N-SMASE ACTIVATION).//3.4e-21:50:100//HOMO SAPIENS (HUMAN).//Q92636
F-HEMBB1001056//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0099:115:35//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341
F-HEMBB1001058//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//1.1e-33:95:76//HOMO SAPIENS (HUMAN).//P39192
F-HEMBB1001060//HYPOTHETICAL 8.2 KD PROTEIN ZC21.7 IN CHROMOSOME III.//1.0:38:36//CAENORHABDITIS ELEGANS.//P34591
F-HEMBB1001063
F-HEMBB1001068
F-HEMBB1001096//NOXIUSTOXIN (NTX) (TOXIN II.11).//0.99:36:38//CENTRUROIDES NOXIUS (MEXICAN SCORPION).//P08815
F-HEMBB1001102//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//1.1e-27:115:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701
F-HEMBB1001105//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR.//0.80:70:40//HOMO SAPIENS (HUMAN).//P28067
F-HEMBB1001112//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.1e-126:287:85//RATTUS NORVEGICUS (RAT).//P38378
F-HEMBB1001114//HYPOTHETICAL 9.6 KD PROTEIN (ORF2).//0.84:62:27//BACTERIOPHAGE L2.//P42537
F-HEMBB1001117
F-HEMBB1001119//COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR.//1.6e-21:50:98//HOMO SAPIENS (HUMAN).//Q99715
F-HEMBB1001126//HYPOTHETICAL 55.9 KD PROTEIN EEED8.6 IN CHROMOSOME II.//1.7e-50:184:53//CAENORHABDITIS ELEGANS.//Q09296
F-HEMBB1001133//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//1.4e-09:53:62//HOMO SAPIENS (HUMAN).//P39192
F-HEMBB1001137//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//2.0e-05:206:27//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414
F-HEMBB1001142//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//4.1e-05:46:56//HOMO SAPIENS (HUMAN).//P39193
F-HEMBB1001151//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I.//2.3e-23:109:44//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10149
F-HEMBB1001153//PROCOLLAGEN ALPHA 2(IV) CHAIN PRECURSOR.//0.75:76:34//ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P27393
F-HEMBB1001169//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.4e-16:71:59//HOMO SAPIENS (HUMAN).//P39195
F-HEMBB1001175//ANKYRIN.//3.2e-12:169:31//MUS MUSCULUS (MOUSE).//Q02357
F-HEMBB1001177//PERIODIC TRYPTOPHAN PROTEIN 2 HOMOLOG.//9.4e-07:148:27//HOMO SAPIENS (HU-

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MAN).//Q15269
F-HEMBB1001182//HYPOTHETICAL 36.0 KD PROTEIN.//1.3e-09:110:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P54858
F-HEMBB1001199
F-HEMBB1001208//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.053:23:47//MUS MUSCULUS (MOUSE).//P15974
F-HEMBB1001209
F-HEMBB1001210//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.14:40:37//MUS MUSCULUS (MOUSE).//P15974
F-HEMBB1001218//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.4e-19:49:67//HOMO SAPIENS (HUMAN).//P39194
F-HEMBB1001221//CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-LIVER PRECURSOR (EC 1.9.3.1).//0.11:44:38//HOMO SAPIENS (HUMAN).//P14406
F-HEMBB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).//2.0e-45:192:53//MUS MUSCULUS (MOUSE).//P46938
F-HEMBB1001242//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN CHROMOSOME I.//5.5e-37:226:41//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09876
F-HEMBB1001249//OXALOACETATE DECARBOXYLASE GAMMA CHAIN (EC 4.1.1.3).//1.0:23:43//KLEBSIELLA PNEUMONIAE.//P13155
F-HEMBB1001253//METALLOTHIONEIN-IH (MT-1H) (METALLOTHIONEIN-0) (MT-0).//0.14:16:43//HOMO SAPIENS (HUMAN).//P80294
F-HEMBB1001254//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.4e-12:40:75//HOMO SAPIENS (HUMAN).//P39195
F-HEMBB1001267//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.0e-12:33:78//HOMO SAPIENS (HUMAN).//P39193
F-HEMBB1001271//HYPOTHETICAL 25.1 KD PROTEIN B0302.5 IN CHROMOSOME X.//1.0:58:37//CAENORHABDITIS ELEGANS.//Q10928
F-HEMBB1001282//ANKYRIN HOMOLOG PRECURSOR.//9.5e-13:206:31//CHROMATIUM VINOSUM.//Q06527
F-HEMBB1001288//COPPER HOMEOSTASIS PROTEIN CUTC.//4.6e-42:163:51//ESCHERICHIA COLI.//P46719
F-HEMBB1001289//HYPOTHETICAL PROTEIN ORF-1137.//1.0e-05:106:26//MUS MUSCULUS (MOUSE).//P11260
F-HEMBB1001294//GTP-BINDING PROTEIN TC10.//1.3e-34:58:94//HOMO SAPIENS (HUMAN).//P17081
F-HEMBB1001302//HOMEOBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEOBOX PROTEIN 2) (CDX-3).//0.24:49:46//HOMO SAPIENS (HUMAN).//Q99626
F-HEMBB1001304//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).//1.0:17:70//LYCOPERSICON ESCULENTUM (TOMATO).//Q01157
F-HEMBB1001314//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.21:104:27//DROSOPHILA ERECTA (FRUIT FLY).//P13730
F-HEMBB1001315//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.3e-24:53:71//HOMO SAPIENS (HUMAN).//P39195
F-HEMBB1001317//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//0.24:90:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09782
F-HEMBB1001326//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.36:26:50//MUS MUSCULUS (MOUSE).//P15974
F-HEMBB1001331//HYPOTHETICAL BHLF1 PROTEIN.//1.0:127:33//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
F-HEMBB1001335//ESCARGOT/SNAIL PROTEIN HOMOLOG (FRAGMENT).//0.85:44:29//SCIARA COPROPHILA (FUNGUS GNAT).//Q01799
F-HEMBB1001337//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//4.2e-20:62:62//HOMO SAPIENS (HUMAN).//P39194
F-HEMBB1001339//HYPOTHETICAL 17.3 KD PROTEIN CY1A11.16C.//8.2e-07:123:34//MYCOBACTERIUM TUBERCULOSIS.//Q50606
F-HEMBB1001346//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.2e-14:60:45//HOMO SAPIENS (HUMAN).//P08547
F-HEMBB1001348//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//5.6e-14:61:62//HOMO SAPIENS (HUMAN).//P39188
F-HEMBB1001356

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F-HEMBB1001364
F-HEMBB1001366/HISTIDINE-RICH PROTEIN.//0.87:26:42//PLASMODIUM FALCIPARUM (ISOLATE FCM17 / SENEGAL).//P14586
F-HEMBB1001367//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//8.6e-40:146:61//HOMO SAPIENS (HUMAN).//P39192
F-HEMBB1001369
F-HEMBB1001380//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!/1.9e-25:49:83//HOMO SAPIENS (HUMAN).//P39193
F-HEMBB1001384//BH3 INTERACTING DOMAIN DEATH AGONIST (BID).//0.80:95:29//MUS MUSCULUS (MOUSE).//P70444
F-HEMBB1001387//PEA2 PROTEIN (PPF2 PROTEIN).//0.022:117:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40091
F-HEMBB1001394//ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA A SUBUNIT).//0.38:85:31//MUS MUSCULUS (MOUSE).//P17426
F-HEMBB1001410
F-HEMBB1001424//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR.//0.99:37:21//ORYZA SATIVA (RICE).//P12162
F-HEMBB1001426//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.0035:40:60//HOMO SAPIENS (HUMAN).//P39195
F-HEMBB1001429//CYTOSOL AMINOPEPTIDASE (EC 3.4.11.1) (LEUCINE AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (EC 3.4.11.5) (PROLYL AMINOPEPTIDASE).//1.1e-99:21:86//BOS TAURUS (BOVINE).//P00727
F-HEMBB1001436//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//3.4e-30:57:78//HOMO SAPIENS (HUMAN).//P39195
F-HEMBB1001443//[PYRUVATE DEHYDROGENASE (LIPOAMIDE)]-PHOSPHATASE PRECURSOR (PDP) (EC 3.1.3.43) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SUBUNIT (PDPC).//2.5e-79:155:97//BOS TAURUS (BOVINE).//P35816
F-HEMBB1001449
F-HEMBB1001454//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//1.1e-05:196:31//HOMO SAPIENS (HUMAN).//P10161
F-HEMBB1001458//24 KD ANTIGEN (FRAGMENT).//0.94:18:50//PLASMODIUM CHABAUDI.//P14592
F-HEMBB1001463
F-HEMBB1001464//PPF2L ANTIGEN (FRAGMENT).//1.0:45:28//PLASMODIUM FALCIPARUM (ISOLATE PALO ALTO / UGANDA).//P07765
F-HEMBB1001482//GASTRULA ZINC FINGER PROTEIN XLCGF16.1 (FRAGMENT).//4.2e-10:37:43//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18712 F-HEMBB1001500
F-HEMBB1001521//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.4e-39:59:72//HOMO SAPIENS (HUMAN).//P39188
F-HEMBB1001527//HOMEOBOX PROTEIN HOX-B5 (XLHBOX-4) (XHOX-1B) (FRAGMENT).//0.21:131:25//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P09019
F-HEMBB1001531//GENE 32 PROTEIN (GP32).//0.88:95:30//MYCOBACTERIOPHAGE L5.//Q05241
F-HEMBB1001535//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:31:38//LUMBRICUS TERRESTRIS (COMMON EARTHWORM).//Q34942
F-HEMBB1001536
F-HEMBB1001537//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//0.0063:52:50//HOMO SAPIENS (HUMAN).//P39191
F-HEMBB1001555//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.9e-23:69:63//HOMO SAPIENS (HUMAN).//P39188
F-HEMBB1001562//RABPHILIN-3A.//0.087:147:27//RATTUS NORVEGICUS (RAT).//P47709
F-HEMBB1001564//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.9e-27:107:54//HOMO SAPIENS (HUMAN).//P08547
F-HEMBB1001565//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.9e-12:51:54//HOMO SAPIENS (HUMAN).//P39194
F-HEMBB1001585
F-HEMBB1001586
F-HEMBB1001588//HYPOTHETICAL 12.3 KD PROTEIN IN GAP1-NAP1 INTERGENIC REGION.//0.0031:31:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36140

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F-HEMBB1001603
F-HEMBB1001618//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE]//0.00076:47:44//MUS MUSCULUS (MOUSE)//P11369
F-HEMBB1001619//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//1.0:52:32//HOMO SAPIENS (HUMAN)//P22531
F-HEMBB1001630
F-HEMBB1001635//METALLOTHIONEIN-LIKE PROTEIN TYPE 2 A//1.0:27:44//LYCOPERSICON ESCULENTUM (TOMATO)//Q40157
F-HEMBB1001637//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.0042:26:73//HOMO SAPIENS (HUMAN)//P39188
F-HEMBB1001641
F-HEMBB1001653//SURVIVAL MOTOR NEURON PROTEIN 1//0.51:36:47//CANIS FAMILIARIS (DOG)//O02771
F-HEMBB1001665//HOMEOBOX PROTEIN ENGRAILED-1 (HU-EN-1)//0.0030:135:34//HOMO SAPIENS (HUMAN)//Q05925
F-HEMBB1001668//PROBABLE 60S RIBOSOMAL PROTEIN L39//0.99:25:44//CAENORHABDITIS ELEGANS//P52814
F-HEMBB1001673//HYPOTHETICAL 46.1 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION//0.0054:128:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38823.
F-HEMBB1001684//SUPPRESSOR PROTEIN SRP40//0.56:81:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32583
F-HEMBB1001685//CYTOCHROME C OXIDASE POLYPEPTIDE VIII-HEART PRECURSOR (EC 1.9.3.1) (VIIIB) (IX)//1.0:21:47//BOS TAURUS (BOVINE)//P10175
F-HEMBB1001695//MYOSIN IC HEAVY CHAIN//8.9e-05:86:40//ACANTHAMOEBA CASTELLANII (AMOEBA)//P10569
F-HEMBB1001704//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//9.0e-08:35:71//HOMO SAPIENS (HUMAN)//P39195
F-HEMBB1001706//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP)//0.91:39:41//SUS SCROFA (PIG)//P35323
F-HEMBB1001707//FERREDOXIN-LIKE PROTEIN IN NIF REGION//1.0:43:23//BRADYRHIZOBIUM JAPONICUM//P27394
F-HEMBB1001717//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3) (FRAGMENT)//1.0:71:25//LEMUR CATTA (RING-TAILED LEMUR)//Q34878
F-HEMBB1001735//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//9.0e-35:97:74//HOMO SAPIENS (HUMAN)//P39194
F-HEMBB1001736//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 BETA SUBUNIT (EIF-3 BETA) (EIF3 P116) (EIF3 P110)//0.00069:180:28//HOMO SAPIENS (HUMAN)//P55884
F-HEMBB1001747
F-HEMBB1001749//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.8e-43:75:70//HOMO SAPIENS (HUMAN)//P39195
F-HEMBB1001753//PROTEIN Q300//0.00091:16:81//MUS MUSCULUS (MOUSE)//Q02722
F-HEMBB1001756//CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 2 (XE-P9)//0.94:35:42//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//Q91879
F-HEMBB1001760
F-HEMBB1001762//GENE 35 PROTEIN (GP35)//0.76:21:47//MYCOBACTERIOPHAGE L5//Q05245
F-HEMBB1001785
F-HEMBB1001797//CHLOROPLAST 50S RIBOSOMAL PROTEIN L35//0.99:41:31//PORPHYRA PURPUREA//P51270
F-HEMBB1001802
F-HEMBB1001812//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//2.2e-39:54:77//HOMO SAPIENS (HUMAN)//P39193
F-HEMBB1001816//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.1e-19:97:57//HOMO SAPIENS (HUMAN)//P39194
F-HEMBB1001831//HYPOTHETICAL 45.6 KD PROTEIN IN COX5A-ALG11 INTERGENIC REGION//0.62:204:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53951
F-HEMBB1001834//GLYCINE-RICH RNA-BINDING PROTEIN 1 (FRAGMENT)//0.0014:40:45//SORGHUM VULGARE (SORGHUM)//Q99069
F-HEMBB1001836//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//7.1e-14:85:61//HOMO SAPIENS (HU-

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MAN).//P39191
F-HEMBB1001839//PROBABLE E4 PROTEIN.//0.61:49:34//HUMAN PAPILLOMAVIRUS TYPE 6C.//P20969
F-HEMBB1001850
F-HEMBB1001863//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.7e-30:57:68//HOMO SAPIENS (HUMAN).//P39194
F-HEMBB1001867
F-HEMBB1001868//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.00036:47:53//NICOTIANA TABACUM (COMMON TOBACCO).//P13983
F-HEMBB1001869//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//7.0e-11:95:45//HOMO SAPIENS (HUMAN).//P39188
F-HEMBB1001872//HYPOTHETICAL 8.2 KD PROTEIN IN LEF8-FP INTERGENIC REGION.//1.0:34:38//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41459
F-HEMBB1001874
F-HEMBB1001875
F-HEMBB1001880
F-HEMBB1001899//GENE 11 PROTEIN.//1.0:45:31//SPIROPLASMA VIRUS SPV1-R8A2 B.//P15902
F-HEMBB1001905//HYPOTHETICAL 81.7 KD PROTEIN IN MOL1-NAT2 INTERGENIC REGION.//8.8e-54:216:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48234
F-HEMBB1001906
F-HEMBB1001908//MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN.//6.3e-51:138:80//HOMO SAPIENS (HUMAN).//Q92794
F-HEMBB1001910
F-HEMBB1001911
F-HEMBB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E).//2.3e-27:71:70//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24574
F-HEMBB1001921//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.8e-13:75:53//HOMO SAPIENS (HUMAN).//P08547
F-HEMBB1001922
F-HEMBB1001925//EPITHELIAL MEMBRANE PROTEIN-1 (EMP-1) (TUMOR-ASSOCIATED MEMBRANE PROTEIN).//1.0:55:30//MUS MUSCULUS (MOUSE).//P47801
F-HEMBB1001930//HYPOTHETICAL 9.6 KD PROTEIN K10D2.7 IN CHROMOSOME III.//0.43:49:26//CAENORHABDITIS ELEGANS.//Q09412
F-HEMBB1001944//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//5.1e-34:63:85//HOMO SAPIENS (HUMAN).//P39189
F-HEMBB1001945//NONSPECIFIC LIPID-TRANSFER PROTEIN (LTP) (PHOSPHOLIPID TRANSFER PROTEIN) (PLTP).//0.28:45:40//AMARANTHUS CAUDATUS (LOVE-LIES-BLEEDING) (INCA-WHEAT).//P80450
F-HEMBB1001947//PROTEIN UL24.//0.48:42:47//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).//P10208
F-HEMBB1001950//HYPOTHETICAL 42.6 KD PROTEIN IN GSHB-ANSB INTERGENIC REGION (O378).//1.6e-24:162:36//ESCHERICHIA COLI.//P52062
F-HEMBB1001952
F-HEMBB1001953
F-HEMBB1001957//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.7e-11:51:60//HOMO SAPIENS (HUMAN).//P39188
F-HEMBB1001962//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//7.6e-24:163:42//HOMO SAPIENS (HUMAN).//P39188
F-HEMBB1001967//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//2.1e-35:55:80//HOMO SAPIENS (HUMAN).//P39189
F-HEMBB1001973//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//2.1e-37:108:75//HOMO SAPIENS (HUMAN).//P39192
F-HEMBB1001983//LYSIS PROTEIN (E PROTEIN) (GPE).//0.84:45:37//BACTERIOPHAGE ALPHA-3.//P31280
F-HEMBB1001988
F-HEMBB1001990
F-HEMBB1001996//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.4e-14:98:40//HOMO SAPIENS (HUMAN).//P08547
F-HEMBB1001997//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.1e-19:38:73//HOMO SAPIENS (HUMAN).//P39188
F-HEMBB1002002//CYTOCHROME C BIOGENESIS PROTEIN CCSA.//1.0:150:25//PORPHYRA PURPUREA.//

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P51369
F-HEMBB1002005//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//7.6e-12:94:40//HOMO SAPIENS (HUMAN).//P39195
F-HEMBB1002009
F-HEMBB1002015//HYPOTHETICAL 7.7 KD PROTEIN IN MRR-TSR INTERGENIC REGION (F67).//1.0:17:47//ESCHERICHIA COLI.//P39395
F-HEMBB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYPIVC1).//2.4e-50:139:55//BLABERUS DISCOIDALIS (TROPICAL COCKROACH).//P29981
F-HEMBB1002043//HYPOTHETICAL 9.5 KD PROTEIN IN DHFR 3'REGION (ORF3).//0.052:40:42//HERPESVIRUS SAIMIRI (SUBGROUP C / STRAIN 488).//P22577
F-HEMBB1002044//CELLULOSE COMPLEMENTING PROTEIN.//0.45:87:33//ACETOBACTER XYLINUM (ACETOBACTER PASTEURIANUS).//P37697
F-HEMBB1002045//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.78:18:55//HOMO SAPIENS (HUMAN).//P03928
F-HEMBB1002049
F-HEMBB1002050//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT).//1.0e-06:188:27//HOMO SAPIENS (HUMAN).//P02812
F-HEMBB1002068//HOMEOBOX PROTEIN HOX-A4 (CHOX-1.4).//0.0023:56:44//GALLUS GALLUS (CHICKEN).//P17277
F-HEMBB1002069//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.0074:134:33//NICOTIANA TABACUM (COMMON TOBACCO).//P13983
F-HEMBB1002092//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: OUTER MEMBRANE PROTEIN GP70; TRANSMEMBRANE PROTEIN P20E].//2.4e-07:75:40//BABOON ENDOGENOUS VIRUS (STRAIN M7).//P10269
F-HEMBB1002094//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//1.9e-24:63:82//HOMO SAPIENS (HUMAN).//P39191
F-HEMBB1002115//EC PROTEIN HOMOLOG (ZINC-METALLOTHIONEIN CLASS II).//0.94:26:42//ZEA MAYS (MAIZE).//P43401
F-HEMBB1002134//ZINC-FINGER PROTEIN NEURO-D4.//4.6e-57:176:67//RATTUS NORVEGICUS (RAT).//P56163
F-HEMBB1002139//CHLOROPLAST 50S RIBOSOMAL PROTEIN L35.//1.0:17:52//PORPHYRA PURPUREA.//P51270
F-HEMBB1002142//EARLY NODULIN 20 PRECURSOR (N-20).//0.087:52:36//MEDICAGO TRUNCATULA (BARREL MEDIC).//P93329
F-HEMBB1002152//HYPOTHETICAL 12.3 KD PROTEIN IN RPL3-RPL33 INTERGENIC REGION (ORF102).//5.8e-05:61:37//CYANOPHORA PARADOXA.//P15811
F-HEMBB1002189//HYPOTHETICAL PROTEIN UL125.//1.0:77:32//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16835
F-HEMBB1002190
F-HEMBB1002193//TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-PROTEIN KINASE DTK).//1.2e-27:59:100//HOMO SAPIENS (HUMAN).//Q06418
F-HEMBB1002217//ZINC FINGER PROTEIN 184 (FRAGMENT).//6.6e-22:106:50//HOMO SAPIENS (HUMAN).//Q99676
F-HEMBB1002218//PROTEIN Q300.//0.85:19:52//MUS MUSCULUS (MOUSE).//Q02722
F-HEMBB1002232//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//9.6e-21:56:71//HOMO SAPIENS (HUMAN).//P39195
F-HEMBB1002247
F-HEMBB1002249//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//7.2e-29:93:69//HOMO SAPIENS (HUMAN).//P39194
F-HEMBB002254//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.0e-29:101:67//HOMO SAPIENS (HUMAN).//P39194
F-HEMBB1002255//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).//1.0:73:28//PARAMECIUM TETRAURELIA.//P15579
F-HEMBB1002266//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//0.0079:151:26//PLASMODIUM FALCIPARUM (ISOLATE FC27 / PAPUA NEW GUINEA).//P13816
F-HEMBB1002280//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.2e-15:182:36//NYCTICEBUS COUCANG (SLOW LORIS).//P08548

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F-HEMBB1002300
F-HEMBB1002306//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.00011:26:84//HOMO SAPIENS (HUMAN).//P39195
F-HEMBB1002327//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//4.1e-11:41:85//HOMO SAPIENS (HUMAN).//P39189
F-HEMBB1002329//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION.//9.9e-17:232:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032
F-HEMBB1002340
F-HEMBB1002342//HYPOTHETICAL 32.5 KD PROTEIN IN MSH6-BMH2 INTERGENIC REGION.//3.6e-40:102:57//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03835
F-HEMBB1002358//THYMIDYLATE KINASE (EC 2.7.4.9) (DTMP KINASE).//6.1e-30:63:96//HOMO SAPIENS (HUMAN).//P23919
F-HEMBB1002359//HYPOTHETICAL 7.1 KD PROTEIN C6G9.01C IN CHROMOSOME I.//0.97:28:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q92346
F-HEMBB1002364//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT).//0.47:119:25//HOMO SAPIENS (HUMAN).//P12895
F-HEMBB1002371//HYPOTHETICAL 15.5 KD PROTEIN C2F7.12 IN CHROMOSOME I PRECURSOR.//3.0e-05:111:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09703
F-HEMBB1002381//PUTATIVE CUTICLE COLLAGEN C09G5.4.//0.34:105:34//CAENORHABDITIS ELEGANS.//Q09455
F-HEMBB1002383//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.049:103:32//AQUIFEX AEOLICUS.//066566
F-HEMBB1002387//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) (HEAT SHOCK PROTEIN 11).//0.18:75:28//RICKETTSIA TSUTSUGAMUSHI.//P16626
F-HEMBB1002409//HIGH MOBILITY GROUP PROTEIN HMG-Y.//0.014:61:36//MUS MUSCULUS (MOUSE).//P17095
F-HEMBB1002415
F-HEMBB1002425//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.8e-18:55:70//HOMO SAPIENS (HUMAN).//P39194
F-HEMBB1002442//LIN-10 PROTEIN.//5.1e-15:121:31//CAENORHABDITIS ELEGANS.//P34692
F-HEMBB1002453//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//1.2e-32:54:75//HOMO SAPIENS (HUMAN).//P39189
F-HEMBB1002457//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.5e-07:31:64//HOMO SAPIENS (HUMAN).//P39188
F-HEMBB1002458//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.92:28:53//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01642
F-HEMBB1002477//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//0.0066:198:27//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414
F-HEMBB1002489//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//0.030:182:28//HOMO SAPIENS (HUMAN).//Q15427
F-HEMBB1002492
F-HEMBB1002495//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//2.1e-08:41:75//HOMO SAPIENS (HUMAN).//P39192
F-HEMBB1002502//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT).//0.00030:31:77//HOMO SAPIENS (HUMAN).//P12895
F-HEMBB1002509
F-HEMBB1002510
F-HEMBB1002520//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.8e-36:162:50//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
F-HEMBB1002522//7 KD PROTEIN (ORF 4).//0.77:32:40//CHRYSANTHEMUM VIRUS B (CVB).//P37990
F-HEMBB1002531
F-HEMBB1002534//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//3.1e-36:80:73//HOMO SAPIENS (HUMAN).//P39195
F-HEMBB1002545
F-HEMBB1002550//HOMEOBOX PROTEIN HOX-D11 (HOX-4.6) (HOX-5.5).//3.8e-05:83:34//MUS MUSCULUS (MOUSE).//P23813
F-HEMBB1002556
F-HEMBB1002579//SPLICING FACTOR U2AF 35 KD SUBUNIT (U2 AUXILIARY FACTOR 35 KD SUBUNIT) (U2

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SNRNP AUXILIARY FACTOR SMALL SUBUNIT) (FRAGMENT).//5.0e-06:27:77//SUS SCROFA (PIG).//Q29350
F-HEMBB1002582//PROTEINASE INHIBITOR.//1.0:27:40//SOLANUM MELONGENA (EGGPLANT) (AUBERGINE).//P01078
F-HEMBB1002590//HYPOTHETICAL PROTEIN IN MMSB 3'REGION (ORF1) (FRAGMENT).//1.9e-20:90:54//PSEUDOMONAS AERUGINOSA.//P28812
F-HEMBB1002596
F-HEMBB1002600//NOVEL ANTIGEN 2 (NAG-2).//1.9e-60:187:59//HOMO SAPIENS (HUMAN).//O14817
F-HEMBB1002601//M PROTEIN, SEROTYPE 6 PRECURSOR.//1.0:71:35//STREPTOCOCCUS PYOGENES.//P08089
F-HEMBB1002603
F-HEMBB1002607//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.0032:142:33//HOMO SAPIENS (HUMAN).//P10162
F-HEMBB1002610//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.0e-11:79:49//HOMO SAPIENS (HUMAN).//P08547
F-HEMBB1002613//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.9e-08:41:60//HOMO SAPIENS (HUMAN).//P39188
F-HEMBB1002614//HYPOTHETICAL 9.5 KD PROTEIN.//1.0:40:35//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20553
F-HEMBB1002617//INSECT TOXIN 1 (BOT IT1).//1.0:44:29//BUTHUS OCCITANUS TUNETANUS (COMMON EUROPEAN SCORPION).//P55902
F-HEMBB1002623//HYPOTHETICAL 9.7 KD PROTEIN (ORF88) (PUTATIVE DNA-BINDING PROTEIN).//0.42:31:54//BACTERIOPHAGE P4.//P12552
F-HEMBB1002635//STRESS-ACTIVATED PROTEIN KINASE JNK3 (EC 2.7.1.-) (C-JUN N-TERMINAL KINASE 3) (MAP KINASE P49 3F12).//6.2e-17:44:95//HOMO SAPIENS (HUMAN).//P53779
F-HEMBB1002664//SMALL NUCLEAR RIBONUCLEOPROTEIN ASSOCIATED PROTEIN B (SM-B) (SNRNP-B) (SM11) (FRAGMENT).//1.0:57:36//RATTUS NORVEGICUS (RAT).//P17136
F-HEMBB1002677//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.9e-06:194:34//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
F-HEMBB1002683//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.96:56:35//LEMUR CATTA (RING-TAILED LEMUR).//Q34879
F-HEMBB1002684//SILLUCIN.//1.0:16:50//RHIZOMUCOR PUSILLUS.//P02885
F-HEMBB1002686
F-HEMBB1002692
F-HEMBB1002697//HELIX-DESTABILIZING PROTEIN (SINGLE-STRANDED DNA BINDING PROTEIN) (GPV).//0.57:36:38//BACTERIOPHAGE FD, BACTERIOPHAGE F1, AND BACTERIOPHAGE M13.//P03669
F-HEMBB1002699
F-HEMBB1002702
F-HEMBB1002705//HYPOTHETICAL 34.8 KD PROTEIN C4H3.04C IN CHROMOSOME I.//3.6e-40:180:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10212
F-HEMBB1002712
F-MAMMA1000009//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//1.2e-32:95:75//HOMO SAPIENS (HUMAN).//P39189
F-MAMMA1000019
F-MAMMA1000020//DIMETHYLANILINE MONOOXYGENASE [N-OXIDE FORMING] 5 (EC 1.14.13.8) (HEPATIC FLAVIN-CONTAINING MONOOXYGENASE 5) (FMO 5) (DIMETHYLANILINE OXIDASE 5).//5.2e-12:24:100//HOMO SAPIENS (HUMAN).//P49326
F-MAMMA1000025//BETA-2-MICROGLOBULIN PRECURSOR.//1.0:73:26//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q04475
F-MAMMA1000043//HYPOTHETICAL PXBL-I PROTEIN (FRAGMENT).//0.057:130:31//BOVINE LEUKEMIA VIRUS (JAPANESE ISOLATE BLV-1) (BLV).//P03412
F-MAMMA1000045
F-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//7.5e-44:138:55//MUS MUSCULUS (MOUSE).//P47226
F-MAMMA1000057//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.2e-39:92:69//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1000069//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0044:96:34//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341
F-MAMMA1000084//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//5.4e-28:94:73//HOMO SAPIENS (HU-

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MAN).//P39195
F-MAMMA1000085//PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.16) (CYSTEINE--TRNA LIGASE) (CYSRS).//6.6e-38:90:51//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09860
F-MAMMA1000092//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//6.4e-30:43:86//HOMO SAPIENS (HUMAN).//P39192
F-MAMMA1000103//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.038:17:52//HOMO SAPIENS (HUMAN).//P22531
F-MAMMA1000117//50S RIBOSOMAL PROTEIN L24E (HL21/HL22).//0.90:25:48//HALOARCULA MARISMORTUI (HALOBACTERIUM MARISMORTUI).//P14116
F-MAMMA1000129//HYPOTHETICAL BHLF1 PROTEIN.//0.0016:75:40//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
F-MAMMA1000133
F-MAMMA1000134//HYPOTHETICAL PROTEIN MJ0647.//1.0:41:41//METHANOCOCCUS JANNASCHII.//Q58063
F-MAMMA1000139//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-3 SUBUNIT.//0.99:69:28//BOS TAURUS (BOVINE), AND MUS MUSCULUS (MOUSE).//P29798
F-MAMMA1000143//CALPAIN INHIBITOR (CALPASTATIN) (FRAGMENT).//0.023:111:27//MUS MUSCULUS (MOUSE).//P51125
F-MAMMA1000155//PUTATIVE CUTICLE COLLAGEN C09G5.5.//0.018:125:34//CAENORHABDITIS ELEGANS.//Q09456
F-MAMMA1000163//MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR (PERIPLASMIC MERCURY ION BINDING PROTEIN) (MERCURY SCAVENGER PROTEIN).//0.11:88:25//SHEWANELLA PUTREFACIENS (PSEUDOMONAS PUTREFACIENS).//Q54463
F-MAMMA1000171
F-MAMMA1000173//DREBRIN E.//7.6e-41:197:43//HOMO SAPIENS (HUMAN).//Q16643
F-MAMMA1000175//GAMMA-THIONIN HOMOLOG PPT PRECURSOR.//0.92:39:38//PETUNIA INTEGRIFOLIA (VIOLET-FLOWERED PETUNIA) (PETUNIA INFLATA).//Q40901
F-MAMMA1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.4e-106:249:61//HOMO SAPIENS (HUMAN).//P51523
F-MAMMA1000198//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.0014:35:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645
F-MAMMA1000221
F-MAMMA1000227//6.8 KD MITOCHONDRIAL PROTEOLIPID.//1.0:30:40//MUS MUSCULUS (MOUSE).//P56379
F-MAMMA1000241//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X (PSI-K).//1.0:40:37//PORPHYRA PURPUREA.//P51370
F-MAMMA1000251//HYPOTHETICAL 6.8 KD PROTEIN IN FIC-PPIA INTERGENIC REGION.//0.99:29:48//SALMONELLA TYPHIMURIUM.//P37771
F-MAMMA1000254//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5'REGION.//1.0:20:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53820
F-MAMMA1000257//HYPOTHETICAL 50.0 KD PROTEIN IN HEML 3'REGION (ORF2).//0.22:50:44//PSEUDOMONAS AERUGINOSA.//Q51470
F-MAMMA1000264//GASTRIN-RELEASING PEPTIDE RECEPTOR (GRP-R) (GRP-PREFERRING BOMBESIN RECEPTOR).//0.80:39:43//HOMO SAPIENS (HUMAN).//P30550
F-MAMMA1000266
F-MAMMA1000270//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//9.5e-42:95:84//HOMO SAPIENS (HUMAN).//P39189
F-MAMMA1000277//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].//0.0062:90:34//MUS MUSCULUS (MOUSE).//P28481
F-MAMMA1000278//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.00096:59:33//HORDEUM VULGARE (BARLEY).//P17991
F-MAMMA1000279//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//8.4e-17:56:76//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1000284//ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2).//0.017:146:30//MUS MUSCULUS (MOUSE).//Q61324
F-MAMMA1000287//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//1.5e-32:84:58//HOMO SAPIENS (HUMAN).//P39189
F-MAMMA1000302//C-HORDEIN (CLONE PC-919) (FRAGMENT).//1.0:42:33//HORDEUM VULGARE (BAR-

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LEY).//P17992
F-MAMMA1000307//PROBABLE E4 PROTEIN.//0.21:71:30//RHESUS PAPILLOMAVIRUS TYPE 1 (RHPV 1).//P24832
F-MAMMA1000309//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN).//0.0026:141:36//HOMO SAPIENS (HUMAN).//P27658
F-MAMMA1000312
F-MAMMA1000313//DNA REPAIR PROTEIN RADC HOMOLOG (25 KD PROTEIN) (FRAGMENT).//0.76:52:32//STAPHYLOCOCCUS AUREUS.//P31337
F-MAMMA1000331
F-MAMMA1000339//50S RIBOSOMAL PROTEIN L29P.//0.78:32:46//METHANOBACTERIUM THERMOAUTOTROPHICUM.//O26117
F-MAMMA1000340//HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION.//1.0:29:58//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36039
F-MAMMA1000348//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//7.5e-09:63:60//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1000356//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.3e-05:42:52//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1000360
F-MAMMA1000361//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//4.4e-33:84:72//HOMO SAPIENS (HUMAN).//P39189
F-MAMMA1000372//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//6.6e-21:53:71//HOMO SAPIENS (HUMAN).//P39193
F-MAMMA1000385
F-MAMMA1000388//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//0.40:72:36//HOMO SAPIENS (HUMAN).//P43489
F-MAMMA1000395//RABPHILIN-3A (FRAGMENT).//0.032:125:25//MUS MUSCULUS (MOUSE).//P47708
F-MAMMA1000402//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.1e-28:266:40//HOMO SAPIENS (HUMAN).//P08547
F-MAMMA1000410//NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-B SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-13KD-B) (CI-13KD-B) (B13).//5.9e-06:32:68//HOMO SAPIENS (HUMAN).//Q16718
F-MAMMA1000413//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//6.7e-05:93:31//MUS MUSCULUS (MOUSE).//P11369
F-MAMMA1000414
F-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//4.1e-28:119:53//CAENORHABDITIS ELEGANS.//Q09232
F-MAMMA1000421//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.7e-23:68:76//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1000422//METALLOTHIONEIN (MT).//0.037:42:42//GADUS MORHUA (ATLANTIC COD).//P51902
F-MAMMA1000423
F-MAMMA1000424//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//0.048:23:73//HOMO SAPIENS (HUMAN).//P39189
F-MAMMA1000429//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5.//2.7e-05:110:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q92331
F-MAMMA1000431//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//9.4e-15:85:58//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1000444//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//4.3e-25:65:76//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1000446//ZYXIN.//0.79:155:29//GALLUS GALLUS (CHICKEN).//Q04584
F-MAMMA1000458//HYPOTHETICAL 37.7 KD PROTEIN C18B11.06 IN CHROMOSOME I.//0.0048:46:43//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09713
F-MAMMA1000468//PERIOD CLOCK PROTEIN (FRAGMENT).//0.50:20:55//DROSOPHILA ROBUSTA (FRUIT FLY).//Q03296
F-MAMMA1000472//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.5e-17:106:55//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1000478//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//3.9e-35:80:68//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1000483//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//2.8e-24:74:77//HOMO SAPIENS (HUMAN).//P39193

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F-MAMMA1000490//TYROSINE-PROTEIN KINASE TXK (EC 2.7.1.112) (PTK-RL-18) (RESTING LYMPHOCYTE KINASE).//0.43:21:57//MUS MUSCULUS (MOUSE).//P42682
F-MAMMA1000500//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.61:33:54//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z2/CDC-Z34 ISOLATE) (HIV-1).//P12506
F-MAMMA1000501//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.1e-32:43:83//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1000516
F-MAMMA1000522//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.0015:113:32//HOMO SAPIENS (HUMAN).//P08547
F-MAMMA1000524//HYPOTHETICAL HOST RANGE 8.5 KD PROTEIN.//1.0:63:31//VACCINIA VIRUS (STRAIN WR).//P17359
F-MAMMA1000559//METALLOTHIONEIN-I (MT-I) (MT-IB/MT-IA).//0.31:16:50//CALLINECTES SAPIDUS (BLUE CRAB).//P55949
F-MAMMA1000565//FERREDOXIN-TYPE PROTEIN NAPF.//0.98:37:35//ESCHERICHIA COLI.//P33939
F-MAMMA1000567//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//5.5e-37:95:76//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1000576//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//4.1e-07:34:64//HOMO SAPIENS (HUMAN).//P39191
F-MAMMA1000583
F-MAMMA1000585//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.5e-28:89:75//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1000594//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//4.8e-24:38:71//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1000597//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.1e-25:74:77//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1000605//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.1e-18:83:50//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1000612//HYPOTHETICAL 34.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION.//4.0e-42:166:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41318
F-MAMMA1000616
F-MAMMA1000621
F-MAMMA1000623//METALLOTHIONEIN-IK (MT-1K).//0.0045:25:48//HOMO SAPIENS (HUMAN).//P80296
F-MAMMA1000625//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.00078:79:35//MUS MUSCULUS (MOUSE).//P05143
F-MAMMA1000643//HYPOTHETICAL 9.3 KD PROTEIN.//1.0:25:28//MAGUARI VIRUS.//P16607
F-MAMMA1000664
F-MAMMA1000669//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.2e-05:186:30//HOMO SAPIENS (HUMAN).//P08547
F-MAMMA1000670//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.6e-06:195:30//MUS MUSCULUS (MOUSE).//P05143
F-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.-).//3.8e-28:184:35//AEDES AEGYPTI (YELLOWFEVER MOSQUITO).//P42660
F-MAMMA1000684//DNA-BINDING PROTEIN (VMW21).//1.1e-07:55:56//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).//P04487
F-MAMMA1000696//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.2e-31:97:74//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1000707//METALLOTHIONEIN-II (MT-II) (MT-IIB/MT-IIA).//0.31:19:42//CALLINECTES SAPIDUS (BLUE CRAB).//P55950
F-MAMMA1000713//XYLULOSE KINASE (EC 2.7.1.17) (XYLULOKINASE).//1.6e-05:88:35//LACTOBACILLUS PENTOSUS.//P21939
F-MAMMA1000714//PROTEIN-LYSINE 6-OXIDASE PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE).//0.44:126:30//RATTUS NORVEGICUS (RAT).//P16636
F-MAMMA1000718//METALLOTHIONEIN-IIE (MT-2E).//1.0:51:31//ORYCTOLAGUS CUNICULUS (RABBIT).//P80292
F-MAMMA1000720//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//3.3e-28:60:71//HOMO SAPIENS (HUMAN).//P39193
F-MAMMA1000723//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.7e-14:63:53//HOMO SAPIENS (HUMAN).//P08547

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F-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2).//1.8e-43:258:43//HOMO SAPIENS (HUMAN).//O14647
F-MAMMA1000732//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//9.9e-12:76:55//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1000733
F-MAMMA1000734//NPL1 PROTEIN (SEC63 PROTEIN).//2.5e-18:181:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P14906
F-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//5.4e-52:196:58//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87115
F-MAMMA1000744//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!//6.3e-36:144:47//HOMO SAPIENS (HUMAN).//P39190
F-MAMMA1000746
F-MAMMA1000752
F-MAMMA1000760//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//6.6e-29:75:72//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1000761//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.6e-09:59:64//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1000775
F-MAMMA1000776//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//3.3e-35:99:74//HOMO SAPIENS (HUMAN).//P39193
F-MAMMA1000778//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.1e-19:65:70//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1000782
F-MAMMA1000798//HYPOTHETICAL PROTEIN ORF-1137.//0.015:59:37//MUS MUSCULUS (MOUSE).//P11260
F-MAMMA1000802//MYOSIN IC HEAVY CHAIN.//0.35:94:41//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569
F-MAMMA1000824//ACTIN 1.//0.046:60:31//ZEA MAYS (MAIZE).//P02582
F-MAMMA1000831//PROBABLE NI/FE-HYDROGENASE 1 B-TYPE CYTOCHROME SUBUNIT.//1.0:30:46//ESCHERICHIA COLI.//P19929
F-MAMMA1000839//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.1e-28:80:58//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4).//1.5e-39:130:36//METHANOBACTERIUM THERMOAUTOTROPHICUM.//O27540
F-MAMMA1000842//C-HORDEIN (CLONE PC-919) (FRAGMENT).//0.064:43:41//HORDEUM VULGARE (BARLEY).//P17992
F-MAMMA1000843
F-MAMMA1000845//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).//0.43:58:34//DROSOPHILA YAKUBA (FRUIT FLY).//P03895
F-MAMMA1000851//CUTICLE COLLAGEN 34.//0.019:107:29//CAENORHABDITIS ELEGANS.//P34687
F-MAMMA1000855//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.00098:149:32//HOMO SAPIENS (HUMAN).//Q15428
F-MAMMA1000856//METALLOTHIONEIN (MT).//0.63:39:41//POTAMON POTAMIOS.//P55952
F-MAMMA1000859//GLYCOPROTEIN X PRECURSOR.//0.014:192:28//EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).//P28968
F-MAMMA1000862//DISINTEGRIN KISTRIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).//1.0:66:27//AGKISTRODON RHODOSTOMA (MALAYAN PIT VIPER) (CALLOSELASMA RHODOSTOMA).//P17494
F-MAMMA1000863//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//5.4e-16:41:68//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1000865//SALIVARY PROUNE-RICH PROTEIN II-1 (FRAGMENT).//0.030:100:32//HOMO SAPIENS (HUMAN).//P81489
F-MAMMA1000867//APTOTOXIN IX (PARALYTIC PEPTIDE IX) (PP IX).//0.98:43:32//APTOSTICHUS SCHLINGERI (TRAP-DOOR SPIDER).//P49272
F-MAMMA1000875//PROLINE-RICH PEPTIDE P-B.//0.18:21:47//HOMO SAPIENS (HUMAN).//P02814
F-MAMMA1000876//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//1.5e-22:85:71//HOMO SAPIENS (HUMAN).//P39189
F-MAMMA1000877//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.2e-38:62:74//HOMO SAPIENS (HUMAN).//P39188

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F-MAMMA1000880//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.49:79:32//BOS TAURUS (BOVINE).//P25508
F-MAMMA1000883//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X.//0.87:15:60//CAENORHABDITIS ELEGANS.//Q11116
F-MAMMA1000897//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR (ITI HEAVY CHAIN H4) (INTER-ALPHA-TRYPSIN INHIBITOR FAMILY HEAVY CHAIN-RELATED PROTEIN) (PLASMA KALLIKREIN SENSITIVE GLYCOPROTEIN 120) (PK-120).//5.3e-17:130:40//HOMO SAPIENS (HUMAN).//Q14624
F-MAMMA1000905
F-MAMMA1000906
F-MAMMA1000908//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//8.0e-17:70:62//HOMO SAPIENS (HUMAN).//P08547
F-MAMMA1000914//HYPOTHETICAL 6.2 KD PROTEIN.//0.97:36:36//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19299
F-MAMMA1000921
F-MAMMA1000931//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//5.6e-10:49:65//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1000940//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L32.//0.42:22:54//RECLINOMONAS AMERICANA.//O21281
F-MAMMA1000941//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.3e-25:55:69//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1000942//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.3e-08:36:75//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1000943
F-MAMMA1000956//SMALL HISTIDINE-ALANINE-RICH PROTEIN PRECURSOR (SHARP) (ANTIGEN 57).//0.041:122:25//PLASMODIUM FALCIPARUM (ISOLATE FC27 / PAPUA NEW GUINEA).//P04930
F-MAMMA1000957//HEAT-STABLE ENTEROTOXIN A2 PRECURSOR (STA2).//0.024:37:37//ESCHERICHIA COLI.//Q47185
F-MAMMA1000962//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//6.0e-39:61:78//HOMO SAPIENS (HUMAN).//P39189
F-MAMMA1000968//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//0.0054:29:72//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1000975//CUTICLE COLLAGEN DPY-2 PRECURSOR.//1.0:93:30//CAENORHABDITIS ELEGANS.//P35799
F-MAMMA1000979//PROLINE-RICH PEPTIDE P-B.//0.012:12:66//HOMO SAPIENS (HUMAN).//P02814
F-MAMMA1000987//HYPOTHETICAL PROTEIN LAMBDA-SP34.//1.0:47:40//MUS MUSCULUS (MOUSE).//P15973
F-MAMMA1000998
F-MAMMA1001003//PROBABLE E5 PROTEIN.//1.0:52:42//HUMAN PAPILLOMAVIRUS TYPE 33.//P06426
F-MAMMA1001008//PROGASTRICSIN PRECURSOR (EC 3.4.23.3) (PEPSINOGEN C) (FRAGMENT).//3.2e-14:131:35//MACACA FUSCATA FUSCATA (JAPANESE MACAQUE).//P03955
F-MAMMA1001021//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.016:61:42//STREPTOMYCES FRADIAE.//P20186
F-MAMMA1001024
F-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CG-R) (LSH-R) (LUTEINIZING HOROMINE RECEPTOR) (FRAGMENT).//2.4e-20:234:29//GALLUS GALLUS (CHICKEN).//Q90674
F-MAMMA1001035//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.7e-15:52:78//HOMO SAPIENS (HUMAN).//P39193
F-MAMMA1001038//NEUROTOXIN II (TOXIN RP-II) (SODIUM CHANNEL TOXIN II).//0.53:25:48//RADIANTHUS PAUMOTENSIS (SEA ANEMONE) (HETERACTIS PAUMOTENSIS).//P01534
F-MAMMA1001041//SPECTRIN BETA CHAIN, ERYTHROCYTE.//6.3e-18:112:43//MUS MUSCULUS (MOUSE).//P15508
F-MAMMA1001050
F-MAMMA1001059//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//1.3e-34:187:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09747
F-MAMMA1001067//PROTEIN Q300.//0.36:12:75//MUS MUSCULUS (MOUSE).//Q02722
F-MAMMA1001073//HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 1 (HFH-1).//1.0:70:37//RATTUS NORVEGICUS (RAT).//Q63244

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F-MAMMA1001074//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.00067:163:32//HOMO SAPIENS (HUMAN).//P08547
F-MAMMA1001075//RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1).//0.53:72:34//HOMO SAPIENS (HUMAN).//P29374
F-MAMMA1001078//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.0e-79:184:73//HOMO SAPIENS (HUMAN).//P08547
F-MAMMA1001080//IG HEAVY CHAIN PRECURSOR V-III REGION (VH26).//1.7e-27:82:71//HOMO SAPIENS (HUMAN).//P01764
F-MAMMA1001082
F-MAMMA1001091//HYPOTHETICAL BHLF1 PROTEIN.//3.1e-05:198:32//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
F-MAMMA1001092//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.1e-21:65:72//HOMO SAPIENS (HUMAN).//P08547
F-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN).//1.0e-18:68:48//DROSOPHILA MELANOGASTER (FRUIT FLY).//P51521
F-MAMMA1001110//PROCOLLAGEN ALPHA 1(IV) CHAIN PRECURSOR.//0.080:108:37//MUS MUSCULUS (MOUSE).//P02463
F-MAMMA1001126//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//2.3e-07:66:45//HOMO SAPIENS (HUMAN).//P39189
F-MAMMA1001133//HYPOTHETICAL 13.2 KD PROTEIN IN RPS4A-BAT2 INTERGENIC REGION.//0.96:43:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47174
F-MAMMA1001139//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.//5.4e-42:81:62//CAENORHABDITIS ELEGANS.//Q09201
F-MAMMA1001143//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.00014:36:66//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1001145
F-MAMMA1001154//CSBA PROTEIN.//1.0:39:38//BACILLUS SUBTILIS.//P37953
F-MAMMA1001161//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//5.2e-23:53:64//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1001162//CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27).//0.69:86:31//MUS MUSCULUS (MOUSE).//P41272
F-MAMMA1001181//HYPOTHETICAL 81.0 KD PROTEIN C35D10.4 IN CHROMOSOME III.//0.00010:74:47//CAENORHABDITIS ELEGANS.//Q18486
F-MAMMA1001186//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//9.0e-32:44:86//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1001191//OCTAMER-BINDING TRANSCRIPTION FACTOR 1 (OTF-1) (NF-A1) (FRAGMENT).//0.096:40:40//MACROPUS EUGENII (TAMMAR WALLABY).//Q28466
F-MAMMA1001198//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN).//2.5e-75:204:70//HOMO SAPIENS (HUMAN).//P42566
F-MAMMA1001202//METALLOTHIONEIN-II (MT-II) (MT-IIB/MT-IIA).//0.52:46:32//CALLINECTES SAPIDUS (BLUE CRAB).//P55950
F-MAMMA1001203//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//7.3e-11:82:58//HOMO SAPIENS (HUMAN).//P39192
F-MAMMA1001206//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.9e-17:67:71//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1001215//9 KD PROTEIN.//1.0:51:33//HOMO SAPIENS (HUMAN).//P13994
F-MAMMA1001220//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//3.4e-37:55:87//HOMO SAPIENS (HUMAN).//P39189
F-MAMMA1001222//HYPOTHETICAL 73.6 KD PROTEIN CY49.21.//3.7e-06:168:38//MYCOBACTERIUM TUBERCULOSIS.//Q10690
F-MAMMA1001243
F-MAMMA1001244//TRP OPERON LEADER PEPTIDE.//1.0:18:55//SERRATIA MARCESCENS.//P03055
F-MAMMA1001249//HYPOTHETICAL 7.2 KD PROTEIN IN RPS2 3'REGION (ORF57).//0.57:23:34//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34774
F-MAMMA1001256//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.3e-07:79:44//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1001259//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-).//0.046:86:32//MYCOPLASMA GENITALIUM.//P47486

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F-MAMMA1001260//MYOSIN HEAVY CHAIN, PERINATAL SKELETAL MUSCLE.//2.7e-05:219:27//HOMO SAPIENS (HUMAN).//P13535
F-MAMMA1001268//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.7e-27:89:67//HOMO SAPIENS (HUMAN).//P08547
F-MAMMA1001271//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//4.0e-06:126:38//HOMO SAPIENS (HUMAN).//P54259
F-MAMMA1001274/!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//7.4e-29:57:66//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1001280//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//0.27:24:54//ESCHERICHIA COLI.//P05834
F-MAMMA1001292//HYPOTHETICAL PROTEIN KIAA0176 (FRAGMENT).//1.3e-73:208:69//HOMO SAPIENS (HUMAN).//Q14681
F-MAMMA1001296//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//6.9e-22:41:80//HOMO SAPIENS (HUMAN).//P39193
F-MAMMA1001298//HYPOTHETICAL PROTEIN HI0371.//0.99:29:37//HAEMOPHILUS INFLUENZAE.//P44668
F-MAMMA1001305//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//9.9e-62:222:54//HOMO SAPIENS (HUMAN).//Q07960
F-MAMMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//2.1e-09:46:60//HOMO SAPIENS (HUMAN).//P20931
F-MAMMA1001324//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)].//2.5e-43:128:50//FRIEND MURINE LEUKEMIA VIRUS (ISOLATE PVC-211) (F-MULV).//P26808
F-MAMMA1001330//HEMOGLOBIN ZETA CHAIN (FRAGMENTS).//0.30:51:37//MACROPUS EUGENII (TAMMAR WALLABY).//P81044
F-MAMMA1001341//TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36) (GROWTH FACTOR- INDUCIBLE NUCLEAR PROTEIN NUP475).//0.024:89:39//HOMO SAPIENS (HUMAN).//P26651
F-MAMMA1001343//PROBABLE E5 PROTEIN.//0.60:64:29//HUMAN PAPILLOMAVIRUS TYPE 16.//P06927
F-MAMMA1001346//PROTEINASE INHIBITOR IIB (FRAGMENTS).//0.97:33:45//SOLANUM TUBEROSUM (POTATO).//P01082
F-MAMMA1001383//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.2e-30:86:77//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//9.2e-91:195:92//HOMO SAPIENS (HUMAN).//P02750
F-MAMMA1001397//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.5e-19:55:69//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1001408//SALIVARY GLUE PROTEIN SGS-7 PRECURSOR.//0.60:45:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P02841
F-MAMMA1001411//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//5.8e-06:153:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
F-MAMMA1001419//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.3e-16:99:51//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1001420//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!//0.0018:23:65//HOMO SAPIENS (HUMAN).//P39190
F-MAMMA1001435//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.7e-22:60:58//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1001442
F-MAMMA1001446//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.2e-23:48:75//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1001452//GENE 35 PROTEIN (GP35).//0.61:31:45//MYCOBACTERIOPHAGE L5.//Q05245
F-MAMMA1001465//HYPOTHETICAL PROTEIN E-115.//0.0026:68:38//HUMAN ADENOVIRUS TYPE 2.//P03290
F-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) (FRAGMENT).//3.7e-94:201:92//MUS MUSCULUS (MOUSE).//P52623
F-MAMMA1001487//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.6e-16:89:41//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
F-MAMMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-

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TRAL PROTEINASE) (CANP) (MU-TYPE).//6.2e-59:86:97//HOMO SAPIENS (HUMAN).//P07384
F-MAMMA1001502//HYPOTHETICAL 11.4 KD PROTEIN (ORF1).//0.21:79:30//STREPTOMYCES FRADIAE.//P26800
F-MAMMA1001510
F-MAMMA1001522//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.67:98:31//STREPTOMYCES FRADIAE.//P20186
F-MAMMA1001547//PROBABLE MOLYBDENUM-PTERIN BINDING PROTEIN.//0.97:35:42//HAEMOPHILUS INFLUENZAE.//P45183
F-MAMMA1001551//HYPOTHETICAL PROTEIN MJ0458.1.//0.038:31:41//METHANOCOCCUS JANNASCHII.//P81308
F-MAMMA1001575
F-MAMMA1001576//TUBULIN GAMMA CHAIN.//1.6e-86:162:99//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P23330
F-MAMMA1001590//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.0035:38:55//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1001600//CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.//0.85:53:33//HOMO SAPIENS (HUMAN).//P29279
F-MAMMA1001604//HYPOTHETICAL 11.1 KD PROTEIN C30D11.02C IN CHROMOSOME I.//0.14:82:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09902
F-MAMMA1001606//HIGH MOBILITY GROUP PROTEIN HMGI-C.//8.2e-05:77:37//HOMO SAPIENS (HUMAN).//P52926
F-MAMMA1001620//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//5.5e-05:24:66//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1001627//CUTICLE COLLAGEN 40.//0.82:131:31//CAENORHABDITIS ELEGANS.//P34804
F-MAMMA1001630//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//8.6e-26:57:78//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1001633//ZINC FINGER PROTEIN 165.//6.9e-38:160:55//HOMO SAPIENS (HUMAN).//P49910
F-MAMMA1001635
F-MAMMA1001649//SPERM PROTAMINE P1.//0.39:31:41//TACHYGLOSSUS ACULEATUS ACULEATUS (AUSTRALIAN ECHIDNA).//P35311
F-MAMMA1001654//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PROTEIN KINASE 1).//5.6e-06:99:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P18160
F-MAMMA1001663//VERY HYPOTHETICAL XYLU PROTEIN.//0.99:27:37//ESCHERICHIA COLI.//P05056
F-MAMMA1001670//CUTICLE COLLAGEN 1.//0.033:97:37//CAENORHABDITIS ELEGANS.//P08124
F-MAMMA1001671
F-MAMMA1001679//PROCOLLAGEN ALPHA 2(IV) CHAIN PRECURSOR.//0.92:32:50//HOMO SAPIENS (HUMAN).//P08572
F-MAMMA1001683//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.00026:147:34//STREPTOMYCES FRADIAE.//P20186
F-MAMMA1001686
F-MAMMA1001692//SMALL HYDROPHOBIC PROTEIN (SMALL PROTEIN 1A).//1.0:34:26//BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN A51908) (BRS).//P24616
F-MAMMA1001711//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.1e-28:56:69//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1001715//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.6e-08:39:71//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1001730//METALLOTHIONEIN-B (MTB).//1.0:17:64//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).//Q27287
F-MAMMA1001735//TUBULIN BETA-5 CHAIN (CLASS-V).//5.1e-121:213:97//GALLUS GALLUS (CHICKEN).//P09653
F-MAMMA1001740
F-MAMMA1001743//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.3e-09:100:42//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1001744//POU DOMAIN PROTEIN 2.//0.97:59:38//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q90270
F-MAMMA1001745//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.1e-43:199:42//HOMO SAPIENS (HUMAN).//P08547
F-MAMMA1001751//TWK-8 PROTEIN.//2.9e-15:77:36//CAENORHABDITIS ELEGANS.//P34410

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F-MAMMA1001754//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.019:20:45//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645
F-MAMMA1001757//HYPOTHETICAL 9.2 KD PROTEIN IN RNPA 3'REGION.//0.94:30:43//PSEUDOMONAS PUTIDA.//P25753
F-MAMMA1001760//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//4.6e-34:103:59//HOMO SAPIENS (HUMAN).//P39191
F-MAMMA1001764
F-MAMMA1001768//HYPOTHETICAL PROTEIN UL61.//0.042:167:33//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818
F-MAMMA1001769//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.0e-29:97:69//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1001771//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//3.3e-09:123:32//HOMO SAPIENS (HUMAN).//P51805
F-MAMMA1001783//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.1e-09:55:61//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1001785//RAS-RELATED PROTEIN RABC.//1.9e-06:120:25//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34143
F-MAMMA1001788//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.3e-29:46:76//HOMO SAPIENS (HUMAN).//P08547
F-MAMMA1001790//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.7e-24:69:69//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1001806//HYPOTHETICAL 21.2 KD PROTEIN IN TOR2-MNN4 INTERGENIC REGION.//0.95:58:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36042
F-MAMMA1001812//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//8.8e-12:53:69//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1001815//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.11:30:70//HOMO SAPIENS (HUMAN).//P08547
F-MAMMA1001817//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.9e-16:86:55//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1001818
F-MAMMA1001820//VITTELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN TU-4) (PROTEIN SV23).//0.0030:63:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13238
F-MAMMA1001824//APTOTOXIN VII (PARALYTIC PEPTIDE VII) (PP VII).//0.99:26:34//APTOSTICHUS SCHLINGERI (TRAP-DOOR SPIDER).//P49271
F-MAMMA1001836//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.6e-35:77:88//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1001837//ZINC FINGER PROTEIN 191.//1.3e-27:106:58//HOMO SAPIENS (HUMAN).//O14754
F-MAMMA1001848//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.0e-19:92:58//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1001851
F-MAMMA1001854
F-MAMMA1001858//ISOTOCIN-NEUROPHYSIN IT 1 PRECURSOR.//0.93:42:38//CATOSTOMUS COMMERSONI (WHITE SUCKER).//P15210
F-MAMMA1001864//PROBABLE ABC TRANSPORTER PERMEASE PROTEIN MG189.//0.77:161:27//MYCOPLASMA GENITALIUM.//P47435
F-MAMMA1001868//FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (EC 5.2.1.8) (PROLINE ROTAMASE) (NUCLEOLAR PROLINE ISOMERASE) (FKBP-70).//0.00013:219:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38911
F-MAMMA1001874//SPERM HISTONE P2 PRECURSOR (PROTAMINE MP2).//0.0075:76:31//MUS MUSCULUS (MOUSE).//P07978
F-MAMMA1001878//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).//0.020:10:80//LYCOPERSICON ESCULENTUM (TOMATO).//Q01157
F-MAMMA1001880
F-MAMMA1001890//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//5.1e-34:56:83//HOMO SAPIENS (HUMAN).//P39192
F-MAMMA1001907//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.7e-12:44:68//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1001908//HYPOTHETICAL 16.2 KD PROTEIN IN PRP24-RRN9 INTERGENIC REGION.//0.00013:77:

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37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03525
F-MAMMA1001931//HYPOTHETICAL 118.2 KD PROTEIN F43C1.1 IN CHROMOSOME III.//0.41:106:29//CAENORHABDITIS ELEGANS.//Q09564
F-MAMMA1001956//OCTAPEPTIDE-REPEAT PROTEIN T2.//0.00053:149:30//MUS MUSCULUS (MOUSE).//Q06666
F-MAMMA1001963//HYPOTHETICAL PROTEIN IN NAC 5'REGION (ORF X) (FRAGMENT).//1.0:46:28//KLEBSIELLA AEROGENES.//Q08600
F-MAMMA1001969//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.7e-34:97:68//HOMO SAPIENS (HUMAN).//P08547
F-MAMMA1001970//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.2e-07:67:37//HOMO SAPIENS (HUMAN).//P08547
F-MAMMA1001992//PROTEIN Q300.//0.53:14:71//MUS MUSCULUS (MOUSE).//Q02722
F-MAMMA1002009//PROBABLE E5 PROTEIN.//0.17:56:32//HUMAN PAPILLOMAVIRUS TYPE 31.//P17385
F-MAMMA1002011//MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MARCKS) (PROTEIN KINASE C SUBSTRATE, 80 KD PROTEIN, LIGHT CHAIN) (PKCSL) (80K-L PROTEIN).//1.0:100:31//HOMO SAPIENS (HUMAN).//P29966
F-MAMMA1002032//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.1e-21:86:65//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1002033//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//8.5e-20:67:58//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1002041//MALE SPECIFIC SPERM PROTEIN MST84DC.//1.0:17:52//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01644
F-MAMMA1002042//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//0.19:45:46//HOMO SAPIENS (HUMAN).//P39192
F-MAMMA1002047//TYROSINE AMINOTRANSFERASE (EC 2.6.1.5) (L-TYROSINE:2-OXOGLUTARATE AMINOTRANSFERASE) (TAT).//0.0017:50:46//RATTUS NORVEGICUS (RAT).//P04694
F-MAMMA1002056//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.2e-37:70:77//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1002058//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.1e-08:26:76//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1002068//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.0e-11:78:46//HOMO SAPIENS (HUMAN).//P08547
F-MAMMA1002078//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.96:26:46//COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).//P50682
F-MAMMA1002082//SUPPRESSOR PROTEIN SRP40.//0.23:95:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
F-MAMMA1002084//HYPOTHETICAL 7.5 KD PROTEIN.//1.0:40:35//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20520
F-MAMMA1002093
F-MAMMA1002108//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.00079:143:33//STREPTOMYCES FRADIAE.//P20186
F-MAMMA1002118//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:43:34//METRIDIUM SENILE (BROWN SEA ANEMONE) (FRILLED SEA ANEMONE).//O47493
F-MAMMA1002125//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//1.9e-14:60:68//HOMO SAPIENS (HUMAN).//P39192
F-MAMMA1002132
F-MAMMA1002140//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.4e-24:69:65//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1002143//SERUM PROTEIN MSE55.//2.1e-16:166:43//HOMO SAPIENS (HUMAN).//Q00587
F-MAMMA1002145//36.4 KD PROLINE-RICH PROTEIN.//0.00014:84:29//LYCOPERSICON ESCULENTUM (TOMATO).//Q00451
F-MAMMA1002153
F-MAMMA1002155
F-MAMMA1002156//METALLOPROTEINASE INHIBITOR PRECURSOR.//0.90:58:34//STREPTOMYCES NIGRESCENS.//P01077
F-MAMMA1002158
F-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN).//6.0e-66:157:70//HOMO SAPIENS (HUMAN).//P15880

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F-MAMMA1002174//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//6.5e-25:56:64//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE 1) (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) (TSA) (PRP) (NATURAL KILLER CELL ENHANCING FACTOR B) (NKEF-B).//9.0e-09:28:100//HOMO SAPIENS (HUMAN).//P32119
F-MAMMA1002209//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.0023:132:33//HOMO SAPIENS (HUMAN).//O00268
F-MAMMA1002215//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//0.00032:68:35//HOMO SAPIENS (HUMAN).//P02452
F-MAMMA1002219//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.0079:224:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25386
F-MAMMA1002230
F-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR).//1.4e-118:151:94//RATTUS NORVEGICUS (RAT).//P70541
F-MAMMA1002243//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).//0.028:112:33//MUS MUSCULUS (MOUSE).//P70315
F-MAMMA1002250//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).//0.0012:80:32//ORYCTOLAGUS CUNICULUS (RABBIT).//P06333
F-MAMMA1002267//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.17:139:28//TRYPANOSOMA BRUCEI BRUCEI.//P24499
F-MAMMA1002268//60S RIBOSOMAL PROTEIN L22.//0.00026:163:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P50887
F-MAMMA1002269//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//0.35:14:57//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//Q48251
F-MAMMA1002282//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//6.1e-05:32:65//HOMO SAPIENS (HUMAN).//P39192
F-MAMMA1002292//TROPOMYOSIN 2.//1.4e-05:100:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40414
F-MAMMA1002293//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//6.8e-25:127:44//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1002294//ALPHA TRANS-INDUCING PROTEIN (ALPHA-TIF).//0.00011:138:38//BOVINE HERPESVIRUS TYPE 1 (STRAIN P8-2).//P30020
F-MAMMA1002297//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.15:144:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
F-MAMMA1002298//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.0e-05:40:50//MUS MUSCULUS (MOUSE).//P05143
F-MAMMA1002299//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.84:65:32//STRUTHIO CAMELUS (OSTRICH).//O21405
F-MAMMA1002308//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.3e-29:61:73//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1002310//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.00016:70:38//MUS MUSCULUS (MOUSE).//P15265
F-MAMMA1002311//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//9.4e-09:84:54//HOMO SAPIENS (HUMAN).//P39189
F-MAMMA1002312//HYPOTHETICAL 10.8 KD PROTEIN IN GP30-RIII INTERGENIC REGION (URF Y).//0.48:48:33//BACTERIOPHAGE T4.//P33084
F-MAMMA1002317
F-MAMMA1002319//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//0.011:128:27//MUS MUSCULUS (MOUSE).//P11369
F-MAMMA1002322//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//5.2e-20:92:57//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1002329//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.051:33:36//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P03931
F-MAMMA1002332//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.5e-20:116:51//HOMO SAPIENS (HUMAN).//P08547
F-MAMMA1002333//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.0017:214:31//BOS TAURUS (BOVINE).//P02453
F-MAMMA1002339//COPPER-METALLOTHIONEIN (CU-MT).//0.59:42:38//HELIX POMATIA (ROMAN SNAIL)

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(EDIBLE SNAIL).//P55947
F-MAMMA1002347//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.43:26:61//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1002351//HYPOTHETICAL PROTEIN MJ0304.//2.3e-07:139:25//METHANOCOCCUS JANNASCHII.//Q57752
F-MAMMA1002352
F-MAMMA1002353//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.00028:31:80//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1002355//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//4.2e-28:87:73//HOMO SAPIENS (HUMAN).//P39193
F-MAMMA1002356//RELAXIN.//0.95:31:35//SQUALUS ACANTHIAS (SPINY DOGFISH).//P11953
F-MAMMA1002359//CHLOROPLAST 50S RIBOSOMAL PROTEIN L33.//0.93:44:36//GUILLARDIA THETA (CRYPTOMONAS PHI).//O78487
F-MAMMA1002360//LATE L2 MU CORE PROTEIN PRECURSOR (PROTEIN X).//0.94:30:43//BOVINE ADENOVIRUS TYPE 2 (MASTADENOVIRUS BOS2).//Q96626
F-MAMMA1002361//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.0e-08:45:68//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1002362//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.58:23:26//LUMBRICUS TERRESTRIS (COMMON EARTHWORM).//Q34942
F-MAMMA1002380//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.23:100:27//DROSOPHILA SIMULANS (FRUIT FLY).//P13729
F-MAMMA1002384
F-MAMMA1002385//HYPOTHETICAL 40.9 KD PROTEIN IN ORC2-TIP1 INTERGENIC REGION.//3.8e-14:125:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38241
F-MAMMA1002392//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:17:58//BRANCHIOSTOMA LANCEOLATUM (COMMON LANCELET) (AMPHIOXUS).//O21003
F-MAMMA1002411//30S RIBOSOMAL PROTEIN S17.//0.85:49:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P73311
F-MAMMA1002413//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRAGMENT).//0.97:41:39//DROSOPHILA AFFINIS (FRUIT FLY).//P51926
F-MAMMA1002417//RFBJ PROTEIN.//0.99:31:35//SHIGELLA FLEXNERI.//P37786
F-MAMMA1002427//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.6e-33:135:59//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1002428//HYPOTHETICAL PROTEIN C18.//0.97:34:44//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//P32217
F-MAMMA1002434//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//3.1e-36:56:78//HOMO SAPIENS (HUMAN).//P39189
F-MAMMA1002446
F-MAMMA1002454//EARLY NODULIN 20 PRECURSOR (N-20).//0.77:57:45//MEDICAGO TRUNCATULA (BAREL MEDIC).//P93329
F-MAMMA1002461//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//1.3e-05:193:32//CANIS FAMILIARIS (DOG).//P50551
F-MAMMA1002470//HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION.//1.0e-75:231:60//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38795
F-MAMMA1002475//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L4 (SNF2-BETA) (BRG-1 PROTEIN) (MITOTIC GROWTH AND TRANSCRIPTION ACTIVATOR) (BRAHMA PROTEIN HOMOLOG 1).//0.013:99:30//HOMO SAPIENS (HUMAN).//P51532
F-MAMMA1002480//NONSTRUCTURAL PROTEIN 5B.//1.0:23:43//HUMAN CORONAVIRUS (STRAIN 229E).//P19741
F-MAMMA1002485//STANNIOCALCIN PRECURSOR.//2.1e-23:88:46//HOMO SAPIENS (HUMAN).//P52823
F-MAMMA1002494//MOLT-INHIBITING HORMONE (MIH).//1.0:32:37//PROCAMBARUS CLARKII (RED SWAMP CRAYFISH).//P55848
F-MAMMA1002498//6.7 KD PROTEIN (ORF 5).//1.0:26:42//BARLEY YELLOW DWARF VIRUS (ISOLATE PAV) (BYDV).//P09517
F-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION.//5.0e-26:222:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43571
F-MAMMA1002530//CYTOSOLIC PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE) / LYSOPHOSPHOLIPASE (EC 3.1.1.5).//4.5e-12:88:44//HOMO SAPIENS (HUMAN).//

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P47712
F-MAMMA1002545//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//4.3e-29:97:71//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1002554//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//0.46:54:40//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414
F-MAMMA1002556//METALLOTHIONEIN 20-I ISOFORMS A AND B (MT-20-IA AND MT-20-IB).//0.99:21:47//MYTILUS EDULIS (BLUE MUSSEL).//P80251
F-MAMMA1002566//TRANSCRIPTION FACTOR P65 (NUCLEAR FACTOR NF-KAPPA-B P65 SUBUNIT).//0.70:130:30//MUS MUSCULUS (MOUSE).//Q04207
F-MAMMA1002571//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (FRAGMENT).//0.54:45:51//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P35084
F-MAMMA1002573//PARATHYMOSIN.//1.5e-07:69:46//HOMO SAPIENS (HUMAN).//P20962
F-MAMMA1002585//MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR ISOFORM (FRAGMENT).//0.38:36:36//MUS MUSCULUS (MOUSE).//P09542
F-MAMMA1002590//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.99:22:77//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1002597//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.1e-18:44:70//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1002598//60S RIBOSOMAL PROTEIN L7.//1.8e-16:40:100//HOMO SAPIENS (HUMAN).//P18124
F-MAMMA1002603
F-MAMMA1002612//30S RIBOSOMAL PROTEIN S16 (FRAGMENT).//1.0:29:37//THERMUS AQUATICUS.//O07348
F-MAMMA1002617//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.00041:81:34//RATTUS NORVEGICUS (RAT).//P10164
F-MAMMA1002618//ESCARGOT/SNAIL PROTEIN HOMOLOG (FRAGMENT).//0.11:18:50//PSYCHODA CINEREA.//Q02027
F-MAMMA1002619//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//1.8e-13:110:40//CAENORHABDITIS ELEGANS.//Q09931
F-MAMMA1002622//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//8.4e-05:53:58//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1002623//PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (EC 1.14.17.3) (PAM).//2.6e-07:37:78//HOMO SAPIENS (HUMAN).//P19021
F-MAMMA1002625
F-MAMMA1002629//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.4e-19:49:73//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1002636//COLLAGEN ALPHA 2(VI) CHAIN (FRAGMENT).//1.7e-07:189:32//HOMO SAPIENS (HUMAN).//P12110
F-MAMMA1002637//KINESIN LIGHT CHAIN (KLC).//7.7e-54:227:52//RATTUS NORVEGICUS (RAT).//P37285
F-MAMMA1002646//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//0.034:199:25//MUS MUSCULUS (MOUSE).//P19246
F-MAMMA1002650//TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOLOG 2).//1.7e-07:104:32//MUS MUSCULUS (MOUSE).//P97303
F-MAMMA1002655//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//1.0:25:44//HOMO SAPIENS (HUMAN).//P22532
F-MAMMA1002662
F-MAMMA1002665//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.3e-07:54:57//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.4e-10:144:31//ESCHERICHIA COLI.//P27550
F-MAMMA1002673//BREVICAN CORE PROTEIN PRECURSOR.//0.76:64:39//BOS TAURUS (BOVINE).//Q28062
F-MAMMA1002684//HYPOTHETICAL 11.8 KD PROTEIN IN GP55-NRDG INTERGENIC REGION.//0.094:77:27/BACTERIOPHAGE T4.//P07079
F-MAMMA1002685//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.0017:177:34//RATTUS NORVEGICUS (RAT).//P02454
F-MAMMA1002698
F-MAMMA1002699//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REGION.//1.2e-28:127:

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47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160
F-MAMMA1002701//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.0:14:92//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1002708//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//7.9e-27:52:65//HOMO SAPIENS (HUMAN).//P39193
F-MAMMA1002711//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.7e-24:54:75//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1002721
F-MAMMA1002727//SOX-13 PROTEIN (FRAGMENT).//0.70:36:38//MUS MUSCULUS (MOUSE).//Q04891
F-MAMMA1002728//HYPOTHETICAL 6.0 KD PROTEIN.//1.0:25:44//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19305
F-MAMMA1002744//HYPOTHETICAL 13.4 KD PROTEIN IN ACT5-YCK1 INTERGENIC REGION.//1.0:52:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38834
F-MAMMA1002746//HYPOTHETICAL 5.6 KD PROTEIN (ORF A-45).//1.0:22:40//SULFOLOBUS VIRUS-LIKE PARTICLE SSV1.//P20198
F-MAMMA1002748
F-MAMMA1002754//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//5.1e-21:56:64//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1002758//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.37:14:64//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645
F-MAMMA1002764//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//4.7e-32:79:60//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1002765//PARATHYMOSIN.//0.79:63:28//BOS TAURUS (BOVINE).//P08814
F-MAMMA1002769//GAR2 PROTEIN.//0.00037:192:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891
F-MAMMA1002775//HYPOTHETICAL 36.7 KD PROTEIN C2F7.14C IN CHROMOSOME I.//5.4e-54:240:49//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09704
F-MAMMA1002780
F-MAMMA1002782//MARGATOXIN (MGTX).//1.0:31:38//CENTRUROIDES MARGARITATUS (SCORPION).//P40755
F-MAMMA1002796//ICE NUCLEATION PROTEIN.//0.0018:100:41//PSEUDOMONAS FLUORESCENS.//P09815
F-MAMMA1002807//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//9.3e-23:100:59//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1002820//NEUROTOXIN IV (LQQ IV).//1.0:18:50//LEIURUS QUINQUESTRIATUS QUINQUESTRIATUS (EGYPTIAN SCORPION).//P01489
F-MAMMA1002830//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//4.7e-24:55:74//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1002833//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//2.6e-31:95:73//HOMO SAPIENS (HUMAN).//P39189
F-MAMMA1002835//HYPOTHETICAL 42.1 KD PROTEIN F13G3.3 IN CHROMOSOME I.//1.0:54:37//CAENORHABDITIS ELEGANS.//Q19417
F-MAMMA1002838//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//2.5e-27:99:70//HOMO SAPIENS (HUMAN).//P39193
F-MAMMA1002842//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.3e-13:65:63//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1002843//METALLOTHIONEIN-II (MT-II).//0.97:19:47//MUS MUSCULUS (MOUSE).//P02798
F-MAMMA1002844//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//4.9e-08:119:36//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479
F-MAMMA1002858//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.98:37:37//PAN TROGLODYTES (CHIMPANZEE).//Q35647
F-MAMMA1002868//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.8e-10:51:62//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1002869//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//1.8e-95:194:78//HOMO SAPIENS (HUMAN).//P48059
F-MAMMA1002871//G-PROTEIN COUPLED RECEPTOR HOMOLOG R33.//1.0:51:35//RAT CYTOMEGALOVIRUS (STRAIN MAASTRICHT).//O12000
F-MAMMA1002880

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F-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN).//3.3e-22:180:35//HOMO SAPIENS (HUMAN).//P48060
F-MAMMA1002886//MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL).//0.00011:148:39//ACANTHAMOEBA CASTELLANII (AMOEBA).//P19706
F-MAMMA1002887
F-MAMMA1002890//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.030:142:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
F-MAMMA1002892
F-MAMMA1002895//HYPOTHETICAL PROTEIN UL61.//0.00099:143:35//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818
F-MAMMA1002908//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).//0.12:44:43//ORYCTOLAGUS CUNICULUS (RABBIT).//P06333
F-MAMMA1002909//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.00011:28:75//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1002930//BOMBYXIN A-7 PRECURSOR (BBX-A7) (4K-PROTHORACICOTROPIC HORMONE) (4K-PTTH).//0.99:45:46//BOMBYX MORI (SILK MOTH).//P26730
F-MAMMA1002937//ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1).//6.5e-24:147:34//HOMO SAPIENS (HUMAN).//P28698
F-MAMMA1002938//CERULOPLASMIN PRECURSOR (EC 1.16.3.1) (FERROXIDASE).//4.7e-11:44:68//MUS MUSCULUS (MOUSE).//Q61147
F-MAMMA1002941//PROTEIN Q300.//0.0076:21:61//MUS MUSCULUS (MOUSE).//Q02722
F-MAMMA1002947//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//1.9e-08:152:38//STREPTOMYCES FRADIAE.//P20186
F-MAMMA1002964
F-MAMMA1002970//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//0.0057:55:43//HOMO SAPIENS (HUMAN).//P39189
F-MAMMA1002972//BRAIN-SPECIFIC HOMEOBOX/POU DOMAIN PROTEIN 3A (BRN-3A) (OCT-T1) (HOMEOBOX/POU DOMAIN PROTEIN RDC-1).//0.84:53:41//HOMO SAPIENS (HUMAN).//Q01851
F-MAMMA1002973//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//4.6e-11:54:68//HOMO SAPIENS (HUMAN).//P39192
F-MAMMA1002982
F-MAMMA1002987//HYPOTHETICAL 11.9 KD PROTEIN IN RPC8-MFA2 INTERGENIC REGION.//0.17:47:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53906
F-MAMMA1003003//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//8.6e-09:30:73//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1003004//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.0071:41:58//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1003007//SPERM PROTAMINE P1.//0.0076:51:37//TACHYGLOSSUS ACULEATUS ACULEATUS (AUSTRALIAN ECHIDNA).//P35311
F-MAMMA1003011//HISTONE MACRO-H2A.1.//1.8e-60:175:70//RATTUS NORVEGICUS (RAT).//Q02874
F-MAMMA1003013//ACTIN BINDING PROTEIN.//0.097:83:31//SACCHAROMYCES EXIGUUS (YEAST).//P38479
F-MAMMA1003015
F-MAMMA1003019//MYOTUBULARIN.//0.022:56:37//HOMO SAPIENS (HUMAN).//Q13496
F-MAMMA1003026//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0014:208:27//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341
F-MAMMA1003031//PROBABLE E4 PROTEIN (E1^E4).//0.14:49:32//HUMAN PAPILLOMAVIRUS TYPE 6B.//P06459
F-MAMMA1003035//HYPOTHETICAL 24.4 KD PROTEIN IN LPD 3'REGION (ORF4).//5.1e-12:112:34//ZYMOMONAS MOBILIS.//O66114
F-MAMMA1003039//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.4e-07:68:54//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1003040//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!//2.8e-39:90:57//HOMO SAPIENS (HUMAN).//P39190
F-MAMMA1003044
F-MAMMA1003047//SPERM HISTONE P2 PRECURSOR (PROTAMINE 2).//0.18:25:44//BOS TAURUS (BOVINE).//P19782
F-MAMMA1003049//PROBABLE E4 PROTEIN.//0.50:67:29//HUMAN PAPILLOMAVIRUS TYPE 6C.//P20969

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F-MAMMA1003055//WEAK TOXIN CM-2.//0.99:23:30//NAJA HAJE HAJE (EGYPTIAN COBRA).//P01415
F-MAMMA1003056//EXPORTED PROTEIN 7 (FRAGMENT).//1.0:52:32//STREPTOCOCCUS PNEUMONIAE.//P35597
F-MAMMA1003057//MD6 PROTEIN.//1.5e-85:168:95//MUS MUSCULUS (MOUSE).//Q60584
F-MAMMA1003066//REGB PROTEIN.//1.0:62:27//PSEUDOMONAS AERUGINOSA.//Q03381
F-MAMMA1003089//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!//5.1e-15:44:77//HOMO SAPIENS (HUMAN).//P39190
F-MAMMA1003099//ENDOTHELIAL ACTIN-BINDING PROTEIN (ABP-280) (NONMUSCLE FILAMIN) (FILAMIN 1).//4.8e-20:80:62//HOMO SAPIENS (HUMAN).//P21333
F-MAMMA1003104//PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII.//0.98:22:40//SYNECHOCOCCUS ELONGATUS NAEGELI.//P25900
F-MAMMA1003113//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS).//0.67:35:45//GALLUS GALLUS (CHICKEN).//P02467
F-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA).//5.2e-34:141:56//MUS MUSCULUS (MOUSE).//P46735
F-MAMMA1003135//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION.//3.6e-05:91:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170
F-MAMMA1003140
F-MAMMA1003146//MALE SPECIFIC SPERM PROTEIN MST87F.//1.0:33:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175
F-MAMMA1003150//HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME II.//4.4e-10:254:30//CAENORHABDITIS ELEGANS.//Q09625
F-MAMMA1003166//BRAIN PROTEIN H5.//4.0e-42:182:48//HOMO SAPIENS (HUMAN).//O43236
F-NT2RM1000001//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70).//0.15:38:34//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779
F-NT2RM1000018
F-NT2RM1000032//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.51:17:41//CYPRINUS CARPIO (COMMON CARP).//P24948
F-NT2RM1000035//3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE (EC 1.1.1.34) (HMG-COA REDUCTASE).//0.00011:114:27//BLATTELLA GERMANICA (GERMAN COCKROACH).//P54960
F-NT2RM1000037//METALLOTHIONEIN-II (MT-II).//0.025:19:47//SCYLLA SERRATA (MUD CRAB).//P02806
F-NT2RM1000039//VITELLINE MEMBRANE VM34CA PROTEIN PRECURSOR.//0.00083:84:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q06521
F-NT2RM1000055//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.//1.1e-07:34:55//PLASMODIUM LOPHURAE.//P04929
F-NT2RM1000059//MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE FACTOR-LIKE PROTEIN 2) (XMEF2) (RSRFR2).//0.18:83:36//HOMO SAPIENS (HUMAN).//Q02080
F-NT2RM1000062//PROLINE-RICH PEPTIDE P-B.//0.54:34:44//HOMO SAPIENS (HUMAN).//P02814
F-NT2RM1000080//HYPOTHETICAL 35.7 KD PROTEIN SLR1128.//2.1e-20:119:40//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P72655
F-NT2RM1000086//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.20:56:35//HOMO SAPIENS (HUMAN).//P10162
F-NT2RM1000092//COLLAGEN-LIKE PROTEIN.//0.0017:44:45//HERPESVIRUS SAIMIRI (SUBGROUP C / STRAIN 488).//P22576
F-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//5.7e-07:109:28//NEUROSPORA CRASSA.//P87072
F-NT2RM1000119//TRANSCRIPTIONAL REGULATOR IE63 (VMW63) (ICP27).//0.0050:135:32//HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).//P28276
F-NT2RM1000127//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.032:68:32//SORGHUM VULGARE (SORGHUM).//P24152
F-NT2RM1000131//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).//0.82:33:39//BOS TAURUS (BOVINE).//P37359
F-NT2RM1000132//NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-A SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-13KD-A) (CI-13KD-A).//2.7e-59:124:91//HOMO SAPIENS (HUMAN).//O75380
F-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//2.5e-08:148:29//HOMO SAPIENS (HUMAN).//P49902
F-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//1.9e-07:109:27//NEUROSPORA CRASSA.//P87072
F-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE

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SPAC10F6.02C.//1.0e-12:94:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O42643
F-NT2RM1000199//CUTICLE COLLAGEN 12 PRECURSOR.//0.46:130:33//CAENORHABDITIS ELEGANS.//P20630
F-NT2RM1000242//PUTATIVE ATP SYNTHASE J CHAIN, MITOCHONDRIAL (EC 3.6.1.34).//0.85:38:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13931
F-NT2RM1000244//HYPOTHETICAL 131.5 KD PROTEIN C02F12.7 IN CHROMOSOME X.//0.0055:98:36//CAENORHABDITIS ELEGANS.//Q11102
F-NT2RM1000252//TRICHOHYALIN.//2.9e-06:88:36//OVIS ARIES (SHEEP).//P22793
F-NT2RM1000256//GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOMERIZING] (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6- PHOSPHATE AMIDOTRANSFERASE) (GFAT).//2.9e-54:153:67//MUS MUSCULUS (MOUSE).//P47856
F-NT2RM1000257//MAGO NASHI PROTEIN.//5.9e-64:136:89//DROSOPHILA MELANOGASTER (FRUIT FLY).//P49028
F-NT2RM1000260
F-NT2RM1000271//GALACTOKINASE (EC 2.7.1.6).//0.99:41:39//BACILLUS SUBTILIS.//P39574
F-NT2RM1000272//HYPOTHETICAL 55.5 KD PROTEIN ZK1128.2 IN CHROMOSOME III.//8.8e-25:131:45//CAENORHABDITIS ELEGANS.//Q09357
F-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V- ATPASE 28 KD ACCESSORY PROTEIN).//2.5e-63:121:94//BOS TAURUS (BOVINE).//P39942
F-NT2RM1000300//TREACLE PROTEIN (TREACHER COLLINS SYNDROME PROTEIN).//0.51:145:26//HOMO SAPIENS (HUMAN).//Q13428
F-NT2RM1000314
F-NT2RM1000318//50S RIBOSOMAL PROTEIN L23.//0.83:28:35//AQUIFEX AEOLICUS.//O66433
F-NT2RM1000341
F-NT2RM1000354//HYPOTHETICAL 5.8 KD PROTEIN IN PUHA 5'REGION (ORF55).//0.95:43:37//RHODOBACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA).//P26159
F-NT2RM1000355//SPERM-SPECIFIC PROTEIN PHI-1.//0.0016:73:43//MYTILUS EDULIS (BLUE MUSSEL).//Q04621
F-NT2RM1000365//HYPOTHETICAL PROTEIN KIAA0140.//3.5e-10:83:49//HOMO SAPIENS (HUMAN).//Q14153
F-NT2RM1000377//DUAL SPECIFICITY PROTEIN PHOSPHATASE 9 (EC 3.1.3.48) (EC 3.1.3.16) (MITOGEN-ACTIVATED PROTEIN KINASE PHOSPHATASE 4) (MAP KINASE PHOSPHATASE 4) (MKP-4).//4.9e-18:113:38//HOMO SAPIENS (HUMAN).//Q99956
F-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.00023:67:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53915
F-NT2RM1000394//HISTONE H3.3 (H3.B) (H3.3Q).//4.7e-52:71:91//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), ORYCTOLAGUS CUNICULUS (RABBIT), GALLUS GALLUS (CHICKEN), SPISULA SOLIDISSIMA (ATLANTIC SURF-CLAM), DROSOPHILA MELANOGASTER (FRUIT FLY), AND DROSOPHILA HYDEI (FRUIT FLY).//P06351
F-NT2RM1000399//ENDOTHELIN-2 PRECURSOR (ET-2) (FRAGMENT).//0.92:24:45//CANIS FAMILIARIS (DOG).//P12064
F-NT2RM1000421//CUTICLE COLLAGEN 2C (FRAGMENT).//0.12:93:33//HAEMONCHUS CONTORTUS.//P16252
F-NT2RM1000430//PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP).//0.13:86:31//NICOTIANA TABACUM (COMMON TOBACCO).//Q03211
F-NT2RM1000499//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT).//2.9e-17:75:49//HOMO SAPIENS (HUMAN).//Q15057
F-NT2RM1000539//HYPOTHETICAL 10.4 KD PROTEIN IN FTR1-SPT15 INTERGENIC REGION.//2.9e-16:82:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40089
F-NT2RM1000553//GLYCOLIPID TRANSFER PROTEIN (GLTP).//6.4e-06:103:33//SUS SCROFA (PIG).//P17403
F-NT2RM1000555//UNR PROTEIN.//8.7e-77:105:95//RATTUS NORVEGICUS (RAT).//P18395
F-NT2RM1000563//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.15:20:50//HOMO SAPIENS (HUMAN).//P30808
F-NT2RM1000623//CLARA CELL PHOSPHOLIPID-BINDING PROTEIN PRECURSOR (CCPBP) (CLARA CELLS 10 KD SECRETORY PROTEIN) (CC10).//0.17:70:34//HOMO SAPIENS (HUMAN).//P11684
F-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//2.0e-22:133:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43636

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F-NT2RM1000661//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF) (GIFB).//0.0060:24:33//HOMO SAPIENS (HUMAN).//P25713
F-NT2RM1000666//COLD SHOCK PROTEIN SCOF//9.1e-07:67:41//STREPTOMYCES COELICOLOR.//P48859
F-NT2RM1000669//CHLOROPLAST 50S RIBOSOMAL PROTEIN L31.//0.071:69:31//PORPHYRA PURPUREA.//P51290
F-NT2RM1000672//SIGNAL RECOGNITION PARTICLE SEC65 SUBUNIT (FRAGMENT).//0.27:42:42//KLUYVEROMYCES LACTIS (YEAST).//O13475
F-NT2RM1000691//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2).//4.3e-42:241:42//HOMO SAPIENS (HUMAN).//P29375
F-NT2RM1000699//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR (EC 2.1.1.32).//0.94:48:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P15565
F-NT2RM1000702//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 1.//0.0013:139:25//DROSOPHILA MELANOGASTER (FRUIT FLY).//P26308
F-NT2RM1000725//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//1.0:15:60//HOMO SAPIENS (HUMAN).//P02811
F-NT2RM1000741//STATHMIN (CLONE XO20) (FRAGMENT).//1.0:53:32//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q09005
F-NT2RM1000742//HYPOTHETICAL 24.1 KD PROTEIN IN DHFR 3'REGION (ORF2).//1.0:54:42//HERPESVIRUS SAIMIRI (STRAIN 484-77).//P25049
F-NT2RM1000746//HYPOTHETICAL 16.8 KD PROTEIN C29E6.04 IN CHROMOSOME I.//0.11:87:21//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09858
F-NT2RM1000770//DXS6673E PROTEIN.//2.0e-38:190:48//HOMO SAPIENS (HUMAN).//Q14202
F-NT2RM1000772//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//4.3e-12:141:30//PODOSPORA ANSERINA.//Q00808
F-NT2RM1000780//MALE SPECIFIC SPERM PROTEIN MST87F.//0.98:34:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175
F-NT2RM1000781
F-NT2RM1000800//24.1 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION.//7.9e-11:135:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P28707
F-NT2RM1000802//ALPHA-AMYLASE INHIBITOR PAIM I (PIG PANCREATIC ALPHA-AMYLASE INHIBITOR OF MICROBES I).//0.43:62:35//STREPTOMYCES OLIVACEOVIRIDIS (STREPTOMYCES CORCHORUSII).//P09921
F-NT2RM1000811
F-NT2RM1000826//UNR PROTEIN.//1.1e-110:144:83//RATTUS NORVEGICUS (RAT).//P18395
F-NT2RM1000829//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:38:34//DROSOPHILA SIMULANS (FRUIT FLY).//P50270
F-NT2RM1000833//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.4e-62:145:841/CANIS FAMILIARIS (DOG).//P38377
F-NT2RM1000850//TESTIS-SPECIFIC PROTEIN KINASE 1 (EC 2.7.1.-).//6.1e-08:136:33//RATTUS NORVEGICUS (RAT).//Q63572
F-NT2RM1000852//ATP-DEPENDENT RNA HELICASE ROK1.//1.6e-34:212:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P45818
F-NT2RM1000857//HISTONE H1.M6.1.//0.76:31:48//TRYPANOSOMA CRUZI.//P40273
F-NT2RM1000867//MICROSOMAL SIGNAL PEPTIDASE 10.8 KD SUBUNIT (EC 3.4.-.-).//0.0082:76:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P46965
F-NT2RM1000874//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.38:12:58//HOMO SAPIENS (HUMAN).//P30808
F-NT2RM1000882//CYTOCHROME B5.//9.0e-13:92:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40312
F-NT2RM1000883//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.79:22:59//HOMO SAPIENS (HUMAN).//P30808
F-NT2RM1000885//HYPOTHETICAL 5.8 KD PROTEIN.//0.76:18:38//CLOVER YELLOW MOSAIC VIRUS (CYMV).//P16485
F-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE I135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT).//6.2e-70:153:88//RATTUS NORVEGICUS (RAT).//O54888
F-NT2RM1000898//ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR).//4.3e-12:159:28//OXYTRICHA FAL-

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LAX.//P02583
F-NT2RM1000905//GLUTATHIONE S-TRANSFERASE 1-1 (EC 2.5.1.18) (CLASS-THETA).//0.98:39:35//LUCILIA CUPRINA (GREENBOTTLE FLY) (AUSTRALIAN SHEEP BLOWFLY).//P42860
F-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//1.3e-11:169:28// CAENORHABDITIS ELEGANS.//P46577
F-NT2RM1000927//CUTICLE COLLAGEN 1.//0.00048:141:31//CAENORHABDITIS ELEGANS.//P08124
F-NT2RM1000962//HYPOTHETICAL 35.8 KD PROTEIN C4F8.04 IN CHROMOSOME I.//7.1e-13:169:31// SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14180
F-NT2RM1000978//HYPOTHETICAL 20.2 KD PROTEIN IN MNN4-PTK1 INTERGENIC REGION.//0.61:82:34// SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36045
F-NT2RM1001003//ALPHA-2 CATENIN (ALPHA N-CATENIN) (NEURAL ALPHA-CATENIN).//1.6e-21:211:31// GALLUS GALLUS (CHICKEN).//P30997
F-NT2RM1001008//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//3.2e-15:119:36// SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701
F-NT2RM1001043//ENDOTHELIN-1 (ET-1) (FRAGMENT).//0.78:32:34//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//Q28469
F-NT2RM1001044
F-NT2RM1001059//LORICRIN.//8.6e-08:108:39//HOMO SAPIENS (HUMAN).//P23490
F-NT2RM1001066//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//0.99:24:50//LYCOPERSICON ESCULENTUM (TOMATO).//Q43513
F-NT2RM1001072//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II) (PLC-148).//4.7e-15:148:33//HOMO SAPIENS (HUMAN).//P19174
F-NT2RM1001074//HYPOTHETICAL PROTEIN F-215.//8.6e-05:126:30//HUMAN ADENOVIRUS TYPE 2.// P03291
F-NT2RM1001082//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//6.5e-19:75:54//HOMO SAPIENS (HUMAN).// P39195
F-NT2RM1001085//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.49:29:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
F-NT2RM1001092//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//2.8e-42:200:38//HOMO SAPIENS (HUMAN).//P51522
F-NT2RM1001102//HYPOTHETICAL 62.8 KD PROTEIN IN TAF145-YOR1 INTERGENIC REGION.//1.7e-18:161:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53331
F-NT2RM1001105//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//4.0e-05:157:35//STREPTOMYCES FRADIAE.//P20186
F-NT2RM1001112//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.18:20:55//BOS TAURUS (BOVINE).//P02313
F-NT2RM1001115
F-NT2RM1001139//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).//2.0e-25:156:46//PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).//P10496
F-NT2RM2000006//MITOCHONDRIAL RIBOSOMAL PROTEIN S12.//0.76:45:35//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//Q34940
F-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//3.9e-87:238:65//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25167
F-NT2RM2000030//TOXINS 1 AND 2.//0.98:21:42//TRIMERESURUS WAGLERI (WAGLER'S PIT VIPER) (TROPIDOLAEMUS WAGLERI).//P24335
F-NT2RM2000032//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.00059:53:49//HOMO SAPIENS (HUMAN).// P39188
F-NT2RM2000042//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//1.0:68:26//HOMO SAPIENS (HUMAN).//P22532
F-NT2RM2000092//HYPOTHETICAL 67.5 KD PROTEIN IN PRPS4-STE20 INTERGENIC REGION.//7.0e-11:80:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38748
F-NT2RM2000093//OVARY MATURATING PARSIN (OMP).//1.0:26:38//LOCUSTA MIGRATORIA (MIGRATORY LOCUST).//P80045
F-NT2RM2000101//HYPOTHETICAL 39.3 KD PROTEIN C02B8.6 IN CHROMOSOME X.//3.3e-09:56:35// CAENORHABDITIS ELEGANS.//Q11096
F-NT2RM2000124//CAMP-DEPENDENT PROTEIN KINASE, ALPHA-CATALYTIC SUBUNIT (EC 2.7.1.37) (PKA C-ALPHA).//3.1e-35:77:96//MUS MUSCULUS (MOUSE).//P05132

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F-NT2RM2000191//3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA).//3.3e-05:181:27//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//Q23917

F-NT2RM2000192//REPLICATION PROTEIN E1 (FRAGMENTS).//0.019:148:25//COTTONTAIL RABBIT (SHOPE) PAPILLOMAVIRUS (STRAIN WASHINGTON B) (CRPV).//P51894

F-NT2RM2000239//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.00032:111:32//MUS MUSCULUS (MOUSE).//P05143

F-nnnnnnnnnnn//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//0.046:59:33//LYCOPERSICON ESCULENTUM (TOMATO).//Q43512

F-NT2RM2000250//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29).//0.054:46:34//RATTUS NORVEGICUS (RAT).//P08699

F-NT2RM2000259//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).//0.27:112:33//BOVINE HERPES VIRUS TYPE 1 (STRAIN JURA).//P29128

F-NT2RM2000260//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//4.7e-22:191:35//MUS MUSCULUS (MOUSE).//P05143

F-NT2RM2000287//HYPOTHETICAL 11.8 KD PROTEIN C1B3.02C IN CHROMOSOME I.//5.0e-19:83:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13868

F-NT2RM2000322//DIAMINOPIMELATE DECARBOXYLASE (EC 4.1.1.20) (DAP DECARBOXYLASE).//0.47:117:29//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//P56129

F-NT2RM2000359//SPORE GERMINATION PROTEIN 270-11.//0.12:83:36//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P22698

F-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN.//1.3e-16:203:30//HOMO SAPIENS (HUMAN).//P11274

F-NT2RM2000368//DEK PROTEIN.//0.00027:100:32//HOMO SAPIENS (HUMAN).//P35659

F-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLEOTIDE PHOSPHORYLASE) (PNPASE).//6.8e-36:170:47//ESCHERICHIA COLI.//P05055

F-NT2RM2000374//NODAL PRECURSOR.//1.1e-32:64:95//MUS MUSCULUS (MOUSE).//P43021

F-NT2RM2000395//IMMEDIATE-EARLY PROTEIN IE180.//0.31:41:43//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675

F-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).//1.2e-30:228:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32802

F-NT2RM2000407//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.032:105:30//HOMO SAPIENS (HUMAN).//P51805

F-NT2RM2000420//METALLOTHIONEIN (MT).//0.88:42:38//PLEURONECTES PLATESSA (PLAICE).//P07216

F-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//2.0e-117:237:87//RATTUS NORVEGICUS (RAT).//Q08469

F-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION.//1.1e-08:157:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36113

F-NT2RM2000469//70 KD ANTIGEN.//0.050:207:23//SHIGELLA FLEXNERI.//P18010

F-NT2RM2000490//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.022:25:44//HOMO SAPIENS (HUMAN).//P02811

F-NT2RM2000502//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.0037:17:58//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645

F-NT2RM2000504//HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17.//1.7e-22:195:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O42908

F-NT2RM2000522//RAS-RELATED PROTEIN RABA (FRAGMENT).//3.6e-05:67:29//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34141

F-NT2RM2000540//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III.//8.4e-33:214:38//CAENORHABDITIS ELEGANS.//Q18262

F-NT2RM2000556//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//1.7e-09:133:36//HOMO SAPIENS (HUMAN).//P56524

F-NT2RM2000566//INTEGRIN ALPHA-6 PRECURSOR (VLA-6) (CD49F).//2.2e-60:244:51//HOMO SAPIENS (HUMAN).//P23229

F-NT2RM2000567//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//2.3e-09:192:34//MUS MUSCULUS (MOUSE).//P05143

F-NT2RM2000569//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//9.0e-08:43:72//HOMO SAPIENS (HUMAN).//P39188

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F-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS).// 9.1e-54:225:45//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P73505
F-NT2RM2000581//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//0.079:111:34//HOMO SAPIENS (HUMAN).//Q15427
F-NT2RM2000588//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//2.3e-09:193:32//HOMO SAPIENS (HUMAN).//P56524
F-NT2RM2000594//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.18:33:42//HOMO SAPIENS (HUMAN).// P02811
F-NT2RM2000599//DNA (CYTOSINE-5)-METHYLTRANSFERASE (EC 2.1.1.37) (DNA METHYLTRANSFERASE) (DNA METASE) (MCMT) (M.MMUI).//1.5e-09:68:45//MUS MUSCULUS (MOUSE).//P13864
F-NT2RM2000609//GRANULIN 2.//0.83:42:35//CYPRINUS CARPIO (COMMON CARP).//P81014
F-NT2RM2000612//ZINC FINGER PROTEIN GCS1.//7.2e-05:155:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35197
F-NT2RM2000623//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//1.8e-09:196:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
F-NT2RM2000624//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.070:113:27//DROSOPHILA ERECTA (FRUIT FLY).//P13730
F-NT2RM2000635//SPERM PROTAMINE P1.//0.54:47:38//ANTECHINUS STUARTII.//P42129
F-NT2RM2000636//OUTER MEMBRANE PROTEIN H.8 PRECURSOR.//0.096:62:35//NEISSERIA GONORRHOEAE.//P11910
F-NT2RM2000639//HYPOTHETICAL PROTEIN MJ0243.//0.99:32:34//METHANOCOCCUS JANNASCHII.// Q57694
F-NT2RM2000649//NEURONAL CALCIUM SENSOR 1 (NCS-1).//0.00049:70:35//RATTUS NORVEGICUS (RAT), AND GALLUS GALLUS (CHICKEN).//P36610
F-NT2RM2000669//50S RIBOSOMAL PROTEIN L34.//1.0:34:44//BACILLUS SUBTILIS.//P05647
F-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//7.0e-116:243:87//HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE).//P32391
F-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-I).//3.8e-21:174:35//HOMO SAPIENS (HUMAN).//Q15404
F-NT2RM2000718//HYPOTHETICAL 52.9 KD SERINE-RICH PROTEIN C11G7.01 IN CHROMOSOME I.//0.0022: 174:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13695
F-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.6e-102:246:74//HOMO SAPIENS (HUMAN).//P28160
F-NT2RM2000740//HYPOTHETICAL 131.1 KD HELICASE IN ALG7-ENP1 INTERGENIC REGION.//8.5e-51:212: 49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38144
F-NT2RM2000795//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//9.0e-41:125:53//HOMO SAPIENS (HUMAN).//P39189
F-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP).//1.1e-128:291:89// RATTUS NORVEGICUS (RAT).//P23514
F-NT2RM2000837//CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITOR P57) (P57KIP2).//3.9e-05:113:36//HOMO SAPIENS (HUMAN).//P49918
F-NT2RM2000951//HYPOTHETICAL 60.3 KD PROTEIN R08D7.7 IN CHROMOSOME III.//2.5e-49:273:39// CAENORHABDITIS ELEGANS.//P30646
F-NT2RM2000952//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H) (FRAGMENT).//0.037:234:23//RATTUS NORVEGICUS (RAT).//P16884
F-NT2RM2000984//HYPOTHETICAL 54.7 KD PROTEIN F37A4.1 IN CHROMOSOME III.//6.3e-44:216:43// CAENORHABDITIS ELEGANS.//P41879
F-NT2RM2001004//SYNAPSINS IA AND IB.//0.15:178:32//RATTUS NORVEGICUS (RAT).//P09951
F-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.4e-87:188:90//MUS MUSCULUS (MOUSE).// Q60809
F-NT2RM2001065//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.53:122:31//TRYPANOSOMA BRUCEI BRUCEI.//P24499
F-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//3.4e-13:171:30// CAENORHABDITIS ELEGANS.//P46577
F-NT2RM2001105//SPORE COAT PROTEIN SP96.//7.8e-06:141:34//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P14328
F-NT2RM2001131//PROBABLE EUKARYOTIC INITIATION FACTOR C17C9.03.//2.3e-18:249:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10475

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F-NT2RM2001141//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.//0.050:134:26//CAENORHABDITIS ELEGANS.//P34681
F-NT2RM2001152
F-NT2RM2001177//COLLAGEN ALPHA 1(XIV) CHAIN PRECURSOR (UNDULIN).//0.86:42:40//GALLUS GALLUS (CHICKEN).//P32018
F-NT2RM2001194//SMOOTHELIN.//4.7e-05:77:32//HOMO SAPIENS (HUMAN).//P53814
F-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.7e-18:218:35//MUS MUSCULUS (MOUSE).//P05143
F-NT2RM2001201//CYSTEINE STRING PROTEIN (CCCS1).//0.041:22:59//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P56101
F-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10).//1.3e-13:183:32//RATTUS NORVEGICUS (RAT).//P97924
F-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMIDOHYDROLASE).//6.5e-121:218:98//RATTUS NORVEGICUS (RAT).//P13264
F-NT2RM2001243//HYPOTHETICAL 200.0 KD PROTEIN IN GZF3-IME2 INTERGENIC REGION.//0.00019:177:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42945
F-NT2RM2001247//LEGUMIN B (FRAGMENT).//0.22:54:35//PISUM SATIVUM (GARDEN PEA).//P14594
F-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.8e-109:207:98//MUS MUSCULUS (MOUSE).//P53995
F-NT2RM2001291//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.016:22:40//HOMO SAPIENS (HUMAN).//P22531
F-NT2RM2001306//REF(2)P PROTEIN.//0.61:51:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//P14199
F-NT2RM2001312//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//7.2e-11:33:72//HOMO SAPIENS (HUMAN).//P39195
F-NT2RM2001319
F-NT2RM2001324//ZYXIN.//5.1e-22:91:38//GALLUS GALLUS (CHICKEN).//Q04584
F-NT2RM2001345//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//7.4e-10:159:27//PODOSPORA ANSERINA.//Q00808
F-NT2RM2001360//ACCESSORY GLAND PEPTIDE PRECURSOR (PARAGONIAL PEPTIDE B).//1.0:27:48//DROSOPHILA MELANOGASTER (FRUIT FLY).//P05623
F-NT2RM2001370//NAPE PROTEIN.//0.98:44:31//PARACOCCUS DENITRIFICANS (SUBSP. THIOSPHAERA PANTOTROPHA).//Q56348
F-NT2RM2001393//VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C; LIPOVITELLIN LV-2].//0.0024:163:31//ICHTHYOMYZON UNICUSPUS (SILVER LAMPREY).//Q91062
F-NT2RM2001420
F-NT2RM2001424//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U).//2.4e-41:140:59//HOMO SAPIENS (HUMAN).//Q00839
F-NT2RM2001499//HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG).//3.7e-71:201:68//HOMO SAPIENS (HUMAN).//P30825
F-NT2RM2001504//CUTICLE COLLAGEN 2.//0.028:41:39//CAENORHABDITIS ELEGANS.//P17656
F-NT2RM2001524//HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III.//6.7e-47:190:42//CAENORHABDITIS ELEGANS.//Q09316
F-NT2RM2001544//TELOMERE-BINDING PROTEIN 51 KD SUBUNIT.//0.0027:136:33//EUPLOTES CRASSUS.//Q06184
F-NT2RM2001547//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION.//8.5e-18:91:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40564
F-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//3.9e-35:212:41//HOMO SAPIENS (HUMAN).//P19474
F-NT2RM2001582//RESA PROTEIN.//0.0033:72:27//BACILLUS SUBTILIS.//P35160
F-NT2RM2001588//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//1.0e-06:115:32//ZEA MAYS (MAIZE).//P14918
F-NT2RM2001592//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.033:156:23//HOMO SAPIENS (HUMAN).//P26371
F-NT2RM2001605//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2).//1.1e-116:249:82//HOMO SAPIENS (HUMAN).//P29375
F-NT2RM2001613//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.2e-97:192:100//RATTUS NORVEGICUS (RAT).//P38378

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F-NT2RM2001632//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.00068:145:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
F-NT2RM2001635//NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145).//1.1e-39:235:47//RATTUS NORVEGICUS (RAT).//P52591
F-NT2RM2001637//HYPOTHETICAL BHLF1 PROTEIN.//0.075:197:29//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
F-NT2RM2001641//NADH-CYTOCHROME B5 REDUCTASE (EC 1.6.2.2) (B5R).//0.013:29:68//HOMO SAPIENS (HUMAN).//P00387
F-NT2RM2001648//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//3.2e-65:132:100//CANIS FAMILIARIS (DOG).//P38377
F-NT2RM2001652//PROTEIN TRANSPORT PROTEIN SEC7.//1.6e-32:261:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11075
F-NT2RM2001659//CARBOXYPEPTIDASE A INHIBITOR.//0.83:30:46//ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P19399
F-NT2RM2001664//IKI3 PROTEIN.//1.3e-31:265:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06706
F-NT2RM2001668//TONB PROTEIN.//0.32:39:41//XANTHOMONAS CAMPESTRIS (PV. CAMPESTRIS).//O34261
F-NT2RM2001670//ZINC FINGER PROTEIN 174.//3.6e-21:172:39//HOMO SAPIENS (HUMAN).//Q15697
F-NT2RM2001671//HYPOTHETICAL 118.6 KD PROTEIN C29E6.03C IN CHROMOSOME I.//1.6e-10:229:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09857
F-NT2RM2001675//DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52) (DHDPS).//1.0:184:21//METHANOCOCCUS JANNASCHII.//Q57695
F-NT2RM2001681//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//0.0039:199:22//DROSOPHILA MELANOGASTER (FRUIT FLY).//P54399
F-NT2RM2001688//HYPOTHETICAL 28.1 KD PROTEIN IN SIPU-PBPC INTERGENIC REGION.//2.6e-21:162:33//BACILLUS SUBTILIS.//P42966
F-NT2RM2001695//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//4.9e-41:60:81//HOMO SAPIENS (HUMAN).//P39194
F-NT2RM2001696//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//9.8e-16:126:38//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479
F-NT2RM2001698//PENAEIDIN-3B PRECURSOR (P3-B).//0.36:52:34//PENAEUS VANNAMEI (PENOEID SHRIMP) (EUROPEAN WHITE SHRIMP).//P81059
F-NT2RM2001699//TRANSCRIPTION INITIATION FACTOR TFIID 30 KD SUBUNIT (TAFII-30) (TAFII30).//0.0012:79:40//HOMO SAPIENS (HUMAN).//Q12962
F-NT2RM2001700//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3.99.-) (VLCAD) (FRAGMENT).//1.0e-30:140:53//MUS MUSCULUS (MOUSE).//P50544
F-NT2RM2001706//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.5e-33:95:75//HOMO SAPIENS (HUMAN).//P39195
F-NT2RM2001716//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.//0.010:116:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47179
F-NT2RM2001718//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB.//0.00029:77:37//BACILLUS SUBTILIS.//P39217
F-NT2RM2001723//POSTERIOR PITUITARY PEPTIDE.//0.94:26:53//BOS TAURUS (BOVINE).//P01154
F-NT2RM2001727//E7 PROTEIN.//0.91:46:34//HUMAN PAPILLOMAVIRUS TYPE 23.//P50781
F-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//4.9e-07:139:29//CAENORHABDITIS ELEGANS.//Q09931
F-NT2RM2001743//PROENKEPHALIN A PRECURSOR.//0.75:65:35//CAVIA PORCELLUS (GUINEA PIG).//P47969
F-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210.//1.5e-14:119:36//HOMO SAPIENS (HUMAN).//Q92609
F-NT2RM2001760//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//8.3e-58:119:99//CANIS FAMILIARIS (DOG).//P38377
F-NT2RM2001768//HYPOTHETICAL PROTEIN UL25.//0.45:77:32//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16761
F-NT2RM2001771//ZINC FINGER PROTEIN 135.//4.6e-80:224:60//HOMO SAPIENS (HUMAN).//P52742
F-NT2RM2001782//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-

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PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//7.0e-06:61:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41940
F-NT2RM2001784//HYPOTHETICAL PROTEIN UL61.//0.00070:145:33//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818
F-NT2RM2001785//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE).//1.5e-08:127:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q08871
F-NT2RM2001797//ZINC FINGER PROTEIN 135.//1.6e-73:267:49//HOMO SAPIENS (HUMAN).//P52742
F-NT2RM2001800//HYPOTHETICAL HELICASE MG018/MG017/MG016 HOMOLOG.//3.9e-12:171:33//MYCOPLASMA PNEUMONIAE.//P75093
F-NT2RM2001803//IKI3 PROTEIN.//1.6e-38:283:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06706
F-NT2RM2001805//COLD SHOCK-LIKE PROTEIN CSPH.//0.51:46:32//SALMONELLA TYPHIMURIUM.//O33793
F-NT2RM2001813//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHROMOSOME III.//5.0e-05:82:32//CAENORHABDITIS ELEGANS.//Q17963
F-NT2RM2001823//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2).//3.6e-49:233:45//HOMO SAPIENS (HUMAN).//O14647
F-NT2RM2001839//RETICULOCALBIN 1 PRECURSOR.//5.2e-65:222:56//HOMO SAPIENS (HUMAN).//Q15293
F-NT2RM2001840//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//9.6e-33:102:68//HOMO SAPIENS (HUMAN).//P39194
F-NT2RM2001855//BASP1 PROTEIN.//0.054:120:30//HOMO SAPIENS (HUMAN).//P80723
F-NT2RM2001867//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//4.1e-19:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867
F-NT2RM2001879//HYPOTHETICAL 47.3 KD PROTEIN C22G7.07C IN CHROMOSOME I.//5.9e-15:76:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09800
F-NT2RM2001886//HYPOTHETICAL 126.9 KD PROTEIN C22G7.04 IN CHROMOSOME I.//1.4e-41:249:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09798
F-NT2RM2001896//HYPOTHETICAL 83.2 KD PROTEIN IN KAR4-PBN1 INTERGENIC REGION.//2.1e-59:197:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25582
F-NT2RM2001903//HYPOTHETICAL PROTEIN MJ0263.//0.070:132:31//METHANOCOCCUS JANNASCHII.//O06917
F-NT2RM2001930//THROMBOSPONDIN 2 PRECURSOR.//7.1e-05:53:47//MUS MUSCULUS (MOUSE).//Q03350
F-NT2RM2001935//PUTATIVE CUTICLE COLLAGEN F55C10.3.//0.00046:116:35//CAENORHABDITIS ELEGANS.//Q21184
F-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//4.5e-27:216:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P28320
F-NT2RM2001950//HIRUDIN HV1 (BUFRUDIN).//0.59:43:34//HIRUDINARIA MANILLENSIS (BUFFALO LEECH).//P81492
F-NT2RM2001982//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-8 SUBUNIT (G GAMMA-C).//0.72:35:42//BOS TAURUS (BOVINE).//P50154
F-NT2RM2001983//PROLINE-RICH PEPTIDE P-B.//0.00035:23:52//HOMO SAPIENS (HUMAN).//P02814
F-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//8.6e-24:197:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P37838
F-NT2RM2001997
F-NT2RM2001998//IMMEDIATE-EARLY PROTEIN IE180.//0.076:92:27//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675
F-NT2RM2002004//SLF1 PROTEIN.//3.5e-06:235:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12034
F-NT2RM2002014//HYPOTHETICAL PROTEIN HI0568.//2.1e-17:235:29//HAEMOPHILUS INFLUENZAE.//P71353
F-NT2RM2002030//GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOMERIZING] (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6- PHOSPHATE AMIDOTRANSFERASE) (GFAT).//9.5e-105:271:76//MUS MUSCULUS (MOUSE).//P47856
F-NT2RM2002049//SMALL PROLINE-RICH PROTEIN 2-1.//0.099:41:41//HOMO SAPIENS (HUMAN).//P35326
F-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.012:217:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q07878
F-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//

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1.1e-09:65:53//MUS MUSCULUS (MOUSE).//Q61990
F-NT2RM2002091//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.072:74:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214
F-NT2RM2002100//ATP-DEPENDENT RNA HELICASE ROK1.//4.5e-50:289:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P45818
F-NT2RM2002109//NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C).//1.4e-14:203:32//RATTUS NORVEGICUS (RAT).//Q03351
F-NT2RM2002128//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.0025:139:31//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437
F-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//9.2e-20:42:73//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//P47805
F-NT2RM2002145//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT 12 PRECURSOR.//0.0085:200:26//TRITICUM AESTIVUM (WHEAT).//P08488
F-NT2RM2002178//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//5.8e-05:56:39//BOS TAURUS (BOVINE).//P25508
F-NT2RM2002580//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//2.9e-14:96:37//PETROMYZON MARINUS (SEA LAMPREY).//P25210
F-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//8.6e-95:271:67//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25167
F-NT2RM4000027//INTERFERON-ACTIVATABLE PROTEIN 202 (IFI-202).//0.99:72:31//MUS MUSCULUS (MOUSE).//P15091
F-NT2RM4000030//LAS1 PROTEIN.//1.4e-14:184:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36146
F-NT2RM4000046//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.99:120:28//RATTUS NORVEGICUS (RAT).//P13941
F-NT2RM4000061
F-NT2RM4000085//ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (NDH II) (DEAD BOX PROTEIN 9) (MHEL-5).//8.5e-40:263:38//MUS MUSCULUS (MOUSE).//O70133
F-NT2RM4000086//HYPOTHETICAL PROTEIN HI1497.//1.0:27:37//HAEMOPHILUS INFLUENZAE.//P44221
F-NT2RM4000104//ZINC FINGER PROTEIN 134.//1.0e-26:64:56//HOMO SAPIENS (HUMAN).//P52741
F-NT2RM4000139//PREPROTEIN TRANSLOCASE SECE SUBUNIT.//0.99:38:42//THERMOTOGA MARITIMA.//P35874
F-NT2RM4000155//THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE--TRNA LIGASE) (THRRS).//6.3e-34:181:40//HOMO SAPIENS (HUMAN).//P26639
F-NT2RM4000156//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//4.6e-12:142:33//NICOTIANA TABACUM (COMMON TOBACCO).//P13983
F-NT2RM4000167//KINESIN-LIKE PROTEIN KIF4.//3.4e-123:269:91//MUS MUSCULUS (MOUSE).//P33174
F-NT2RM4000169//M PROTEIN, SEROTYPE 2.2 PRECURSOR.//9.7e-10:229:26//STREPTOCOCCUS PYOGENES.//P50469
F-NT2RM4000191//P68-LIKE PROTEIN.//2.1e-11:104:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P24783
F-NT2RM4000197//CUTICLE PROTEIN CP463 (CPCP463).//0.84:29:37//CANCER PAGURUS (ROCK CRAB).//P81587
F-NT2RM4000199//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//1.8e-06:187:34//HOMO SAPIENS (HUMAN).//P10162
F-NT2RM4000200//HYPOTHETICAL 9.4 KD PROTEIN IN FLAL 3'REGION (ORF3).//0.52:42:40//BACILLUS LICHENIFORMIS.//P22754
F-NT2RM4000202//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN).//0.00044:168:32//ORYCTOLAGUS CUNICULUS (RABBIT).//P14282
F-NT2RM4000210//EXTENSIN PRECURSOR.//0.27:129:27//DAUCUS CAROTA (CARROT).//P06599
F-NT2RM4000215//MAK16 PROTEIN.//2.0e-65:234:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P10962
F-NT2RM4000229//GAR2 PROTEIN.//0.13:217:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891
F-NT2RM4000233//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.047:108:30//HOMO SAPIENS (HUMAN).//P51805
F-NT2RM4000244//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.67:59:27//BALAENOPTERA

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PHYSALUS (FINBACK WHALE) (COMMON RORQUAL).//P24947
F-NT2RM4000251//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.0059:108:35//MUS MUSCULUS (MOUSE).//P05143
F-NT2RM4000265//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//8.1e-38:70:70//HOMO SAPIENS (HUMAN).//P39188
F-NT2RM4000290//TRANSDUCIN-LIKE ENHANCER PROTEIN 3 (ESG3).//1.6e-115:209:94//HOMO SAPIENS (HUMAN).//Q04726
F-NT2RM4000324//PRESPORE PROTEIN DP87 PRECURSOR.//0.14:136:30//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//Q04503
F-NT2RM4000327//HYPOTHETICAL 8.9 KD PROTEIN IN IE0-IE1 INTERGENIC REGION.//0.91:73:28//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41703
F-NT2RM4000344//YME1 PROTEIN HOMOLOG (EC 3.4.24.-).//9.4e-78:241:55//CAENORHABDITIS ELEGANS.//P54813
F-NT2RM4000349//CYSTEINE STRING PROTEIN (CCCS1).//0.055:22:59//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P56101
F-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//4.6e-26:208:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24371
F-NT2RM4000356//COAT PROTEIN.//0.11:105:36//SATELLITE TOBACCO MOSAIC VIRUS (STMV).//P17574
F-NT2RM4000366//IMMEDIATE-EARLY PROTEIN.//1.2e-05:215:24//HERPES VIRUS SAIMIRI (STRAIN 11).//Q01042
F-NT2RM4000368//HYPOTHETICAL 7.3 KD PROTEIN IN RPBA-GP46 INTERGENIC REGION.//0.54:46:36//BACTERIOPHAGE RB69.//O64300
F-NT2RM4000386//RHSC PROTEIN PRECURSOR.//0.0096:162:29//ESCHERICHIA COLI.//P16918
F-NT2RM4000395//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION.//4.5e-66:256:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43616
F-NT2RM4000414//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5'REGION.//0.13:33:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53820
F-NT2RM4000421//MRNA TRANSPORT REGULATOR MTR10.//5.0e-13:171:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q99189
F-NT2RM4000425//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//2.1e-25:46:80//HOMO SAPIENS (HUMAN).//P39193
F-NT2RM4000433//CUTICLE COLLAGEN 3A3.//2.5e-06:77:38//HAEMONCHUS CONTORTUS.//P16253
F-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//4.3e-09:215:22//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10297
F-NT2RM4000471//TRNA SPLICING PROTEIN SPL1.//6.7e-73:163:65//CANDIDA ALBICANS (YEAST).//P87185
F-NT2RM4000486//COLLAGEN ALPHA 2(VI) CHAIN PRECURSOR.//0.0012:121:34//GALLUS GALLUS (CHICKEN).//P15988
F-NT2RM4000496//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RNA POLYMERASE II SUBUNIT 1).//5.9e-09:175:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P36594
F-NT2RM4000511//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.020:122:31//DROSOPHILA SIMULANS (FRUIT FLY).//P13729
F-NT2RM4000514//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.46:68:32//ARTEMIA SANFRANCISCANA (BRINE SHRIMP) (ARTEMIA FRANCISCANA).//Q37708
F-NT2RM4000515//GAR2 PROTEIN.//3.2e-05:198:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891
F-NT2RM4000520//HYPOTHETICAL 7.5 KD PROTEIN (ORF 63).//0.011:55:38//SPINACIA OLERACEA (SPINACH).//P08974
F-NT2RM4000531//ZINC FINGER PROTEIN 169 (FRAGMENT).//3.6e-44:244:42//HOMO SAPIENS (HUMAN).//Q14929
F-NT2RM4000532//PUTATIVE MEMBRANE PROTEIN 53.//1.0:47:34//HERPES VIRUS SAIMIRI (STRAIN 11).//Q01049
F-NT2RM4000534//HYPOTHETICAL 5.9 KD PROTEIN IN WRBA-PUTA INTERGENIC REGION.//0.75:26:46//ESCHERICHIA COLI.//P56614
F-NT2RM4000585//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P16; CORE PROTEIN P26].//0.019:86:34//HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE SBLIS Y) (HIV-2).//P12450
F-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).//5.0e-23:224:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

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F-NT2RM4000595//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III.//3.8e-62:226:50// CAENORHABDITIS ELEGANS.//P34284
F-NT2RM4000603//SRC SUBSTRATE CORTACTIN (AMPLAXIN) (EMS1 ONCOGENE).//0.077:132:22//HOMO SAPIENS (HUMAN).//Q14247
F-NT2RM4000611//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHROMOSOME III.//1.9e-06:82:32//CAENORHABDITIS ELEGANS.//Q17963
F-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//5.3e-79:213:62//ESCHERICHIA COLI.//P27550
F-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL1374.//1.3e-11:147:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P74168
F-NT2RM4000689
F-NT2RM4000698//CHORION CLASS HIGH-CYSTEINE HCA PROTEIN 12 PRECURSOR (HC-A.12).//0.26:45:33//BOMBYX MORI (SILK MOTH).//P05687
F-NT2RM4000700//THIOPHENE AND FURAN OXIDATION PROTEIN THDF.//0.95:165:25//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//P53364
F-NT2RM4000712//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//2.2e-82:152:63//CAENORHABDITIS ELEGANS.//P34547
F-NT2RM4000717//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.80:54:40//DROSOPHILA SIMULANS (FRUIT FLY).//P13729
F-NT2RM4000733//OCTAPEPTIDE-REPEAT PROTEIN T2.//1.5e-08:139:28//MUS MUSCULUS (MOUSE).//Q06666
F-NT2RM4000734//GASTRULA ZINC FINGER PROTEIN XLCGF26.1 (FRAGMENT).//7.2e-20:205:28//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18715
F-NT2RM4000741//SPERM PROTAMINE P1.//0.89:52:38//ISOODON MACROURUS (SHORT-NOSED BANDICOOT).//P42136
F-NT2RM4000751//ZINC FINGER PROTEIN 26 (ZFP-26) (MKR3 PROTEIN) (FRAGMENT).//5.2e-77:246:52// MUS MUSCULUS (MOUSE).//P10076
F-NT2RM4000764//KERATIN, GLYCINE/TYROSINE-RICH OF HAIR.//0.062:33:42//OVIS ARIES (SHEEP).//Q02958
F-NT2RM4000778
F-NT2RM4000779//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.014:53:45//VOLVOX CARTERI.//P21997
F-NT2RM4000787//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).//0.00011:73:39//MUS MUSCULUS (MOUSE).//P98063
F-NT2RM4000790//SPORE COAT PROTEIN SP96.//0.00083:157:29//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P14328
F-NT2RM4000795//CHOLINESTERASE PRECURSOR (EC 3.1.1.8) (ACYLCHOLINE ACYLHYDROLASE) (CHOLINE ESTERASE II) (BUTYRYLCHOLINE ESTERASE) (PSEUDOCHOLINESTERASE).//7.4e-41:271:36// HOMO SAPIENS (HUMAN).//P06276
F-NT2RM4000796//5-METHYLCYTOSINE-SPECIFIC RESTRICTION ENZYME B (EC 3.1.21.-).//0.28:82:30//ESCHERICHIA COLI.//P15005
F-NT2RM4000798//PROTEIN TRANSPORT PROTEIN SEC7.//4.7e-38:165:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11075
F-NT2RM4000813//METALLOTHIONEIN-IB.//0.0025:25:44//OVIS ARIES (SHEEP).//P09577
F-NT2RM4000820
F-NT2RM4000833//HYPOTHETICAL PROTEIN MJ1136.//6.5e-42:206:41//METHANOCOCCUS JANNASCHII.//Q58536
F-NT2RM4000848//BRAIN-SPECIFIC HOMEOBOX/POU DOMAIN PROTEIN 3A (BRN-3A) (BRN-3.0).//0.00060:159:33//MUS MUSCULUS (MOUSE).//P17208
F-NT2RM4000852//SMALL PROLINE-RICH PROTEIN 2B (SPR-2B).//0.0076:13:69//HOMO SAPIENS (HUMAN).//P35325
F-NT2RM4000855//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//0.0060:68:44//HOMO SAPIENS (HUMAN).//P39194
F-NT2RM4000887//RTS1 PROTEIN (SCS1 PROTEIN).//0.23:153:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38903
F-NT2RM4000895//HYPOTHETICAL 53.5 KD PROTEIN IN PHO2-POL3 INTERGENIC REGION.//3.3e-09:80:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43123

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F-NT2RM4000950//HYPOTHETICAL PROTEIN MJ0572.//0.090:68:29//METHANOCOCCUS JANNASCHII.// Q57992
F-NT2RM4000971//KINESIN LIGHT CHAIN (KLC).//0.79:201:24//LOLIGO PEALEII (LONGFIN SQUID).//P46825
F-NT2RM4000979//MYOSIN REGULATORY LIGHT CHAIN 2, NONSARCOMERIC (MYOSIN RLC).//1.2e-07:25:96//HOMO SAPIENS (HUMAN).//P19105
F-NT2RM4000996//ZINC FINGER PROTEIN 37 (ZFP-37) (MALE GERM CELL SPECIFIC ZINC FINGER PROTEIN).//1.4e-56:253:46//MUS MUSCULUS (MOUSE).//P17141
F-NT2RM4001002
F-NT2RM4001016//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30].//0.25:101:31//FBR MURINE OSTEOSARCOMA VIRUS.//P29175
F-NT2RM4001032//CUTICLE COLLAGEN 2.//2.6e-07:130:39//CAENORHABDITIS ELEGANS.//P17656
F-NT2RM4001047//MO25 PROTEIN.//5.6e-107:252:80//MUS MUSCULUS (MOUSE).//Q06138
F-NT2RM4001054//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//9.0e-109:209:94//CANIS FAMILIARIS (DOG).//P38377
F-NT2RM4001084//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN UXUR-IADA INTERGENIC REGION.//0.57:95:30//ESCHERICHIA COLI.//P39376
F-NT2RM4001092//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//2.5e-47:231:47// CAENORHABDITIS ELEGANS.//Q09531
F-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME II.//1.3e-08:243:23// CAENORHABDITIS ELEGANS.//Q09417
F-NT2RM4001140//HOMEOBOX PROTEIN MSH-D.//7.1e-13:103:38//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q01704
F-NT2RM4001151//SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1).//0.26:96:34//HOMO SAPIENS (HUMAN).// P17600
F-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN.//3.6e-103:201:91//BOS TAURUS (BOVINE).// Q27969
F-NT2RM4001160//GLUTATHIONE S-TRANSFERASE (EC 2.5.1.18) (CLASS-PHI) (FRAGMENTS).//1.0:33:36// BRASSICA OLERACEA (CAULIFLOWER).//P48438 F-NT2RM4001187//PREPROTEIN TRANSLOCASE SECA SUBUNIT.//0.44:158:27//MYCOPLASMA GENITALIUM.//P47318
F-NT2RM4001191//LONG NEUROTOXIN 2 (TOXIN C).//0.99:44:43//ASTROTIA STOKESI (STOKES'S SEA SNAKE) (DISTEIRA STOKESI).//P01381
F-NT2RM4001200//ZINC FINGER PROTEIN 135.//2.2e-82:245:59//HOMO SAPIENS (HUMAN).//P52742
F-NT2RM4001203//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.028:94:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214
F-NT2RM4001204//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.0096:182:34//HOMO SAPIENS (HUMAN).//Q15428
F-NT2RM4001217//RING CANAL PROTEIN (KELCH PROTEIN).//2.1e-21:221:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
F-NT2RM4001256//CBP3 PROTEIN PRECURSOR.//0.30:55:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P21560
F-NT2RM4001258//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.00031:132:39//STREPTOMYCES FRADIAE.//P20186
F-NT2RM4001309//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT).//0.048:132:28//HOMO SAPIENS (HUMAN).//P02812
F-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-LIKE (EC 2.7.1.137) (PI3-KINASE) (PTDINS-3-KINASE) (PI3K).//2.6e-37:124:65//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P54676
F-NT2RM4001316//ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.3) (MCAD).//1.7e-10:185:30//RATTUS NORVEGICUS (RAT).//P08503
F-NT2RM4001320//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//1.5e-08:197:26//MUS MUSCULUS (MOUSE).//P52734
F-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).//7.7e-14:82:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32626
F-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HOL1 INTERGENIC REGION.//3.3e-16:128:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53742
F-NT2RM4001347//HYPOTHETICAL 76.9 KD PROTEIN IN RPM2-TUB1 INTERGENIC REGION.//0.067:111:33// SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04511
F-NT2RM4001371
F-NT2RM4001382//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.//1.0e-08:82:39//PLASMODIUM LOPHU-

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RAE.//P04929
F-NT2RM4001384
F-NT2RM4001410//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//2.1e-08:185:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
F-NT2RM4001411//EARLY NODULIN 20 PRECURSOR (N-20).//5.3e-05:105:38//MEDICAGO TRUNCATULA (BARREL MEDIC).//P93329
F-NT2RM4001412//GTPASE-ACTIVATING PROTEIN (GAP) (RAS P21 PROTEIN ACTIVATOR) (P120GAP) (RASGAP).//6.2e-17:109:41//RATTUS NORVEGICUS (RAT).//P50904
F-NT2RM4001414//ZINC FINGER PROTEIN 177.//8.3e-06:54:50//HOMO SAPIENS (HUMAN).//Q13360
F-NT2RM4001437//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//2.1e-24:87:65//HOMO SAPIENS (HUMAN).//P39192
F-NT2RM4001444//PROBABLE ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS) (FRAGMENT).//2.6e-45:197:47//CIONA INTESTINALIS.//Q94425
F-NT2RM4001454//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT).//0.0060:95:29//HOMO SAPIENS (HUMAN).//Q15057
F-NT2RM4001455//PROBABLE E5B PROTEIN.//0.41:44:36//HUMAN PAPILLOMAVIRUS TYPE 6B.//P06461
F-NT2RM4001483//ZINC FINGER PROTEIN 136.//1.7e-28:85:64//HOMO SAPIENS (HUMAN).//P52737
F-NT2RM4001489//PTB-ASSOCIATED SPLICING FACTOR (PSF).//0.086:111:34//HOMO SAPIENS (HUMAN).//P23246
F-NT2RM4001519//ACID UREASE ALPHA SUBUNIT (EC 3.5.1.5) (UREA AMIDOHYDROLASE).//0.82:51:47//LACTOBACILLUS FERMENTUM.//P26929
F-NT2RM4001522//TROPOMYOSIN.//0.030:117:23//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q02088
F-NT2RM4001557
F-NT2RM4001565//HYPOTHETICAL 44.3 KD PROTEIN C1F7.07C IN CHROMOSOME I.//0.99:42:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09919
F-NT2RM4001566//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//0.054:190:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
F-NT2RM4001569//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (ACTIVATED PROTEIN KINASE C RECEPTOR HOMOLOG).//0.72:64:31//TRYPANOSOMA BRUCEI BRUCEI.//Q94775
F-NT2RM4001582
F-NT2RM4001592//DNA REPAIR PROTEIN RAD9.//0.00037:198:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P14737
F-NT2RM4001594//IMMEDIATE-EARLY PROTEIN IE180.//1.9e-05:147:34//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479
F-NT2RM4001597//THIOL:DISULFIDE INTERCHANGE PROTEIN TLPA (CYTOCHROME C BIOGENESIS PROTEIN TLPA).//5.7e-06:122:29//BRADYRHIZOBIUM JAPONICUM.//P43221
F-NT2RM4001605//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//1.7e-128:249:96//RATTUS NORVEGICUS (RAT).//P37199
F-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).//1.5e-35:128:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36024
F-NT2RM4001629//MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LARGE HOMOLOG 3).//5.8e-42:254:37//HOMO SAPIENS (HUMAN).//Q13368
F-NT2RM4001650//HOMEOBOX PROTEIN HOX-A4 (CHOX-1.4).//0.62:19:57//GALLUS GALLUS (CHICKEN).//P17277
F-NT2RM4001662//PROTEIN KINASE C, ALPHA TYPE (EC 2.7.1.-) (PKC-ALPHA).//0.29:90:32//HOMO SAPIENS (HUMAN).//P17252
F-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REGION.//1.1e-31:137:44//ESCHERICHIA COLI.//P37339
F-NT2RM4001682//PROBABLE 60S RIBOSOMAL PROTEIN L22.//0.98:55:29//CAENORHABDITIS ELEGANS.//P52819
F-NT2RM4001710//HYPOTHETICAL PROTEIN KIAA0039 (FRAGMENT).//0.56:113:28//HOMO SAPIENS (HUMAN).//Q15054
F-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT).//1.4e-108:255:77//HOMO SAPIENS (HUMAN).//Q14141
F-NT2RM4001715//HYPOTHETICAL PROTEIN C19G10.16 IN CHROMOSOME I (FRAGMENT).//2.1e-36:148:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10342

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F-NT2RM4001731//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III.//1.1e-05:90:33// CAENORHABDITIS ELEGANS.//P34284
F-NT2RM4001741//TALIN.//1.1e-106:208:99//MUS MUSCULUS (MOUSE).//P26039
F-NT2RM4001746//EBNA-1 NUCLEAR PROTEIN.//1.6e-09:155:38//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03211
F-NT2RM4001754//COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR.//0.93:158:33//HOMO SAPIENS (HUMAN).// P29400
F-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).//5.1e-113:277:79// HOMO SAPIENS (HUMAN).//P27448
F-NT2RM4001776//MYOSIN I ALPHA (MMI-ALPHA).//2.2e-73:262:54//MUS MUSCULUS (MOUSE).//P46735
F-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1) (FRAGMENT).//5.3e-26:169:39//MUS MUSCULUS (MOUSE).//P55200
F-NT2RM4001810//MALE SPECIFIC SPERM PROTEIN MST84DB.//2.3e-05:68:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
F-NT2RM4001813//RHODOCETIN ALPHA SUBUNIT.//2.3e-05:115:34//AGKISTRODON RHODOSTOMA (MALAYAN PIT VIPER) (CALLOSELASMA RHODOSTOMA).//P81397
F-NT2RM4001819//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR) (CELL SURFACE GLYCOPROTEIN F4/80).//1.7e-06:159:25//MUS MUSCULUS (MOUSE).//Q61549
F-NT2RM4001823//ZINC FINGER PROTEIN ZIC1 (ZINC FINGER PROTEIN OF THE CEREBELLUM 1).//2.6e-18:114:40//MUS MUSCULUS (MOUSE).//P46684
F-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//4.0e-81:253:59//HOMO SAPIENS (HUMAN).//P51523
F-NT2RM4001836//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//0.21:176:30//NEPHILA CLAVIPES (ORB SPIDER).//P46804
F-NT2RM4001841//PROLINE-RICH PEPTIDE P-B.//0.046:27:40//HOMO SAPIENS (HUMAN).//P02814
F-NT2RM4001842//HYPOTHETICAL 7.0 KD PROTEIN B03B8.1 IN CHROMOSOME III.//0.98:35:42// CAENORHABDITIS ELEGANS.//Q11104
F-NT2RM4001856//HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION.//2.3e-37:242:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39722
F-NT2RM4001858//T-BOX PROTEIN VEGT (T-BOX PROTEIN BRAT) (T-BOX PROTEIN ANTIPODEAN).//1.8e-23:78:64//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P87377
F-NT2RM4001865//NEURONAL CALCIUM SENSOR 2 (NCS-2).//0.012:83:28//CAENORHABDITIS ELEGANS.// P36609
F-NT2RM4001876//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.//3.8e-10:242:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47179
F-NT2RM4001880//EC PROTEIN HOMOLOG.//0.22:59:32//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).// P93746
F-NT2RM4001905//60S RIBOSOMAL PROTEIN L40 (CEP52).//0.57:20:60//HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND GALLUS GALLUS (CHICKEN).//P14793
F-NT2RM4001922
F-NT2RM4001930//PUTATIVE GLUCOSYLTRANSFERASE C08B11.8 (EC 2.4.1.-).//5.5e-45:167:53// CAENORHABDITIS ELEGANS.//Q09226
F-NT2RM4001938//RTOA PROTEIN (RATIO-A).//0.0036:120:32//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P54681
F-NT2RM4001940//IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-1 (FRAGMENT).//0.32:31:48//HOMO SAPIENS (HUMAN).//P78415
F-NT2RM4001953//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//2.2e-43:56:85//HOMO SAPIENS (HUMAN).// P39192
F-NT2RM4001965//IG ALPHA-1 CHAIN C REGION.//0.56:73:34//GORILLA GORILLA GORILLA (LOWLAND GORILLA).//P20758
F-NT2RM4001969//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//0.0016:140:27//HOMO SAPIENS (HUMAN).//P04280
F-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.9e-21:103:51//HOMO SAPIENS (HUMAN).//P51523
F-NT2RM4001984//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.0034:50:40//MUS MUSCULUS (MOUSE).// P15974
F-NT2RM4001987//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN).//6.9e-17:115:31//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q08180

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F-NT2RM4002013//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHROMOSOME V.//0.0062:117:28//CAENORHABDITIS ELEGANS.//Q23256
F-NT2RM4002018//SPORE COAT PROTEIN SP96.//4.3e-06:203:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P14328
F-NT2RM4002034//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//0.78:132:25//HOMO SAPIENS (HUMAN).//P98171
F-NT2RM4002044//VITELLOGENIN I PRECURSOR (MINOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LVI); PHOSVITIN (PV); LIPOVITELLIN II (LVII); YGP42].//0.062:201:24//GALLUS GALLUS (CHICKEN).//P87498
F-NT2RM4002054//DUPLICATE PROCYCLIN.//0.0079:44:52//TRYPANOSOMA BRUCEI BRUCEI.//P14044
F-NT2RM4002055//PUTATIVE Z PROTEIN.//0.82:39:30//OVIS ARIES (SHEEP).//P08105
F-NT2RM4002062//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//7.0e-37:80:52//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P36419
F-NT2RM4002063//SARCOSINE OXIDASE (EC 1.5.3.1).//2.2e-25:216:31//BACILLUS SP. (STRAIN NS-129).//P23342
F-NT2RM4002066//HYPOTHETICAL PROTEIN KIAA0192 (FRAGMENT).//1.1e-94:260:71//HOMO SAPIENS (HUMAN).//Q93074
F-NT2RM4002067//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.5e-15:51:70//HOMO SAPIENS (HUMAN).//P39188
F-NT2RM4002073//ELASTIN PRECURSOR (TROPOELASTIN).//4.9e-05:88:36//HOMO SAPIENS (HUMAN).//P15502
F-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//7.2e-43:220:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
F-NT2RM4002093//POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I) (57 KD RNA-BINDING PROTEIN PPTB-1).//1.8e-93:255:72//HOMO SAPIENS (HUMAN).//P26599
F-NT2RM4002109//KINESIN-LIKE PROTEIN KIF4.//3.7e-101:260:78//MUS MUSCULUS (MOUSE).//P33174
F-NT2RM4002128//HYPOTHETICAL PROTEIN IN CYCB 3'REGION PRECURSOR (ORF2) (FRAGMENT).//0.91:49:32//PARACOCCUS DENITRIFICANS.//P29969
F-NT2RM4002140//GROUCHO PROTEIN (ENHANCER OF SPLIT M9/10).//0.36:104:22//DROSOPHILA MELANOGASTER (FRUIT FLY).//P16371
F-NT2RM4002145//SLIT PROTEIN PRECURSOR.//8.6e-13:127:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//P24014
F-NT2RM4002146//MAGO NASHI PROTEIN.//7.9e-69:143:91//DROSOPHILA MELANOGASTER (FRUIT FLY).//P49028
F-NT2RM4002161//DUAL SPECIFICITY PROTEIN PHOSPHATASE (EC 3.1.3.48) (EC 3.1.3.16).//0.0062:99:26//CHLAMYDOMONAS EUGAMETOS.//Q39491
F-NT2RM4002174//MRP PROTEIN.//4.5e-50:183:55//ESCHERICHIA COLI.//P21590
F-NT2RM4002189//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//2.6e-14:233:29//HOMO SAPIENS (HUMAN).//Q02817
F-NT2RM4002194//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.92:108:28//HOMO SAPIENS (HUMAN).//P51805
F-NT2RM4002205//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//5.8e-39:122:72//RATTUS NORVEGICUS (RAT).//Q07803
F-NT2RM4002213//HYPOTHETICAL 88.4 KD PROTEIN B0464.7 IN CHROMOSOME III.//9.9e-27:110:43//CAENORHABDITIS ELEGANS.//Q03565
F-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//1.3e-21:147:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//P40809
F-NT2RM4002251//PROTEIN EF-7 (FRAGMENT).//0.00082:45:42//MUS MUSCULUS (MOUSE).//P97805
F-NT2RM4002256//COLD-REGULATED PROTEIN 1 (FRAGMENT).//0.00015:114:42//HORDEUM VULGARE (BARLEY).//P23251
F-NT2RM4002266//CUTICLE COLLAGEN 2.//0.00013:142:33//CAENORHABDITIS ELEGANS.//P17656
F-NT2RM4002278//HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC REGION.//1.0:40:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53288
F-NT2RM4002281
F-NT2RM4002287//GAR2 PROTEIN.//0.00055:225:23//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891
F-NT2RM4002294//HYPOTHETICAL PROTEIN KIAA0281 (HA6725).//1.1e-60:152:75//HOMO SAPIENS (HUMAN).//Q92556

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F-NT2RM4002301//GENERAL STRESS PROTEIN CTC (FRAGMENT).//0.56:43:39//BACILLUS CALDOLYTICUS.//P42832
F-NT2RM4002323//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.0080:73:35//BOS TAURUS (BOVINE).//P02313
F-NT2RM4002339//METALLOTHIONEIN 10-III (MT-10-III).//0.67:34:38//MYTILUS EDULIS (BLUE MUSSEL).//P80248
F-NT2RM4002344//METALLOTHIONEIN-I (MT-I).//0.84:41:31//MUS MUSCULUS (MOUSE).//P02802
F-NT2RM4002373//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT DY10 PRECURSOR.//0.0019:190:28//TRITICUM AESTIVUM (WHEAT).//P10387
F-NT2RM4002374//5E5 ANTIGEN.//0.0059:170:32//RATTUS NORVEGICUS (RAT).//Q63003
F-NT2RM4002383//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//0.13:17:88//HOMO SAPIENS (HUMAN).//P39193
F-NT2RM4002390
F-NT2RM4002398//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN).//0.034:110:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38074
F-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//4.0e-20:179:31//METHANOTHRIX SOEHNGENII.//P27095
F-NT2RM4002438//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.7e-15:41:95//HOMO SAPIENS (HUMAN).//P39194
F-NT2RM4002446//CRYPTDIN-RELATED PROTEIN 4C-1 PRECURSOR (CRS4C).//0.0058:24:50//MUS MUSCULUS (MOUSE).//P17534
F-NT2RM4002452//METALLOTHIONEIN 10-II (MT-10-II).//0.83:48:37//MYTILUS EDULIS (BLUE MUSSEL).//P80247
F-NT2RM4002457//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//4.9c-07:52:63//HOMO SAPIENS (HUMAN).//P39192
F-NT2RM4002460//C-HORDEIN (CLONE PC-919) (FRAGMENT).//0.92:43:30//HORDEUM VULGARE (BARLEY).//P17992
F-NT2RM4002479//RNA HELICASE-LIKE PROTEIN DB10.//1.7e-28:200:41//NICOTIANA SYLVESTRIS (WOOD TOBACCO).//P46942
F-NT2RM4002482//HYPOTHETICAL 65.9 KD PROTEIN YPR065W.//8.8e-26:123:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12514 F-NT2RM4002493//LARVAL CUTICLE PROTEIN I PRECURSOR.//0.17:126:27//DROSOPHILA MIRANDA (FRUIT FLY).//P91627
F-NT2RM4002499//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//9.4e-34:92:80//HOMO SAPIENS (HUMAN).//P39194
F-NT2RM4002504//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//3.4e-19:55:83//HOMO SAPIENS (HUMAN).//P39189
F-NT2RM4002527//WD-40 REPEAT PROTEIN MSI2.//3.0e-07:193:27//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//O22468
F-NT2RM4002532//AEROLYSIN REGULATORY PROTEIN.//0.97:19:47//AEROMONAS SOBRIA.//P09165
F-NT2RM4002534//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L32 PRECURSOR (YML32).//0.76:86:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25348
F-NT2RM4002558//LONG-CHAIN FATTY ACID TRANSPORT PROTEIN (FATP).//4.2e-55:204:50//MUS MUSCULUS (MOUSE).//Q60714
F-NT2RM4002565//CHYMOTRYPSIN/ELASTASE ISOINHIBITORS 2 TO 5.//1.0:16:62//ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P07852
F-NT2RM4002567//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION.//2.7e-10:184:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032
F-NT2RM4002571//POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1).//2.4e-25:124:47//HOMO SAPIENS (HUMAN).//Q10472
F-NT2RM4002593//HYPOTHETICAL 9.1 KD PROTEIN IN TETB-EXOA INTERGENIC REGION.//0.95:36:38//BACILLUS SUBTILIS.//P37509
F-NT2RM4002594//MSP1 PROTEIN HOMOLOG.//9.0e-68:227:60//CAENORHABDITIS ELEGANS.//P54815
F-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//3.3e-54:243:47//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P73851
F-NT2RP1000018//SUPPRESSOR PROTEIN SRP40.//0.0023:131:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
F-NT2RP1000035//RING CANAL PROTEIN (KELCH PROTEIN).//1.0e-06:63:34//DROSOPHILA MELA-

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NOGASTER (FRUIT FLY).//Q04652
F-NT2RP1000040//LETHAL NEUROTOXIN TX1.//0.69:21:47//PHONEUTRIA NIGRIVENTER (BRAZILIAN ARMED SPIDER).//P17727
F-NT2RP1000063//HYPOTHETICAL 25.1 KD PROTEIN IN SMC3-MRPL8 INTERGENIC REGION.//3.8e-14:130:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40359
F-NT2RP1000086//HYPOTHETICAL 9.4 KD PROTEIN IN RNPA-THDF INTERGENIC REGION.//0.16:44:40//ESCHERICHIA COLI.//P22847
F-NT2RP1000101//45.8 KD PROTEIN IN SHM1-MRPL37 INTERGENIC REGION.//1.9e-06:74:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38344
F-NT2RP1000111//COP1 REGULATORY PROTEIN (FUSCA PROTEIN FUS1).//2.7e-19:135:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P43254
F-NT2RP1000112//DUAL SPECIFICITY PROTEIN KINASE TTK (EC 2.7.1.-) (PYT).//1.2e-39:91:62//HOMO SAPIENS (HUMAN).//P33981
F-NT2RP1000124//ATP-DEPENDENT PROTEASE LA 2 (EC 3.4.21.53).//0.074:131:24//MYXOCOCCUS XANTHUS.//P36774
F-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//1.5e-49:186:56//MUS MUSCULUS (MOUSE).//P51859
F-NT2RP1000163//METALLOTHIONEIN (MT).//0.98:41:34//PLEURONECTES PLATESSA (PLAICE).//P07216
F-NT2RP1000170//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.85:64:35//HOMO SAPIENS (HUMAN).//P10162
F-NT2RP1000174//IMMEDIATE-EARLY PROTEIN IE180.//0.00056:89:37//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479
F-NT2RP1000191//NIFU PROTEIN.//0.53:78:35//FRANKIA ALNI.//P46045
F-NT2RP1000202//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//9.1e-21:148:39//HOMO SAPIENS (HUMAN).//Q01485
F-NT2RP1000243//HYPOTHETICAL PROTEIN MJ1136.//1.4e-37:219:36//METHANOCOCCUS JANNASCHII.//Q58536
F-NT2RP1000259//HYPOTHETICAL PROTEIN TP0318.//0.18:25:44//TREPONEMA PALLIDUM.//O83338
F-NT2RP1000272//SPLICING FACTOR, ARGININE/SERINE-RICH 3 (PRE-MRNA SPLICING FACTOR SRP20) (X16 PROTEIN).//1.6e-18:133:36//HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE).//P23152
F-NT2RP1000324
F-NT2RP1000326//HYPOTHETICAL 29.8 KD PROTEIN ZC97.1 IN CHROMOSOME III.//1.0e-23:129:36//CAENORHABDITIS ELEGANS.//P34599
F-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//2.5e-45:147:57//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32447
F-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//4.8e-14:119:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25343
F-NT2RP1000357//TRYPOMASTIGOTE DECAY-ACCELERATING FACTOR (T-DAF) (FRAGMENT).//1.0:43:32//TRYPANOSOMA CRUZI.//Q26327
F-NT2RP1000358//HYPOTHETICAL 84.4 KD PROTEIN IN RPC2/RET1 3'REGION.//7.9e-28:244:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39744
F-NT2RP1000363//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//2.2e-07:178:30//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437
F-NT2RP1000376//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//1.5e-20:254:31//HOMO SAPIENS (HUMAN).//P16157
F-NT2RP1000409//CYTOCHROME C3 (CYTOCHROME C7) (C551.5).//1.0:34:26//DESULFUROMONAS ACETOXIDANS (CHLOROPSEUDOMONAS ETHYLICA).//P00137
F-NT2RP1000413//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN).//3.7e-131:230:97//RATTUS NORVEGICUS (RAT).//P55161
F-NT2RP1000416//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.83:54:40//DROSOPHILA SIMULANS (FRUIT FLY).//P13729
F-NT2RP1000418//HYPOTHETICAL 9.9 KD PROTEIN IN GCVT-SPOIIIAA INTERGENIC REGION.//0.24:91:35//BACILLUS SUBTILIS.//P49779
F-NT2RP1000439//HYPOTHETICAL 100.5 KD PROTEIN C1B9.04 IN CHROMOSOME I.//0.13:172:22//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10429
F-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN).//1.9e-08:167:24//HOMO SAPIENS (HUMAN).//Q08257
F-NT2RP1000460//NUCLEAR MOVEMENT PROTEIN NUDC.//1.0e-18:149:34//EMERICELLA NIDULANS (AS-

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PERGILLUS NIDULANS).//P17624
F-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//1.3e-43:180:47//CAENORHABDITIS ELEGANS.//P34580
F-NT2RP1000478//TUBULIN BETA-6 CHAIN (CLASS-VI).//1.5e-45:85:63//GALLUS GALLUS (CHICKEN).//P09207
F-NT2RP1000481//HYPOTHETICAL 5.8 KD PROTEIN IN PUHA 5'REGION (ORF55).//0.083:21:47//RHODOBACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA).//P26159
F-NT2RP1000493//POSSIBLE DNA-REPAIR PROTEIN XP-E (POSSIBLE XERODERMA PIGMENTOSUM GROUP E PROTEIN) (UV-DAMAGED DNA-BINDING PROTEIN) (UV-DDB).//6.6e-11:139:31//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).//P33194
F-NT2RP1000513//60S RIBOSOMAL PROTEIN L22.//0.017:92:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P50887
F-NT2RP1000522//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//0.0055:86:36//MUS MUSCULUS (MOUSE).//Q61068
F-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.2e-09:69:36//CRICETULUS GRISEUS (CHINESE HAMSTER).//P49020
F-NT2RP1000574//HOMEOBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//6.0e-39:141:65//MUS MUSCULUS (MOUSE).//P97367
F-NT2RP1000577//PUTATIVE ATP-DEPENDENT RNA HELICASE YDL031W.//0.00016:48:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12389
F-NT2RP1000581//VON WILLEBRAND FACTOR PRECURSOR.//0.00017:61:50//HOMO SAPIENS (HUMAN).//P04275
F-NT2RP1000609//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE).//4.4e-07:128:31//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q08871
F-NT2RP1000629//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//4.2e-70:167:86//MUS MUSCULUS (MOUSE).//P35585
F-NT2RP1000630//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.//0.0011:238:21//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47179
F-NT2RP1000677//COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR.//0.99:71:33//HOMO SAPIENS (HUMAN).//Q07092
F-NT2RP1000688//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//0.0024:19:94//HOMO SAPIENS (HUMAN).//P39193
F-NT2RP1000695//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III.//2.2e-30:185:37//CAENORHABDITIS ELEGANS.//Q18262
F-NT2RP1000701//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.2e-65:128:93//RATTUS NORVEGICUS (RAT).//P54319
F-NT2RP1000721//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//2.3e-06:139:34//HOMO SAPIENS (HUMAN).//O00268
F-NT2RP1000730//MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR ISOFORM (FRAGMENT).//0.89:40:40//MUS MUSCULUS (MOUSE).//P09542
F-NT2RP1000733//METALLOTHIONEIN-LIKE PROTEIN CRS5.//0.024:24:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41902
F-NT2RP1000738//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1 / PRP-3) (PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C) [CONTAINS: PEPTIDE P-C].//0.040:82:36//HOMO SAPIENS (HUMAN).//P02810
F-NT2RP1000746//HYPOTHETICAL 27.1 KD PROTEIN UFD4-CAP1 INTERGENIC REGION.//2.0e-30:170:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33201
F-NT2RP1000767//PSEUDOMONAPEPSIN PRECURSOR (EC 3.4.23.37) (PEPSTATIN-INSENSITIVE CARBOXYL PROTEINASE).//0.99:75:34//PSEUDOMONAS SP. (STRAIN 101).//P42790
F-NT2RP1000782//CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1).//2.3e-23:159:35//HOMO SAPIENS (HUMAN).//P41732
F-NT2RP1000796//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).//0.00018:79:32//SUS SCROFA (PIG).//P35323
F-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//3.1e-37:89:64//HOMO SAPIENS (HU-

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MAN).//Q07960
F-NT2RP1000833//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.32:29:48//HOMO SAPIENS (HUMAN).//P22531
F-NT2RP1000834//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-).//6.4e-67:202:68//RATTUS NORVEGICUS (RAT).//P70473
F-NT2RP1000836//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION.//1.0:35:54//HUMAN ADENOVIRUS TYPE 41.//P23691
F-NT2RP1000846//SMALL PROLINE-RICH PROTEIN 2-1.//0.013:35:48//HOMO SAPIENS (HUMAN).//P35326
F-NT2RP1000851//PERIOD CLOCK PROTEIN (FRAGMENT).//0.082:28:57//DROSOPHILA SALTANS (FRUIT FLY).//Q04536
F-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//2.5e-26:190:30//MUS MUSCULUS (MOUSE).//O35566
F-NT2RP1000860//POTENTIAL TRANSCRIPTIONAL ADAPTOR.//0.13:86:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q02336
F-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//7.6e-11:200:35//CAENORHABDITIS ELEGANS.//Q09531
F-NT2RP1000915//HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTERGENIC REGION.//1.4e-06:88:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40010
F-NT2RP1000916//SUPPRESSOR PROTEIN SRP40.//0.40:90:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
F-NT2RP1000943//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//0.099:75:34//HOMO SAPIENS (HUMAN).//Q02817
F-NT2RP1000944//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//7.6e-06:65:41//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341
F-NT2RP1000947//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//3.6e-12:27:77//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P51669
F-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//2.8e-15:169:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
F-NT2RP1000958//HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTERGENIC REGION.//4.2e-16:162:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40010
F-NT2RP1000959//CORNIFIN A (SMALL PROLINE-RICH PROTEIN IA) (SPR-IA) (SPRK).//0.0031:34:44//HOMO SAPIENS (HUMAN).//P35321
F-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//1.5e-52:110:95//HOMO SAPIENS (HUMAN).//P19338
F-NT2RP1000980//LIGHT-HARVESTING PROTEIN B-1015, ALPHA CHAIN PRECURSOR (ANTENNA PIGMENT PROTEIN, ALPHA CHAIN).//0.87:37:45//RHODOPSEUDOMONAS VIRIDIS.//P04123
F-NT2RP1000988
F-NT2RP1001011//PROTEIN P19.//0.96:30:50//BACTERIOPHAGE PRD1.//P17638
F-NT2RP1001013//DNA-BINDING PROTEIN 65 (PROTEIN GP65).//1.0:20:45//BACTERIOPHAGE T4.//P16012
F-NT2RP1001014
F-NT2RP1001033//TUBULIN GAMMA CHAIN.//2.5e-16:112:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P25295
F-NT2RP1001073//HYPOTHETICAL 10.4 KD PROTEIN IN FTR1-SPT15 INTERGENIC REGION.//7.6e-16:82:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40089
F-NT2RP1001079//SARCOSINE OXIDASE (EC 1.5.3.1).//4.8e-15:95:40//ARTHROBACTER SP. (STRAIN TE1826).//P40873
F-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9.//2.4e-29:126:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06218
F-NT2RP1001113//SMALL PROLINE-RICH PROTEIN 2-1.//0.49:38:39//HOMO SAPIENS (HUMAN).//P35326
F-NT2RP1001173//RHOMBOTIN-1 (CYSTEINE RICH PROTEIN TTG-1) (T-CELL TRANSLOCATION PROTEIN 1) (LIM-ONLY PROTEIN 1).//0.99:54:37//HOMO SAPIENS (HUMAN).//P25800
F-NT2RP1001177//HISTONE MACRO-H2A.1.//1.6e-29:85:76//RATTUS NORVEGICUS (RAT).//Q02874
F-NT2RP1001185
F-NT2RP1001199//NEUROTOXIN I.//1.0:23:47//CENTRUROIDES SCULPTURATUS (BARK SCORPION).//P01491
F-NT2RP1001247//TRANSFORMING GROWTH FACTOR BETA 4 PRECURSOR (TGF-BETA 4) (ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR).//3.3e-08:28:89//HOMO SAPIENS (HUMAN).//O00292

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F-NT2RP1001248//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.33:49:28//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18804
F-NT2RP1001253//GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10) (GLUCOSAMINE-6- PHOSPHATE DEAMINASE) (GNPDA) (OSCILLIN) (KIAA0060).//3.8e-46:115:81//HOMO SAPIENS (HUMAN).//P46926
F-NT2RP1001286//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-34 GALACTOSIDE-BINDING LECTIN).//0.16:48:37//MUS MUSCULUS (MOUSE).//P16110
F-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//6.1e-05:92:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12024
F-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.2e-05:92:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12024
F-NT2RP1001310//PROBABLE E4 PROTEIN.//0.99:109:26//HUMAN PAPILLOMAVIRUS TYPE 5.//P06924
F-NT2RP1001311//SODIUM/HYDROGEN EXCHANGER 5 (NA(+)/H(+) EXCHANGER 5) (NHE-5) (FRAGMENT).//0.99:94:31//HOMO SAPIENS (HUMAN).//Q14940
F-NT2RP1001313//CYTOCHROME B5.//9.0e-13:92:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40312
F-NT2RP1001361//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B).//1.2e-47:117:74//BOS TAURUS (BOVINE).//Q02827
F-NT2RP1001385//CELL DIVISION PROTEIN FTSN.//0.64:107:28//ESCHERICHIA COLI.//P29131
F-NT2RP1001395//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS).//0.25:35:45//GALLUS GALLUS (CHICKEN).//P02467
F-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//2.2e-41:129:67//CAENORHABDITIS ELEGANS.//P91917
F-NT2RP1001424//UREASE ACCESSORY PROTEIN UREF (FRAGMENT).//0.87:24:45//ESCHERICHIA COLI.//Q03286
F-NT2RP1001432//CYSTEINE PROTEINASE INHIBITOR B (CYSTATIN B) (SCB).//1.0:35:42//HELIANTHUS ANNUUS (COMMON SUNFLOWER).//Q10993
F-NT2RP1001449//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.053:37:37//OVIS ARIES (SHEEP).//P26372
F-NT2RP1001457//HYPOTHETICAL 57.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN CPR4-SSK22 INTERGENIC REGION.//2.9e-16:159:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25382
F-NT2RP1001466//HYPOTHETICAL PROTEIN MJ0284.//5.3e-15:162:35//METHANOCOCCUS JANNASCHII.//Q57732
F-NT2RP1001475//HYPOTHETICAL 195.1 KD PROTEIN IN DNA43-UBI1 INTERGENIC REGION.//0.69:119:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40457
F-NT2RP1001482//PROTEASOME COMPONENT C9 (EC 3.4.99.46) (MACROPAIN SUBUNIT C9) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C9).//1.0:58:32//HOMO SAPIENS (HUMAN).//P25789
F-NT2RP1001494//MALE STERILITY PROTEIN 2.//2.4e-12:84:42//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q08891
F-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//6.3e-37:94:52//SPIRODELA POLYRRHIZA.//P42803
F-NT2RP1001546//LEUKOCYTE SURFACE ANTIGEN CD53 (CELL SURFACE GLYCOPROTEIN CD53).//9.3e-11:98:29//HOMO SAPIENS (HUMAN).//P19397
F-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//2.2e-64:159:84//MUS MUSCULUS (MOUSE).//P47758
F-NT2RP1001616//HYPOTHETICAL 13.5 KD PROTEIN C45G9.7 IN CHROMOSOME III.//9.2e-05:49:42//CAENORHABDITIS ELEGANS.//Q09506
F-NT2RP1001665//REGB PROTEIN.//0.99:29:37//PSEUDOMONAS AERUGINOSA.//Q03381
F-NT2RP2000001//SMALL PROLINE-RICH PROTEIN 2-1.//0.64:36:41//HOMO SAPIENS (HUMAN).//P35326
F-NT2RP2000006//DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40).//1.7e-19:74:52//HOMO SAPIENS (HUMAN).//P25685
F-NT2RP2000007//TROPOMYOSIN, FIBROBLAST AND EPITHELIAL MUSCLE-TYPE (TM36) (TME1) (TM1).//0.93:126:23//HOMO SAPIENS (HUMAN).//P06468
F-NT2RP2000008//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) (FRAGMENT).//4.2e-35:156:54//HOMO SAPIENS (HUMAN).//Q06730
F-NT2RP2000027//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.95:41:39//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//P50665
F-NT2RP2000032//BAX PROTEIN, CYTOPLASMIC ISOFORM GAMMA.//1.0:35:34//HOMO SAPIENS (HU-

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MAN).//Q07815
F-NT2RP2000040//BASIC PROLINE-RICH PEPTIDE IB-1.//0.0024:58:36//HOMO SAPIENS (HUMAN).//P04281
F-NT2RP2000045//DNAJ PROTEIN.//1.1e-12:42:66//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//Q56237
F-NT2RP2000054//GONADOLIBERIN III PRECURSOR (GONADOTROPIN-RELEASING HORMONE III) (GN-RH-III) (LH-RH III) (LULIBERIN III).//0.20:46:36//ONCORHYNCHUS MASOU (CHERRY SALMON) (MASU SALMON).//P30973
F-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EPSILON).//1.3e-18:45:100//MUS MUSCULUS (MOUSE).//P49446
F-NT2RP2000067//HOMEOBOX PROTEIN HOX-A5 (S12-B) (FRAGMENT).//0.71:44:40//SALMO SALAR (ATLANTIC SALMON).//P09637
F-NT2RP2000070//INSULIN.//0.94:30:43//HYSTRIX CRISTATA (CRESTED PORCUPINE).//P01328
F-NT2RP2000076//ETS-LIKE PROTEIN POINTED P1 (D-ETS-2).//0.0013:76:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P51022
F-NT2RP2000077//U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (U1-C).//0.24:49:40//HOMO SAPIENS (HUMAN).//P09234
F-NT2RP2000079//PLATELET FACTOR 4 (PF-4).//0.15:52:30//SUS SCROFA (PIG).//P30034
F-NT2RP2000088//HYPOTHETICAL 13.6 KD PROTEIN IN SPT4-ROM1 INTERGENIC REGION.//1.0:36:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53245
F-NT2RP2000091//HYPOTHETICAL PROTEIN HI0149 PRECURSOR.//0.22:38:47//HAEMOPHILUS INFLUENZAE.//P43953
F-NT2RP2000097//VIRUS ATTACHMENT PROTEIN (O61R).//0.75:33:36//AFRICAN SWINE FEVER VIRUS (STRAIN BA71V) (ASFV).//P32510
F-NT2RP2000098
F-NT2RP2000108//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.4e-09:50:70//HOMO SAPIENS (HUMAN).//P39195
F-NT2RP2000114//WISKOTT-ALDRICH SYNDROME PROTEIN (WASP).//0.024:52:44//HOMO SAPIENS (HUMAN).//P42768
F-NT2RP2000120//5.8 KD PROTEIN IN HMC OPERON (ORF 4).//0.67:37:32//DESULFOVIBRIO VULGARIS (STRAIN HILDENBOROUGH).//P33391
F-NT2RP2000126//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//1.5e-23:94:47//HOMO SAPIENS (HUMAN).//O14646
F-NT2RP2000133//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//5.6e-10:82:39//HOMO SAPIENS (HUMAN).//Q15427
F-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//6.7e-89:96:98//MUS MUSCULUS (MOUSE).//P35585
F-NT2RP2000153//PEPTIDYLPROLYL ISOMERASE CYP-1 (EC 5.2.1.8) (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE).//1.7e-05:136:33//BRUGIA MALAYI.//Q27450
F-NT2RP2000157//MLO2 PROTEIN.//2.7e-06:62:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09329
F-NT2RP2000161//DIS3 PROTEIN HOMOLOG.//2.7e-33:173:45//CAENORHABDITIS ELEGANS.//Q17632
F-NT2RP2000173//HYPOTHETICAL 10.5 KD PROTEIN IN SODA-COMGA INTERGENIC REGION.//0.99:62:25//BACILLUS SUBTILIS.//P54499
F-NT2RP2000175//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.19:41:43//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
F-NT2RP2000183//DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL SPECIFIC PROTEIN NSP60).//4.1e-19:114:44//BOS TAURUS (BOVINE).//O02675
F-NT2RP2000195//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:30:33//MICROTUS PENNSYLVANICUS (MEADOW VOLE).//P24949
F-NT2RP2000205//MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR (PERIPLASMIC MERCURY ION BINDING PROTEIN) (MERCURY SCAVENGER PROTEIN).//0.098:88:25//SHEWANELLA PUTREFACIENS (PSEUDOMONAS PUTREFACIENS).//Q54463
F-NT2RP2000208//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.020:19:57//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645
F-NT2RP2000224//PUTATIVE CUTICLE COLLAGEN C09G5.4.//0.0058:159:32//CAENORHABDITIS ELEGANS.//Q09455
F-NT2RP2000232//P55-C-FOS PROTO-ONCOGENE PROTEIN (FRAGMENT).//1.0:44:38//OVIS ARIES

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(SHEEP).//O02761
F-NT2RP2000233//GASTRIN/CHOLECYSTOKININ TYPE B RECEPTOR (CCK-B RECEPTOR) (CCK-BR).//0.34:53:43//CANIS FAMILIARIS (DOG).//P30552
F-NT2RP2000239//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.019:69:33//RATTUS NORVEGICUS (RAT).//P10164
F-NT2RP2000248//OVOMUCOID (FRAGMENT).//0.88:18:55//POLYPLECTRON EMPHANUM (PALAWAN PEACOCK-PHEASANT).//P52250
F-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//6.4e-09:83:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40556
F-NT2RP2000258//MYOSIN II HEAVY CHAIN, NON MUSCLE.//0.081:217:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P08799
F-NT2RP2000270//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.4e-17:80:57//HOMO SAPIENS (HUMAN).//P39188
F-NT2RP2000274//HYPOTHETICAL 5.8 KD PROTEIN.//0.082:22:45//CLOVER YELLOW MOSAIC VIRUS (CYMV).//P16485
F-NT2RP2000283//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III.//0.39:38:34//CAENORHABDITIS ELEGANS.//P34535
F-NT2RP2000288
F-NT2RP2000289//HYPOTHETICAL 9.4 KD PROTEIN IN RNPA-THDF INTERGENIC REGION.//0.40:38:42//ESCHERICHIA COLI.//P22847
F-NT2RP2000297//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//2.3e-62:206:47//HOMO SAPIENS (HUMAN).//Q03923
F-NT2RP2000298//CUTICLE COLLAGEN 12 PRECURSOR.//0.55:81:40//CAENORHABDITIS ELEGANS.//P20630
F-NT2RP2000310//RUBREDOXIN (RD).//0.13:43:41//TREPONEMA PALLIDUM.//O83956
F-NT2RP2000327//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:46:30//GADUS MORHUA (ATLANTIC COD).//P15996
F-NT2RP2000328//HYPOTHETICAL 86.6 KD PROTEIN IN PFK1-TDS4 INTERGENIC REGION.//2.0e-21:198:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53313
F-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//1.8e-91:155:92//BOS TAURUS (BOVINE).//P08760
F-NT2RP2000337//PROTEIN A54.//0.75:48:35//VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPENHAGEN).//P21072
F-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//9.7e-13:114:42//MUS MUSCULUS (MOUSE).//P17564
F-NT2RP2000369//CALTRIN (CALCIUM TRANSPORT INHIBITOR).//0.98:47:34//MUS MUSCULUS (MOUSE).//Q09098
F-NT2RP2000412//SHORT NEUROTOXIN D PRECURSOR.//0.66:57:36//AIPYSURUS LAEVIS (OLIVE SEA SNAKE).//P19960
F-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F).//1.0e-27:96:67//HOMO SAPIENS (HUMAN).//P52597
F-NT2RP2000420//ZINC FINGER PROTEIN 191.//0.16:47:38//HOMO SAPIENS (HUMAN).//O14754
F-NT2RP2000422//PUTATIVE PHOSPHOACETYLGLUCOSAMINE MUTASE (EC 5.4.2.3) (ACETYLGLUCOSAMINE PHOSPHOMUTASE) (N-ACETYLGLUCOSAMINE-PHOSPHATE MUTASE).//3.6e-19:148:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09687
F-NT2RP2000438//TUBULIN GAMMA CHAIN.//0.86:190:27//RETICULOMYXA FILOSA.//P54405
F-NT2RP2000448//OXYSTEROL-BINDING PROTEIN.//3.7e-13:140:42//HOMO SAPIENS (HUMAN).//P22059
F-NT2RP2000459//NEURONAL PROTEIN 3.1 (P311 PROTEIN).//1.0:45:35//HOMO SAPIENS (HUMAN).//Q16612
F-NT2RP2000498//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//0.062:25:68//HOMO SAPIENS (HUMAN).//P39194
F-NT2RP2000503
F-NT2RP2000510//TOXIN IV-5.//1.0:51:33//TITYUS BAHIENSIS (BRAZILIAN SCORPION).//P56608
F-NT2RP2000516//SLYX PROTEIN.//1.0:52:32//ESCHERICHIA COLI.//P30857
F-NT2RP2000523//PHORBOLIN I (FRAGMENTS).//1.4e-06:36:47//HOMO-SAPIENS (HUMAN).//P31941
F-NT2RP2000603//ALPHA/BETA-GLIADIN PRECURSOR (PROLAMIN) (CLASS A-III).//0.93:119:26//TRITICUM AESTIVUM (WHEAT).//P04723
F-NT2RP2000617//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.056:16:62//OVIS ARIES

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(SHEEP), AND CAPRA HIRCUS (GOAT).//P04102
F-NT2RP2000634//NEDD-4 PROTEIN (EC 6.3.2.-) (KIAA0093) (FRAGMENT).//1.8e-05:128:28//HOMO SAPIENS (HUMAN).//P46934
F-NT2RP2000644//HYPOTHETICAL PROTEIN HI1566 PRECURSOR.//0.85:48:39//HAEMOPHILUS INFLUENZAE.//P44257
F-NT2RP2000656//EARLY GROWTH RESPONSE PROTEIN 1 (EGR-1) (NERVE GROWTH FACTOR-INDUCED PROTEIN A) (NGFI-A).//1.0:111:24//RATTUS NORVEGICUS (RAT).//P08154
F-NT2RP2000658//URONATE ISOMERASE (EC 5.3.1.12) (GLUCURONATE ISOMERASE) (URONIC ISOMERASE).//0.49:79:31//ESCHERICHIA COLI.//P42607
F-NT2RP2000668//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (45 KD MEROZOITE SURFACE ANTIGEN).//0.020:115:30//PLASMODIUM FALCIPARUM (ISOLATE 3D7).//P50498
F-NT2RP2000678//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.00085:38:68//HOMO SAPIENS (HUMAN).//P39188
F-NT2RP2000704//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.2e-17:55:74//HOMO SAPIENS (HUMAN).//P39188
F-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//8.9e-47:106:59//TREPONEMA PALLIDUM.//O83950
F-NT2RP2000715
F-NT2RP2000731//CONIDIATION-SPECIFIC PROTEIN 10.//0.094:31:41//NEUROSPORA CRASSA.//P10713
F-NT2RP2000758//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.00027:31:74//HOMO SAPIENS (HUMAN).//P39188
F-NT2RP2000764//NIFS PROTEIN.//2.7e-27:175:47//ANABAENA SP. (STRAIN PCC 7120).//P12623
F-NT2RP2000809//HYPOTHETICAL PROTEIN MG381 HOMOLOG.//0.91:85:25//MYCOPLASMA PNEUMONIAE.//P75219
F-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//2.8e-07:133:31//MUS MUSCULUS (MOUSE).//Q99104
F-NT2RP2000814//40S RIBOSOMAL PROTEIN S27A.//0.93:44:38//LYCOPERSICON ESCULENTUM (TOMATO), AND SOLANUM TUBEROSUM (POTATO).//P27083
F-NT2RP2000816//HYPOTHETICAL 88.4 KD PROTEIN B0464.7 IN CHROMOSOME III.//3.3e-21:123:39//CAENORHABDITIS ELEGANS.//Q03565
F-NT2RP2000819//TROPOMYOSIN 5, CYTOSKELETAL TYPE.//1.0:71:30//MUS MUSCULUS (MOUSE).//P21107
F-NT2RP2000841//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//0.0011:133:26//MUS MUSCULUS (MOUSE).//P27671
F-NT2RP2000842//LYSOPHOSPHATIDIC ACID RECEPTOR (EDG-2).//6.4e-13:22:95//HOMO SAPIENS (HUMAN).//Q92633
F-NT2RP2000845//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (MSTI).//0.92:24:41//MEDICAGO SCUTELLATA (SNAIL MEDIC).//P80321
F-NT2RP2000863//N-MYC PROTO-ONCOGENE PROTEIN.//0.010:148:27//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P24793
F-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2.//4.0e-100:199:94//HOMO SAPIENS (HUMAN).//O60841
F-NT2RP2000892//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].//0.43:45:44//MUS MUSCULUS (MOUSE).//P28481
F-NT2RP2000931//MATRIN 3.//2.8e-46:104:92//RATTUS NORVEGICUS (RAT).//P43244
F-NT2RP2000932//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).//3.9e-07:113:31//MUS MUSCULUS (MOUSE).//Q05921
F-NT2RP2000938//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIIID).//0.026:59:45//RATTUS NORVEGICUS (RAT).//Q01956
F-NT2RP2000943//HYPOTHETICAL PROTEIN KIAA0079 (HA3543).//5.9e-18:161:42//HOMO SAPIENS (HUMAN).//P53992
F-NT2RP2000965//INNER CENTROMERE PROTEIN (INCENP).//0.062:156:25//GALLUS GALLUS (CHICKEN).//P53352
F-NT2RP2000970//EC PROTEIN HOMOLOG.//1.0:50:30//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P93746
F-NT2RP2000985//HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION.//2.5e-06:53:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36159
F-NT2RP2000987//INSECT TOXIN 4 (INSECT TOXIN AAH IT4).//1.0:32:34//ANDROCTONUS AUSTRALIS HEC-

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TOR (SAHARA SCORPION).//P21150
F-NT2RP2001036//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.2e-33:65:81//HOMO SAPIENS (HUMAN).//P39193
F-NT2RP2001044//HIRUSTASIN.//0.97:15:66//HIRUDO MEDICINALIS (MEDICINAL LEECH).//P80302
F-NT2RP2001056//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.0e-24:85:65//HOMO SAPIENS (HUMAN).//P39194
F-NT2RP2001065//BOWMAN-BIRK TYPE SEED TRYPSIN AND CHYMOTRYPSIN INHIBITOR (BTCI).//0.41:50:32//VIGNA UNGUICULATA (COWPEA).//P17734
F-NT2RP2001070//PROBABLE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE) (FPRA PROTEIN).//6.2e-18:64:48//MYXOCOCCUS XANTHUS.//P21159
F-NT2RP2001081//SYNAPTOTAGMIN IV.//7.8e-16:94:46//RATTUS NORVEGICUS (RAT).//P50232
F-NT2RP2001094//METALLOTHIONEIN-I (MT-I).//1.0:24:33//RATTUS NORVEGICUS (RAT).//P02803
F-NT2RP2001119//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//7.5e-11:61:63//HOMO SAPIENS (HUMAN).//P39195
F-NT2RP2001127//XE169 PROTEIN (SMCX PROTEIN) (FRAGMENTS).//1.0e-47:155:58//MUS MUSCULUS (MOUSE).//P41230
F-NT2RP2001137//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.10:68:39//BOS TAURUS (BOVINE).//P25508
F-NT2RP2001149//!!!! ALU SUBFAMILY J WARNING ENTRY!!!!//1.1e-13:81:59//HOMO SAPIENS (HUMAN).//P39188
F-NT2RP2001168//PROTEIN KINASE C SUBSTRATE 80 KD PROTEIN (FRAGMENTS).//0.0071:77:33//RATTUS NORVEGICUS (RAT).//P20468
F-NT2RP2001173//CYTOSKELETON-ASSOCIATED PROTEIN CKAPI (TUBULIN FOLDING COFACTOR B).//1.0:36:41//HOMO SAPIENS (HUMAN).//Q99426
F-NT2RP2001174//ZINC FINGER PROTEIN 137.//7.2e-11:65:43//HOMO SAPIENS (HUMAN).//P52743
F-NT2RP2001196//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).//1.0:95:26//CAPRA HIRCUS (GOAT).//Q36346
F-NT2RP2001218//HYPOTHETICAL 59.2 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION.//0.00024:80:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40486
F-NT2RP2001226//RABPHILIN-3A (FRAGMENT).//4.6e-05:121:39//MUS MUSCULUS (MOUSE).//P47708
F-NT2RP2001233//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.2e-61:153:56//HOMO SAPIENS (HUMAN).//P16415
F-NT2RP2001245//SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN).//4.9e-05:230:21//HOMO SAPIENS (HUMAN).//Q15431
F-NT2RP2001268//HOMEOBOX PROTEIN CEH-32.//0.23:159:25//CAENORHABDITIS ELEGANS.//Q23175
F-NT2RP2001277
F-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-ALPHA HOMOLOG) (BRAIN PROTEIN I47) (FRAGMENT).//1.0e-86:131:97//MUS MUSCULUS (MOUSE).//P28663
F-NT2RP2001295
F-NT2RP2001312//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).//0.64:80:33//CAPRA HIRCUS (GOAT).//P50426
F-NT2RP2001327//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//1.0e-36:118:65//HOMO SAPIENS (HUMAN).//Q13829
F-NT2RP2001328//PROBABLE E5 PROTEIN.//1.0:46:41//HUMAN PAPILLOMAVIRUS TYPE 33.//P06426
F-NT2RP2001347//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//4.5e-19:66:62//HOMO SAPIENS (HUMAN).//P39193
F-NT2RP2001366//SPERM-SPECIFIC PROTEIN PHI-1.//0.66:55:32//MYTILUS EDULIS (BLUE MUSSEL).//Q04621
F-NT2RP2001378//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIIID) (FRAGMENT).//0.060:78:33//HOMO SAPIENS (HUMAN).//Q14003
F-NT2RP2001381//26S PROTEASE REGULATORY SUBUNIT 8 (SUG1 HOMOLOG) (XSUG1).//1.0:167:26//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P46470
F-NT2RP2001392//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIA3.//0.0080:82:32//OVIS ARIES (SHEEP).//P02441
F-NT2RP2001394//POLYHOMEOTIC-PROXIMAL CHROMATIN PROTEIN.//0.024:39:53//DROSOPHILA MELANOGASTER (FRUIT FLY).//P39769
F-NT2RP2001397//G2/MITOTIC-SPECIFIC CYCLIN B2.//1.4e-46:125:78//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//P37883

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F-NT2RP2001420//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//0.00018:113:38//HOMO SAPIENS (HUMAN).//P04280
F-NT2RP2001423//HYPOTHETICAL 9.4 KD PROTEIN IN GP31-CD INTERGENIC REGION (ORF A).//0.90:23:43//BACTERIOPHAGE T4.//P17307
F-NT2RP2001427//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.2e-11:38:68//HOMO SAPIENS (HUMAN).//P39188
F-NT2RP2001436//DYNEIN LIGHT INTERMEDIATE CHAIN 2, CYTOSOLIC (LIC53/55) (LIC-2).//0.25:124:28//RATTUS NORVEGICUS (RAT).//Q62698
F-NT2RP2001440//14-3-3 PROTEIN GAMMA (PROTEIN KINASE C INHIBITOR PROTEIN-1) (KCIP-1).//4.8e-62:145:90//RATTUS NORVEGICUS (RAT).//P35214
F-NT2RP2001445
F-NT2RP2001449//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//9.5e-118:226:95//BOS TAURUS (BOVINE).//Q10568
F-NT2RP2001450
F-NT2RP2001467//SHORT NEUROTOXIN 1 (TOXIN V-II-1).//1.0:25:40//BUNGARUS FASCIATUS (BANDED KRAIT).//P10808
F-NT2RP2001506
F-NT2RP2001511//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.//0.49:124:29//CAENORHABDITIS ELEGANS.//P34681
F-NT2RP2001520//VITAMIN D-DEPENDENT CALCIUM-BINDING PROTEIN, INTESTINAL (CABP) (CALBINDIN D9K).//0.035:71:33//HOMO SAPIENS (HUMAN).//P29377
F-NT2RP2001526
F-NT2RP2001536//METALLOTHIONEIN-I (MT-1).//1.0:19:42//COLUMBA LIVIA (DOMESTIC PIGEON).//P15786
F-NT2RP2001560//CUTICLE COLLAGEN 12 PRECURSOR.//0.0018:144:35//CAENORHABDITIS ELEGANS.//P20630
F-NT2RP2001569//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.7e-31:102:67//HOMO SAPIENS (HUMAN).//P39194
F-NT2RP2001576//SMP3 PROTEIN.//0.00016:75:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04174
F-NT2RP2001581//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.040:46:36//HOMO SAPIENS (HUMAN).//P51805
F-NT2RP2001597//PROBABLE E4 PROTEIN.//0.00042:113:34//HUMAN PAPILLOMAVIRUS TYPE 5.//P06924
F-NT2RP2001601
F-NT2RP2001613//HOMEOBOX PROTEIN SAX-1 (CHOX-3) (FRAGMENT).//0.14:59:32//GALLUS GALLUS (CHICKEN).//P19601
F-NT2RP2001628//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.056:140:33//SACCHAROMYCES CEREVISIAE (BAKER'S
YEAST).//P32323
F-NT2RP2001634//ALPHA-CATENIN.//7.1e-12:152:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P35220
F-NT2RP2001660//HYPOTHETICAL 80.4 KD PROTEIN IN SMC3-MRPL8 INTERGENIC REGION.//0.43:119:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40358
F-NT2RP2001663//ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE).//1.2e-26:126:56//HOMO SAPIENS (HUMAN).//P06733
F-NT2RP2001675//HYPOTHETICAL 107.7 KD PROTEIN IN RPSO 5'REGION (ORF1).//0.25:148:25//CAMPYLOBACTER JEJUNI.//Q46089
F-NT2RP2001677//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.010:101:31//RATTUS NORVEGICUS (RAT).//P10164
F-NT2RP2001678//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.6e-18:83:61//HOMO SAPIENS (HUMAN).//P39188
F-NT2RP2001699//PROTEIN C14.//0:98:51:31//VACCINIA VIRUS (STRAIN COPENHAGEN).//P21045
F-NT2RP2001720//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (ALLELIC FORM 1).//0.16:145:30//PLASMODIUM FALCIPARUM (ISOLATE CAMP / MALAYSIA).//Q99317
F-NT2RP2001721//MALE-SPECIFIC LETHAL-2 PROTEIN.//0.00090:48:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//P50534
F-NT2RP2001740//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.50:43:25//BOS TAURUS (BOVINE).//P20072
F-NT2RP2001748//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-

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MENT).//0.77:111:28//HOMO SAPIENS (HUMAN).//P10162
F-NT2RP2001762
F-NT2RP2001813//PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII (PSI-I).//1.0:22:40//PICEA ABIES (NORWAY SPRUCE) (PICEA EXCELSA).//O47040
F-NT2RP2001839//SCY1 PROTEIN.//6.8e-17:204:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53009
F-NT2RP2001861//D15KZ1 PROTEIN (FRAGMENT).//0.31:56:39//MUS MUSCULUS (MOUSE).//Q61466
F-NT2RP2001869//CORNEODESMOSIN (S PROTEIN) (FRAGMENT).//0.97:78:30//SUS SCROFA (PIG).//O19084
F-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AIF-1) (IONIZED CALCIUM BINDING ADAPTER MOLECULE 1).//3.5e-36:106:66//HOMO SAPIENS (HUMAN).//P55008
F-NT2RP2001883//CATHEPSIN L (EC 3.4.22.15).//0.95:29:41//OVIS ARIES (SHEEP).//Q10991
F-NT2RP2001898//TYPE II INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) (FRAGMENT).//1.6e-84:185:88//HOMO SAPIENS (HUMAN).//P32019
F-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5.//1.1e-17:180:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53946
F-NT2RP2001907//HYPHAL WALL PROTEIN 1 (CELL ELONGATION PROTEIN 2).//0.13:108:27//CANDIDA ALBICANS (YEAST).//P46593
F-NT2RP2001926//HYPOTHETICAL 7.6 KD PROTEIN YCF33.//0.55:57:26//CYANOPHORA PARADOXA.//P48273
F-NT2RP2001936
F-NT2RP2001943//HYPOTHETICAL 57.7 KD PROTEIN IN AIP1-CTF13 INTERGENIC REGION.//1.8e-13:208:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04305
F-NT2RP2001946//HYPOTHETICAL 13.0 KD PROTEIN IN ALGR3 3'REGION.//0.59:76:28//PSEUDOMONAS AERUGINOSA.//P21485
F-NT2RP2001947//ZINC FINGER PROTEIN DAN (N03).//0.53:68:29//RATTUS NORVEGICUS (RAT).//Q06880
F-NT2RP2001969//CHLOROPLAST 30S RIBOSOMAL PROTEIN S18.//0.0015:52:34//CHLORELLA VULGARIS.//P56353
F-NT2RP2001976//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//9.5e-07:201:22//MUS MUSCULUS (MOUSE).//Q99104
F-NT2RP2001985//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.016:90:32//MUS MUSCULUS (MOUSE).//P05142
F-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//8.0e-14:47:76//RATTUS NORVEGICUS (RAT).//Q08469
F-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//2.9e-30:211:42//GALLUS GALLUS (CHICKEN).//P35331
F-NT2RP2002032//FLOCCULANT-ACTIVE PROTEINS MO2.1 AND MO2.2.//0.23:20:40//MORINGA OLEIFERA (HORSERADISH TREE) (MORINGA PTERYGOSPERMA).//P24303
F-NT2RP2002033//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//0.88:27:62//HOMO SAPIENS (HUMAN).//P39193
F-NT2RP2002041
F-NT2RP2002046//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1) (PROTEIN KINASE A INTERFERENCE PROTEIN).//1.0:85:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36027
F-NT2RP2002047
F-NT2RP2002058//DOM34 INTERACTING PROTEIN 2.//9.4e-25:165:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12220
F-NT2RP2002066//TIGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1).//5.7e-12:108:41//HOMO SAPIENS (HUMAN).//Q07157
F-NT2RP2002070//CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) (FRAGMENT).//0.88:28:50//ASTERINA PECTINIFERA (STARFISH).//P11958
F-NT2RP2002076//TRP-ASP REPEATS CONTAINING PROTEIN RBA-2.//0.0031:124:27//CAENORHABDITIS ELEGANS.//P90916
F-NT2RP2002078//KERATIN, GLYCINE/TYROSINE-RICH OF HAIR.//0.82:30:40//OVIS ARIES (SHEEP).//Q02958
F-NT2RP2002079//OUTER DENSE FIBER PROTEIN.//0.34:41:39//HOMO SAPIENS (HUMAN).//Q14990
F-NT2RP2002099//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U).//5.2e-08:81:48//HOMO SAPIENS (HUMAN).//Q00839
F-NT2RP2002105//COLLAGEN 1(X) CHAIN PRECURSOR.//0.0012:100:34//BOS TAURUS (BOVINE).//P23206

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F-NT2RP2002124//EARLY GROWTH RESPONSE PROTEIN 1 (EGR-1) (KROX24) (TRANSCRIPTION FACTOR ETR103) (ZINC FINGER PROTEIN 225) (AT225).//0.74:72:31//HOMO SAPIENS (HUMAN).//P18146
F-NT2RP2002137//NEUROTOXIN B-II.//1.0:27:44//CEREBRATULUS LACTEUS (MILKY RIBBON WORM).//P01526
F-NT2RP2002154//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-34 GALACTOSIDE-BINDING LECTIN).//0.0029:112:34//MUS MUSCULUS (MOUSE).//P16110
F-NT2RP2002172
F-NT2RP2002185//UBIQUITIN-LIKE PROTEIN DSK2.//1.8e-07:87:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48510
F-NT2RP2002192
F-NT2RP2002193//CUTICLE COLLAGEN 40.//0.0062:70:37//CAENORHABDITIS ELEGANS.//P34804
F-NT2RP2002208//PEROXISOME ASSEMBLY PROTEIN PEX10 (PEROXIN-10).//0.00011:45:40//HOMO SAPIENS (HUMAN).//060683
F-NT2RP2002219
F-NT2RP2002231//V-TYPE SODIUM ATP SYNTHASE SUBUNIT E (EC 3.6.1.34) (NA(+)-TRANSLOCATING ATPASE SUBUNIT E).//1.0:68:32//ENTEROCOCCUS HIRAE.//P43436
F-NT2RP2002235//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP34.5).//0.0022:66:45//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN CVG-2).//P37318
F-NT2RP2002252//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//0.071:110:31//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414
F-NT2RP2002256//CYTOCHROME P450 26 (EC 1.14.-.-) (RETINOIC ACID-METABOLIZING CYTOCHROME) (P450RAI) (RETINOIC ACID 4-HYDROXYLASE).//3.1e-31:75:84//MUS MUSCULUS (MOUSE).//O55127
F-NT2RP2002259//L-MYC-1 PROTO-ONCOGENE PROTEIN.//1.9e-17:41:90//HOMO SAPIENS (HUMAN).//P12524
F-NT2RP2002270//HYPOTHETICAL 26.0 KD PROTEIN IN CYB5-LEU4 INTERGENIC REGION.//2.1e-27:164:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53930
F-NT2RP2002292//IMMEDIATE-EARLY PROTEIN RSP40.//0.018:107:23//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P24827
F-NT2RP2002312//PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41) (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE).//1.4e-52:174:55//HOMO SAPIENS (HUMAN).//Q92903
F-NT2RP2002316//HISTONE H1.C6/H1.C9.//1.0:40:40//TRYPANOSOMA CRUZI.//P40269
F-NT2RP2002325//PEROXISOMAL MEMBRANE PROTEIN PMP30A (PMP31) (PEROXIN 11A).//2.2e-06:145:26//CANDIDA BOIDINII (YEAST).//Q00316
F-NT2RP2002333//HYPOTHETICAL 39.1 KD PROTEIN IN RNPB-SOHA INTERGENIC REGION (ORF 3).//0.30:86:32//ESCHERICHIA COLI.//P23524
F-NT2RP2002373//SYNAPSINS IA AND IB.//0.080:145:31//BOS TAURUS (BOVINE).//P17599
F-NT2RP2002385//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: KNOB PROTEIN GP70; SPIKE PROTEIN P15E; R PROTEIN].//0.021:66:28//MINK CELL FOCUS-FORMING MURINE LEUKEMIA VIRUS (ISOLATE CI-3).//P03388
F-NT2RP2002394
F-NT2RP2002408//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.00030:107:37//BOS TAURUS (BOVINE).//P02453
F-NT2RP2002426
F-NT2RP2002439//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//0.00032:79:32//PLASMODIUM BERGHEI (STRAIN ANKA).//P23093
F-NT2RP2002442//HESA PROTEIN.//6.0e-16:163:30//PLECTONEMA BORYANUM.//P46037
F-NT2RP2002457
F-NT2RP2002464//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME I.//9.3e-18:165:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10264
F-NT2RP2002475//CYSTEINE-RICH HEART PROTEIN (HCRHP).//0.91:45:35//HOMO SAPIENS (HUMAN).//P50238
F-NT2RP2002479//ATP-BINDING CASSETTE TRANSPORTER 7 PRECURSOR (ABC TRANSPORTER 7 PROTEIN).//6.8e-96:186:94//HOMO SAPIENS (HUMAN).//O75027
F-NT2RP2002498//HYPOTHETICAL MERCURIC RESISTANCE PROTEIN MERC.//0.65:37:45//PSEUDOMONAS AERUGINOSA.//P04139

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F-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC1744).//1.3e-31:124:59//HOMO SAPIENS (HUMAN).//Q02386
F-NT2RP2002504//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//1.2e-123:240:92//RATTUS NORVEGICUS (RAT).//P37199
F-NT2RP2002520//ACIDIC PROLINE-RICH PROTEIN HP43A PRECURSOR.//0.94:83:28//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//P06680
F-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//4.0e-10:194:23//CAENORHABDITIS ELEGANS.//Q11073
F-NT2RP2002546
F-NT2RP2002549//G2/MITOTIC-SPECIFIC CYCLIN C13-1 (A-LIKE CYCLIN) (FRAGMENT).//0.98:65:30//DAUCUS CAROTA (CARROT).//P25010
F-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.6e-19:60:61//HOMO SAPIENS (HUMAN).//P51523
F-NT2RP2002595//ANNEXIN VII (SYNEXIN).//1.2e-15:121:49//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q92125
F-NT2RP2002606//PROTEIN TRANSPORT PROTEIN SEC2.//0.00034:98:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P17065
F-NT2RP2002609//HYPOTHETICAL 52.0 KD PROTEIN IN CLB6-SPT6 INTERGENIC REGION.//0.00022:79:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53264
F-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 1 (EC 2.1.1.-).//6.2e-37:180:44//RATTUS NORVEGICUS (RAT).//Q63009
F-NT2RP2002621//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.98:37:35//LEMUR CATTA (RING-TAILED LEMUR).//Q34879
F-NT2RP2002643//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP34.5).//0.042:77:32//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN MGH-10).//P37319
F-NT2RP2002672//PROTEIN Q300.//0.0018:41:43//MUS MUSCULUS (MOUSE).//Q02722
F-NT2RP2002701//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//3.6e-17:100:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701
F-NT2RP2002706//IMMEDIATE-EARLY PROTEIN IE180.//0.00027:139:33//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479
F-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1.//6.9e-09:96:40//MUS MUSCULUS (MOUSE).//P55194
F-NT2RP2002727//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).//3.6e-20:160:36//RATTUS NORVEGICUS (RAT).//P49816
F-NT2RP2002736
F-NT2RP2002740
F-NT2RP2002741//RHO1 GDP-GTP EXCHANGE PROTEIN 2.//2.0e-07:178:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P51862
F-NT2RP2002750//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//1.6e-09:43:72//HOMO SAPIENS (HUMAN).//P39191
F-NT2RP2002752//LOW CALCIUM RESPONSE LOCUS PROTEIN T.//0.95:33:39//YERSINIA PSEUDOTUBERCULOSIS.//Q00932
F-NT2RP2002753//ENDOGLUCANASE EG-1 PRECURSOR (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE) (CELLULASE).//0.71:78:33//TRICHODERMA LONGIBRACHIATUM.//Q12714
F-NT2RP2002769//50 KD SPICULE MATRIX PROTEIN PRECURSOR.//0.44:76:32//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).//P11994
F-NT2RP2002778
F-NT2RP2002800//CRAMBIN.//0.99:20:50//CRAMBE ABYSSINICA (ABYSSINIAN CRAMBE).//P01542
F-NT2RP2002839//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT).//0.010:87:31//HOMO SAPIENS (HUMAN).//P02812
F-NT2RP2002857//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).//0.00018:57:45//RATTUS NORVEGICUS (RAT).//P04474
F-NT2RP2002862//HYPOTHETICAL 27.1 KD PROTEIN UFD4-CAP1 INTERGENIC REGION.//7.2e-27:140:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33201
F-NT2RP2002880//DNA REPAIR PROTEIN RAD32.//0.83:67:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09683
F-NT2RP2002891//HOMEOBOX PROTEIN DLX-2 (DLX-5) (FRAGMENT).//0.99:70:24//RATTUS NORVEGICUS (RAT).//Q64204
F-NT2RP2002925//ALPHA-1D ADRENERGIC RECEPTOR (ALPHA 1D-ADRENOCEPTOR) (ALPHA-1A

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ADRENERGIC RECEPTOR).//0.31:48:43//HOMO SAPIENS (HUMAN).//P25100
F-NT2RP2002928//CELL DIVISION CONTROL PROTEIN 40.//2.8e-26:142:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40968
F-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II.//2.0e-31:186:35//CAENORHABDITIS ELEGANS.//Q18964
F-NT2RP2002939//ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-INHIBITABLE ADENYLYL CYCLASE).//0.0022:98:39//CANIS FAMILIARIS (DOG).//P30803
F-NT2RP2002954//U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A').//0.0019:107:30//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P43333
F-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//2.8e-11:33:81//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P51669
F-NT2RP2002979
F-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//1.1e-09:98:36//MYCOPLASMA CAPRICOLUM.//P10129
F-NT2RP2002986//RING CANAL PROTEIN (KELCH PROTEIN).//1.1e-19:141:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
F-NT2RP2002987//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//1.3e-07:78:47//HOMO SAPIENS (HUMAN).//P39192
F-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT).//8.0e-77:165:85//RATTUS NORVEGICUS (RAT).//O54888
F-NT2RP2003000//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.8e-19:62:64//HOMO SAPIENS (HUMAN).//P39194
F-NT2RP2003034//HYPOTHETICAL PROTEIN HI1458.//1.0:42:35//HAEMOPHILUS INFLUENZAE.//P44204
F-NT2RP2003073//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//0.0051:16:87//HOMO SAPIENS (HUMAN).//P39189
F-NT2RP2003099
F-NT2RP2003108//BASIC PROLINE-RICH PEPTIDE IB-1.//0.84:47:34//HOMO SAPIENS (HUMAN).//P04281
F-NT2RP2003117
F-NT2RP2003121//HYPOTHETICAL 96.7 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION.//9.0e-08:99:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43572
F-NT2RP2003125//TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOLOG 2).//9.2e-08:134:28//MUS MUSCULUS (MOUSE).//P97303
F-NT2RP2003129
F-NT2RP2003137//UBIQUITIN.//3.4e-06:70:30//NEUROSPORA CRASSA.//P13117
F-NT2RP2003157//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//7.8e-13:84:40//CAENORHABDITIS ELEGANS.//Q09217
F-NT2RP2003158//26S PROTEASOME REGULATORY SUBUNIT S3 (PROTEASOME SUBUNIT P58).//3.1e-65:155:84//HOMO SAPIENS (HUMAN).//O43242
F-NT2RP2003161//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.0011:59:42//MUS MUSCULUS (MOUSE).//P05142
F-NT2RP2003164//ZYXIN.//0.0037:85:36//MUS MUSCULUS (MOUSE).//Q62523
F-NT2RP2003165//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.2e-24:77:64//HOMO SAPIENS (HUMAN).//P39194
F-NT2RP2003177//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.55:38:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
F-NT2RP2003194//HYPOTHETICAL 12.5 KD PROTEIN ZK637.2 IN CHROMOSOME III.//2.3e-14:87:37//CAENORHABDITIS ELEGANS.//P30629
F-NT2RP2003206//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).//1.0:100:28//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM).//P41306
F-NT2RP2003228//DNA REPLICATION LICENSING FACTOR MCM4 (CDC21 HOMOLOG) (P1-CDC21).//9.3e-82:211:81//HOMO SAPIENS (HUMAN).//P33991
F-NT2RP2003230//SEC14 CYTOSOLIC FACTOR (PHOSPHATIDYLINOSITOL/PHOSPHATIDYLCHOLINE TRANSFER PROTEIN) (PI/PC TP).//1.0:51:31//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA).//P53989
F-NT2RP2003237//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//5.1e-44:66:84//HOMO SAPIENS (HUMAN).//P39194

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F-NT2RP2003243//M PROTEIN, SEROTYPE 5 PRECURSOR.//0.027:204:23//STREPTOCOCCUS PYOGENES.//P02977
F-NT2RP2003265//BP4A PROTEIN.//0.95:35:34//BRASSICA NAPUS (RAPE).//P41505
F-NT2RP2003272//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT).//5.5e-06:78:35//BRASSICA NAPUS (RAPE).//P40603
F-NT2RP2003277//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1).//1.9e-19:145:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P30771
F-NT2RP2003280
F-NT2RP2003286//RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4) (RNA-3'-PHOSPHATE CYCLASE) (RNA CYCLASE).//2.1e-32:137:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q08096
F-NT2RP2003293//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.7e-12:175:33//HOMO SAPIENS (HUMAN).//P51522
F-NT2RP2003295//PTB-ASSOCIATED SPLICING FACTOR (PSF).//0.055:44:45//HOMO SAPIENS (HUMAN).//P23246
F-NT2RP2003297
F-NT2RP2003307//KINESIN LIGHT CHAIN (KLC).//2.0e-18:87:49//RATTUS NORVEGICUS (RAT).//P37285
F-NT2RP2003308//CROOKED NECK PROTEIN.//2.1e-91:244:67//DROSOPHILA MELANOGASTER (FRUIT FLY).//P17886
F-NT2RP2003329//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III.//5.8e-57:186:55//CAENORHABDITIS ELEGANS.//P34284
F-NT2RP2003339//SHORT NEUROTOXIN 1 (NEUROTOXIN ALPHA).//0.98:11:72//DENDROASPIS POLYLEPIS POLYLEPIS (BLACK MAMBA).//P01416
F-NT2RP2003347//60S RIBOSOMAL PROTEIN L38.//0.83:42:33//OSTERTAGIA OSTERTAGI.//O61570
F-NT2RP2003367//SYNERGISTIC-TYPE VENOM PROTEIN C9S3, CHAIN 1.//1.0:37:35//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P01408
F-NT2RP2003391//MRNA TRANSPORT REGULATOR MTR10.//3.3e-11:229:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q99189
F-NT2RP2003393//PROTOCHLOROPHYLLIDE REDUCTASE CHLB SUBUNIT (EC 1.3.1.33) (NADPH- PROTOCHLOROPHYLLIDE OXIDOREDUCTASE CHLB SUBUNIT) (FRAGMENT).//0.94:29:34//ARAUCARIA HETEROPHYLLA.//P37843
F-NT2RP2003394
F-NT2RP2003401//60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN).//0.95:125:28//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P45746
F-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//9.8e-78:178:84//RATTUS NORVEGICUS (RAT).//P38378
F-NT2RP2003445
F-NT2RP2003446//HYPOTHETICAL PROTEIN E-115.//0.00030:106:33//HUMAN ADENOVIRUS TYPE 2.//P03290
F-NT2RP2003456//PHOTOSYSTEM II REACTION CENTRE M PROTEIN.//1.0:27:51//MARCHANTIA POLYMORPHA (LIVERWORT).//P12168
F-NT2RP2003466//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE).//6.7e-06:108:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q08871
F-NT2RP2003480//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (CBF-2) (T-14-6).//7.2e-15:38:50//GALLUS GALLUS (CHICKEN).//Q98937
F-NT2RP2003499//5E5 ANTIGEN.//0.090:114:32//RATTUS NORVEGICUS (RAT).//Q63003
F-NT2RP2003506//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//2.0e-11:91:43//SUS SCROFA (PIG).//P04175
F-NT2RP2003511//PARAMYOSIN, SHORT FORM (MIMIPARAMYOSIN).//0.0020:108:25//DROSOPHILA MELANOGASTER (FRUIT FLY).//P35416
F-NT2RP2003513//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.2e-05:96:36//HOMO SAPIENS (HUMAN).//P23246
F-NT2RP2003517//HYPOTHETICAL 12.9 KD PROTEIN CY49.27.//0.0059:22:31//MYCOBACTERIUM TUBERCULOSIS.//Q10696
F-NT2RP2003522//HYPOTHETICAL 10.0 KD PROTEIN.//1.0:65:30//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19283
F-NT2RP2003533//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//8.7e-18:94:54//HOMO SAPIENS (HUMAN).//P08547
F-NT2RP2003543//SYNAPSINS IA AND IB.//0.045:101:35//RATTUS NORVEGICUS (RAT).//P09951

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F-NT2RP2003559//ITBA2 PROTEIN (DXS9879E).//0.98:37:37//HOMO SAPIENS (HUMAN).//Q14657
F-NT2RP2003564//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//6.4e-35:175:44//HOMO SAPIENS (HUMAN).//P19474
F-NT2RP2003567//HYPOTHETICAL 11.2 KD PROTEIN T18D3.7 IN CHROMOSOME X.//0.72:82:34//CAENORHABDITIS ELEGANS.//Q22544
F-NT2RP2003581//HOMEOBOX PROTEIN OTX1.//0.90:61:37//MUS MUSCULUS (MOUSE).//P80205
F-NT2RP2003596//ELONGATION FACTOR P (EF-P).//0.83:61:32//MYCOPLASMA GENITALIUM.//P47272
F-NT2RP2003604//ALPHA-CATENIN.//1.5e-11:152:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//P35220
F-NT2RP2003629//PHOSPHOLIPASE A2 ALPHA (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE).//0.97:85:27//CROTALUS ADAMANTEUS (EASTERN DIAMONDBACK RATTLESNAKE).//P00623
F-NT2RP2003643//ACYLNEURAMINATE CYTIDYLYLTRANSFERASE (EC 2.7.7.43) (CMP-N- ACETYLNEURAMINIC ACID SYNTHETASE) (CMP-NEUNAC SYNTHETASE) (CMP-SIALIC ACID SYNTHETASE).//3.9e-12:84:40//NEISSERIA MENINGITIDIS.//Q57385
F-NT2RP2003668//!!!! ALU-SUBFAMILY SX WARNING ENTRY !!!!//5.0e-33:74:81//HOMO SAPIENS (HUMAN).//P39195
F-NT2RP2003687//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//5.7e-05:40:67//HOMO SAPIENS (HUMAN).//P39188
F-NT2RP2003691//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.5e-37:56:67//HOMO SAPIENS (HUMAN).//P39194
F-NT2RP2003702//HYPOTHETICAL OXIDOREDUCTASE IN INLA 5'REGION (EC 1.-.-.-) (ORFA).//1.3e-07:98:37//LISTERIA MONOCYTOGENES.//P25145
F-NT2RP2003704//GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (EC 2.3.2.2) (GAMMA-GLUTAMYLTRANSFERASE 5) (GGT-REL).//0.66:23:52//HOMO SAPIENS (HUMAN).//P36269
F-NT2RP2003706//GLUTAMYL AMINOPEPTIDASE (EC 3.4.11.7) (EAP) (AMINOPEPTIDASE A) (APA) (DIFFERENTIATION ANTIGEN GP160).//1.2e-22:187:35//HOMO SAPIENS (HUMAN).//Q07075
F-NT2RP2003713//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 6 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 6) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 6) (DEUBIQUITINATING ENZYME 6) (PROTO-ONCOGENE TRE-2).//2.7e-06:119:34//HOMO SAPIENS (HUMAN).//P35125
F-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//6.7e-27:68:75//HOMO SAPIENS (HUMAN).//Q05481
F-NT2RP2003727//HYPOTHETICAL PROTEIN MG007 HOMOLOG.//0.64:110:30//MYCOPLASMA PNEUMONIAE.//P75105
F-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//1.2e-72:147:90//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P51669
F-NT2RP2003751//EXTRACELLULAR GLOBIN PRECURSOR.//0.67:68:30//PSEUDOTERRANOVA DECIPIENS (COD WORM).//P26914
F-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.0e-98:235:82//BOS TAURUS (BOVINE).//P53620
F-NT2RP2003764//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.011:69:34//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341
F-NT2RP2003769//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:33:36//EQUUS CABALLUS (HORSE).//P48663
F-NT2RP2003770//PHOSPHATE REGULON SENSOR PROTEIN PHOR (EC 2.7.3.-) (FRAGMENT).//0.029:35:42//PSEUDOMONAS AERUGINOSA.//P23621
F-NT2RP2003777/HYPOTHETICAL 82 KD AVIRULENCE PROTEIN IN AVRBS3 REGION.//0.041:67:34//XANTHOMONAS CAMPESTRIS (PV. VESICATORIA).//P14728
F-NT2RP2003781//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.//4.7e-54:204:47//CAENORHABDITIS ELEGANS.//Q09201
F-NT2RP2003793//PSEUDO-HEVEIN (MINOR HEVEIN).//0.61:30:36//HEVEA BRASILIENSIS (PARA RUBBER TREE).//P80359
F-NT2RP2003825//ENDOTHELIN-1 PRECURSOR (ET-1) (FRAGMENT).//1.0:35:37//CANIS FAMILIARIS (DOG).//P13206
F-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//2.5e-05:80:38//CAENORHABDITIS ELEGANS.//Q11076
F-NT2RP2003857//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//0.54:28:50//ESCHERICHIA CO-

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LI.//P05834
F-NT2RP2003859//DROSOCIN PRECURSOR.//1.0:37:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P36193
F-NT2RP2003871
F-NT2RP2003885//CUTICLE PROTEIN 32 (LM-32) (LM-ACP 32) (FRAGMENT).//1.0:28:50//LOCUSTA MIGRATORIA (MIGRATORY LOCUST).//P11736
F-NT2RP2003912//SERINE/THREONINE-PROTEIN KINASE NEK1 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 1).//4.8e-110:268:80//MUS MUSCULUS (MOUSE).//P51954
F-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//0.00024:92:31//RATTUS NORVEGICUS (RAT).//O09175
F-NT2RP2003968//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//9.2e-05:101:36//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437
F-NT2RP2003976//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.7e-21:62:62//HOMO SAPIENS (HUMAN).//P39188
F-NT2RP2003981//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS8.//2.7e-08:165:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39702
F-NT2RP2003984//UNC-87 PROTEIN.//0.75:71:28//CAENORHABDITIS ELEGANS.//P37806
F-NT2RP2003986//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//5.3e-19:47:70//HOMO SAPIENS (HUMAN).//P39193
F-NT2RP2003988//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.2e-18:80:58//HOMO SAPIENS (HUMAN).//P39195
F-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//1.0e-52:141:77//HOMO SAPIENS (HUMAN).//P20290
F-NT2RP2004014//MACROPHAGE INFLAMMATORY PROTEIN-2-ALPHA (MIP2-ALPHA) (CINC-2-ALPHA).//0.99:45:26//RATTUS NORVEGICUS (RAT).//Q10746
F-NT2RP2004041//SYNAPSINS IA AND IB.//0.0022:51:37//BOS TAURUS (BOVINE).//P17599
F-NT2RP2004042//CRUSTACEAN HYPERGLYCEMIC HORMONE PRECURSOR (CHH) (FRAGMENT).//1.0:49:28//PENAEUS VANNAMEI (PENOEID SHRIMP) (EUROPEAN WHITE SHRIMP).//Q26181
F-NT2RP2004066//CALDESMON (CDM).//2.9e-05:175:21//GALLUS GALLUS (CHICKEN).//P12957
F-NT2RP2004081//CADMIUM-METALLOTHIONEIN (CD-MT).//0.93:59:23//HELIX POMATIA (ROMAN SNAIL) (EDIBLE SNAIL).//P33187
F-NT2RP2004098//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//4.6e-09:121:30//HOMO SAPIENS (HUMAN).//Q15404
F-NT2RP2004124//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.068:63:31//GALLUS GALLUS (CHICKEN).//P02314
F-NT2RP2004142//HYPOTHETICAL 59.1 KD PROTEIN IN VPS15-YMC2 INTERGENIC REGION.//7.9e-05:94:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38262
F-NT2RP2004152//LAMIN L(I).//0.25:167:19//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P09010
F-NT2RP2004165//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.0014:124:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214
F-NT2RP2004170//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.012:125:30//MUS MUSCULUS (MOUSE).//P05143
F-NT2RP2004172//HYPOTHETICAL 105.7 KD PROTEIN IN TPK3-PIR1 INTERGENIC REGION.//4.1e-26:214:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36051
F-NT2RP2004187//ZINC FINGER PROTEIN 174.//3.7e-12:76:47//HOMO SAPIENS (HUMAN).//Q15697
F-NT2RP2004194//HYPOTHETICAL 10.5 KD PROTEIN C31A2.13C IN CHROMOSOME I.//0.0013:92:23//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09730
F-NT2RP2004196//METALLOTHIONEIN 10-II (MT-10-II).//0.92:36:36//MYTILUS EDULIS (BLUE MUSSEL).//P80247
F-NT2RP2004207//MALE ACCESSORY GLAND SECRETORY PROTEIN 355A PRECURSOR.//0.92:62:35//DROSOPHILA SIMULANS (FRUIT FLY).//P33737
F-NT2RP2004226//66 KD STRESS PROTEIN (P66).//0.030:113:26//PHYSARUM POLYCEPHALUM (SLIME MOLD).//P90587
F-NT2RP2004232//PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).//2.0e-48:211:51//HOMO SAPIENS (HUMAN).//Q15139
F-NT2RP2004239//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR.//0.00038:111:36//TRITICUM AESTIVUM (WHEAT).//P08489

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F-NT2RP2004240//METALLOTHIONEIN-II (MT-II) (METALLOTHIONEIN-LIKE PROTEIN) (MT-CE).//1.0:39:28//CAENORHABDITIS ELEGANS.//P17512
F-NT2RP2004242//RAS-RELATED PROTEIN RGP1 (GTP-BINDING REGULATORY PROTEIN RGP1).//0.0036:64:28//ORYZA SATIVA (RICE).//P25766
F-NT2RP2004245//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:21:42//PONGO PYGMAEUS PYGMAEUS (BORNEAN ORANGUTAN).//P92896
F-NT2RP2004270//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//0.00023:118:33//NEPHILA CLAVIPES (ORB SPIDER).//P46804
F-NT2RP2004300//PROBABLE E4 PROTEIN.//0.18:77:40//HUMAN PAPILLOMAVIRUS TYPE 8.//P06425
F-NT2RP2004316
F-NT2RP2004321//HYPOTHETICAL 10.8 KD PROTEIN SSR2439.//1.0:50:28//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q01904
F-NT2RP2004339//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//5.0e-33:84:77//HOMO SAPIENS (HUMAN).//P39195
F-NT2RP2004347//HYPOTHETICAL 40.9 KD PROTEIN F33H1.3 FROM CHROMOSOME II.//0.78:96:30//CAENORHABDITIS ELEGANS.//Q09556
F-NT2RP2004364//MINOR OUTER CAPSID PROTEIN (NS26) (NONSTRUCTURAL PROTEIN VP9).//0.059:143:30//BOVINE ROTAVIRUS (STRAIN UK).//P04515
F-NT2RP2004365//EAMZP30-47 PROTEIN (FRAGMENT).//0.27:38:39//EIMERIA ACERVULINA.//P21959
F-NT2RP2004366//GLYCOPROTEIN L PRECURSOR.//0.64:71:28//MAREK'S DISEASE HERPESVIRUS (STRAIN GA) (MDHV).//P52510
F-NT2RP2004373//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR (HISTIDINE-PROLINE RICH GLYCOPROTEIN) (HPRG) (FRAGMENT).//0.59:50:40//ORYCTOLAGUS CUNICULUS (RABBIT).//Q28640
F-NT2RP2004389//HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III.//4.0e-16:89:43//CAENORHABDITIS ELEGANS.//P34388
F-NT2RP2004392
F-NT2RP2004396//SINGLE-STRANDED NUCLEIC ACID-BINDING PROTEIN.//0.42:89:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P10080
F-NT2RP2004399//SOMATOTROPIN PRECURSOR (GROWTH HORMONE).//1.0:72:34//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//P37886
F-NT2RP2004400
F-NT2RP2004412//SPERM PROTAMINE P1.//0.24:38:31//NOTORYCTES TYPHLOPS (MARSUPIAL MOLE).//P42143
F-NT2RP2004425//SUPPRESSOR PROTEIN SRP40.//0.0087:197:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
F-NT2RP2004463//ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR).//1.3e-05:121:37//MUS MUSCULUS (MOUSE).//Q01338
F-NT2RP2004476//NICKEL-SENSITIVE T-TYPE CALCIUM CHANNEL ALPHA-1 SUBUNIT (RBE-II).//0.20:68:36//RATTUS NORVEGICUS (RAT).//Q07652
F-NT2RP2004490//FOS-RELATED ANTIGEN 1.//0.94:59:33//HOMO SAPIENS (HUMAN).//P15407
F-NT2RP2004512//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3) (FRAGMENTS).//1.0:37:32//PISASTER OCHRACEUS (SEA STAR).//P24998
F-NT2RP2004523//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.1e-15:57:71//HOMO SAPIENS (HUMAN).//P39194
F-NT2RP2004538//KINESIN-LIKE PROTEIN KIF1A (AXONAL TRANSPORTER OF SYNAPTIC VESICLES).//1.2e-48:121:60//HOMO SAPIENS (HUMAN).//Q12756
F-NT2RP2004551//HYPOTHETICAL 7.6 KD PROTEIN (ORF 65).//1.0:20:50//EUGLENA GRACILIS.//P32095
F-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03.//5.2e-07:150:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09903
F-NT2RP2004580//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//3.7e-37:100:78//HOMO SAPIENS (HUMAN).//P39192
F-NT2RP2004587//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//8.2e-06:150:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214
F-NT2RP2004594//HYPOTHETICAL 45.3 KD PROTEIN C09F5.7 IN CHROMOSOME II.//0.84:105:24//CAENORHABDITIS ELEGANS.//Q09458
F-NT2RP2004600//MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MARCKS).//0.17:127:29//RATTUS NORVEGICUS (RAT).//P30009
F-NT2RP2004602//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.1e-05:50:58//HOMO SAPIENS (HUMAN).//

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P39188
F-NT2RP2004614//HYPOTHETICAL 11.6 KD PROTEIN.//1.0:68:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20561
F-NT2RP2004655//GLYCINE-RICH RNA-BINDING PROTEIN 7.//7.0e-05:70:42//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q03250
F-NT2RP2004664//HYPOTHETICAL 104.0 KD PROTEIN C32A11.03C IN CHROMOSOME I.//0.30:78:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10328
F-NT2RP2004675
F-NT2RP2004681
F-NT2RP2004689//HYPOTHETICAL 78.3 KD PROTEIN IN RAM2-ATP7 INTERGENIC REGION.//0.021:179:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P34243
F-NT2RP2004709//HYPOTHETICAL PROTEIN MJ0647.//0.90:39:43//METHANOCOCCUS JANNASCHII.//Q58063
F-NT2RP2004710//GAR2 PROTEIN.//0.085:60:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891
F-NT2RP2004736//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.4e-15:97:49//HOMO SAPIENS (HUMAN).//P39188
F-NT2RP2004743//MALE SPECIFIC SPERM PROTEIN MST87F.//0.43:24:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175
F-NT2RP2004767//36.4 KD PROLINE-RICH PROTEIN.//0.0051:88:27//LYCOPERSICON ESCULENTUM (TOMATO).//Q00451
F-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).//9.0e-29:166:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38692
F-NT2RP2004775
F-NT2RP2004791//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//7.4e-60:226:53//CAENORHABDITIS ELEGANS.//Q09996
F-NT2RP2004799//SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//2.2e-42:133:57//NEOCALLIMASTIX FRONTALIS (RUMEN FUNGUS).//P53587
F-NT2RP2004802//HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION.//0.018:86:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38898
F-NT2RP2004816//H<BETA>58 PROTEIN.//1.0e-68:145:93//MUS MUSCULUS (MOUSE).//P40336
F-NT2RP2004841//DSRD PROTEIN.//0.83:33:39//ARCHAEOGLOBUS FULGIDUS.//P70742
F-NT2RP2004861//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIA3A.//0.0072:41:39//OVIS ARIES (SHEEP).//P02443
F-NT2RP2004897//METALLOTHIONEIN-LIKE PROTEIN 1.//0.99:41:41//CASUARINA GLAUCA (SWAMP OAK).//Q39511
F-NT2RP2004933//DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1).//8.4e-34:102:67//HOMO SAPIENS (HUMAN).//P53355
F-NT2RP2004936//HIGH POTENTIAL IRON-SULFUR PROTEIN, ISOZYME 2 (HIPIP 2).//0.87:36:33//ECTOTHIORHODOSPIRA VACUOLATA.//P38524
F-NT2RP2004959//STEM CELL FACTOR PRECURSOR (SCF) (MAST CELL GROWTH FACTOR) (MGF) (C-KIT LIGAND).//1.0:69:28//CANIS FAMILIARIS (DOG).//Q06220
F-NT2RP2004961//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) (FRAGMENT).//2.1e-21:73:58//HOMO SAPIENS (HUMAN).//Q06730
F-NT2RP2004962//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//0.17:28:57//HOMO SAPIENS (HUMAN).//P39189
F-NT2RP2004967//HYPOTHETICAL 7.3 KD PROTEIN.//0.76:41:31//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19301
F-NT2RP2004978//SPERMATID-SPECIFIC PROTEIN T2 [CONTAINS: SPERM PROTAMINE SP2].//0.44:40:45//SEPIA OFFICINALIS (COMMON CUTTLEFISH).//P80002
F-NT2RP2004982
F-NT2RP2004985//HYPOTHETICAL PROTEIN KIAA0144.//1.2e-51:204:57//HOMO SAPIENS (HUMAN).//Q14157
F-NT2RP2004999//LONG NEUROTOXIN 1 (ALPHA-BUNGAROTOXIN) (BGTX).//0.23:73:26//BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT).//P01378
F-NT2RP2005000//ATPASE STABILIZING FACTOR 15 KD PROTEIN.//0.12:37:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P16965

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F-NT2RP2005001//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.90:54:31//HOMO SAPIENS (HUMAN).//P22531
F-NT2RP2005003//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//1.6e-30:78:56//MUS MUSCULUS (MOUSE).//P15533
F-NT2RP2005012//NPL1 PROTEIN (SEC63 PROTEIN).//0.00024:94:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P14906
F-NT2RP2005018//GAG POLYPROTEIN (CORE POLYPROTEIN) [CONTAINS: CORE PROTEINS P19, P10] (FRAGMENT).//1.0:91:28//AVIAN ENDOGENOUS ROUS-ASSOCIATED VIRUS-0 (EV-2) (AVIAN RETROVIRUS RAV-0).//P06937
F-NT2RP2005020
F-NT2RP2005022//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//4.9e-11:106:35//PODOSPORA ANSERINA.//Q00808
F-NT2RP2005031
F-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//2.2e-32:117:55//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32447
F-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL ADDITION ENZYME) (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFERASE).//9.3e-28:187:40//AMBYSTOMA MEXICANUM (AXOLOTL).//O57486
F-NT2RP2005108//CUTICLE COLLAGEN 2.//0.33:62:38//CAENORHABDITIS ELEGANS.//P17656
F-NT2RP2005116//PUTATIVE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 ALPHA SUBUNIT (EIF-3 ALPHA).//4.0e-54:161:63//CAENORHABDITIS ELEGANS.//P34466
F-NT2RP2005126//CHLOROPLAST 50S RIBOSOMAL PROTEIN L27 (FRAGMENT).//0.23:46:39//PLEUROCHRYSIS HAPTONEMOFERA.//P41552
F-NT2RP2005139//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.016:43:37//BOS TAURUS (BOVINE).//P25508
F-NT2RP2005140//HYPOTHETICAL 7.4 KD PROTEIN YCF33.//0.96:51:39//GUILLARDIA THETA (CRYPTOMONAS PHI).//O78517
F-NT2RP2005144//TUBBY PROTEIN.//5.6e-08:66:45//MUS MUSCULUS (MOUSE).//P50586
F-NT2RP2005147
F-NT2RP2005159//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR.//0.94:57:29//NICOTIANA TABACUM (COMMON TOBACCO), AND SPINACIA OLERACEA (SPINACH).//P12164
F-NT2RP2005162//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION.//1.2e-33:139:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38821
F-NT2RP2005168//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U).//2.8e-33:102:61//HOMO SAPIENS (HUMAN).//Q00839
F-NT2RP2005204//DNA DAMAGE TOLERANCE PROTEIN RHC31 (RAD31 HOMOLOG).//3.9e-28:141:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06624
F-NT2RP2005227
F-NT2RP2005239//TRNA SPLICING PROTEIN SPL1.//2.0e-38:117:64//CANDIDA ALBICANS (YEAST).//P87185
F-NT2RP2005254//OMEGA-AGATOXIN IB (OMEGA-AGA-IB) (FRAGMENT).//0.26:29:48//AGELENOPSIS APERTA (FUNNEL-WEB SPIDER).//P15970
F-NT2RP2005270//HOMEOBOX PROTEIN HOX-A4 (CHOX-1.4).//0.037:82:34//GALLUS GALLUS (CHICKEN).//P17277
F-NT2RP2005276//LONG-CHAIN-FATTY-ACID--COA LIGASE 4 (EC 6.2.1.3) (LONG-CHAIN ACYL-COA SYNTHETASE 4) (LACS 4).//2.0e-59:174:61//RATTUS NORVEGICUS (RAT).//O35547
F-NT2RP2005287//ZINC FINGER PROTEIN 26 (ZINC FINGER PROTEIN KOX20) (FRAGMENT).//1.5e-05:27:70//HOMO SAPIENS (HUMAN).//P17031
F-NT2RP2005288//PROBABLE RUBREDOXIN HUPI.//1.0:42:28//RHIZOBIUM LEGUMINOSARUM (BIOVAR VICIAE).//P28151
F-NT2RP2005289//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.1e-21:75:70//HOMO SAPIENS (HUMAN).//P39193
F-NT2RP2005293//TRANSLATION INITIATION FACTOR IF-2.//0.58:170:24//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//P55972
F-NT2RP2005315//CUTICLE COLLAGEN 7 (FRAGMENT).//0.091:65:38//CAENORHABDITIS ELEGANS.//P18832
F-NT2RP2005325//CHROMOGRANIN A PRECURSOR (CGA) (PITUITARY SECRETORY PROTEIN I) (SP-I) [CONTAINS: PANCREASTATIN; WE-14].//9.5e-09:98:39//HOMO SAPIENS (HUMAN).//P10645
F-NT2RP2005336//HYPOTHETICAL 68.7 KD PROTEIN IN STB1-MCK1 INTERGENIC REGION.//0.00011:124:

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28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42846
F-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPASE 4 (EC 3.6.1.38).//4.7e-21:92:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12675
F-NT2RP2005354
F-NT2RP2005358//MYOSIN IC HEAVY CHAIN.//0.012:91:39//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569
F-NT2RP2005360//ACROSIN PRECURSOR (EC 3.4.21.10).//0.0022:73:36//ORYCTOLAGUS CUNICULUS (RABBIT).//P48038
F-NT2RP2005393//HYPOTHETICAL 25.9 KD PROTEIN AH6.3 IN CHROMOSOME II.//0.00085:135:28//CAENORHABDITIS ELEGANS .//Q09202
F-NT2RP2005407//SQUALENE MONOOXYGENASE (EC 1.14.99.7) (SQUALENE EPOXIDASE) (SE).//0.96:109:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32476
F-NT2RP2005436//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.0011:54:42//ZEA MAYS (MAIZE).//P14918
F-NT2RP2005441//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.039:182:29//MUS MUSCULUS (MOUSE).//P05142
F-NT2RP2005453
F-NT2RP2005457//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B).//4.0e-10:124:37//BOS TAURUS (BOVINE).//Q02827
F-NT2RP2005464//HYPOTHETICAL 9.5 KD PROTEIN.//0.96:42:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20553
F-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2.//4.6e-09:92:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38127
F-NT2RP2005472//HYPOTHETICAL PROTEIN BB0129.//0.76:80:32//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//O51155
F-NT2RP2005476//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.0e-31:39:89//HOMO SAPIENS (HUMAN).//P39193
F-NT2RP2005490//METALLOTHIONEIN-II (MT-II).//0.14:27:33//SCYLLA SERRATA (MUD CRAB).//P02806
F-NT2RP2005491//DNA-DIRECTED RNA POLYMERASE SUBUNIT I (EC 2.7.7.6).//0.95:45:31//METHANOCOCCUS JANNASCHII.//Q58785
F-NT2RP2005495//HYPOTHETICAL 10.8 KD PROTEIN IN GP30-RIII INTERGENIC REGION.//0.99:68:30//BACTERIOPHAGE T4.//Q02407
F-NT2RP2005496//ZINC FINGER PROTEIN 135.//1.4e-54:120:59//HOMO SAPIENS (HUMAN).//P52742
F-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55).//9.5e-76:146:86//RATTUS NORVEGICUS (RAT).//P36876
F-NT2RP2005501//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP).//0.025:70:40//HOMO SAPIENS (HUMAN).//P17931
F-NT2RP2005509//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//1.0:166:27//GALLUS GALLUS (CHICKEN).//P02457
F-NT2RP2005520//CHROMOSOME ASSEMBLY PROTEIN XCAP-E.//7.9e-45:118:79//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P50533
F-NT2RP2005525//50S RIBOSOMAL PROTEIN L11.//1.0:47:27//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//O51354
F-NT2RP2005531//PROTEIN-TYROSINE PHOSPHATASE MEG1 (EC 3.1.3.48) (PTPASE-MEG1) (MEG).//9.8e-13:84:45//HOMO SAPIENS (HUMAN).//P29074
F-NT2RP2005539//RING CANAL PROTEIN (KELCH PROTEIN).//4.9e-10:90:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
F-NT2RP2005540//NUCLEOTIDE BINDING PROTEIN EXPZ.//0.36:119:21//BACILLUS SUBTILIS.//P39115
F-NT2RP2005549//HYPOTHETICAL 32.0 KD PROTEIN C16C10.10 IN CHROMOSOME III.//6.0e-39:179:46//CAENORHABDITIS ELEGANS.//Q09253
F-NT2RP2005555
F-NT2RP2005557//HYPOTHETICAL 23.7 KD PROTEIN C13G6.14 IN CHROMOSOME I.//4.9e-06:90:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09790
F-NT2RP2005581
F-NT2RP2005600//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.014:37:40//HOMO SAPIENS (HUMAN).//

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P02811
F-NT2RP2005605//GONADOLIBERIN I PRECURSOR (LHRH I) (LUTEINIZING HORMONE RELEASING HORMONE I) (GONADOTROPIN RELEASING HORMONE I) (GNRH I) (LULIBERIN I) (FRAGMENT).//0.64:26:42//MACACA MULATTA (RHESUS MACAQUE).//P55247
F-NT2RP2005620//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REGION.//8.7e-31:138:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160
F-NT2RP2005622//NEUROTOXIN-LIKE PROTEIN STR1 (ANATOXIN AAH STR1).//0.39:22:40//ANDROCTONUS AUSTRALIS HECTOR (SAHARA SCORPION).//P80950
F-NT2RP2005635//HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION.//5.8e-43:144:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38795
F-NT2RP2005637//VPU PROTEIN (U ORF PROTEIN).//0.91:33:45//CHIMPANZEE IMMUNODEFICIENCY VIRUS (SIV(CPZ)) (CIV).//P17286
F-NT2RP2005640//METALLOTHIONEIN-LIKE PROTEIN LSC54.//0.63:41:31//BRASSICA NAPUS (RAPE).//P43402
F-NT2RP2005645
F-NT2RP2005651//OCTAMER-BINDING TRANSCRIPTION FACTOR 3A (OCT-3A) (OCT-4).//0.0023:50:42//HOMO SAPIENS (HUMAN).//Q01860
F-NT2RP2005654//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION.//6.1e-16:76:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40564
F-NT2RP2005669//METALLOTHIONEIN-II (MT-II).//0.76:16:50//SCYLLA SERRATA (MUD CRAB).//P02806
F-NT2RP2005675//PUTATIVE ORAL CANCER SUPPRESSOR (DELETED IN ORAL CANCER-1).//6.5e-26:116:54//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//P49119
F-NT2RP2005683//HYPOTHETICAL PROTEIN HI0275.//0.17:50:40//HAEMOPHILUS INFLUENZAE.//P43975
F-NT2RP2005690//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//1.3e-16:75:30//PISUM SATIVUM (GARDEN PEA).//Q04708
F-NT2RP2005694//HYPOTHETICAL PROTEIN KIAA0032.//9.6e-11:135:34//HOMO SAPIENS (HUMAN).//Q15034
F-NT2RP2005701//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.084:158:32//HOMO SAPIENS (HUMAN).//P10161
F-NT2RP2005712//METALLOTHIONEIN-II (MT-II).//0.19:14:50//STENELLA COERULEOALBA (STRIPED DOLPHIN).//P14425
F-NT2RP2005719//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).//1.0:36:41//ORYCTOLAGUS CUNICULUS (RABBIT).//P02456
F-NT2RP2005722//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//7.8e-37:131:62//HOMO SAPIENS (HUMAN).//P16415
F-NT2RP2005723//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//0.98:23:60//HOMO SAPIENS (HUMAN).//P39192
F-NT2RP2005726//HYPOTHETICAL PROTEIN TP0375.//0.98:30:43//TREPONEMA PALLIDUM.//O83390
F-NT2RP2005732//PERIOD CLOCK PROTEIN (FRAGMENT).//0.41:20:55//DROSOPHILA ROBUSTA (FRUIT FLY).//Q03296
F-NT2RP2005741//SMR1 PROTEIN PRECURSOR (VCS-ALPHA 1).//0.38:58:36//RATTUS NORVEGICUS (RAT).//P13432
F-NT2RP2005748//ZINC FINGER PROTEIN KOX23 (FRAGMENT).//0.026:19:68//HOMO SAPIENS (HUMAN).//P17034
F-NT2RP2005752//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//0.90:101:31//HOMO SAPIENS (HUMAN).//P02461
F-NT2RP2005753//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.50:22:59//HOMO SAPIENS (HUMAN).//P30808
F-NT2RP2005763//PUTATIVE ATP-DEPENDENT RNA HELICASE STE13.//4.7e-14:108:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09181
F-NT2RP2005767//NONHISTONE CHROMOSOMAL PROTEIN 6B.//4.1e-08:65:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11633
F-NT2RP2005773//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//1.2e-14:65:61//HOMO SAPIENS (HUMAN).//P32322
F-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP).//1.3e-103:199:90//ORYCTOLAGUS CUNICULUS (RABBIT).//P42675
F-NT2RP2005781//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1 / PRP-

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3) (PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C) [CONTAINS: PEPTIDE P-C].//0.090:73:36//HOMO SAPIENS (HUMAN).//P02810

F-NT2RP2005784//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).//3.5e-06:79:37//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).// P08393

F-NT2RP2005804//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//1.8e-07:43:55//OWENIA FUSIFORMIS.//P21260

F-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//6.3e-14:143:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40004

F-NT2RP2005815//FERROCHELATASE (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE).//0.0017:123:37//MYCOBACTERIUM AVIUM.//O07401

F-NT2RP2005835//SHP1 PROTEIN.//1.2e-08:135:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P34223

F-NT2RP2005841//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.23:28:53//HOMO SAPIENS (HUMAN).//P22532

F-NT2RP2005853//HYPOTHETICAL 8.5 KD PROTEIN IN ASIA-MOTA INTERGENIC REGION.//0.99:33:48//BACTERIOPHAGE T4.//P22917

F-NT2RP2005857//CHROMOSOME ASSEMBLY PROTEIN XCAP-C.//8.6e-84:235:66//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P50532

F-NT2RP2005859//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.017:60:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643

F-NT2RP2005868//ATP SYNTHASE B' CHAIN PRECURSOR (EC 3.6.1.34) (SUBUNIT II).//0.28:121:28//SPINACIA OLERACEA (SPINACH).//P31853

F-NT2RP2005886//MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA].//0.80:130:28//TETRAHYMENA THERMOPHILA.//P40631

F-NT2RP2005890

F-NT2RP2005901//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.35:18:44//DROSOPHILA YAKUBA (FRUIT FLY).//P03933

F-NT2RP2005908//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.0e-28:61:65//HOMO SAPIENS (HUMAN).//P39194

F-NT2RP2005933//PERIOD CLOCK PROTEIN (P230) (FRAGMENT).//1.7e-11:85:49//ACETABULARIA MEDITERRANEA (MERMAID'S WINE GLASS).//P12347

F-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//7.2e-59:216:58//BOS TAURUS (BOVINE).//P25500

F-NT2RP2005980//HYPOTHETICAL 11.5 KD PROTEIN IN RSP8A-AST1 INTERGENIC REGION.//1.0:49:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38185

F-NT2RP2006023//DNA REPAIR PROTEIN RECN (RECOMBINATION PROTEIN N) (FRAGMENT).//1.0:40:45//VIBRIO CHOLERAE.//P52118

F-NT2RP2006038//HYPOTHETICAL 30.2 KD PROTEIN C02F5.4 IN CHROMOSOME III.//4.0e-11:90:34//CAENORHABDITIS ELEGANS.//P34281

F-NT2RP2006043//LAMININ BETA-1 CHAIN VARIANT (LAMININ BETA-1-2 CHAIN) (FRAGMENT).//0.00067:73:38//GALLUS GALLUS (CHICKEN).//Q01636

F-NT2RP2006052//METALLOTHIONEIN-I (MT-I).//0.19:31:38//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).//P02797

F-NT2RP2006069//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENTS).//1.0:66:34//RATTUS NORVEGICUS (RAT).//P02466

F-NT2RP2006071//RESTIN.//0.40:156:29//GALLUS GALLUS (CHICKEN).//O42184

F-NT2RP2006098//HYPOTHETICAL 21.7 KD PROTEIN IN TUP1-ABP1 INTERGENIC REGION.//0.99:95:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25651

F-NT2RP2006100//LONG NEUROTOXIN 4 (ALPHA-NEUROTOXIN).//0.94:43:34//OPHIOPHAGUS HANNAH (KING COBRA) (NAJA HANNAH).//P80156

F-NT2RP2006103//50S RIBOSOMAL PROTEIN L32.//0.40:36:38//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P73014

F-NT2RP2006106//CUTICLE COLLAGEN 1.//0.28:85:29//CAENORHABDITIS ELEGANS.//P08124

F-NT2RP2006141//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//1.9e-08:57:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701

F-NT2RP2006166

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F-NT2RP2006184//HYPOTHETICAL 11.2 KD PROTEIN IN CSGC-MDOG INTERGENIC REGION PRECURSOR.//0.95:87:26//ESCHERICHIA COLI.//P75917
F-NT2RP2006186//MICROTUBULE-ASSOCIATED PROTEIN 2.//0.088:124:33//MUS MUSCULUS (MOUSE).//P20357
F-NT2RP2006196//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//4.0e-05:49:61//HOMO SAPIENS (HUMAN).//P39193
F-NT2RP2006200//PROCOLLAGEN ALPHA 2(V) CHAIN PRECURSOR.//0.0013:205:32//HOMO SAPIENS (HUMAN).//P05997
F-NT2RP2006219//GONADAL PROTEIN GDL.//3.5e-18:158:37//DROSOPHILA MELANOGASTER (FRUIT FLY).//P22468
F-NT2RP2006237//FIBRINOGEN- AND IG-BINDING PROTEIN PRECURSOR (MRP PROTEIN).//0.79:103:28//STREPTOCOCCUS PYOGENES.//P30141
F-NT2RP2006238//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//4.7e-07:127:39//MUS MUSCULUS (MOUSE).//P05143
F-NT2RP2006258//PROBABLE E5 PROTEIN.//0.78:47:34//RHESUS PAPILLOMAVIRUS TYPE 1 (RHPV 1).//P24834
F-NT2RP2006261//PENAEIDIN-3A PRECURSOR (P3-A).//0.61:35:40//PENAEUS VANNAMEI (PENOEID SHRIMP) (EUROPEAN WHITE SHRIMP).//P81058
F-NT2RP2006275//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 2 (FRAGMENT).//1.2e-28:59:57//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P14401
F-NT2RP2006312//HIGH-MOBILITY-GROUP PROTEIN (NONHISTONE CHROMOSOMAL PROTEIN).//1.6e-06:53:35//TETRAHYMENA PYRIFORMIS.//P40625
F-NT2RP2006320//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).//0.90:24:41//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1).//P04612
F-NT2RP2006321//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//0.0051:25:76//HOMO SAPIENS (HUMAN).//P39193
F-NT2RP2006323//WISKOTT-ALDRICH SYNDROME PROTEIN (WASP).//0.84:33:39//HOMO SAPIENS (HUMAN).//P42768
F-NT2RP2006333//MYOTOXIN 3 PRECURSOR (CROTAMINE 3).//0.56:37:40//CROTALUS DURISSUS TERRIFICUS (SOUTH AMERICAN RATTLESNAKE).//P24333
F-NT2RP2006334//SUCCINYL-COA LIGASE [GDP-FORMING], ALPHA-CHAIN 3 PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN 3).//0.00097:46:41//TRICHOMONAS VAGINALIS.//P53401
F-NT2RP2006365//NONSPECIFIC LIPID-TRANSFER PROTEIN 4.3 PRECURSOR (LTP 4.3).//0.18:75:29//HORDEUM VULGARE (BARLEY).//Q42842
F-NT2RP2006393//OMEGA-CONOTOXIN MVIIC PRECURSOR (FRAGMENT).//0.82:15:66//CONUS MAGUS (MAGUS CONE).//P37300
F-NT2RP2006436//ANTERIOR-RESTRICTED HOMEOBOX PROTEIN (RATHKE POUCH HOMEO BOX).//1.4e-08:50:50//MUS MUSCULUS (MOUSE).//Q61658
F-NT2RP2006441//METALLOTHIONEIN-LIKE PROTEIN 1.//0.99:22:54//MIMULUS GUTTATUS (SPOTTED MONKEY FLOWER) (YELLOW MONKEY FLOWER).//P20238
F-NT2RP2006454//SPERM PROTAMINE P1.//0.60:47:36//TACHYGLOSSUS ACULEATUS ACULEATUS (AUSTRALIAN ECHIDNA).//P35311
F-NT2RP2006456
F-NT2RP2006464//PHOTOSYSTEM I IRON-SULFUR CENTER (PHOTOSYSTEM I SUBUNIT VII) (9 KD POLYPEPTIDE) (PSI-C).//0.91:79:30//SYNECHOCOCCUS SP. (STRAIN PCC 7002) (AGMENELLUM QUADRUPLICATUM).//P31087
F-NT2RP2006467//PUTATIVE CUTICLE COLLAGEN F55C10.3.//0.15:53:35//CAENORHABDITIS ELEGANS.//Q21184
F-NT2RP2006472//HYPOTHETICAL 19 KD PROTEIN (ORF 167).//0.33:98:26//MARCHANTIA POLYMORPHA (LIVERWORT).//P12202
F-NT2RP2006534
F-NT2RP2006554//ANTI-SIGMA F FACTOR ANTAGONIST (STAGE II SPORULATION PROTEIN AA).//0.91:50:34//BACILLUS SPHAERICUS.//O32723
F-NT2RP2006565//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 1 (SCAMP 37).//6.0e-66:93:96//RATTUS NORVEGICUS (RAT).//P56603
F-NT2RP2006571//CYTOCHROME P450 2B10 (EC 1.14.14.1) (CYPIIB10) (TESTOSTERONE 16-ALPHA HYDROXYLASE) (P450-16-ALPHA) (CLONE PF3/46).//4.5e-40:138:57//MUS MUSCULUS (MOUSE).//P12791
F-NT2RP2006573//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.53:46:39//BOS TAURUS (BO-

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VINE).//P02318
F-NT2RP2006598//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.3e-12:44:77//HOMO SAPIENS (HUMAN).//P39195
F-NT2RP3000002//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//1.4e-19:60:63//HOMO SAPIENS (HUMAN).//P39192
F-NT2RP3000031//HYPOTHETICAL 89.8 KD PROTEIN F41H10.6 IN CHROMOSOME IV.//2.1e-39:210:42//CAENORHABDITIS ELEGANS.//Q20296
F-NT2RP3000046//POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF.//1.4e-25:149:44//PSEUDOMONAS PUTIDA.//P25755
F-NT2RP3000047//NPL4 PROTEIN.//4.7e-48:275:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33755
F-NT2RP3000050//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//3.2e-72:232:59//HOMO SAPIENS (HUMAN).//P51522
F-NT2RP3000055//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.26:57:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
F-NT2RP3000068//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION.//0.0014:66:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170
F-NT2RP3000072//HYPOTHETICAL 6.7 KD PROTEIN IN NOHA-CSPI INTERGENIC REGION.//0.95:49:30//ESCHERICHIA COLI.//P77695
F-NT2RP3000080//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//5.1e-17:64:68//HOMO SAPIENS (HUMAN).//P39188
F-NT2RP3000085//BIOTIN CARBOXYLASE (EC 6.3.4.14) (A SUBUNIT OF ACETYL-COA CARBOXYLASE (EC 6.4.1.2)) (ACC).//4.4e-43:169:51//BACILLUS SUBTILIS.//P49787
F-NT2RP3000092//CELL DIVISION CONTROL PROTEIN 1.//0.00016:103:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40986
F-NT2RP3000109//ACYL CARRIER PROTEIN HOMOLOG (ACP).//0.76:83:28//MYCOPLASMA GENITALIUM.//P47529
F-NT2RP3000134
F-NT2RP3000142//GAR2 PROTEIN.//0.00098:241:20//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891
F-NT2RP3000149//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.0014:33:36//PONGO PYGMAEUS ABELII (SUMATRAN ORANGUTAN).//P92694
F-NT2RP3000186//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//8.3e-15:36:83//HOMO SAPIENS (HUMAN).//P39188
F-NT2RP3000197//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5'REGION.//0.91:21:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53820
F-NT2RP3000207//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//0.026:209:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
F-NT2RP3000220//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//1.0:26:42//HOMO SAPIENS (HUMAN).//P30808
F-NT2RP3000233//RING CANAL PROTEIN (KELCH PROTEIN).//2.1e-42:249:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
F-NT2RP3000235//HOMEOBOX PROTEIN H40 (FRAGMENT).//0.55:45:40//APIS MELLIFERA (HONEYBEE).//P15858
F-NT2RP3000247//HYPOTHETICAL PROTEIN KIAA0218.//1.7e-82:123:69//HOMO SAPIENS (HUMAN).//Q93075
F-NT2RP3000251//SERINE PROTEINASE STUBBLE (EC 3.4.21.-) (STUBBLE-STUBBLOID PROTEIN).//1.0:53:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q05319
F-NT2RP3000252//HYPOTHETICAL 40 KD GTP-BINDING PROTEIN IN RIBOSOMAL PROTEIN GENE CLUSTER 5'REGION.//2.2e-06:96:32//HALOBACTERIUM CUTIRUBRUM.//P17103
F-NT2RP3000255//HISTONE H1.1 (FRAGMENT).//0.95:71:33//BOS TAURUS (BOVINE).//P02253
F-NT2RP3000267//HYPOTHETICAL 21.1 KD PROTEIN IN SSR-SERA INTERGENIC REGION (O182).//0.38:77:33//ESCHERICHIA COLI.//P09160
F-NT2RP3000299//MYOSIN IC HEAVY CHAIN.//1.2e-11:147:34//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569
F-NT2RP3000312//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.64:216:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214

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F-NT2RP3000320//TRANSLATION INITIATION FACTOR IF-2.//5.2e-05:184:22//AQUIFEX AEOLICUS.//O67825
F-NT2RP3000324//HYPOTHETICAL PROTEIN HI1036.//0.69:64:35//HAEMOPHILUS INFLUENZAE.//P44097
F-NT2RP3000333//WIR1A PROTEIN.//0.35:51:41//TRITICUM AESTIVUM (WHEAT).//Q01482
F-NT2RP3000341//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//2.1e-30:57:80//HOMO SAPIENS (HUMAN).//P39189
F-NT2RP3000348
F-NT2RP3000350//HYPOTHETICAL 40 KD GTP-BINDING PROTEIN IN RIBOSOMAL PROTEIN GENE CLUSTER 5'REGION.//0.0011:77:35//HALOBACTERIUM CUTIRUBRUM.//P17103
F-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//1.2e-97:222:84//BOS TAURUS (BOVINE).//P08760
F-NT2RP3000361//PRE-MRNA SPLICING FACTOR PRP6.//2.2e-08:128:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P19735
F-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.1e-107:206:99//MUS MUSCULUS (MOUSE).//P35293
F-NT2RP3000393//HOMEOBOX PROTEIN HOX-C4 (HOX-3E) (CP19).//0.0023:36:52//HOMO SAPIENS (HUMAN).//P09017
F-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13).//5.5e-27:116:44//MUS MUSCULUS (MOUSE).//O35286
F-NT2RP3000403//PRE-MRNA PROCESSING PROTEIN PRP40.//0.00044:67:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33203
F-NT2RP3000418//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//2.2e-16:228:34//MUS MUSCULUS (MOUSE).//P11369
F-NT2RP3000433//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.7e-17:79:55//HOMO SAPIENS (HUMAN).//P39188
F-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//9.8e-10:201:26//ESCHERICHIA COLI.//P37908
F-NT2RP3000441//PROTEIN-EXPORT MEMBRANE PROTEIN SECG HOMOLOG.//0.91:48:35//MYCOBACTERIUM LEPRAE.//P38388
F-NT2RP3000449//HOMEOBOX PROTEIN HOX-B8 (CHOX-2.4) (FRAGMENT).//1.0:42:33//GALLUS GALLUS (CHICKEN).//P23681
F-NT2RP3000451
F-NT2RP3000456//COLLAGEN ALPHA 1(I) CHAIN
(FRAGMENTS).//0.00018:178:36//RATTUS NORVEGICUS (RAT).//P02454
F-NT2RP3000484//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).//0.098:40:27//BOS TAURUS (BOVINE).//P37359
F-NT2RP3000487//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.00037:16:81//VOLVOX CARTERI.//P21997
F-NT2RP3000512
F-NT2RP3000526//HYPOTHETICAL NIN REGION PROTEIN ORF56.//0.51:37:43//BACTERIOPHAGE LAMBDA.//P03769
F-NT2RP3000527//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.0e-16:234:30//HOMO SAPIENS (HUMAN).//P51522
F-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//3.4e-15:192:30//HOMO SAPIENS (HUMAN).//P15151
F-NT2RP3000542//CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) (FRAGMENT).//0.60:51:39//ASTERINA PECTINIFERA (STARFISH).//P11958
F-NT2RP3000561//HYPOTHETICAL ATP-BINDING PROTEIN MJ0423.//0.79:53:32//METHANOCOCCUS JANNASCHII.//Q57866
F-NT2RP3000562//ACCESSORY GLAND PEPTIDE PRECURSOR (PARAGONIAL PEPTIDE B).//0.99:26:34//DROSOPHILA MAURITIANA (FRUIT FLY), AND DROSOPHILA SIMULANS (FRUIT FLY).//O18666
F-NT2RP3000578//HYPOTHETICAL 49.8 KD PROTEIN IN RPL14B-GPA1 INTERGENIC REGION.//1.5e-26:127:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38755
F-NT2RP3000582
F-NT2RP3000584//METALLOTHIONEIN-II (MT-II).//0.28:27:29//MUS MUSCULUS (MOUSE).//P02798
F-NT2RP3000590//UVS-2 PROTEIN.//4.8e-10:113:33//NEUROSPORA CRASSA.//P33288
F-NT2RP3000592//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.00087:178:31//HOMO SAPIENS (HUMAN).//O00268
F-NT2RP3000596//YEMANUCLEIN-ALPHA.//1.8e-05:98:34//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25992

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F-NT2RP3000599//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.00095:90:37//HOMO SAPIENS (HUMAN).//Q15428
F-NT2RP3000603//5E5 ANTIGEN.//1.0e-09:181:34//RATTUS NORVEGICUS (RAT).//Q63003
F-NT2RP3000605//STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT-BINDING TRANSCRIPTION FACTOR 1).//0.00098:76:34//HOMO SAPIENS (HUMAN).//P36956
F-NT2RP3000622//HYPOTHETICAL PROTEIN MG096 HOMOLOG 5 (P02_ORF427).//0.15:52:36//MYCOPLASMA PNEUMONIAE.//P75277
F-NT2RP3000624//HYPOTHETICAL PROTEIN KIAA0256.//5.4e-16:222:31//HOMO SAPIENS (HUMAN).//Q93073
F-NT2RP3000628
F-NT2RP3000632//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).//2.0e-16:52:63//MUS MUSCULUS (MOUSE).//Q61967
F-NT2RP3000644//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//6.7e-40:102:79//HOMO SAPIENS (HUMAN).//P39194
F-NT2RP3000661//HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN CHROMOSOME II.//6.0e-08:83:36//CAENORHABDITIS ELEGANS.//Q09441
F-NT2RP3000665//HOMEOBOX PROTEIN PROPHET OF PIT-1 (PROP-1) (PITUITARY SPECIFIC HOMEODOMAIN FACTOR).//0.13:48:35//HOMO SAPIENS (HUMAN).//O75360
F-NT2RP3000685//HYPOTHETICAL 33.5 KD PROTEIN IN CAT1 5'REGION (ORFY).//0.26:202:23//CLOSTRIDIUM KLUYVERI.//P38943
F-NT2RP3000690//INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO- HYDROLASE) (PPASE).//0.99:131:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P00817
F-NT2RP3000736//HYPOTHETICAL 28.7 KD PROTEIN IN RNR3-ARC15 INTERGENIC REGION.//3.5e-27:211:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40516
F-NT2RP3000739//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I.//6.0e-23:114:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10149
F-NT2RP3000742//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III).//6.7e-12:85:36//RATTUS NORVEGICUS (RAT).//P10688
F-NT2RP3000753//CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1).//0.00011:208:28//CLOSTRIDIUM THERMOCELLUM.//Q06852
F-NT2RP3000759//ADP-RIBOSYLATION FACTOR 6.//8.1e-28:141:38//GALLUS GALLUS (CHICKEN).//P26990
F-NT2RP3000815//CYTOCHROME C-551 (C551) (CYTOCHROME C8).//0.24:45:37//PSEUDOMONAS DENITRIFICANS.//P00103
F-NT2RP3000825//ALPHA-LACTALBUMIN (LACTOSE SYNTHASE B PROTEIN (EC 2.4.1.22)).//0.82:51:39//MACROPUS RUFOGRISEUS (RED-NECKED WALLABY).//P07458
F-NT2RP3000826//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.025:79:37//BOS TAURUS (BOVINE).//P25508
F-NT2RP3000836//HYPOTHETICAL PROTEIN IN KSGA 3'REGION (ORF L5) (FRAGMENT).//0.85:36:47//MYCOPLASMA CAPRICOLUM.//P43040
F-NT2RP3000841//UDP-GLUCURONOSYLTRANSFERASE 1-7 PRECURSOR, MICROSOMAL (EC 2.4.1.17) (UDPGT) (UGT1*7) (UGT1-07) (UGT1.7) (UGT1A7) (UGTP4) (FRAGMENT).//1.0:70:34//MUS MUSCULUS (MOUSE).//Q62452
F-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).//5.2e-72:247:61//HOMO SAPIENS (HUMAN).//P27448
F-NT2RP3000847//HYPOTHETICAL PROTEIN KIAA0161.//0.037:55:30//HOMO SAPIENS (HUMAN).//P50876
F-NT2RP3000850//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//7.4e-31:90:75//HOMO SAPIENS (HUMAN).//P39194
F-NT2RP3000852//HYDROPHOBIC SEED PROTEIN (HPS).//0.33:23:69//GLYCINE MAX (SOYBEAN).//P24337
F-NT2RP3000859//IMMEDIATE-EARLY PROTEIN.//3.6e-07:189:25//HERPESVIRUS SAIMIRI (STRAIN 11).//Q01042
F-NT2RP3000865
F-NT2RP3000868//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ISOFORM (FRAGMENT).//1.4e-09:232:28//GALLUS GALLUS (CHICKEN).//P29616
F-NT2RP3000869//CUTICLE COLLAGEN 2.//4.5e-08:58:46//CAENORHABDITIS ELEGANS.//P17656
F-NT2RP3000875//HOMEOBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEOBOX PROTEIN 2).//0.90:62:37//MUS MUSCULUS (MOUSE).//P43241

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F-NT2RP3000901//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.99:124:33//BOS TAURUS (BOVINE).// P02453
F-NT2RP3000904
F-NT2RP3000917//DHP1 PROTEIN.//6.5e-60:229:55//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P40848
F-NT2RP3000919//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I.//2.4e-19:159:34// SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10149
F-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A.//3.7e-48:73:98//HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT).//P39027
F-NT2RP3000980//COPA/INCA PROTEIN (REPA3 PROTEIN).//0.24:19:47//ESCHERICHIA COLI//P13946
F-NT2RP3000994//MATERNAL EFFECT PROTEIN STAUFEN.//1.4e-10:78:48//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25159
F-NT2RP3001004//HYPOTHETICAL 7.6 KD PROTEIN B0563.8 IN CHROMOSOME X.//0.70:50:32// CAENORHABDITIS ELEGANS.//Q11084
F-NT2RP3001007
F-NT2RP3001055//N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG.//1.3e-05: 138:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P36416
F-NT2RP3001057//ZINC FINGER PROTEIN 45 (BRC1744).//4.0e-28:141:51//HOMO SAPIENS (HUMAN).// Q02386
F-NT2RP3001081//HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMOSOME III.//3.8e-08:144:29// CAENORHABDITIS ELEGANS.//P34568
F-NT2RP3001084//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//3.4e-06:217:32//NEPHILA CLAVIPES (ORB SPIDER).//P46804
F-NT2RP3001096//SYNAPTONEMAL COMPLEX PROTEIN SC65.//1.1e-30:244:33//RATTUS NORVEGICUS (RAT).//Q64375
F-NT2RP3001107//ARYLSULFATASE F (EC 3.1.6.-) (ASF) (FRAGMENT).//0.041:47:44//HOMO SAPIENS (HUMAN).//P54793
F-NT2RP3001109
F-NT2RP3001111//MALE SPECIFIC SPERM PROTEIN MST84DC.//0.17:28:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01644
F-NT2RP3001113//INVOLUCRIN.//0.00036:192:23//MUS MUSCULUS (MOUSE).//P48997
F-NT2RP3001115
F-NT2RP3001116//AMINOPEPTIDASE G (EC 3.4.11.-) (FRAGMENT).//0.99:29:51//STREPTOMYCES LIVIDANS.//Q54340
F-NT2RP3001119//COLLAGEN ALPHA 4(IV) CHAIN (FRAGMENT).//0.0015:73:39//BOS TAURUS (BOVINE).// Q29442
F-NT2RP3001120//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//1.3e-57:229:52//HOMO SAPIENS (HUMAN).//P16415
F-NT2RP3001126//HYPOTHETICAL 91.2 KD PROTEIN IN RPS4B-SCH9 INTERGENIC REGION.//2.8e-07:83: 34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38888
F-NT2RP3001133//CALCIUM BINDING PROTEIN.//2.0e-08:171:32//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P35085
F-NT2RP3001140//F-SPONDIN PRECURSOR.//2.0e-147:244:97//RATTUS NORVEGICUS (RAT).//P35446
F-NT2RP3001147//TROPOMYOSIN 2 (TMII).//0.11:159:23//SCHISTOSOMA MANSONI (BLOOD FLUKE).// P42638
F-NT2RP3001150//OCTAPEPTIDE-REPEAT PROTEIN T2.//6.2e-09:163:25//MUS MUSCULUS (MOUSE).// Q06666
F-NT2RP3001155//DNA POLYMERASE ALPHA-BINDING PROTEIN (POB1/CTF4 PROTEIN) (CHROMOSOME REPLICATION PROTEIN CHL15).//4.1e-05:244:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).// Q01454
F-NT2RP3001176//LEUKOSIALIN PRECURSOR (LEUCOCYTE SIALOGLYCOPROTEIN) (SIALOPHORIN) (CD43) (LY 48) (B CELL DIFFERENTIATION ANTIGEN LP-3).//0.21:136:26//MUS MUSCULUS (MOUSE).// P15702
F-NT2RP3001214//SAP1 PROTEIN.//0.058:133:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).// P39955
F-NT2RP3001216//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT).//2.1e-08:137:33//HOMO SAPIENS (HUMAN).//P35663
F-NT2RP3001221//GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-

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BUTYROBETAINE HYDROXYLASE).//4.2e-05:131:26//PSEUDOMONAS SP. (STRAIN AK-1).//P80193
F-NT2RP3001232//HYPOTHETICAL PROTEIN PRECURSOR IN CS5 3'REGION (FRAGMENT).//0.75:57:31//ESCHERICHIA COLI.//P33792
F-NT2RP3001236//TRANSFORMING PROTEIN MAF.//0.017:136:30//AVIAN MUSCULOAPONEUROTIC FIBROSARCOMA VIRUS AS42.//P23091
F-NT2RP3001239//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 1 (FRAGMENT).//4.2e-55:221:49//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P14400
F-NT2RP3001245
F-NT2RP3001253//TROPOMYOSIN 2, MUSCLE THORACIC ISOFORM (TROPOMYOSIN I).//0.0042:142:24//DROSOPHILA MELANOGASTER (FRUIT FLY).//P09491
F-NT2RP3001260//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.//0.0011:89:43//HOMO SAPIENS (HUMAN).//P53420
F-NT2RP3001268//ZINC FINGER PROTEIN 45 (BRC1744).//9.0e-29:194:44//HOMO SAPIENS (HUMAN).//Q02386
F-NT2RP3001272//HYPOTHETICAL 75.2 KD PROTEIN C13F4.08C IN CHROMOSOME I.//8.2e-17:183:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10199
F-NT2RP3001274//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PPT) (FRAGMENT).//1.7e-09:78:39//MUS MUSCULUS (MOUSE).//Q60676
F-NT2RP3001281//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//7.7e-08:38:71//HOMO SAPIENS (HUMAN).//P39188
F-NT2RP3001297//HYPOTHETICAL PROTEIN KIAA0281 (HA6725).//2.2e-57:159:70//HOMO SAPIENS (HUMAN).//Q92556
F-NT2RP3001307//SPERM PROTAMINE P1.//0.21:46:39//ORNITHORHYNCHUS ANATINUS (DUCKBILL PLATYPUS).//P35307
F-NT2RP3001318
F-NT2RP3001325//ENHANCER OF RUDIMENTARY HOMOLOG.//1.0:73:24//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q98874
F-NT2RP3001338//ZINC FINGER PROTEIN 29 (ZINC FINGER PROTEIN KOX26) (FRAGMENT).//0.0021:56:35//HOMO SAPIENS (HUMAN).//P17037
F-NT2RP3001339//CITRON PROTEIN.//3.6e-06:90:33//MUS MUSCULUS (MOUSE).//P49025
F-NT2RP3001340//HYPOTHETICAL PROTEIN UL61.//7.2e-11:202:34//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818
F-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN).//7.7e-16:129:33//HOMO SAPIENS (HUMAN).//P53007
F-NT2RP3001356//RAS-RELATED PROTEIN RABA (FRAGMENT).//0.00041:66:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34141
F-NT2RP3001374
F-NT2RP3001383//PTB-ASSOCIATED SPLICING FACTOR (PSF).//2.5e-06:190:32//HOMO SAPIENS (HUMAN).//P23246
F-NT2RP3001384//CHORION PROTEIN S15.//0.00079:94:37//DROSOPHILA VIRILIS (FRUIT FLY).//P13424
F-NT2RP3001392//VPU PROTEIN (ORF-X PROTEIN) (UPX PROTEIN).//1.0:22:45//CAPRINE ARTHRITIS ENCEPHALITIS VIRUS (CAEV).//P31834
F-NT2RP3001396//HYPOTHETICAL 8.1 KD PROTEIN (ORF4).//1.0:37:32//STRAWBERRY MILD YELLOW EDGE-ASSOCIATED VIRUS (SMYEAV).//Q00848
F-NT2RP3001398//KRUEPPEL-RELATED ZINC FINGER PROTEIN 2 (HKR2 PROTEIN) (FRAGMENT).//1.9e-08:45:37//HOMO SAPIENS (HUMAN).//P10073
F-NT2RP3001399//SSU72 PROTEIN.//7.3e-18:84:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53538
F-NT2RP3001407//SCY1 PROTEIN.//1.5e-08:143:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53009
F-NT2RP3001420//HYPOTHETICAL 7.9 KD PROTEIN.//0.25:41:26//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20542
F-NT2RP3001426//DNAJ PROTEIN.//7.5e-15:78:43//HAEMOPHILUS INFLUENZAE.//P43735
F-NT2RP3001427//WERNER SYNDROME HELICASE.//3.6e-13:159:33//HOMO SAPIENS (HUMAN).//Q14191
F-NT2RP3001428//NUCLEOPROTEIN TPR.//1.8e-53:117:99//HOMO SAPIENS (HUMAN).//P12270
F-NT2RP3001432//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.96:52:21//TARSIUS SYRICHTA (TARSIER).//Q36151
F-NT2RP3001447//HYPOTHETICAL 5.5 KD PROTEIN IN REPLICATION ORIGIN REGION (ORF1).//0.96:45:35//

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ESCHERICHIA COLI.//P14505
F-NT2RP3001449//HOMEOBOX PROTEIN SAX-1 (CHOX-3) (FRAGMENT).//0.0043:53:43//GALLUS GALLUS (CHICKEN).//P19601
F-NT2RP3001453//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.0048:65:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
F-NT2RP3001457//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS28.//0.55:121:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q02767
F-NT2RP3001459//MYOSIN IC HEAVY CHAIN.//0.10:126:34//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569
F-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A.//3.0e-14:87:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11632
F-NT2RP3001490//METALLOTHIONEIN-LIKE PROTEIN LSC54.//1.0:39:35//BRASSICA NAPUS (RAPE).//P43402
F-NT2RP3001495//UBIQUITIN--PROTEIN LIGASE RSP5 (EC 6.3.2.-).//3.3e-14:148:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39940
F-NT2RP3001497//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.13:44:38//BOS TAURUS (BOVINE).//P25508
F-NT2RP3001527//SPERM PROTAMINE P1.//0.35:29:37//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM), AND MONODELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM).//P35305
F-NT2RP3001529//HYPOTHETICAL 43.3 KD GTP-BINDING PROTEIN IN DACB-RPMA INTERGENIC REGION.//3.3e-21:125:37//ESCHERICHIA COLI.//P42641
F-NT2RP3001538//HNF3/FH TRANSCRIPTION FACTOR GENESIS (WINGED HELIX PROTEIN CWH-3).//0.13:53:39//GALLUS GALLUS (CHICKEN).//P79772
F-NT2RP3001554//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 2 (FRAGMENT).//2.3e-48:137:52//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P14401
F-NT2RP3001580//GERM CELL-LESS PROTEIN.//8.2e-18:100:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01820
F-NT2RP3001587//UBIQUITIN-ACTIVATING ENZYME E1-LIKE (POLYMERASE-INTERACTING PROTEIN 2).//2.0e-47:188:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P52488
F-NT2RP3001589//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//7.4e-41:87:80//HOMO SAPIENS (HUMAN).//P39193
F-NT2RP3001607//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:49:32//DICENTRARCHUS LABRAX (EUROPEAN SEA BASS).//Q36362
F-NT2RP3001608//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.0013:177:25//ZEA MAYS (MAIZE).//P14918
F-NT2RP3001621//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.84:29:37//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645
F-NT2RP3001629//RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 (P21-RAC1) (FRAGMENTS).//0.91:57:24//CAVIA PORCELLUS (GUINEA PIG).//P80236
F-NT2RP3001634//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//8.9e-11:73:54//HOMO SAPIENS (HUMAN).//P39189
F-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210.//1.1e-12:117:29//HOMO SAPIENS (HUMAN).//Q92609
F-NT2RP3001646//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0092:69:34//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341
F-NT2RP3001671//RING CANAL PROTEIN (KELCH PROTEIN).//0.0042:55:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
F-NT2RP3001672
F-NT2RP3001676//GTP-BINDING PROTEIN LEPA (FRAGMENT).//1.2e-15:56:62//PSEUDOMONAS FLUORESCENS.//P26843
F-NT2RP3001678//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//0.054:187:31//NEPHILA CLAVIPES (ORB SPIDER).//P46804
F-NT2RP3001679//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.//1.5e-07:63:44//CAENORHABDITIS ELEGANS.//P34679
F-NT2RP3001688//GLUCOAMYLASE S1 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) (GAI).//1.0:83:28//SACCHAROMYCES DIASTATICUS (YEAST).//P04065
F-NT2RP3001690//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//0.021:247:24//HOMO SA-

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PIENS (HUMAN).//P12883
F-NT2RP3001698
F-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR.//7.7e-12:73:43//DROSOPHILA MELANOGASTER (FRUIT FLY).//P54356
F-NT2RP3001712//CEC-1 PROTEIN.//1.9e-07:121:29//CAENORHABDITIS ELEGANS.//P34618
F-NT2RP3001716//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.89:54:40//DROSOPHILA SIMULANS (FRUIT FLY).//P13729
F-NT2RP3001724//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//7.5e-41:164:48//HOMO SAPIENS (HUMAN).//O14646
F-NT2RP3001727//HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III.//1.5e-51:240:41//CAENORHABDITIS ELEGANS.//P34669
F-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT).//2.4e-122:267:86//HOMO SAPIENS (HUMAN).//Q14141
F-NT2RP3001739//INTESTINAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER).//0.99:63:34//RATTUS NORVEGICUS (RAT).//P70545
F-NT2RP3001752//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//4.0e-21:60:85//HOMO SAPIENS (HUMAN).//P39193
F-NT2RP3001753//HYPOTHETICAL PROTEIN KIAA0127.//7.9e-12:83:44//HOMO SAPIENS (HUMAN).//Q14140
F-NT2RP3001764//DUAL SPECIFICITY PROTEIN PHOSPHATASE 6 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE PYST1).//7.7e-25:146:36//HOMO SAPIENS (HUMAN).//Q16828
F-NT2RP3001777//SERINE/THREONINE-PROTEIN KINASE STE20 HOMOLOG (EC 2.7.1.-).//0.0096:204:25//CANDIDA ALBICANS (YEAST).//Q92212
F-NT2RP3001782//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.91:34:44//PONGO PYGMAEUS ABELII (SUMATRAN ORANGUTAN).//P92694
F-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.8e-33:159:53//HOMO SAPIENS (HUMAN).//P52272
F-NT2RP3001799//LIGHT-HARVESTING PROTEIN B800/830/1020, ALPHA-2 CHAIN (EHS-ALPHA-2) (ANTENNA PIGMENT PROTEIN, ALPHA-2 CHAIN).//0.14:46:28//ECTOTHIORHODOSPIRA HALOCHLORIS.//P80103
F-NT2RP3001819//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.//0.00030:77:36//HOMO SAPIENS (HUMAN).//P08123
F-NT2RP3001844//OCTAMER-BINDING TRANSCRIPTION FACTOR 1 (OTF-1) (NF-A1) (FRAGMENT).//0.99:43:34//MACROPUS EUGENII (TAMMAR WALLABY).//Q28466
F-NT2RP3001854//FIBRINOGEN- AND IG-BINDING PROTEIN PRECURSOR (MRP PROTEIN).//9.3e-10:213:24//STREPTOCOCCUS PYOGENES.//P30141
F-NT2RP3001855//HOMEOBOX PROTEIN PKNOX1 (HOMEOBOX PROTEIN PREP-1).//2.6e-61:220:60//HOMO SAPIENS (HUMAN).//P55347
F-NT2RP3001857//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.0e-13:213:24//PODOSPORA ANSERINA.//Q00808
F-NT2RP3001896//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//0.074:124:34//HOMO SAPIENS (HUMAN).//Q15428
F-NT2RP3001898//REGULATORY PROTEIN E2.//0.36:131:29//CANINE ORAL PAPILLOMAVIRUS (COPV).//Q89420
F-NT2RP3001915//CHITIN BIOSYNTHESIS PROTEIN CHS5 (CAL3 PROTEIN).//0.0021:237:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12114
F-NT2RP3001926//HYPOTHETICAL 14.0 KD PROTEIN IN RPL15B-GCR3 INTERGENIC REGION.//1.0:63:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03880
F-NT2RP3001929//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.4e-14:35:60//HOMO SAPIENS (HUMAN).//P39195
F-NT2RP3001931//HYPOTHETICAL 59.3 KD PROTEIN IN TAP42-ARP9 INTERGENIC REGION.//0.86:162:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q05040
F-NT2RP3001938//GLYCOPROTEIN GP50.//0.0036:54:40//PSEUDORABIES VIRUS (STRAIN RICE) (PRV).//P07645
F-NT2RP3001943//33.2 KD PROTEIN IN DIND-RPH INTERGENIC REGION (ORF X).//1.0:113:27//ESCHERICHIA COLI.//P23839
F-NT2RP3001944//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//4.1e-56:208:47//CAENORHABDITIS ELEGANS.//Q09251
F-NT2RP3001969//PUFF II/9-2 PROTEIN PRECURSOR.//0.0078:149:26//SCIARA COPROPHILA (FUNGUS

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GNAT).//P22312
F-NT2RP3001989//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//1.0:41:31//MUS MUSCULUS (MOUSE).//P02319
F-NT2RP3002002//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.2e-44:69:79//HOMO SAPIENS (HUMAN).//P39195
F-NT2RP3002004//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2).//0.00024:45:40//MUS MUSCULUS (MOUSE).//Q61345
F-NT2RP3002007//TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C).//0.21:115:28//HOMO SAPIENS (HUMAN).//P24821
F-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//1.7e-25:139:48//CAENORHABDITIS ELEGANS.//Q09232
F-NT2RP3002033//ACTIVATOR OF APOPTOSIS HARAKIRI (NEURONAL DEATH PROTEIN DP5).//0.14:65:41//HOMO SAPIENS (HUMAN).//O00198
F-NT2RP3002045//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//8.1e-108:192:98//MUS MUSCULUS (MOUSE).//P17427
F-NT2RP3002054//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.046:176:31//STREPTOMYCES FRADIAE.//P20186
F-NT2RP3002056//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140).//1.4e-07:245:25//RATTUS NORVEGICUS (RAT).//P41777
F-NT2RP3002057//SMALL HYDROPHOBIC PROTEIN.//1.0:12:66//SIMIAN VIRUS 5 (STRAIN W3) (SV5).//P07577
F-NT2RP3002062//PROTEASE A INHIBITOR 3 (PROTEINASE INHIBITOR I(A)3).//1.0:49:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P01094
F-NT2RP3002063//ACYL CARRIER PROTEIN (ACP).//0.99:38:31//HAEMOPHILUS INFLUENZAE.//P43709
F-NT2RP3002081//HYPOTHETICAL 100.5 KD PROTEIN C1B9.04 IN CHROMOSOME I.//5.8e-35:253:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10429
F-NT2RP3002097//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC REGION.//6.2e-06:99:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40164
F-NT2RP3002102//HYPOTHETICAL 7.4 KD PROTEIN.//0.68:34:47//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19302
F-NT2RP3002108//HYPOTHETICAL 105.5 KD PROTEIN R13F6.10 IN CHROMOSOME III.//7.9e-19:179:34//CAENORHABDITIS ELEGANS.//Q21986
F-NT2RP3002142//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.6e-17:37:75//HOMO SAPIENS (HUMAN).//P39188
F-NT2RP3002146//CUTICLE COLLAGEN 40.//0.00034:90:37//CAENORHABDITIS ELEGANS.//P34804
F-NT2RP3002147//SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S).//0.011:166:28//HOMO SAPIENS (HUMAN).//P10163
F-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING PROTEIN GST1-HS).//4.8e-11:60:53//HOMO SAPIENS (HUMAN).//P15170
F-NT2RP3002163//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TARII130).//0.028:191:29//HOMO SAPIENS (HUMAN).//O00268
F-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP.//2.3e-131:223:91//MUS MUSCULUS (MOUSE).//Q02614
F-NT2RP3002166//D-ALANYL CARRIER PROTEIN (DCP).//1.0:65:33//LACTOBACILLUS CASEI.//P55153
F-NT2RP3002173//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.4e-26:114:62//HOMO SAPIENS (HUMAN).//P39194
F-NT2RP3002181//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.25:31:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645
F-NT2RP3002244//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.069:16:62//OVIS ARIES (SHEEP), AND CAPRA HIRCUS (GOAT).//P04102
F-NT2RP3002248//MICROFIBRILLAR-ASSOCIATED PROTEIN 1 (ASSOCIATED MICROFIBRIL PROTEIN) (AMF).//0.0079:187:24//GALLUS GALLUS (CHICKEN).//P55080
F-NT2RP3002255//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//4.6e-10:168:34//MUS MUSCULUS (MOUSE).//P05143
F-NT2RP3002273//SCD6 PROTEIN.//1.5e-11:160:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P45978

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F-NT2RP3002276//PROBABLE E4 PROTEIN.//0.91:54:29//HUMAN PAPILLOMAVIRUS TYPE 16.//P06922
F-NT2RP3002303//HYPOTHETICAL 30.2 KD PROTEIN C4D7.04C IN CHROMOSOME I.//1.7e-42:191:43// SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14171
F-NT2RP3002304
F-NT2RP3002330//NNP-1 PROTEIN.//0.52:140:18//MUS MUSCULUS (MOUSE).//P56183
F-NT2RP3002343//5E5 ANTIGEN.//0.0056:189:30//RATTUS NORVEGICUS (RAT).//Q63003
F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.15) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) MITOCHONDRIAL PRECURSOR.// 1.0e-66:196:68//HOMO SAPIENS (HUMAN).//P13995
F-NT2RP3002352//PRESYNAPTIC PROTEIN SAP102 (SYNAPSE-ASSOCIATED PROTEIN 102) (NEUROENDOCRINE-DLG) (NE-DLG).//0.79:173:27//HOMO SAPIENS (HUMAN).//Q92796
F-NT2RP3002377//PUTATIVE HELICASE YGR271W.//1.0e-56:216:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53327
F-NT2RP3002399//MINICHROMOSOME MAINTENANCE PROTEIN 6.//1.4e-19:136:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53091
F-NT2RP3002402//EBNA-6 NUCLEAR PROTEIN (EBNA-3C) (EBNA-4B).//0.74:107:36//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03204
F-NT2RP3002455//DNAJ PROTEIN (FRAGMENT).//5.6e-06:57:42//AGROBACTERIUM TUMEFACIENS.// P50018
F-NT2RP3002484//HYPOTHETICAL 46.5 KD PROTEIN C12B10.04 IN CHROMOSOME I.//0.00032:52:48// SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10438
F-NT2RP3002501//HYPOTHETICAL 34.9 KD PROTEIN IN FRE2-JEN1 INTERGENIC REGION.//9.4e-42:209: 42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36007
F-NT2RP3002512//HYPOTHETICAL 37.4 KD PROTEIN IN GPM1-MCR1 INTERGENIC REGION.//7.7e-32:162: 37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36059
F-NT2RP3002529//PUTATIVE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN C2G11.03C.//2.1e-45: 241:43//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09805
F-NT2RP3002545
F-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III.//2.8e-41:161:52// CAENORHABDITIS ELEGANS.//Q10010
F-NT2RP3002566//IMMEDIATE-EARLY PROTEIN IE180.//0.56:130:24//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479
F-NT2RP3002587
F-NT2RP3002590
F-NT2RP3002602//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1) (THIOREDOXIN- RELATED GLYCOPROTEIN 1).//0.00091:111:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P17967
F-NT2RP3002603//HYPOTHETICAL 14.2 KD PROTEIN IN BLAB 3'REGION.//1.0:65:40//STREPTOMYCES CACAOI.//P33654
F-NT2RP3002628//DNAJ-LIKE PROTEIN SLR0093.//2.4e-17:101:44//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P50027
F-NT2RP3002631//METALLOTHIONEIN-IB (MT-1B).//0.092:36:33//HOMO SAPIENS (HUMAN).//P07438
F-NT2RP3002650//DUALIN.//3.0e-21:184:37//GALLUS GALLUS (CHICKEN).//Q90830
F-NT2RP3002659//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.//0.00016:223:33//HOMO SAPIENS (HUMAN).//P08123
F-NT2RP3002660//40S RIBOSOMAL PROTEIN S27A.//0.16:72:31//CAENORHABDITIS ELEGANS.//P37165
F-NT2RP3002663//OXYSTEROL-BINDING PROTEIN.//5.4e-23:168:41//HOMO SAPIENS (HUMAN).//P22059
F-NT2RP3002671//HYPOTHETICAL 124.5 KD PROTEIN IN SKO1-RPL44A INTERGENIC REGION.//6.0e-38: 203:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53893
F-NT2RP3002682//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.25:63:31//ARTEMIA SALINA (BRINE SHRIMP).//P19049
F-NT2RP3002687//HYPOTHETICAL 30.4 KD PROTEIN IN LEF3-IAP2 INTERGENIC REGION.//0.029:60:36// AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41469
F-NT2RP3002688//KINESIN-LIKE PROTEIN KIF1B.//5.3e-61:130:88//MUS MUSCULUS (MOUSE).//Q60575
F-NT2RP3002701//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//7.4e-05:109:33//MUS MUSCULUS (MOUSE).//P15265
F-NT2RP3002713//PROBABLE ATP-DEPENDENT RNA HELICASE DDX10 (DEAH BOX PROTEIN 10).//0.77: 70:32//HOMO SAPIENS (HUMAN).//Q13206
F-NT2RP3002763//HYPOTHETICAL 11.3 KD PROTEIN C2C6.07 IN CHROMOSOME I.//6.7e-11:66:40//

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SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14056
F-NT2RP3002770//COLLAGEN ALPHA 1(IX) CHAIN (FRAGMENT).//0.33:87:34//MUS MUSCULUS (MOUSE).//Q05722
F-NT2RP3002785//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//9.7e-36:187:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24371
F-NT2RP3002799//!!!! ALU SUBFAMILY J WARNING ENTRY!!!!//5.6e-08:41:73//HOMO SAPIENS (HUMAN).//P39188
F-NT2RP3002810//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//0.0034:35:65//HOMO SAPIENS (HUMAN).//P39193
F-NT2RP3002818//MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B).//3.2e-17:148:37//MUS MUSCULUS (MOUSE).//P27790
F-NT2RP3002861//HYPOTHETICAL 70.2 KD PROTEIN IN GSH1-CHS6 INTERGENIC REGION.//1.7e-05:95:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42951
F-NT2RP3002869//TRYPSIN INHIBITOR II (BDTI-II).//0.97:23:39//BRYONIA DIOICA (RED BRYONY).//P11968
F-NT2RP3002876//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).//0.00017:140:31//RATTUS NORVEGICUS (RAT).//P04474
F-NT2RP3002877//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.5e-06:55:60//HOMO SAPIENS (HUMAN).//P39194
F-NT2RP3002909//P53-BINDING PROTEIN 53BP2 (BCL2-BINDING PROTEIN) (BBP).//4.6e-08:129:38//HOMO SAPIENS (HUMAN).//Q13625
F-NT2RP3002911//HYPOTHETICAL PROTEIN C18.//0.99:26:50//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//P32217
F-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-23:113:47//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
F-NT2RP3002953//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//0.55:116:27//DROSOPHILA MELANOGASTER (FRUIT FLY).//P33450
F-NT2RP3002955//HYPOTHETICAL 16.5 KD PROTEIN IN BLTR-SPOIIIC INTERGENIC REGION.//0.87:67:37//BACILLUS SUBTILIS.//P54445
F-NT2RP3002969//LONG-CHAIN-FATTY-ACID--COA LIGASE 4 (EC 6.2.1.3) (LONG-CHAIN ACYL-COA SYNTHETASE 4) (LACS 4).//6.7e-56:189:59//HOMO SAPIENS (HUMAN).//O60488
F-NT2RP3002972//HYPOTHETICAL 73.0 KD PROTEIN IN CLA4-MID1 INTERGENIC REGION.//0.0028:147:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48566
F-NT2RP3002978//PROBABLE E5 PROTEIN.//0.15:55:36//HUMAN PAPILLOMAVIRUS TYPE 51.//P26553
F-NT2RP3002985//METALLOTHIONEIN (MT).//0.0031:49:42//PLEURONECTES PLATESSA (PLAICE).//P07216
F-NT2RP3002988//NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR (MOTCH PROTEIN).//1.0:111:29//MUS MUSCULUS (MOUSE).//Q01705
F-NT2RP3003008//HYPOTHETICAL 54.7 KD PROTEIN F37A4.1 IN CHROMOSOME III.//0.96:112:25//CAENORHABDITIS ELEGANS.//P41879
F-NT2RP3003032
F-NT2RP3003059//HYPOTHETICAL 52.3 KD PROTEIN C56F8.06C IN CHROMOSOME I PRECURSOR.//9.7e-27:216:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10254
F-NT2RP3003061//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//3.7e-25:167:34//HOMO SAPIENS (HUMAN).//P16157
F-NT2RP3003068//SERYL-TRNA SYNTHETASE (EC 6.1.1.11) (SERINE--TRNA LIGASE) (SERRS) (FRAGMENT).//0.074:82:39//SULFOLOBUS SOLFATARICUS.//O33780
F-NT2RP3003071//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.0085:128:30//HOMO SAPIENS (HUMAN).//P50552
F-NT2RP3003078//SPERM ACROSOMAL PROTEIN FSA-ACR.1 PRECURSOR (FRAGMENT).//0.028:165:31//VULPES VULPES (RED FOX).//P53353
F-NT2RP3003101//TETRACYCLINE RESISTANCE PROTEIN, CLASS C (TETA(C)).//1.0e-14:243:25//ESCHERICHIA COLI.//P02981
F-NT2RP3003121//SUPPRESSOR PROTEIN SRP40.//7.4e-05:143:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
F-NT2RP3003133//65 KD YES-ASSOCIATED PROTEIN (YAP65).//0.024:61:42//GALLUS GALLUS (CHICKEN).//P46936
F-NT2RP3003138//KINESIN-LIKE PROTEIN KIF4.//1.1e-118:151:93//MUS MUSCULUS (MOUSE).//P33174
F-NT2RP3003139//ATP-BINDING CASSETTE TRANSPORTER ABC1.//1.0:70:30//SCHIZOSACCHAROMYCES

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POMBE (FISSION YEAST).//Q92337
F-NT2RP3003145//MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (HMFG) (BREAST EPITHELIAL ANTIGEN BA46) (MFGM).//2.0e-12:121:37//HOMO SAPIENS (HUMAN).//Q08431
F-NT2RP3003150
F-NT2RP3003157//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//4.0e-79:260:54//HOMO SAPIENS (HUMAN).//P51522
F-NT2RP3003185//TROPOMYOSIN.//0.077:122:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q02088
F-NT2RP3003193//ZINC FINGER PROTEIN 135.//7.2e-91:239:65//HOMO SAPIENS (HUMAN).//P52742
F-NT2RP3003197//HYPOTHETICAL 28.1 KD PROTEIN IN SIPU-PBPC INTERGENIC REGION.//1.3e-07:117:34//BACILLUS SUBTILIS.//P42966
F-NT2RP3003203//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I.//9.9e-23:132:39//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10149
F-NT2RP3003204//RAS-LIKE PROTEIN RASB.//0.92:103:27//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P32252
F-NT2RP3003210//VERY HYPOTHETICAL 13.2 KD PROTEIN IN PTC3-SAS3 INTERGENIC REGION.//0.23:106:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38190
F-NT2RP3003212//SUPPRESSOR PROTEIN SRP40.//0.019:171:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
F-NT2RP3003230//CORONIN-LIKE PROTEIN P57.//8.3e-74:183:73//BOS TAURUS (BOVINE).//Q92176
F-NT2RP3003242//STANNIOCALCIN PRECURSOR.//1.4e-21:127:37//HOMO SAPIENS (HUMAN).//P52823
F-NT2RP3003251//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//3.1e-51:198:52//MUS MUSCULUS (MOUSE).//P15533
F-NT2RP3003264//E6 PROTEIN.//1.0:31:41//HUMAN PAPILLOMAVIRUS TYPE 48.//Q80920
F-NT2RP3003278//45.8 KD PROTEIN IN SHM1-MRPL37 INTERGENIC REGION.//8.6e-07:80:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38344
F-NT2RP3003282//DYNAMIN 2 (DYNAMIN UDNM).//8.0e-108:226:88//MUS MUSCULUS (MOUSE).//P39054
F-NT2RP3003290//BIOH PROTEIN.//0.0055:107:30//ESCHERICHIA COLI.//P13001
F-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//1.3e-69:200:55//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//O64948
F-NT2RP3003302//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.4e-69:102:66//HOMO SAPIENS (HUMAN).//P08547
F-NT2RP3003311//MYOSIN II HEAVY CHAIN, NON MUSCLE.//0.18:225:26//ACANTHAMOEBA CASTELLANII (AMOEBA).//P05659
F-NT2RP3003313//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.0014:142:33//HOMO SAPIENS (HUMAN).//P10162
F-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52).//8.8e-18:94:43//MUS MUSCULUS (MOUSE).//Q62191
F-NT2RP3003330//HYPOTHETICAL PROTEIN KIAA0176 (FRAGMENT).//1.3e-20:123:44//HOMO SAPIENS (HUMAN).//Q14681
F-NT2RP3003344//HYPOTHETICAL 8.8 KD PROTEIN IN ICDC-MINE INTERGENIC REGION.//1.0:28:42//ESCHERICHIA COLI.//P75991
F-NT2RP3003346//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//6.9e-26:74:78//HOMO SAPIENS (HUMAN).//P39191
F-NT2RP3003353//HYPOTHETICAL 52.4 KD PROTEIN R08D7.2 IN CHROMOSOME III.//3.7e-10:118:33//CAENORHABDITIS ELEGANS.//P30641
F-NT2RP3003377//PUTATIVE CUTICLE COLLAGEN F09G8.6.//1.5e-05:102:37//CAENORHABDITIS ELEGANS.//P34391
F-NT2RP3003384
F-NT2RP3003385//SKD3 PROTEIN.//5.1e-83:210:69//MUS MUSCULUS (MOUSE).//Q60649
F-NT2RP3003403
F-NT2RP3003409//SOX-22 PROTEIN.//0.042:173:28//HOMO SAPIENS (HUMAN).//O15370
F-NT2RP3003411//PROBABLE E3 PROTEIN.//0.17:91:31//BOVINE PAPILLOMAVIRUS TYPE 2.//P11300
F-NT2RP3003427//HOLOTRICIN 3 PRECURSOR.//0.012:36:41//HOLOTRICHIA DIOMPHALIA.//Q25055
F-NT2RP3003433
F-NT2RP3003464//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.0042:110:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214
F-NT2RP3003490

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F-NT2RP3003491//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) (HEAT SHOCK 10 KD PROTEIN).//0.99:49:34//LEPTOSPIRA INTERROGANS.//P35472
F-NT2RP3003500//SCY1 PROTEIN.//6.8e-14:192:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53009
F-NT2RP3003543//COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR.//0.0026:175:30//HOMO SAPIENS (HUMAN).//P29400
F-NT2RP3003552//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.19:21:47//BOS TAURUS (BOVINE).//P20072
F-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC REGION.//7.3e-27:159:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40529
F-NT2RP3003564//RNA REPLICASE POLYPROTEIN (EC 2.7.7.48).//1.0:99:30//TURNIP YELLOW MOSAIC VIRUS.//P10358
F-NT2RP3003572//PUTATIVE CUTICLE COLLAGEN F09G8.6.//0.33:128:32//CAENORHABDITIS ELEGANS.//P34391
F-NT2RP3003576//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//7.1e-28:58:77//HOMO SAPIENS (HUMAN).//P39195
F-NT2RP3003589//RAS-RELATED PROTEIN RAB-10.//5.4e-54:114:94//CANIS FAMILIARIS (DOG).//P24409
F-NT2RP3003621//COAGULATION FACTOR XII PRECURSOR (EC 3.4.21.38) (HAGEMAN FACTOR) (HAF).//2.0e-15:89:40//HOMO SAPIENS (HUMAN).//P00748
F-NT2RP3003625//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.99:22:50//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645
F-NT2RP3003656//HOMEOBOX PROTEIN OTX3 (ZOTX3).//0.30:111:25//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q90267
F-NT2RP3003659//HYPOTHETICAL 49.8 KD PROTEIN IN RPL14B-GPA1 INTERGENIC REGION.//1.1e-20:127:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38755
F-NT2RP3003665//PENAEIDIN-3C PRECURSOR (P3-C).//0.34:52:34//PENAEUS VANNAMEI (PENOEID SHRIMP) (EUROPEAN WHITE SHRIMP).//P81060
F-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//8.7e-15:146:42//HOMO SAPIENS (HUMAN).//P14209
F-NT2RP3003680//HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION.//4.3e-25:159:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43601
F-NT2RP3003686//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.067:63:31//GALLUS GALLUS (CHICKEN).//P02314
F-NT2RP3003701//F-SPONDIN PRECURSOR.//1.8e-13:193:27//RATTUS NORVEGICUS (RAT).//P35446
F-NT2RP3003716//SLIT PROTEIN PRECURSOR.//1.3e-12:150:34//DROSOPHILA MELANOGASTER (FRUIT FLY).//P24014
F-NT2RP3003726//INSERTION ELEMENT IS136 HYPOTHETICAL 16.9 KD PROTEIN).//0.47:109:28//AGROBACTERIUM TUMEFACIENS.//P05680
F-NT2RP3003746//HYPOTHETICAL 7.7 KD PROTEIN IN FIXX 3'REGION (ORF1).//0.57:34:38//AZORHIZOBIUM CAULINODANS.//P26486
F-NT2RP3003795//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//4.3e-10:40:90//HOMO SAPIENS (HUMAN).//P39195
F-NT2RP3003799//MATING-TYPE PHEROMONE BBP1(3) PRECURSOR.//0.75:60:36//SCHIZOPHYLLUM COMMUNE (BRACKET FUNGUS).//P78744
F-NT2RP3003800//PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC (EC 2.7.1.112) (P60-SRC).//4.2e-51:72:95//GALLUS GALLUS (CHICKEN).//P00523
F-NT2RP3003805//HYPOTHETICAL 32.1 KD PROTEIN IN DBP7-GCN3 INTERGENIC REGION.//0.00069:160:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36121
F-NT2RP3003809//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENTS).//0.028:135:35//GALLUS GALLUS (CHICKEN).//P12105
F-NT2RP3003819//C-HORDEIN (PCP387) (FRAGMENT).//0.0026:90:33//HORDEUM VULGARE (BARLEY).//P06472
F-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP).//5.6e-20:174:31//BOS TAURUS (BOVINE).//P02720
F-NT2RP3003828//ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-INHIBITABLE ADENYLYL CYCLASE).//0.0017:111:38//CANIS FAMILIARIS (DOG).//P30803
F-NT2RP3003831//ENDONUCLEASE G PRECURSOR (EC 3.1.30.-) (ENDO G).//1.1e-37:187:42//MUS MUSCULUS (MOUSE).//O08600
F-NT2RP3003833//HYPOTHETICAL 6.4 KD PROTEIN IN INTE-PIN INTERGENIC REGION.//1.0:38:39//ES-

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CHERICHIA COLI.//P75979
F-NT2RP3003842
F-NT2RP3003846//RETINAL DEGENERATION B PROTEIN (PROBABLE CALCIUM TRANSPORTER RDGB).// 0.61:54:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P43125
F-NT2RP3003870//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.83:51:37//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
F-NT2RP3003876//PROTEIN TRANSPORT PROTEIN SEC2.//0.0017:151:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P17065
F-NT2RP3003914//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//3.3e-23:76:64//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q09332
F-NT2RP3003918//VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPTOBREVIN BINDING PROTEIN (VAP-33).//5.5e-45:127:69//APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).//Q16943
F-NT2RP3003932
F-NT2RP3003989//PREPROTEIN TRANSLOCASE SECE SUBUNIT.//0.96:46:32//THERMOTOGA MARITIMA.// P35874
F-NT2RP3003992//NUCLEAR LOCALIZATION SEQUENCE BINDING PROTEIN (P67).//0.0011:170:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P27476
F-NT2RP3004013//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//3.6e-21:134:45//RATTUS NORVEGICUS (RAT).//P51400
F-NT2RP3004016//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//0.00021:64:40// AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479
F-NT2RP3004041//SPERM PROTAMINE P1.//0.0028:43:46//ORNITHORHYNCHUS ANATINUS (DUCKBILL PLATYPUS).//P35307
F-NT2RP3004051//MICROBIAL COLLAGENASE PRECURSOR (EC 3.4.24.3) (120 KD COLLAGENASE).// 0.0079:194:24//CLOSTRIDIUM PERFRINGENS.//P43153
F-NT2RP3004070//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.4e-11:51:72//HOMO SAPIENS (HUMAN).// P39188
F-NT2RP3004078//DNA BINDING PROTEIN RFX2.//2.7e-114:243:87//MUS MUSCULUS (MOUSE).//P48379
F-NT2RP3004093//HYPOTHETICAL 32.3 KD PROTEIN IN RHSE-NARV INTERGENIC REGION (ORFB).//8.0e-13:111:41//ESCHERICHIA COLI.//P37757
F-NT2RP3004095//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.5e-17:72:65//HOMO SAPIENS (HUMAN).// P39188
F-NT2RP3004110//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.6e-10:51:72//HOMO SAPIENS (HUMAN).// P39195
F-NT2RP3004125//ZINC FINGER PROTEIN 75.//1.1e-28:118:47//HOMO SAPIENS (HUMAN).//P51815
F-NT2RP3004145//AEROLYSIN REGULATORY PROTEIN.//0.012:45:33//AEROMONAS SOBRIA.//P09165
F-NT2RP3004148//METALLOTHIONEIN-I (MT-1).//0.055:18:50//COLUMBA LIVIA (DOMESTIC PIGEON).// P15786
F-NT2RP3004155//UBIQUINONE BIOSYNTHESIS PROTEIN COQ7 HOMOLOG.//1.7e-82:178:89//RATTUS NORVEGICUS (RAT).//Q63619
F-NT2RP3004189//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.7e-11:215:24//PODOSPORA ANSERINA.//Q00808
F-NT2RP3004206//CROOKED NECK PROTEIN.//3.8e-101:241:73//DROSOPHILA MELANOGASTER (FRUIT FLY).//P17886
F-NT2RP3004207//CUTICLE COLLAGEN 12 PRECURSOR.//0.13:130:33//CAENORHABDITIS ELEGANS.// P20630
F-NT2RP3004209//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//6.5e-16:207:29//HOMO SAPIENS (HUMAN).//Q13107
F-NT2RP3004215//PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT.//1.0:69:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35179
F-NT2RP3004242//HYPOTHETICAL 30.2 KD PROTEIN ZK632.12 IN CHROMOSOME III.//1.1e-64:191:63// CAENORHABDITIS ELEGANS.//P34657
F-NT2RP3004246//RING3 PROTEIN (KIAA9001).//0.060:101:28//HOMO SAPIENS (HUMAN).//P25440
F-NT2RP3004253//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//1.1e-07:184:35//BOS TAURUS (BOVINE).// P02453
F-NT2RP3004258//SUPPRESSOR PROTEIN SRP40.//4.9e-08:98:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583

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F-NT2RP3004262//DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40).//1.6e-63:210:61//HOMO SAPIENS (HUMAN).//P25685
F-NT2RP3004282//HYPOTHETICAL PROTEIN F44G4.1 IN CHROMOSOME II (FRAGMENT).//1.6e-29:177:38//CAENORHABDITIS ELEGANS.//P54073
F-NT2RP3004332//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//0.030:118:36//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414
F-NT2RP3004334
F-NT2RP3004341//ALPHA-INTERNEXIN (ALPHA-INX).//0.91:110:26//MUS MUSCULUS (MOUSE).//P46660
F-NT2RP3004348//HYPOTHETICAL 105.3 KD PROTEIN C01G6.5 IN CHROMOSOME III.//0.60:198:24//CAENORHABDITIS ELEGANS.//P46012
F-NT2RP3004349//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.0e-37:60:76//HOMO SAPIENS (HUMAN).//P39193
F-NT2RP3004378//HYPOTHETICAL 18.8 KD PROTEIN IN GNTR-GGT INTERGENIC REGION (O162).//0.0026:76:28//ESCHERICHIA COLI.//P46854
F-NT2RP3004399//LEUCINE-RICH PRIMARY RESPONSE PROTEIN 1 (FOLLICLE-STIMULATING HORMONE PRIMARY RESPONSE PROTEIN).//4.4e-109:212:96//HOMO SAPIENS (HUMAN).//Q92674
F-NT2RP3004424//JTV-1 PROTEIN.//4.5e-18:60:70//HOMO SAPIENS (HUMAN).//Q13155 F-NT2RP3004428//METALLOTHIONEIN-A (MTA).//0.0010:36:47//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).//P04734
F-NT2RP3004451//MYOSIN IC HEAVY CHAIN.//0.00072:113:34//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569
F-NT2RP3004454//VERPROLIN.//3.3e-07:156:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P37370
F-NT2RP3004466//HYPOTHETICAL PROTEIN F-215.//0.0013:125:32//HUMAN ADENOVIRUS TYPE 2.//P03291
F-NT2RP3004470//HYPOTHETICAL 15.4 KD PROTEIN C16C10.11 IN CHROMOSOME III.//1.0:33:51//CAENORHABDITIS ELEGANS.//Q09254
F-NT2RP3004472//GERM CELL-LESS PROTEIN.//7.3e-33:170:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01820
F-NT2RP3004475//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//8.4e-54:214:46//HOMO SAPIENS (HUMAN).//P98171
F-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//3.9e-47:199:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P34110
F-NT2RP3004490//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.0013:121:33//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437
F-NT2RP3004498//HYPOTHETICAL 43.5 KD PROTEIN IN COTD-KDUD INTERGENIC REGION PRECURSOR.//0.066:87:35//BACILLUS SUBTILIS.//P50840
F-NT2RP3004503//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.0e-34:102:69//HOMO SAPIENS (HUMAN).//P39194
F-NT2RP3004504//SUPPRESSOR PROTEIN SRP40.//0.64:93:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
F-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).//2.2e-16:90:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40484
F-NT2RP3004527
F-NT2RP3004534//S-PHASE ENTRY CYCLIN 6.//0.38:148:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32943
F-NT2RP3004539//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (IGFBP-1) (IBP-1) (IGF-BINDING PROTEIN 1).//0.38:89:38//RATTUS NORVEGICUS (RAT).//P21743
F-NT2RP3004544//CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 2 (CYTADHERENCE ACCESSORY PROTEIN 2).//0.0024:200:24//MYCOPLASMA PNEUMONIAE.//P75471
F-NT2RP3004566//GASTRULA ZINC FINGER PROTEIN XLCGF17.1 (FRAGMENT).//4.6e-25:126:43//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18713
F-NT2RP3004569//ANKYRIN.//8.3e-07:150:28//MUS MUSCULUS (MOUSE).//Q02357
F-NT2RP3004572//TRANSCRIPTION INITIATION FACTOR TFIID 150 KD SUBUNIT (TAFII-150) (TAFII150).//1.6e-70:247:54//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24325
F-NT2RP3004578//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//1.5e-10:210:26//HOMO SAPIENS (HUMAN).//Q02224
F-NT2RP3004594//P54 PROTEIN PRECURSOR.//0.0044:230:24//ENTEROCOCCUS FAECIUM (STREPTO-

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COCCUS FAECIUM).//P13692
F-NT2RP3004617//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//1.5e-14:113:34//MUS MUSCULUS (MOUSE).//P15533
F-NT2RP3004618//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.//4.5e-08:149:30// CAENORHABDITIS ELEGANS.//P34681
F-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN).//1.0e-24:75:48// DROSOPHILA MELANOGASTER (FRUIT FLY).//P54352
F-NT2RP3004670//CUTICLE COLLAGEN 21/0.00090:159:29//CAENORHABDITIS ELEGANS.//P17656
F-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64.//4.0e-79:243:62//BOS TAURUS (BOVINE).//P35526
F-NT2RP4000023
F-NT2RP4000035//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.6e-06:46:67//HOMO SAPIENS (HUMAN).// P39194
F-NT2RP4000049//CALDESMON (CDM).//0.41:63:34//GALLUS GALLUS (CHICKEN).//P12957
F-NT2RP4000051//DUALIN.//2.3e-23:195:37//GALLUS GALLUS (CHICKEN).//Q90830
F-NT2RP4000078//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-24:182:31//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
F-NT2RP4000102//XPAR7 PROTEIN.//1.0:54:33//BACILLUS LICHENIFORMIS.//Q99166
F-NT2RP4000109//SLIT PROTEIN PRECURSOR.//1.9e-60:230:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//P24014
F-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//1.4e-91:157:100//BOS TAURUS (BOVINE).//Q10568
F-NT2RP4000129//5E5 ANTIGEN.//0.00072:124:37//RATTUS NORVEGICUS (RAT).//Q63003
F-NT2RP4000147//ZINC FINGER PROTEIN GCS1.//1.5e-26:119:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35197
F-NT2RP4000150
F-NT2RP4000151//HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III.//4.2e-31:180:47// CAENORHABDITIS ELEGANS .//P32740
F-NT2RP4000159//SPORE COAT PROTEIN SP96.//0.84:107:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P14328
F-NT2RP4000167//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC REGION.//2.4e-08:133: 32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40164
F-NT2RP4000185//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).//5.4e-05:143: 32//HERBES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).//P28284
F-NT2RP4000210//PAIRED AMPHIPATHIC HELIX PROTEIN.//1.8e-40:258:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P22579
F-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//1.4e-20:104:40//APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).//P15287
F-NT2RP4000214//FERREDOXIN.//1.0:19:42//MOORELLA THERMOACETICA (CLOSTRIDIUM THERMOACETICUM).//P00203
F-NT2RP4000218//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.7e-15:48:60//HOMO SAPIENS (HUMAN).// P39188
F-NT2RP4000243//DUALIN.//5.8e-78:192:70//GALLUS GALLUS (CHICKEN).//Q90830
F-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//3.1e-83:207:76//MUS MUSCULUS (MOUSE).//Q03173
F-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).//5.5e-29:153:43//HELIANTHUS ANNUUS (COMMON SUNFLOWER).//O23968
F-NT2RP4000263//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.98:42:40//BOS TAURUS (BOVINE).//P20072
F-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//3.5e-71:209:66// SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87115
F-NT2RP4000312//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//8.9e-22:166:37//HOMO SAPIENS (HUMAN).//Q15404
F-NT2RP4000321//VERPROLIN.//0.00018:260:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).// P37370
F-NT2RP4000323//ANTHOPLEURIN B (TOXIN AP-B).//0.42:15:46//ANTHOPLEURA XANTHOGRAMMICA (GIANT GREEN SEA ANEMONE).//P01531
F-NT2RP4000355//HYPOTHETICAL 90.9 KD PROTEIN IN GCN20-CMK1 INTERGENIC REGION.//0.75:125:29// SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43596
F-NT2RP4000360//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.27:92:

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33//RATTUS NORVEGICUS (RAT).//P10164
F-NT2RP4000367//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION.//0.99:52:32//HUMAN ADENOVIRUS TYPE 41.//P23691
F-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1).//4.1e-40:163:52//HOMO SAPIENS (HUMAN).//O75570
F-NT2RP4000376//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//4.2e-59:125:80//RATTUS NORVEGICUS (RAT).//P54319
F-NT2RP4000381//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//0.00058:194:30//MUS MUSCULUS (MOUSE).//P19246
F-NT2RP4000398//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.2e-45:153:39//HOMO SAPIENS (HUMAN).//Q99676
F-NT2RP4000415//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.//0.00066:201:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47179
F-NT2RP4000417//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).//1.8e-25:196:40//MUS MUSCULUS (MOUSE).//P39098
F-NT2RP4000424//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.0e-15:72:61//HOMO SAPIENS (HUMAN).//P39195
F-NT2RP4000448//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//7.0e-23:63:82//HOMO SAPIENS (HUMAN).//P39192
F-NT2RP4000449//REGULATORY PROTEIN SIR2 (SILENT INFORMATION REGULATOR 2).//1.3e-41:102:45//KLUYVEROMYCES LACTIS (YEAST).//P33294
F-NT2RP4000455//HOMEOBOX PROTEIN SAX-1 (CHOX-3) (FRAGMENT).//0.00014:92:30//GALLUS GALLUS (CHICKEN).//P19601
F-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 7 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 7) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 7) (DEUBIQUITINATING ENZYME 7) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE).//1.0e-29:218:38//HOMO SAPIENS (HUMAN).//Q93009
F-NT2RP4000480//TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3).//0.049:117:29//PSEUDOMONAS AERUGINOSA.//P15276
F-NT2RP4000481//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//2.3e-05:152:23//CAENORHABDITIS ELEGANS.//Q09475
F-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//2.3e-48:172:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40484
F-NT2RP4000500//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III.//1.3e-23:165:35//CAENORHABDITIS ELEGANS.//P34535
F-NT2RP4000515//PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE) (5'-NUCLEOTIDE PHOSPHODIESTERASE) (FRAGMENT).//1.0:48:37//BOS TAURUS (BOVINE).//P15396
F-NT2RP4000517//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//1.0:41:36//VICIA FABA (BROAD BEAN).//Q41657
F-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.1e-11:93:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P45818
F-NT2RP4000519//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.68:55:40//BOS TAURUS (BOVINE).//P25508
F-NT2RP4000524//IGA FC RECEPTOR PRECURSOR (BETA ANTIGEN) (B ANTIGEN).//0.37:187:24//STREPTOCOCCUS AGALACTIAE.//P27951
F-NT2RP4000528//NPL4 PROTEIN.//2.1e-45:305:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33755
F-NT2RP4000541//HOMEOBOX PROTEIN CHOX-1 (FRAGMENT).//0.23:28:50//GALLUS GALLUS (CHICKEN).//P13544
F-NT2RP4000556//HYPOTHETICAL 34.1 KD PROTEIN C40H1.4 IN CHROMOSOME III.//4.3e-14:174:34//CAENORHABDITIS ELEGANS.//Q03574
F-NT2RP4000560//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.//2.1e-19:155:36//CAENORHABDITIS ELEGANS.//P34679
F-NT2RP4000588//HYPOTHETICAL PROTEIN E-115.//0.014:64:35//HUMAN ADENOVIRUS TYPE 2.//P03290
F-NT2RP4000614//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//2.7e-27:188:44//GALLUS GALLUS (CHICKEN).//P30352
F-NT2RP4000638//EARLY NODULIN 55-1 PRECURSOR (N-55-1) (FRAGMENT).//0.55:40:40//GLYCINE MAX (SOYBEAN).//Q05544
F-NT2RP4000648//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.4e-06:31:74//HOMO SAPIENS (HUMAN).//

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P39188
F-NT2RP46000657//HYPOTHETICAL PROTEIN MJ1065.//2.5e-40:237:40//METHANOCOCCUS JANNASCHII.//Q58465
F-NT2RP4000704
F-NT2RP4000713//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//4.0e-07:134:40//STREPTOMYCES FRADIAE.//P20186
F-NT2RP4000724//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//1.1e-62:109:88//HOMO SAPIENS (HUMAN).//P10266
F-NT2RP4000728//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.0033:190:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
F-NT2RP4000737//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.0e-05:114:34//HOMO SAPIENS (HUMAN).//P23246
F-NT2RP4000739//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:20:50//ANAS PLATYRHYNCHOS (DOMESTIC DUCK).//P50655
F-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.0013:67:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53915
F-NT2RP4000787//POLLEN SPECIFIC PROTEIN SF3.//1.3e-13:79:39//HELIANTHUS ANNUUS (COMMON SUNFLOWER).//P29675
F-NT2RP4000817//SUPPRESSOR PROTEIN SRP40.//1.3e-05:255:21//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
F-NT2RP4000833
F-NT2RP4000837//MALE SPECIFIC SPERM PROTEIN MSTS4DB.//0.18:38:44//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
F-NT2RP4000839//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAFII-90).//0.026:38:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38129
F-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//2.8e-64:229:53//RATTUS NORVEGICUS (RAT).//O09175
F-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.6e-84:174:54//HOMO SAPIENS (HUMAN).//P16415
F-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//8.2e-88:227:74//MUS MUSCULUS (MOUSE).//O35682
F-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN).//9.1e-55:268:43//HOMO SAPIENS (HUMAN).//P22314
F-NT2RP4000907//BDNF / NT-3 GROWTH FACTORS RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKB TYROSINE KINASE) (GP145-TRKB) (TRK-B).//5.4e-10:220:25//HOMO SAPIENS (HUMAN).//Q16620
F-NT2RP4000915//60S ACIDIC RIBOSOMAL PROTEIN P2 (FRAGMENT).//0.46:23:60//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P51407
F-NT2RP4000918//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB.//0.00010:148:32//BACILLUS SUBTILIS.//P39217
F-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//3.5e-27:220:36//HOMO SAPIENS (HUMAN).//Q06828
F-NT2RP4000927//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).//0.64:75:37//BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).//P29128
F-NT2RP4000928//PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41) (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE).//3.1e-104:263:66//HOMO SAPIENS (HUMAN).//Q92903
F-NT2RP4000929//HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC REGION.//0.93:107:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53288
F-NT2RP4000955//PUTATIVE CUTICLE COLLAGEN F09G8.6.//2.0e-05:102:37//CAENORHABDITIS ELEGANS.//P34391
F-NT2RP4000973//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION.//2.3e-17:78:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40564
F-NT2RP4000975//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.0041:142:33//HOMO SAPIENS (HUMAN).//P10162
F-NT2RP4000979//HYPOTHETICAL 14.5 KD PROTEIN.//0.77:106:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20517

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F-NT2RP4000984//HYPOTHETICAL 124.8 KD PROTEIN C29E4.4 IN CHROMOSOME III.//0.90:94:25// CAENORHABDITIS ELEGANS.//P34343
F-NT2RP4000989//ANTHOPLEURIN B (TOXIN AP-B).//0.76:41:41//ANTHOPLEURA XANTHOGRAMMICA (GIANT GREEN SEA ANEMONE).//P01531
F-NT2RP4000996//PROTEIN Q300.//0.00024:41:53//MUS MUSCULUS (MOUSE).//Q02722
F-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT).//8.7e-115:261:82//RATTUS NORVEGICUS (RAT).//O54888
F-NT2RP4001004//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.50:61:34//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q42377
F-NT2RP4001006//HYPOTHETICAL 43.5 KD PROTEIN IN COTD-KDUD INTERGENIC REGION PRECURSOR.//0.010:152:29//BACILLUS SUBTILIS.//P50840
F-NT2RP4001010//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.9e-05:247:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
F-NT2RP4001029//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//1.1e-14:175:31//DROSOPHILA MELANOGASTER (FRUIT FLY).// P13002
F-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//1.5e-74:272:55//CAENORHABDITIS ELEGANS.//Q09996
F-NT2RP4001057//HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III.//0.0064:76:38// CAENORHABDITIS ELEGANS.//P34664
F-NT2RP4001064//DUALIN.//2.5e-24:199:38//GALLUS GALLUS (CHICKEN).//Q90830
F-NT2RP4001078//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.11:139:38//HOMO SAPIENS (HUMAN).//O00268
F-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE).//1.5e-22:242:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P13586
F-NT2RP4001080//POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I).//1.7e-82:178:69//SUS SCROFA (PIG).//Q29099
F-NT2RP4001086//LEUCINE-RICH ACIDIC NUCLEAR PROTEIN.//0.00039:141:26//RATTUS NORVEGICUS (RAT).//P49911
F-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//9.9e-07:79:43//HOMO SAPIENS (HUMAN).//P78563
F-NT2RP4001100//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION.//4.4e-16:207:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032
F-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//8.1e-115:224:99//RATTUS NORVEGICUS (RAT).//P38378
F-NT2RP4001122//TIPD PROTEIN://7.5e-11:129:31//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//O15736
F-NT2RP4001126//TRICHOHYALIN.//1.4e-19:257:28//OVIS ARIES (SHEEP).//P22793
F-NT2RP4001138//PUTATIVE F420-DEPENDENT NADP REDUCTASE (EC 1.-.-.-).//0.00010:204:25//METHANOCOCCUS JANNASCHII.//Q58896
F-NT2RP4001143//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION.//4.5e-34:168:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43616
F-NT2RP4001148//SOF1 PROTEIN.//2.4e-41:158:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).// P33750
F-NT2RP4001149//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//1.3e-08:106:41//VOLVOX CARTERI.//P21997
F-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).// 3.6e-24:194:32//GALLUS GALLUS (CHICKEN).//P35331
F-NT2RP4001159//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2).//0.0056:117:25//PLASMODIUM FALCIPARUM (ISOLATE K1 / THAILAND).//Q03643
F-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).// 5.9e-24:184:34//BRASSICA OLERACEA (CAULIFLOWER).//P52178
F-NT2RP4001206//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2).//0.0029:117:26//PLASMODIUM FALCIPARUM (ISOLATE K1 / THAILAND).//Q03643
F-NT2RP4001207//CHROMOSOME SEGREGATION PROTEIN CSE1.//1.0e-07:144:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33307
F-NT2RP4001210//DERMORPHIN 1 PRECURSOR [CONTAINS: DELTORPHIN (DERMENKEPHALIN); DER-

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MORPHIN).//0.019:130:30//PHYLLOMEDUSA SAUVAGEI (SAUVAGE'S LEAF FROG).//P05422
F-NT2RP4001213//ZINC FINGER PROTEIN 177.//3.2e-28:176:39//HOMO SAPIENS (HUMAN).//Q13360
F-NT2RP4001219//DISULFIDE ISOMERASE MPD1 PRECURSOR (EC 5.3.4.1).//2.4e-13:108:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12404
F-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//2.7e-56:242:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
F-NT2RP4001235//REGULATORY PROTEIN E2.//0.0080:100:38//HUMAN PAPILLOMAVIRUS TYPE 25.//P36787
F-NT2RP4001256//CUTICLE COLLAGEN 1.//0.014:104:31//CAENORHABDITIS ELEGANS.//P08124
F-NT2RP4001260//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//0.00077:16:68//ESCHERICHIA COLI.//P05834
F-NT2RP4001274//HISTONE H1.M6.1.//0.98:65:35//TRYPANOSOMA CRUZI.//P40273
F-NT2RP4001276//ELAV PROTEIN.//0.00054:134:33//DROSOPHILA VIRILIS (FRUIT FLY).//P23241
F-NT2RP4001313//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.014:71:35//NICOTIANA TABACUM (COMMON TOBACCO).//P13983
F-NT2RP4001315//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.//2.3e-12:190:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P54787
F-NT2RP4001336//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//0.0037:108:31//PODOSPORA ANSERINA.//Q00808
F-NT2RP4001339//HYPOTHETICAL PROTEIN MJ0810.//1.2e-09:150:34//METHANOCOCCUS JANNASCHII.//Q58220
F-NT2RP4001343//HYPOTHETICAL 85.2 KD PROTEIN F52C9.3 IN CHROMOSOME III.//1.4e-18:244:27//CAENORHABDITIS ELEGANS.//Q10123
F-NT2RP4001345//PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43) (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE) (FRAGMENT).//4.0e-49:212:50//GALLUS GALLUS (CHICKEN).//P53760
F-NT2RP4001351//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//5.7e-11:229:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25386
F-NT2RP4001353//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//0.00088:84:28//HOMO SAPIENS (HUMAN).//Q15404
F-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN).//1.0e-22:222:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q08180
F-NT2RP4001373//OV-17 ANTIGEN PRECURSOR (IMMUNODOMINANT HYPODERMAL ANTIGEN).//0.51:92:26//ONCHOCERCA VOLVULUS.//P36991
F-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PROTEIN KINASE 1).//3.5e-13:146:35//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P18160
F-NT2RP4001379//HYPOTHETICAL 64.2 KD PROTEIN IN SLT2-PUT2 INTERGENIC REGION.//1.2e-14:207:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38767
F-NT2RP4001389//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//0.073:112:33//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414
F-NT2RP4001407//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//0.0019:233:24//HOMO SAPIENS (HUMAN).//Q02224
F-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//6.2e-89:195:81//HOMO SAPIENS (HUMAN).//Q14141
F-NT2RP4001433//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.5e-85:216:56//HOMO SAPIENS (HUMAN).//P28160
F-NT2RP4001442//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (VERSION 1).//0.012:107:35//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P18616
F-NT2RP4001447//60S ACIDIC RIBOSOMAL PROTEIN P2 (EL12).//0.0046:69:33//ARTEMIA SALINA (BRINE SHRIMP).//P02399
F-NT2RP4001474//CBP3 PROTEIN PRECURSOR.//0.0011:111:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P21560
F-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE).//6.2e-60:146:61//HOMO SAPIENS (HUMAN).//Q02218
F-NT2RP4001498//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//2.3e-24:137:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701
F-NT2RP4001502//HYPOTHETICAL 24.7 KD PROTEIN IN POM152-REC114 INTERGENIC REGION.//6.0e-22:148:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40206
F-NT2RP4001507//CUTICLE COLLAGEN 40.//0.00029:166:31//CAENORHABDITIS ELEGANS.//P34804

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F-NT2RP4001524//LACTOCOCCIN A IMMUNITY PROTEIN.//0.74:96:30//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS), AND LACTOCOCCUS LACTIS (SUBSP. CREMORIS) (STREPTOCOCCUS CREMORIS).//Q00561

F-NT2RP4001529//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//2.8e-06:79:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13002

F-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENIC REGION.//5.4e-34:88:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25656

F-NT2RP4001551//CELL DIVISION CONTROL PROTEIN 68.//1.5e-18:243:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32558

F-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//0.00030:158:24//MYCOBACTERIUM TUBERCULOSIS.//P96902

F-NT2RP4001567//IMPORTIN ALPHA-1 SUBUNIT (KARYOPHERIN ALPHA-1 SUBUNIT).//0.00013:147:29//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P52170

F-NT2RP4001568//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT).//8.0e-22:119:42//HOMO SAPIENS (HUMAN).//Q15057

F-NT2RP4001571//NEUROMODULIN (AXONAL MEMBRANE PROTEIN GAP-43) (PP46) (B-50) (PROTEIN F1) (CALMODULIN-BINDING PROTEIN P-57).//0.012:167:28//BOS TAURUS (BOVINE).//P06836

F-NT2RP4001574//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//6.8e-115:208:98//BOS TAURUS (BOVINE).//P53620

F-NT2RP4001575//M-RELATED PROTEIN PRECURSOR.//0.22:184:25//STREPTOCOCCUS PYOGENES.//P16946

F-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS).//7.4c-45:229:39//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P73505

F-NT2RP4001610//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII).//0.41:74:28//SUS SCROFA (PIG).//P27917

F-NT2RP4001614//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//1.0:29:37//HOMO SAPIENS (HUMAN).//P02811

F-NT2RP4001634//MYOSIN HEAVY CHAIN, PERINATAL SKELETAL MUSCLE (FRAGMENT).//0.16:233:23//RATTUS NORVEGICUS (RAT).//P04462

F-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/34MS19.//4.2e-21:249:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40469

F-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//4.5e-18:111:44//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P25323

F-NT2RP4001656//HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II.//3.4e-13:175:32//CAENORHABDITIS ELEGANS.//Q09600

F-NT2RP4001677//HYPOTHETICAL 73.6 KD PROTEIN CY49.21.//0.065:66:43//MYCOBACTERIUM TUBERCULOSIS.//Q10690

F-NT2RP4001679//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.3e-36:103:72//HOMO SAPIENS (HUMAN).//P39194

F-NT2RP4001696//PHOTOSYSTEM II REACTION CENTRE J PROTEIN.//0.93:37:37//CHLORELLA VULGARIS.//P56338

F-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//4.3e-11:128:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10282

F-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//4.1e-22:201:27//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q09332

F-NT2RP4001739//HOMEOBOX PROTEIN HOX-A10 (HOX-1H) (HOX-1.8) (PL).//1.0:67:34//HOMO SAPIENS (HUMAN).//P31260

F-NT2RP4001753//ZINC FINGER PROTEIN 10 (ZINC FINGER PROTEIN KOX1) (FRAGMENT).//1.2e-19:72:62//HOMO SAPIENS (HUMAN).//P21506

F-NT2RP4001760//BREAKPOINT CLUSTER REGION PROTEIN.//1.8e-13:179:28//HOMO SAPIENS (HUMAN).//P11274

F-NT2RP4001790//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).//7.9e-38:147:49//MUS MUSCULUS (MOUSE).//Q07231

F-NT2RP4001803//CUTICLE COLLAGEN 12 PRECURSOR.//0.40:48:39//CAENORHABDITIS ELEGANS.//P20630

F-NT2RP4001822//NOVEL ANTIGEN 2 (NAG-2).//2.7e-27:173:36//HOMO SAPIENS (HUMAN).//O14817

F-NT2RP4001823//PUTATIVE CUTICLE COLLAGEN F09G8.6.//3.3e-16:152:42//CAENORHABDITIS ELE-

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GANS.//P34391
F-NT2RP4001828//HOLIN.//0.99:33:36//BACTERIOPHAGE HP1.//P51727
F-NT2RP4001838//METASTASIS-ASSOCIATED PROTEIN MTA1.//1.2e-07:95:31//HOMO SAPIENS (HUMAN).//Q13330
F-NT2RP4001841//INTESTINAL MUCIN-LIKE PROTEIN (MLP) (FRAGMENT).//0.94:141:22//RATTUS NORVEGICUS (RAT).//P98089
F-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1.//5.6e-52:276:45//MUS MUSCULUS (MOUSE).//P55194
F-NT2RP4001861//HYPOTHETICAL 10.6 KD PROTEIN IN GALE-PEPT INTERGENIC REGION.//0.92:39:51//BACILLUS SUBTILIS.//P55185
F-NT2RP4001889//HYPOTHETICAL BHLF1 PROTEIN.//0.32:97:31//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
F-NT2RP4001893//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).//3.6e-07:124:29//MUS MUSCULUS (MOUSE).//Q05921
F-NT2RP4001896//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1 INTERGENIC REGION.//3.9e-10:210:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42935
F-NT2RP4001901//ACROSIN PRECURSOR (EC 3.4.21.10).//2.4e-07:53:45//ORYCTOLAGUS CUNICULUS (RABBIT).//P48038
F-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//3.1e-19:170:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12024
F-NT2RP4001938//ZINC FINGER PROTEIN MOK-2.//1.3e-28:72:50//MUS MUSCULUS (MOUSE).//P24399
F-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE).//4.8e-14:183:30//TRITICUM AESTIVUM (WHEAT).//Q43209
F-NT2RP4001950//HYPOTHETICAL PROTEIN ORF-1137.//3.7e-07:115:29//MUS MUSCULUS (MOUSE).//P11260
F-NT2RP4001953
F-NT2RP4001966//WALL-ASSOCIATED PROTEIN PRECURSOR.//0.13:151:27//BACILLUS SUBTILIS.//Q07833
F-NT2RP4001975//FIBRIL-FORMING COLLAGEN ALPHA CHAIN.//0.00031:190:31//RIFTIA PACHYPTILA (TUBE WORM).//P30754
F-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//3.5e-18:185:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
F-NT2RP4002047//GTP-BINDING PROTEIN GUF1 (GTPASE GUF1).//4.0e-49:158:65//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P46943
F-NT2RP4002052//HYPOTHETICAL 54.3 KD PROTEIN C23D3.03C IN CHROMOSOME I.//0.0047:148:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09844
F-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE F56D2.6.//0.057:66:30//CAENORHABDITIS ELEGANS.//Q20875
F-NT2RP4002071//VERY HYPOTHETICAL 13.2 KD PROTEIN CY251.09.//0.94:45:46//MYCOBACTERIUM TUBERCULOSIS.//Q10888
F-NT2RP4002075//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.44:36:38//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18804
F-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.6e-19:46:76//HOMO SAPIENS (HUMAN).//Q05481
F-NT2RP4002081//MHC CLASS II REGULATORY FACTOR RFX1 (RFX) (ENHANCER FACTOR C) (EF-C).//2.8e-05:196:31//HOMO SAPIENS (HUMAN).//P22670
F-NT2RP4002083//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//0.0064:29:55//OWENIA FUSIFORMIS.//P21260
F-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.1e-37:159:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P38938
F-NT2RP4002791//30S RIBOSOMAL PROTEIN S20.//1.0:73:26//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//P56027
F-NT2RP4002888//HYPOTHETICAL PROTEIN TP0352.//0.98:52:26//TREPONEMA PALLIDUM.//O83371
F-NT2RP4002905//G2/MITOTIC-SPECIFIC CYCLIN S13-7 (B-LIKE CYCLIN) (FRAGMENT).//5.9e-05:138:27//GLYCINE MAX (SOYBEAN).//P25012
F-NT2RP5003459//HOMEOBOX PROTEIN HOX-A3 (HOX-1.5) (MO-10).//0.027:40:40//MUS MUSCULUS (MOUSE).//P02831

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F-NT2RP5003461//HYPOTHETICAL PROTEIN C22F3.14C IN CHROMOSOME I (FRAGMENT).//1.1e-12:142:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09779
F-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.3e-13:215:28//PODOSPORA ANSERINA.//Q00808
F-NT2RP5003492//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//0.0055:144:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
F-NT2RP5003500//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//9.0e-05:103:38//MUS MUSCULUS (MOUSE).//P05142
F-NT2RP5003506//MALE SPECIFIC SPERM PROTEIN MST87F.//0.53:21:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175
F-NT2RP5003512//HYPOTHETICAL PROTEIN IN CYCB 3'REGION PRECURSOR (ORF2) (FRAGMENT).//0.92:49:32//PARACOCCUS DENITRIFICANS.//P29969
F-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//2.7e-18:165:39//PHASEOLUS AUREUS (MUNG BEAN) (VIGNA RADIATA).//P37116
F-NT2RP5003524//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//6.0e-08:125:41//RATTUS NORVEGICUS (RAT).//P02454
F-NT2RP5003534//ATP SYNTHASE, SUBUNIT F (EC 3.6.1.34).//0.88:37:45//HALOBACTERIUM VOLCANII (HALOFERAX VOLCANII).//Q48331
F-OVARC1000001//GAR22 PROTEIN.//1.9e-05:41:58//HOMO SAPIENS (HUMAN).//Q99501
F-OVARC1000004//70 KD EXOCYST COMPLEX PROTEIN.//3.7e-08:186:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P19658
F-OVARC1000006//HISTONE H2A.1.//4.7e-55:117:98//RATTUS NORVEGICUS (RAT).//P02262
F-OVARC1000013//WD-REPEAT PROTEIN POP1.//0.00022:126:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87060
F-OVARC1000014//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//2.3e-05:220:30//GALLUS GALLUS (CHICKEN).//P02457
F-OVARC1000017//CUTICLE COLLAGEN DPY-13.//2.6e-05:97:30//CAENORHABDITIS ELEGANS.//P17657
F-OVARC1000035
F-OVARC1000058//RAS-RELATED PROTEIN RABC.//0.00015:110:24//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34143
F-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE).//6.8e-09:60:45//LYCOPERSICON ESCULENTUM (TOMATO).//P80022
F-OVARC1000068//CYTOTOXIN 4 (CARDIOTOXIN V-II-4).//1.0:27:44//NAJA MOSSAMBICA (MOZAMBIQUE COBRA).//P01452
F-OVARC1000071//NUCLEAR TRANSPORT FACTOR 2 (NTF-2) (PLACENTAL PROTEIN 15) (PP15).//5.2e-06:115:29//HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT).//P13662
F-OVARC1000085
F-OVARC1000087//HISTONE MACRO-H2A.1.//1.2e-13:174:26//RATTUS NORVEGICUS (RAT).//Q02874
F-OVARC1000091//OCTAPEPTIDE-REPEAT PROTEIN T2.//0.0013:137:32//MUS MUSCULUS (MOUSE).//Q06666
F-OVARC1000092//MITOCHONDRIAL RIBOSOMAL PROTEIN S7.//0.97:46:39//ACANTHAMOEBA CASTELLANII (AMOEBA).//P46756
F-OVARC1000106//HYPOTHETICAL 141.5 KD PROTEIN IN YPT53-RHO2 INTERGENIC REGION.//0.0012:165:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53935
F-OVARC1000109//PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR (FRAGMENT).//0.18:35:34//DAUCUS CAROTA (CARROT).//P06600
F-OVARC1000113//HYPOTHETICAL PROTEIN C18.//1.0:26:26//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//P32217
F-OVARC1000114//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.6e-28:57:63//HOMO SAPIENS (HUMAN).//P39194
F-OVARC1000133
F-OVARC1000139//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//1.9e-09:200:29//HOMO SAPIENS (HUMAN).//Q13107
F-OVARC1000145//HOMEOBOX PROTEIN DLX-3.//1.0:65:30//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q01702
F-OVARC1000148//HYPHAL WALL PROTEIN 1 (CELL ELONGATION PROTEIN 2).//0.12:175:29//CANDIDA AL-

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BICANS (YEAST).//P46593
F-OVARC1000151//HYPOTHETICAL PROTEIN KIAA0161.//5.6e-20:197:30//HOMO SAPIENS (HUMAN).// P50876
F-OVARC1000168//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.0030:77:38//HOMO SAPIENS (HUMAN).// P39188
F-OVARC1000191//COLANIC ACID BIOSYNTHESIS PROTEIN WCAH.//0.95:56:35//ESCHERICHIA COLI.// P32056
F-OVARC1000198//HISTONE H1.C2.//0.96:70:25//TRYPANOSOMA CRUZI.//P40268
F-OVARC1000209//HYPOTHETICAL 20.9 KD PROTEIN IN PLB1-HXT2 INTERGENIC REGION.//2.5e-33:178:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03677
F-OVARC1000212//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//1.7e-05:66:46//MUS MUSCULUS (MOUSE).//P05142
F-OVARC1000240//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.8e-10:41:78//HOMO SAPIENS (HUMAN).// P39193
F-OVARC1000241//ENDOTHELIAL PAS DOMAIN PROTEIN 1 (EPAS-1) (HIF-1 ALPHA-LIKE FACTOR) (MHLF) (HIF-RELATED FACTOR) (HRF).//7.4e-54:177:54//MUS MUSCULUS (MOUSE).//P97481
F-OVARC1000288//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION.//2.9e-20:115:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38821
F-OVARC1000302//CORTICOSTEROID-BINDING GLOBULIN PRECURSOR (CBG) (TRANSCORTIN).//1.0:79:25//MUS MUSCULUS (MOUSE).//Q06770
F-OVARC1000304//PROTEIN MOV-10.//1.6e-79:181:83//MUS MUSCULUS (MOUSE).//P23249
F-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//6.9e-36:156:42//ASHBYA GOSSYPII (EREMOTHECIUM GOSSYPII).//Q00063
F-OVARC1000321//HYPOTHETICAL 28.1 KD PROTEIN C4F8.03 IN CHROMOSOME I.//5.2e-45:159:53// SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14179
F-OVARC1000326//BASIC PROLINE-RICH PEPTIDE IB-1.//0.036:67:35//HOMO SAPIENS (HUMAN).//P04281
F-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//1.2e-16:200:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40004
F-OVARC1000347//HYPOTHETICAL 7.6 KD PROTEIN YCF33.//0.69:41:43//CYANOPHORA PARADOXA.// P48273
F-OVARC1000384//ANTIFREEZE PEPTIDE 4 PRECURSOR.//0.98:49:34//PSEUDOPLEURONECTA AMERICANUS (WINTER FLOUNDER).//P02734
F-OVARC1000408//INTEGUMENTARY MUCIN C.1 (FIM-C.1) (FRAGMENT).//8.1e-05:115:33//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q05049
F-OVARC1000411//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP-150) (DAP-150) (P150-GLUED).//0.00076:100:29//RATTUS NORVEGICUS (RAT).//P28023
F-OVARC1000414//HYPOTHETICAL 7.0 KD PROTEIN IN BLTR-SPOIIIC INTERGENIC REGION.//1.0:46:34// BACILLUS SUBTILIS.//P54431
F-OVARC1000420//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT).//0.0028:97:37//HOMO SAPIENS (HUMAN).//P25067
F-OVARC1000427//HYPOTHETICAL 13.9 KD PROTEIN IN PRFA-SPOIIR INTERGENIC REGION.//0.70:21:47// BACILLUS SUBTILIS.//P39150
F-OVARC1000431
F-OVARC1000437//TENSIN.//9.2e-42:195:52//GALLUS GALLUS (CHICKEN).//Q04205
F-OVARC1000440//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//3.4e-31:37:97//HOMO SAPIENS (HUMAN).//P48059
F-OVARC1000442
F-OVARC1000443//CUTICLE COLLAGEN 2C (FRAGMENT).//0.0056:163:34//HAEMONCHUS CONTORTUS.// P16252
F-OVARC1000461//FIXU PROTEIN.//0.36:36:44//RHIZOBIUM LEGUMINOSARUM (BIOVAR TRIFOLII).// P42710
F-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//2.4e-14:222:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11075
F-OVARC1000466//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//2.3e-08:29:93//HOMO SAPIENS (HUMAN).// P39192
F-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 7 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE MKP-X) (FRAGMENT).//2.8e-06:96:36//RATTUS NORVEGICUS (RAT).// Q63340

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F-OVARC1000479//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X (PSI-K).//0.99:48:37//CYANIDIUM CALDARIUM (GALDIERIA SULPHURARIA).//P31567 F-OVARC1000486
F-OVARC1000496//HYPOTHETICAL PROTEIN MJ1213.//1.0:62:32//METHANOCOCCUS JANNASCHII.// Q58610
F-OVARC1000520//MEROZOITE SURFACE PROTEIN CMZ-8 (FRAGMENT).//0.0011:66:40//EIMERIA ACERVULINA.//P09125
F-OVARC1000526//PROTEIN Q300.//1.2e-05:51:43//MUS MUSCULUS (MOUSE).//Q02722
F-OVARC1000533//NEURONAL PROTEIN 3.1 (P311 PROTEIN).//0.74:43:41//HOMO SAPIENS (HUMAN).// Q16612
F-OVARC1000543//POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1).//2.3e-23:192:35//HOMO SAPIENS (HUMAN).//Q10472
F-OVARC1000556
F-OVARC1000557//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.6e-08:80:47//HOMO SAPIENS (HUMAN).// P39188
F-OVARC1000564//VPX PROTEIN (X ORF PROTEIN) (VIRAL ACCESSORY PROTEIN).//0.45:32:50//HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D194) (HIV-2).//P17760
F-OVARC1000573
F-OVARC1000576//BETA-DEFENSIN 1 (BNDB-1).//0.47:29:41//BOS TAURUS (BOVINE).//P46159
F-OVARC1000578//COLLAGEN ALPHA 1(II) CHAIN (FRAGMENTS).//0.023:96:36//BOS TAURUS (BOVINE).// P02459
F-OVARC1000588//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3.//0.75:57:29//HOMO SAPIENS (HUMAN).//P09001
F-OVARC1000605//AUTOLYSIN PRECURSOR (EC 3.4.24.38) (GAMETE LYTIC ENZYME) (GLE).//0.91:134:28// CHLAMYDOMONAS REINHARDTII.//P31178
F-OVARC1000622//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//2.6e-36:100:80//HOMO SAPIENS (HUMAN).//P39189
F-OVARC1000640//HYPOTHETICAL 8.5 KD PROTEIN YCF40 (ORF73).//0.96:34:38//ODONTELLA SINENSIS.// P49535
F-OVARC1000649//ANTHER-SPECIFIC PROTEIN SF18 PRECURSOR (FRAGMENT).//0.0036:64:37//HELIANTHUS ANNUUS (COMMON SUNFLOWER).//P22357
F-OVARC1000661//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENTS).//0.21:53:47//RATTUS NORVEGICUS (RAT).//P02466
F-OVARC1000678//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//1.0:17:58//ESCHERICHIA COLI.// P05834
F-OVARC1000679//DNA-DIRECTED RNA POLYMERASE OMEGA CHAIN (EC 2.7.7.6) (TRANSCRIPTASE OMEGA CHAIN) (RNA POLYMERASE OMEGA SUBUNIT).//0.096:67:29//ESCHERICHIA COLI.//P08374
F-OVARC1000681//PROTEIN Q300.//0.72:16:43//MUS MUSCULUS (MOUSE).//Q02722
F-OVARC1000682//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).// 7.6e-70:102:99//MUS MUSCULUS (MOUSE).//P39098
F-OVARC1000689//CADMIUM-METALLOTHIONEIN (CD-MT).//0.032:30:40//HELIX POMATIA (ROMAN SNAIL) (EDIBLE SNAIL).//P33187
F-OVARC1000700//BRAIN NEURON CYTOPLASMIC PROTEIN 2.//0.17:60:40//RATTUS NORVEGICUS (RAT).// P02684
F-OVARC1000703//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.57:42:42//HOMO SAPIENS (HUMAN).// P02811
F-OVARC1000722//N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1->4)GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT).//1.1e-20:44:70//BOS TAURUS (BOVINE).//P08037
F-OVARC1000730//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III.//5.2e-29:224:36// CAENORHABDITIS ELEGANS.//Q18262
F-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN.//6.2e-12:78:48//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25159
F-OVARC1000769
F-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.1e-46:121:79//HOMO SAPIENS (HUMAN), AND CANIS FAMILIARIS (DOG).//P08886
F-OVARC1000781//HOMEOBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEOBOX PROTEIN 2).//0.81:36:52//HOMO SAPIENS (HUMAN).//P52951

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F-OVARC1000787//40S RIBOSOMAL PROTEIN S14 (FRAGMENT).//0.96:37:48//SUS SCROFA (PIG).//Q29303
F-OVARC1000800//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//2.5e-31:47:82//HOMO SAPIENS (HUMAN).//P39189
F-OVARC1000802//HYPOTHETICAL 8.8 KD PROTEIN B0302.2 IN CHROMOSOME X.//0.16:55:40//CAENORHABDITIS ELEGANS.//Q10926
F-OVARC1000834//SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA (EC 2.7.1.-) (P68-PAK) (P21- ACTIVATED KINASE) (ALPHA-PAK) (PROTEIN KINASE MUK2).//0.87:140:31//RATTUS NORVEGICUS (RAT).//P35465
F-OVARC1000846//NUCLEOLIN (PROTEIN C23).//7.0e-07:109:30//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//P08199
F-OVARC1000850//HYPOTHETICAL 56.2 KD PROTEIN IN ERG8-UBP8 INTERGENIC REGION.//6.9e-09:180:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04991
F-OVARC1000862//UBIQUITIN-CONJUGATING ENZYME E2-17.5 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).//0.0020:74:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P52490
F-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).//9.8e-39:154:55//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40484
F-OVARC1000883//METALLOTHIONEIN-I.//0.87:38:36//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA).//P15113
F-OVARC1000885//OXIDOREDUCTASE UCPA (EC 1.-.-.-).//2.8e-18:170:34//ESCHERICHIA COLI.//P37440
F-OVARC1000886//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//0.00033:60:45//BOS TAURUS (BOVINE).//P02465
F-OVARC1000890//PROBABLE E5 PROTEIN.//0.92:7:71//HUMAN PAPILLOMAVIRUS TYPE 70.//P50774
F-OVARC1000891//HYPOTHETICAL 8.3 KD PROTEIN (ORF5).//1.0:36:36//PARAMECIUM TETRAURELIA.//P15606
F-OVARC1000897//HYPOTHETICAL 6.1 KD PROTEIN PRECURSOR (ORF87).//1.0:34:44//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10337
F-OVARC1000912//PUTATIVE CUTICLE COLLAGEN C09G5.4.//4.0e-07:98:35//CAENORHABDITIS ELEGANS.//Q09455
F-OVARC1000915//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//1.7e-47:115:76//HOMO SAPIENS (HUMAN).//P56524
F-OVARC1000924//CYTOCHROME B (EC 1.10.2.2) (FRAGMENT).//0.99:54:24//BOA CONSTRICTOR (BOA).//P92848
F-OVARC1000936//HYPOTHETICAL 7.5 KD PROTEIN IN INAA-GLPQ INTERGENIC REGION.//1.0:48:33//ESCHERICHIA COLI.//P45505
F-OVARC1000937//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//1.0:135:31//HOMO SAPIENS (HUMAN).//P02452
F-OVARC1000945//EARLY E1A 11 KD PROTEIN.//0.087:81:24//MOUSE ADENOVIRUS TYPE 1 (MAV-1).//P12533
F-OVARC1000948
F-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//0.99:67:28//METHANOCOCCUS JANNASCHII.//Q58343
F-OVARC1000960//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.8e-32:56:75//HOMO SAPIENS (HUMAN).//P39193
F-OVARC1000964//MAMBIN (GLYCOPROTEIN IIB-IIA ANTAGONIST) (PLATELET AGGREGATION INHIBITOR) (DENDROASPIN).//1.0:30:36//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S MAMBA).//P28375
F-OVARC1000971
F-OVARC1000984//HYPOTHETICAL 52.3 KD PROTEIN IN MRPL10-ERG24 INTERGENIC REGION PRECURSOR.//0.093:36:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53832
F-OVARC1000996//MO25 PROTEIN.//1.9e-39:80:95//MUS MUSCULUS (MOUSE).//Q06138
F-OVARC1000999//BRAIN-SPECIFIC HOMEOBOX/POU DOMAIN PROTEIN 1 (BRN-1 PROTEIN).//0.00020:50:40//HOMO SAPIENS (HUMAN).//P20264
F-OVARC1001000//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.4e-16:43:90//HOMO SAPIENS (HUMAN).//P39195
F-OVARC1001004//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.95:33:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01642
F-OVARC1001010//HYPOTHETICAL PROTEIN MJ0926.//0.50:71:23//METHANOCOCCUS JANNASCHII.//

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Q58336
F-OVARC1001011//CORTISTATIN PRECURSOR.//0.81:45:37//RATTUS NORVEGICUS (RAT).//Q62949
F-OVARC1001032//FERREDOXIN LIKE PROTEIN.//1.0:26:46//RHIZOBIUM LEGUMINOSARUM (BIOVAR PHASEOLI).//Q05561
F-OVARC1001034//METALLOTHIONEIN-IG (MT-1G).//0.14:9:77//HOMO SAPIENS (HUMAN).//P13640
F-OVARC1001038//NUCLEOLIN (PROTEIN C23).//3.2e-07:36:80//HOMO SAPIENS (HUMAN).//P19338
F-OVARC1001040//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.5e-18:45:60//HOMO SAPIENS (HUMAN).//P39194
F-OVARC1001044//BIS(5'-NUCLEOSYL)-TETRAPHOSPHATASE (SYMMETRICAL) (EC 3.6.1.41) (DIADENOSINE TETRAPHOSPHATASE).//0.88:43:39//ESCHERICHIA COLI.//P05637
F-OVARC1001051//SERINE PROTEINASE STUBBLE (EC 3.4.21.-) (STUBBLE-STUBBLOID PROTEIN).//0.34:117:25//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q05319
F-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSOR.//1.6e-33:43:97//HOMO SAPIENS (HUMAN).//P43490
F-OVARC1001062
F-OVARC1001065//METHIONYL-TRNA SYNTHETASE (EC 6.1.1.10) (METHIONINE--TRNA LIGASE) (METRS).//0.79:76:39//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//Q44951
F-OVARC1001068//GTP-BINDING PROTEIN ERA HOMOLOG (FRAGMENT).//5.3e-15:100:44//BRADYRHIZOBIUM JAPONICUM.//O69162
F-OVARC1001072//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.0076:41:56//HOMO SAPIENS (HUMAN).//P39188
F-OVARC1001074//60S RIBOSOMAL PROTEIN L38.//1.0:32:40//LYCOPERSICON ESCULENTUM (TOMATO).//P46291
F-OVARC1001085//HYPOTHETICAL 126.5 KD PROTEIN C13F4.06 IN CHROMOSOME I.//0.73:135:25//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10197
F-OVARC1001092//HYPOTHETICAL 51.2 KD PROTEIN IN PET54-DIE2 INTERGENIC REGION.//5.6e-05:30:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P50079
F-OVARC1001107//SHK1 KINASE-BINDING PROTEIN 1.//1.8e-08:52:51//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P78963
F-OVARC1001113//DIAPHANOUS PROTEIN.//1.9e-33:218:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48608
F-OVARC1001117//GENE 7 PROTEIN.//0.68:12:50//SPIROPLASMA VIRUS 4 (SPV4).//P11339
F-OVARC1001118
F-OVARC1001129//30S RIBOSOMAL PROTEIN S17.//0.15:57:22//AQUIFEX AEOLICUS.//O66439
F-OVARC1001154//GRANULINS PRECURSOR (ACROGRANIN).//2.3e-95:99:77//MUS MUSCULUS (MOUSE).//P28798
F-OVARC1001161//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//0.17:87:34//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P49177
F-OVARC1001162
F-OVARC1001167//TRBD PROTEIN.//0.92:24:45//ESCHERICHIA COLI.//P41070
F-OVARC1001169//FRUCTOSE-1,6-BISPHOSPHATASE (EC 3.1.3.11) (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) (FRAGMENT).//0.82:35:40//MUS MUSCULUS (MOUSE).//P97323
F-OVARC1001170//PROLINE-RICH PEPTIDE P-B.//0.17:27:37//HOMO SAPIENS (HUMAN).//P02814
F-OVARC1001171//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.00023:28:75//HOMO SAPIENS (HUMAN).//P39188
F-OVARC1001173
F-OVARC1001176//HYPOTHETICAL BHLF1 PROTEIN.//2.7e-05:158:31//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
F-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2.//1.4e-12:208:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48510
F-OVARC1001188//HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//3.3e-31:129:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53215
F-OVARC1001200//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION.//0.018:148:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47057
F-OVARC1001232//HYPOTHETICAL PROTEIN MJ1236.//2.5e-27:141:39//METHANOCOCCUS JANNASCHII.//Q58633
F-OVARC1001240
F-OVARC1001243

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F-OVARC1001244//RING3 PROTEIN (KIAA9001).//1.7e-13:37:91//HOMO SAPIENS (HUMAN).//P25440
F-OVARC1001261//OCTAPEPTIDE-REPEAT PROTEIN T2.//1.3e-07:109:35//MUS MUSCULUS (MOUSE).//Q06666
F-OVARC1001268//HYPOTHETICAL 57.4 KD PROTEIN IN PILT REGION (ORF4).//0.71:43:41//PSEUDOMONAS AERUGINOSA.//P24563
F-OVARC1001270//HYPOTHETICAL 9.0 KD PROTEIN IN UVSW-UVSY INTERGENIC REGION.//1.0:44:29//BACTERIOPHAGE T4.//P32281
F-OVARC1001271//HYPOTHETICAL 104.7 KD PROTEIN F23F12.8 IN CHROMOSOME III PRECURSOR.//0.00015:188:23//CAENORHABDITIS ELEGANS.//P46504
F-OVARC1001282
F-OVARC1001296//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//0.022:101:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38968
F-OVARC1001306//HYPOTHETICAL 52.9 KD SERINE-RICH PROTEIN C11G7.01 IN CHROMOSOME I.//0.023:134:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13695
F-OVARC1001329//CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//1.3e-14:150:28//ZEA MAYS (MAIZE).//P49133
F-OVARC1001330
F-OVARC1001339//RIBONUCLEOPROTEIN RB97D.//0.0013:55:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q02926
F-OVARC1001341//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION.//4.9e-17:110:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032
F-OVARC1001342
F-OVARC1001344//PREPROTEIN TRANSLOCASE SECE SUBUNIT.//0.99:39:23//STAPHYLOCOCCUS CARNOSUS.//P36253
F-OVARC1001357//METALLOTHIONEIN.//0.99:28:42//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q05890
F-OVARC1001360//LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2).//0.86:109:31//HOMO SAPIENS (HUMAN).//P48634
F-OVARC1001369//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//6.7e-05:124:36//BOS TAURUS (BOVINE).//P02465
F-OVARC1001372//HYPOTHETICAL 34.5 KD PROTEIN IN CLCB-CLCD INTERGENIC REGION PRECURSOR.//0.75:33:48//PSEUDOMONAS PUTIDA, AND PSEUDOMONAS SP. (STRAIN B13).//Q47100
F-OVARC1001376//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.8e-24:96:61//HOMO SAPIENS (HUMAN).//P39188
F-OVARC1001381//MEMBRANE-ASSOCIATED ATPASE EPSILON CHAIN (EC 3.6.1.34) (SUL-ATPASE EPSILON).//0.96:46:39//SULFOLOBUS ACIDOCALDARIUS.//P23039
F-OVARC1001391//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.00024:189:29//HOMO SAPIENS (HUMAN).//P10162
F-OVARC1001399//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.062:18:77//HOMO SAPIENS (HUMAN).//P39195
F-OVARC1001417//HYPOTHETICAL 157.0 KD PROTEIN C38C10.5 IN CHROMOSOME III.//0.010:185:23//CAENORHABDITIS ELEGANS.//Q03570
F-OVARC1001419//A-TYPE INCLUSION PROTEIN (ATI).//0.50:135:28//CAMELPOX VIRUS (STRAIN CP-1).//Q05482
F-OVARC1001425//COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.//0.43:85:40//HOMO SAPIENS (HUMAN).//Q03692
F-OVARC1001436//HYPOTHETICAL 11.4 KD PROTEIN (C4 PROTEIN).//0.031:100:30//TOMATO YELLOW LEAF CURL VIRUS (STRAIN AUSTRALIA) (TYLCV).//P36283
F-OVARC1001442//HOMEOBOX PROTEIN HTR-A2 (FRAGMENT).//1.0:32:34//HELOBDELLA TRISERIALIS (LEECH).//P17138
F-OVARC1001453//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).//0.74:19:47//MUS MUSCULUS (MOUSE).//P28184
F-OVARC1001476//GTP-BINDING PROTEIN GTR2.//3.0e-12:114:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53290
F-OVARC1001480//COLLAGEN ALPHA 2(VI) CHAIN PRECURSOR.//0.00019:134:32//MUS MUSCULUS (MOUSE).//Q02788
F-OVARC1001489//HYPOTHETICAL PROTEIN HI1270.//0.98:30:43//HAEMOPHILUS INFLUENZAE.//P44149
F-OVARC1001496//C-TERMINAL BINDING PROTEIN 2.//4.0e-65:132:100//HOMO SAPIENS (HUMAN).//

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P56545
F-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE PROTEIN 1).//3.2e-70:159:94//HOMO SAPIENS (HUMAN).//P98161
F-OVARC1001525//FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 14 (FIN14).//1.0:36:33//MUS MUSCULUS (MOUSE).//Q61077
F-OVARC1001542//SMALL PROLINE-RICH PROTEIN 2B (SPR-2B).//0.69:57:33//HOMO SAPIENS (HUMAN).//P35325
F-OVARC1001547
F-OVARC1001555//NGG1-INTERACTING FACTOR 3.//7.6e-16:148:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53081
F-OVARC1001577//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//8.8e-38:94:81//GALLUS GALLUS (CHICKEN).//P30352
F-OVARC1001600//GENE 7 PROTEIN.//0.80:38:39//SPIROPLASMA VIRUS SPV1-R8A2 B.//P15898
F-OVARC1001610//DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE (EC 2.7.8.2) (SN-1,2- DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE) (CHOPT).//1.6e-22:122:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P17898
F-OVARC1001611
F-OVARC1001615//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X.//0.30:43:34//CAENORHABDITIS ELEGANS.//Q11116
F-OVARC1001668//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//1.0e-19:45:82//HOMO SAPIENS (HUMAN).//P39192
F-OVARC1001702//SOX-20 PROTEIN.//2.4e-28:71:83//HOMO SAPIENS (HUMAN).//O60248
F-OVARC1001703//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-BINDING PROTEIN 1) (INTERFERON-GAMMA INDUCIBLE PROTEIN MAG-1).//0.00018:88:36//MUS MUSCULUS (MOUSE).//Q01514
F-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).//2.7e-05:98:32//MUS MUSCULUS (MOUSE).//Q62267
F-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).//4.5e-20:46:67//BOS TAURUS (BOVINE).//P07106
F-OVARC1001726//ALPHA-AMYLASE INHIBITOR PAIM I (PIG PANCREATIC ALPHA-AMYLASE INHIBITOR OF MICROBES I).//0.59:23:56//STREPTOMYCES OLIVACEOVIRIDIS (STREPTOMYCES CORCHORUSII).//P09921
F-OVARC1001731//TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE.//2.1e-75:176:87//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q01173
F-OVARC1001745//GENE 11 PROTEIN.//0.31:36:52//SPIROPLASMA VIRUS SPV1-R8A2 B.//P15902
F-OVARC1001762//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMINO, ACETYLTRANSFERASE 1).//2.8e-23:197:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P12945
F-OVARC1001766//FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (EC 5.2.1.8) (PROLINE ROTAMASE) (NUCLEOLAR PROLINE ISOMERASE) (FKBP-70).//2.2e-06:99:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38911
F-OVARC1001767//33.2 KD PROTEIN IN DIND-RPH INTERGENIC REGION (ORF X).//0.99:113:27//ESCHERICHIA COLI.//P23839
F-OVARC1001768
F-OVARC1001791//HYPOTHETICAL 63.3 KD PROTEIN IN MPT5-SAE2 INTERGENIC REGION.//0.090:75:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P46945
F-OVARC1001795//HYPOTHETICAL 7.5 KD PROTEIN IN RPBA-GP46 INTERGENIC REGION.//0.81:21:38//BACTERIOPHAGE T4.//P07878
F-OVARC1001802//PLECTOXIN VIII (PLT-VIII) (PLTVIII).//0.41:19:36//PLECTREURYS TRISTIS (SPIDER).//P36984
F-OVARC1001805//60S RIBOSOMAL PROTEIN L40 (CEP52).//0.67:24:58//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P14796
F-OVARC1001809//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.23:111:31//RATTUS NORVEGICUS (RAT).//P02454
F-OVARC1001812//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:28:42//HALICHOERUS GRYPUS (GRAY SEAL).//P38592
F-OVARC1001813//HYPOTHETICAL 9.9 KD PROTEIN.//0.41:36:30//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20562

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F-OVARC1001820//HYPOTHETICAL PROTEIN ORF-1137.//0.80:58:29//MUS MUSCULUS (MOUSE).//P11260
F-OVARC1001828
F-OVARC1001846
F-OVARC1001861//METALLOTHIONEIN (MT).//0.18:11:54//PLEURONECTES PLATESSA (PLAICE).//P07216
F-OVARC1001873
F-OVARC1001879//HYPOTHETICAL 55.9 KD PROTEIN EEED8.6 IN CHROMOSOME II.//2.3e-05:73:31//CAENORHABDITIS ELEGANS.//Q09296
F-OVARC1001880//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT).//2.4e-11:203:32//HOMO SAPIENS (HUMAN).//P02812
F-OVARC1001883//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.3e-16:86:59//HOMO SAPIENS (HUMAN).//P39188
F-OVARC1001900//HYPOTHETICAL 105.9 KD PROTEIN F22B7.5 IN CHROMOSOME III.//0.0053:48:47//CAENORHABDITIS ELEGANS.//P34408
F-OVARC1001901
F-OVARC1001911//40S RIBOSOMAL PROTEIN S28.//1.0:33:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P34789
F-OVARC1001916//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN).//0.00082:114:27//HOMO SAPIENS (HUMAN).//P98174
F-OVARC1001928//FERREDOXIN III (FDIII).//1.0:64:29//ANABAENA VARIABILIS.//P46050
F-OVARC1001942//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMINO, ACETYLTRANSFERASE 1).//3.0e-07:93:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P12945
F-OVARC1001943//HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III.//1.7e-23:147:43//CAENORHABDITIS ELEGANS.//P34664
F-OVARC1001949//ZINC FINGER PROTEIN 177.//2.0e-23:56:66//HOMO SAPIENS (HUMAN).//Q13360
F-OVARC1001950//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.011:57:47//HOMO SAPIENS (HUMAN).//P39188
F-OVARC1001987//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.39:14:64//MUS MUSCULUS (MOUSE).//P02319
F-OVARC1001989//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.4e-13:55:72//HOMO SAPIENS (HUMAN).//P39188
F-OVARC1002044
F-OVARC1002050//UTROPHIN (DYSTROPHIN-RELATED PROTEIN 1) (DRP1) (DRP).//3.6e-12:221:25//HOMO SAPIENS (HUMAN).//P46939
F-OVARC1002066
F-OVARC1002082
F-OVARC1002107//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.99:149:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25386
F-OVARC1002112//HISTONE MACRO-H2A.1.//2.8e-64:133:98//RATTUS NORVEGICUS (RAT).//Q02874
F-OVARC1002127//60S RIBOSOMAL PROTEIN L22.//0.0023:95:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P50887
F-OVARC1002138//PROBABLE 26S PROTEASE SUBUNIT YTA6 (TAT-BINDING HOMOLOG 6).//6.4e-51:198:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40328
F-OVARC1002143
F-OVARC1002156//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.00010:64:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53915
F-OVARC1002158//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//8.2e-07:119:35//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479
F-OVARC1002165//EBNA-6 NUCLEAR PROTEIN (EBNA-3C) (EBNA-4B).//0.00023:90:45//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03204
F-OVARC1002182//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II.//1.3e-34:165:35//CAENORHABDITIS ELEGANS.//Q18964
F-PLACE1000004//HYPOTHETICAL 180.2 KD PROTEIN C31A2.05C IN CHROMOSOME I.//8.8e-05:148:25//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09725
F-PLACE1000005//PROTEIN Q300.//0.30:10:100//MUS MUSCULUS (MOUSE).//Q02722
F-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//2.3e-39:134:62//CAENORHABDITIS ELEGANS.//P34547

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F-PLACE1000014//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))./// 0.00036:63:39//HOMO SAPIENS (HUMAN).//P19474
F-PLACE1000031
F-PLACE1000040//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//4.4e-12:97:41//HOMO SAPIENS (HUMAN).// P39194
F-PLACE1000048//50S RIBOSOMAL PROTEIN L15 (FRAGMENT).//0.98:31:38//BACILLUS SP. (STRAIN C-125).//P38373
F-PLACE1000050//COLLAGEN ALPHA 1(III) CHAIN.//0.00062:190:33//BOS TAURUS (BOVINE).//P04258
F-PLACE1000061//60S RIBOSOMAL PROTEIN L37A.//6.4e-19:51:86//GALLUS GALLUS (CHICKEN).//P32046
F-PLACE1000066//SSU72 PROTEIN.//2.3e-39:165:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).// P53538
F-PLACE1000078//BAD PROTEIN (BCL-2 BINDING COMPONENT 6).//1.7e-06:21:95//HOMO SAPIENS (HUMAN).//Q92934
F-PLACE1000081//HOMEOBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3).//0.0053:146:33//MUS MUSCULUS (MOUSE).//P06798
F-PLACE1000094
F-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).// 1.8e-62:158:81//HOMO SAPIENS (HUMAN).//P20290
F-PLACE1000142//ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR (EC 4.2.1.17) (SHORT CHAIN ENOYL-COA HYDRATASE) (SCEH) (ENOYL-COA HYDRATASE 1).//9.8e-12:104:34//HOMO SAPIENS (HUMAN).//P30084
F-PLACE1000184//AC PROTEIN.//0.44:31:29//BACTERIOPHAGE T4.//P18924
F-PLACE1000185//HYPOTHETICAL GLYCINE-RICH 49.6 KD PROTEIN CY130.10C PRECURSOR.//0.11:48:33//MYCOBACTERIUM TUBERCULOSIS.//Q10637
F-PLACE1000213//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//3.4e-05:194:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
F-PLACE1000214
F-PLACE1000236//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//0.027:63:34//GALLUS GALLUS (CHICKEN).//P02457
F-PLACE1000246//TEGUMENT PROTEIN (GENE 11 PROTEIN).//0.78:100:26//EQUINE HERPESVIRUS TYPE 4 (STRAIN 1942) (EHV-4) (EQUINE HERPESVIRUS TYPE 1 SUBTYPE 2).//Q00039
F-PLACE1000292
F-PLACE1000308//EARLY NODULIN 75 (N-75) (NGM-75) (FRAGMENT).//0.049:28:42//MEDICAGO SATIVA (ALFALFA).//P11728
F-PLACE1000332
F-PLACE1000347//HYPOTHETICAL PROTEIN TP0420.//0.15:24:54//TREPONEMA PALLIDUM.//O83435
F-PLACE1000374//LYSOZYME C (EC 3.2.1.17) (1,4-BETA-N-ACETYLMURAMIDASE C).//1.0:63:25//ORYCTOLAGUS CUNICULUS (RABBIT).//P16973
F-PLACE1000380//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1) (PROTEIN KINASE A INTERFERENCE PROTEIN).//0.018:169:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36027
F-PLACE1000383//MYOTUBULARIN.//1.2e-65:215:57//HOMO SAPIENS (HUMAN).//Q13496
F-PLACE1000401//ELASTIN PRECURSOR (TROPOELASTIN).//0.00023:145:30//MUS MUSCULUS (MOUSE).//P54320
F-PLACE1000406//54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)).//3.4e-27:90:63//HOMO SAPIENS (HUMAN).//Q15233
F-PLACE1000420//7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE).//4.7e-07:134:29//MUS MUSCULUS (MOUSE).//P53368
F-PLACE1000421//HYPOTHETICAL 8.8 KD PROTEIN C11D3.01C IN CHROMOSOME I.//0.48:72:27// SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10080
F-PLACE1000424
F-PLACE1000435
F-PLACE1000444//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.0e-31:129:63//HOMO SAPIENS (HUMAN).//P39195
F-PLACE1000453//PROTEIN Q300.//0.013:16:68//MUS MUSCULUS (MOUSE).//Q02722
F-PLACE1000481//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.14:63:36//HOMO SAPIENS (HUMAN).//P08547
F-PLACE1000492//BASP1 PROTEIN.//0.17:114:28//HOMO SAPIENS (HUMAN).//P80723

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F-PLACE1000540
F-PLACE1000547//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//1.8e-21:87:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41940
F-PLACE1000562//HYPOTHETICAL PROTEIN MJ0562.//1.0:35:34//METHANOCOCCUS JANNASCHII.//Q57982
F-PLACE1000564//ADRENAL SPECIFIC 30 KD PROTEIN (CLONE PG2).//0.13:66:37//HOMO SAPIENS (HUMAN).//P15803
F-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.0e-45:192:47//HOMO SAPIENS (HUMAN).//P51522
F-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-BINDING PROTEIN 1).//5.3e-63:122:88//HOMO SAPIENS (HUMAN).//P32455
F-PLACE1000596//RING CANAL PROTEIN (KELCH PROTEIN).//2.6e-12:120:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
F-PLACE1000599//EARLY E3B 12.7 KD PROTEIN PRECURSOR.//0.83:53:32//HUMAN ADENOVIRUS TYPE 12.//P36707
F-PLACE1000610
F-PLACE1000611//HYPOTHETICAL 33.6 KD PROTEIN IN MCK1-RPS19B INTERGENIC REGION.//9.4e-07:64:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48558
F-PLACE1000636//MALE STERILITY PROTEIN 2.//3.7e-09:83:43//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q08891
F-PLACE1000653//PUTATIVE PHOSPHOACETYLGLUCOSAMINE MUTASE (EC 5.4.2.3) (ACETYLGLUCOSAMINE PHOSPHOMUTASE) (N-ACETYLGLUCOSAMINE-PHOSPHATE MUTASE).//1.9e-30:203:41//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09687
F-PLACE1000656//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.0029:75:33//NICOTIANA TABACUM (COMMON TOBACCO).//P13983
F-PLACE1000706//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1).//1.1e-38:180:42//HOMO SAPIENS (HUMAN).//Q13263
F-PLACE1000712//VERY HYPOTHETICAL 8.9 KD PROTEIN CY441.05 PRECURSOR.//0.93:49:34//MYCOBACTERIUM TUBERCULOSIS.//P71934
F-PLACE1000716
F-PLACE1000748//HYPOTHETICAL 10.4 KD PROTEIN IN SPAT 3'REGION (ORF-11).//0.90:53:37//SHIGELLA FLEXNERI.//P55794
F-PLACE1000749//HYPOTHETICAL PROTEIN MG148.//0.0014:142:27//MYCOPLASMA GENITALIUM.//P47394
F-PLACE1000755//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//1.1e-15:98:48//CAENORHABDITIS ELEGANS.//P34529
F-PLACE1000769//VIGILIN.//0.51:60:33//GALLUS GALLUS (CHICKEN).//P81021
F-PLACE1000785//PROBABLE COLD SHOCK PROTEIN CY15C10.04.//1.0:22:45//MYCOBACTERIUM TUBERCULOSIS.//O06360
F-PLACE1000786//HYPOTHETICAL 30.2 KD PROTEIN ZK632.12 IN CHROMOSOME III.//2.6e-38:159:51//CAENORHABDITIS ELEGANS.//P34657
F-PLACE1000793//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.0097:128:30//HOMO SAPIENS (HUMAN).//P50552
F-PLACE1000798//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//9.4e-07:47:61//HOMO SAPIENS (HUMAN).//P39188
F-PLACE1000841
F-PLACE1000849//ELAV PROTEIN.//3.5e-05:140:35//DROSOPHILA VIRILIS (FRUIT FLY).//P23241
F-PLACE1000856//HYPOTHETICAL PROTEIN MJ0008.//0.95:100:23//METHANOCOCCUS JANNASCHII.//Q60319
F-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR148W.//2.3e-46:172:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32899
F-PLACE1000909//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//0.00022:105:35//HOMO SAPIENS (HUMAN).//P16157
F-PLACE1000931//KILLER TOXIN HM-1.//0.95:24:33//WILLIOPSIS MRAKII (YEAST) (HANSENULA MRAKII).//P10410
F-PLACE1000948//SL CYTOKINE PRECURSOR (FLT3 LIGAND).//0.97:52:40//HOMO SAPIENS (HUMAN).//P49771

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F-PLACE1000972//MYOSIN ID HEAVY CHAIN.//1.9e-06:79:43//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34109
F-PLACE1000977//HYPOTHETICAL 94.2 KD PROTEIN C38D4.5 IN CHROMOSOME III.//2.5e-23:105:41// CAENORHABDITIS ELEGANS.//P46941
F-PLACE1000979//ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4) (ZINC FINGER PROTEIN HF. 16).//0.91:83:30//HOMO SAPIENS (HUMAN).//P17097
F-PLACE1000987//HYPOTHETICAL 111.5 KD PROTEIN C22G7.02 IN CHROMOSOME I.//0.10:128:24// SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09796
F-PLACE1001000
F-PLACE1001007//ZYXIN.//2.2e-05:135:30//GALLUS GALLUS (CHICKEN).//Q04584
F-PLACE1001010//BETA-1 BUNGAROTOXIN B CHAIN, MAJOR COMPONENT PRECURSOR (BUNGAROTOXIN, B1 CHAIN).//1.0:30:40//BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT).//P00987
F-PLACE1001015
F-PLACE1001024
F-PLACE1001036
F-PLACE1001054//HOLOTRICIN 3 PRECURSOR.//0.0044:56:39//HOLOTRICHIA DIOMPHALIA.//Q25055
F-PLACE1001062//SACCHAROPINE DEHYDROGENASE [NADP+, L-GLUTAMATE FORMING] (EC 1.5.1.10).// 0.0013:38:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38999
F-PLACE1001076
F-PLACE1001088//EARLY NODULIN 75 (N-75) (NGM-75) (FRAGMENT).//0.95:32:50//MEDICAGO SATIVA (ALFALFA).//P11728
F-PLACE1001092//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION.//0.0026:81:35// SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47057
F-PLACE1001104//HYPOTHETICAL 131.5 KD PROTEIN C02F12.7 IN CHROMOSOME X.//0.00063:125:32// CAENORHABDITIS ELEGANS.//Q11102
F-PLACE1001118//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46).//2.6e-77:209:63//MUS MUSCULUS (MOUSE).//Q03309
F-PLACE1001136//ALPHA-N-ACETYLGALACTOSAMINIDASE PRECURSOR (EC 3.2.1.49) (ALPHA- GALACTOSIDASE B).//0.99:107:30//HOMO SAPIENS (HUMAN).//P17050
F-PLACE1001168
F-PLACE1001171//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT).//0.00012:37:59//HOMO SAPIENS (HUMAN).//P12895
F-PLACE1001185//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//3.6e-12:88: 36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867
F-PLACE1001238
F-PLACE1001241//METALLOTHIONEIN B (MTB) (FRAGMENT).//0.13:30:53//COLINUS VIRGINIANUS (BOBWHITE QUAIL) (COMMON BOBWHITE).//P27087
F-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.1e-24:125:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
F-PLACE1001272//HYPOTHETICAL PROTEIN IN KSGA 3'REGION (ORF L5) (FRAGMENT).//1.0:24:45//MYCOPLASMA CAPRICOLUM.//P43040
F-PLACE1001279//CYTOTOXIN 3 (CYTOTOXIN V-II-3).//0.98:31:41//NAJA MOSSAMBICA (MOZAMBIQUE COBRA).//P01470
F-PLACE1001280//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].// 0.0051:156:32//MUS MUSCULUS (MOUSE).//P28481
F-PLACE1001294//GAMETOGENESIS EXPRESSED PROTEIN GEG-154.//3.7e-56:109:93//MUS MUSCULUS (MOUSE).//P50636
F-PLACE1001304//ZINC FINGER PROTEIN 35 (ZFP-35).//3.2e-30:75:57//MUS MUSCULUS (MOUSE).//P15620
F-PLACE1001311//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//2.7e-31:66:66//HOMO SAPIENS (HUMAN).// P39189
F-PLACE1001323
F-PLACE1001351//REV PROTEIN (ANTI-REPRESSION TRANSACTIVATOR PROTEIN) (ART/TRS).//0.11:66: 27//SIMIAN IMMUNODEFICIENCY VIRUS (AGM155 ISOLATE) (SIV-AGM).//P27971
F-PLACE1001366//SHORT NEUROTOXIN 2 (TOXIN CM-14) (TOXIN V-N-I2).//0.070:18:33//NAJA HAJE ANNULIFERA (BANDED EGYPTIAN COBRA).//P01422
F-PLACE1001377//DISINTEGRIN TRIGRAMIN BETA (PLATELET AGGREGATION ACTIVATION INHIBITOR).// 4.9e-06:50:46//TRIMERESURUS GRAMINEUS (INDIAN GREEN TREE VIPER) (GREEN HABU SNAKE).// P17495

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F-PLACE1001383//M PROTEIN, SEROTYPE 49 PRECURSOR.//0.080:136:24//STREPTOCOCCUS PYOGENES.//P16947
F-PLACE1001384
F-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//1.9e-22:142:39//HOMO SAPIENS (HUMAN).//Q12929
F-PLACE1001395//HYPOTHETICAL 8.5 KD PROTEIN IN ASIA-MOTA INTERGENIC REGION.//0.98:67:34//BACTERIOPHAGE T4.//P22917
F-PLACE1001399//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.1e-32:47:74//HOMO SAPIENS (HUMAN).//P39194
F-PLACE1001412//GLYCOPHORIN C (PAS-2') (GLYCOPROTEIN BETA) (GLPC) (GLYCOCONNECTIN) (SIALOGLYCOPROTEIN D) (GLYCOPHORIN D) (GPD).//0.00021:125:36//HOMO SAPIENS (HUMAN).//P04921
F-PLACE1001414//CHYMOTRYPSIN/ELASTASE ISOINHIBITORS 2 TO 5.//0.99:37:35//ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P07852
F-PLACE1001440//PROLINE-RICH PEPTIDE P-B.//0.35:16:50//HOMO SAPIENS (HUMAN).//P02814
F-PLACE1001456//RELAXIN.//0.48:38:36//BALAENOPTERA ACUTOROSTRATA (MINKE WHALE) (LESSER RORQUAL).//P11184
F-PLACE1001468//HYPOTHETICAL PROTEIN MJ0602.//0.10:86:32//METHANOCOCCUS JANNASCHII.//Q58019
F-PLACE1001484//HYPOTHETICAL 7.5 KD PROTEIN IN DNAC-RPLI INTERGENIC REGION.//1.0:47:34//BACILLUS SUBTILIS.//P37480
F-PLACE1001502//COLLAGEN 1(X) CHAIN PRECURSOR.//0.00029:118:34//BOS TAURUS (BOVINE).//P23206
F-PLACE1001503//HYPOTHETICAL 77.3 KD PROTEIN T05G5.8 IN CHROMOSOME III.//2.2e-07:107:30//CAENORHABDITIS ELEGANS.//P34561
F-PLACE1001517//SMALL PROTEIN INHIBITOR OF INSECT ALPHA-AMYLASES 2 (SI ALPHA-2).//0.56:22:45//SORGHUM BICOLOR MILO (SORGHUM).//P21924
F-PLACE1001534//PUTATIVE GENE PROTEIN 54.//0.43:44:40//BACTERIOPHAGE SP01.//O48408
F-PLACE1001545//HYPOTHETICAL 7.9 KD PROTEIN IN CELF-KATE INTERGENIC REGION.//0.99:70:32//ESCHERICHIA COLI.//P37795
F-PLACE1001551//CHLOROPLAST 50S RIBOSOMAL PROTEIN L32.//1.0:66:28//MARCHANTIA POLYMORPHA (LIVERWORT).//P12196
F-PLACE1001570//SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN).//0.024:120:27//HOMO SAPIENS (HUMAN).//Q15431
F-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.1e-30:90:78//MUS MUSCULUS (MOUSE).//Q60809
F-PLACE1001603//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.054:77:33//RATTUS NORVEGICUS (RAT).//P10164
F-PLACE1001608
F-PLACE1001610//PROBABLE E4 PROTEIN.//0.90:58:29//HUMAN PAPILLOMAVIRUS TYPE 28.//P51896
F-PLACE1001611//METALLOTHIONEIN-IG (MT-1G).//0.35:30:40//HOMO SAPIENS (HUMAN).//P13640
F-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.6e-28:144:43//HOMO SAPIENS (HUMAN).//P51523
F-PLACE1001634//PHOTOSYSTEM II REACTION CENTRE N PROTEIN.//1.0:36:41//CYANIDIUM CALDARIUM (GALDIERIA SULPHURARIA).//O19926
F-PLACE1001640//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.24:47:38//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18804
F-PLACE1001672//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.0:27:66//HOMO SAPIENS (HUMAN).//P39188
F-PLACE1001691//HYPOTHETICAL 15.5 KD PROTEIN IN PIK1-POL2 INTERGENIC REGION.//0.40:81:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53842
F-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//8.3e-41:103:55//RATTUS NORVEGICUS (RAT).//P08635
F-PLACE1001705
F-PLACE1001716//HYPOTHETICAL 138.5 KD PROTEIN C17H9.01 IN CHROMOSOME I.//6.1e-07:157:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13798
F-PLACE1001720
F-PLACE1001729//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//6.5e-05:196:32//MUS MUSCULUS (MOUSE).//P05143
F-PLACE1001739//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//

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0.00050:213:23//RATTUS NORVEGICUS (RAT).//P12839
F-PLACE1001740//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.4e-17:90:56//HOMO SAPIENS (HUMAN).//P39188
F-PLACE1001745//HYPOTHETICAL PROTEIN KIAA0125.//0.96:38:36//HOMO SAPIENS (HUMAN).//Q14138
F-PLACE1001746//CONGLUTIN DELTA-2 SMALL CHAIN.//0.98:23:43//LUPINUS ANGUSTIFOLIUS (NARROW-LEAVED BLUE LUPINE).//P09930
F-PLACE1001748//HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17.//2.9e-28:167:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O42908
F-PLACE1001756//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//9.2e-43:126:77//HOMO SAPIENS (HUMAN).//P39189
F-PLACE1001761//50S RIBOSOMAL PROTEIN L35.//0.26:42:38//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//P56057
F-PLACE1001771//TRANSIENT-RECEPTOR-POTENTIAL LIKE PROTEIN.//4.8e-35:223:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48994
F-PLACE1001781//HYPOTHETICAL 71.1 KD PROTEIN IN DSK2-CAT8 INTERGENIC REGION.//9.5e-41:194:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03262
F-PLACE1001799
F-PLACE1001810
F-PLACE1001817//SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//2.8e-40:115:61//NEOCALLIMASTIX FRONTALIS (RUMEN FUNGUS).//P53587
F-PLACE1001821
F-PLACE1001844//IG KAPPA CHAIN V-I REGION (HAU).//0.59:89:35//HOMO SAPIENS (HUMAN).//P01600
F-PLACE1001845
F-PLACE1001869//MPA43 PROTEIN.//3.5e-14:153:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53583
F-PLACE1001897//LIGATOXIN A.//1.0:43:27//PHORADENDRON LIGA (ARGENTINE MISTLETOE).//P01540
F-PLACE1001912//LONG NEUROTOXIN 2 (TOXIN C).//0.57:44:45//ASTROTIA STOKESI (STOKES'S SEA SNAKE) (DISTEIRA STOKESI).//P01381
F-PLACE1001920//LATE GENES ACTIVATOR (EARLY PROTEIN GP4) (GPF).//0.89:75:29/BACTERIOPHAGE NF.//P09877
F-PLACE1001928
F-PLACE1001983//IMMEDIATE-EARLY PROTEIN IE180.//0.0049:51:45//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479
F-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//8.9e-08:125:36//MORAXELLA CATARRHALIS.//Q49091
F-PLACE1002004
F-PLACE1002046//LIGATIN (FRAGMENT).//1.6e-84:191:84//MUS MUSCULUS (MOUSE).//Q61211
F-PLACE1002052
F-PLACE1002066
F-PLACE1002072//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.//0.16:77:31//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P40602
F-PLACE1002073//HYPOTHETICAL 118.2 KD PROTEIN F43C1.1 IN CHROMOSOME III.//4.0e-11:174:28//CAENORHABDITIS ELEGANS.//Q09564
F-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).//2.8e-57:112:99//HOMO SAPIENS (HUMAN).//O76094
F-PLACE1002115//P8 MTCP-1 PROTEIN (MATURE T-CELL PROLIFERATION-1 TYPE A) (MTCP-1 TYPE A) (P8MTCP1).//1.0:49:30//MUS MUSCULUS (MOUSE).//Q61908
F-PLACE1002119//T-LYMPHOCYTE ACTIVATED PROTEIN (CYCLOHEXIMIDE-INDUCED) (CHX1) (IMMEDIATE EARLY RESPONSE 2 PROTEIN).//2.7e-11:118:36//MUS MUSCULUS (MOUSE).//P17950
F-PLACE1002140//HYPOTHETICAL 12.3 KD PROTEIN IN MOBL 3'REGION (ORF 4).//0.0086:39:46//THIOBACILLUS FERROOXIDANS.//P20088
F-PLACE1002150
F-PLACE1002157//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//2.4e-34:56:82//HOMO SAPIENS (HUMAN).//P39189
F-PLACE1002163//NEUROTOXIN 1.//1.0:17:52//CENTRUROIDES SCULPTURATUS (BARK SCORPION).//P01492
F-PLACE1002170
F-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX COMPONENT

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SWI3) (TRANSCRIPTION FACTOR
TYE2).//0.00023:179:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32591
F-PLACE1002205//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION.//0.77:21:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40490
F-PLACE1002213//HISTONE H4 (FRAGMENT).//0.62:31:32//BLEPHARISMA JAPONICUM.//P80738
F-PLACE1002227//HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION.//0.41:49:36//RHIZOBIUM LEGUMINOSARUM.//P14310
F-PLACE1002256//CYTOCHROME B (EC 1.10.2.2).//0.61:95:29//CAENORHABDITIS ELEGANS.//P24890
F-PLACE1002259//HYPOTHETICAL 9.2 KD PROTEIN IN SPS1-QCR7 INTERGENIC REGION.//0.99:22:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P56508
F-PLACE1002319//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//0.91:18:72//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867
F-PLACE1002342//HYPOTHETICAL PROTEIN C16.//1.0:53:32//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//P32219
F-PLACE1002395//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//6.4e-05:127:37//PLASMODIUM VIVAX.//P08677
F-PLACE1002399
F-PLACE1002433//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP-150) (DAP-150) (P150-GLUED).//0.00094:182:25//RATTUS NORVEGICUS (RAT).//P28023
F-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1.//4.5e-19:62:77//MUS MUSCULUS (MOUSE).//P41233
F-PLACE1002438//HYPOTHETICAL 141.5 KD ZINC FINGER PROTEIN IN TUB1-CPR3 INTERGENIC REGION.//0.014:63:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04545
F-PLACE1002450//OOCYTE ZINC FINGER PROTEIN XLCOF6 (FRAGMENT).//3.9e-28:159:38//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18749
F-PLACE1002465//LARIAT DEBRANCHING ENZYME (EC 3.1.-.-).//0.0014:148:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13765
F-PLACE1002474//FIBRILLIN 2 PRECURSOR.//2.1e-24:203:33//MUS MUSCULUS (MOUSE).//Q61555
F-PLACE1002477//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//0.15:65:41//HOMO SAPIENS (HUMAN).//P39193
F-PLACE1002493//SEMENOGELIN II PRECURSOR (SGII).//1.0:72:31//MACACA MULATTA (RHESUS MACAQUE).//Q95196
F-PLACE1002499//HYPOTHETICAL 39.3 KD PROTEIN C02B8.6 IN CHROMOSOME X.//2.9e-11:67:35//CAENORHABDITIS ELEGANS.//Q11096
F-PLACE1002500//COBALT-ZINC-CADMIUM RESISTANCE PROTEIN CZCD (CATION EFFLUX SYSTEM PROTEIN CZCD).//8.4e-11:143:32//ALCALIGENES EUTROPHUS.//P13512
F-PLACE1002514//HYPOTHETICAL 8.1 KD PROTEIN IN SPEA-METK INTERGENIC REGION (O71).//1.0:15:60//ESCHERICHIA COLI.//P46878
F-PLACE1002529
F-PLACE1002532//HOMEOBOX PROTEIN DLX-5.//1.1e-76:183:81//MUS MUSCULUS (MOUSE).//P70396
F-PLACE1002537//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.6e-18:51:86//HOMO SAPIENS (HUMAN).//P39195
F-PLACE1002571//ACTIN-LIKE PROTEIN 13E.//6.0e-56:140:47//DROSOPHILA MELANOGASTER (FRUIT FLY).//P45890
F-PLACE1002578
F-PLACE1002583
F-PLACE1002591//CORONIN-LIKE PROTEIN P57.//5.5e-26:78:69//BOS TAURUS (BOVINE).//Q92176
F-PLACE1002598
F-PLACE1002604
F-PLACE1002625//HYPOTHETICAL 180.2 KD PROTEIN IN FAA4-HOR7 INTERGENIC REGION.//6.4e-08:193:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04781
F-PLACE1002655//ADSEVERIN (GELSOLIN-LIKE PROTEIN).//7.1e-100:210:89//MUS MUSCULUS (MOUSE).//Q60604
F-PLACE1002665//MOBILIZATION PROTEIN MOBS.//0.35:60:30//THIOBACILLUS FERROOXIDANS.//P20086
F-PLACE1002685//ACTIN BINDING PROTEIN.//0.052:115:29//SACCHAROMYCES EXIGUUS (YEAST).//P38479
F-PLACE1002714//CIS-GOLGI MATRIX PROTEIN GM130.//1.8e-06:214:30//RATTUS NORVEGICUS (RAT).//Q62839

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F-PLACE1002722//THROMBIN RECEPTOR PRECURSOR.//2.0e-19:134:38//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P47749
F-PLACE1002768//FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) (FRAGMENT).//0.43:40:35//MUS MUSCULUS (MOUSE).//P35378
F-PLACE1002772
F-PLACE1002775//CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5 (CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5).//4.8e-07:96:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14007
F-PLACE1002782//COBALT-ZINC-CADMIUM RESISTANCE PROTEIN CZCD (CATION EFFLUX SYSTEM PROTEIN CZCD).//1.1e-07:114:35//ALCALIGENES EUTROPHUS.//P13512
F-PLACE1002794//CUTICLE COLLAGEN 12 PRECURSOR.//0.0068:98:39//CAENORHABDITIS ELEGANS.//P20630
F-PLACE1002811//CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT KINASE 4 INHIBITOR C) (P18-INK4C).//1.1e-09:137:34//MUS MUSCULUS (MOUSE).//Q60772
F-PLACE1002815//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.46:35:42//HORDEUM VULGARE (BARLEY).//P17991
F-PLACE1002816//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//1.0e-86:201:74//HOMO SAPIENS (HUMAN).//P56524
F-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.6e-30:54:96//HOMO SAPIENS (HUMAN).//P51522
F-PLACE1002839//METALLOTHIONEIN-I (MT-I).//1.0:43:37//MUS MUSCULUS (MOUSE).//P02802
F-PLACE1002851//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (VAI).//0.77:35:37//VICIA ANGUSTIFOLIA (COMMON VETCH).//P01065
F-PLACE1002853//HYPOTHETICAL 7.9 KD PROTEIN IN PE 5'REGION (ORF1).//1.0:18:55//LYMANTRIA DISPAR MULTICAPSID NUCLEAR POLYHEDROSIS VIRUS (LDMNPV).//P36866
F-PLACE1002881//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.1e-27:91:70//HOMO SAPIENS (HUMAN).//P39188
F-PLACE1002908//HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOME III.//2.0e-31:148:46//CAENORHABDITIS ELEGANS.//P34548
F-PLACE1002941//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.6e-11:40:85//HOMO SAPIENS (HUMAN).//P39195
F-PLACE1002962//ENDOTHELIN-1 PRECURSOR (ET-1) (FRAGMENT).//0.90:38:36//CANIS FAMILIARIS (DOG).//P13206
F-PLACE1002968//TOXIN IV-5 PRECURSOR (TITYUSTOXIN) (FRAGMENT).//0.97:26:38//TITYUS SERRULATUS (BRAZILIAN SCORPION).//P01496
F-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4).//3.3e-20:120:41//METHANOCOCCUS JANNASCHII.//Q58560
F-PLACE1002993//HYPOTHETICAL 17.8 KD PROTEIN IN SMPA-SMPB INTERGENIC REGION (F158).//0.00045:93:23//ESCHERICHIA COLI.//P52121
F-PLACE1002996//PUTATIVE REGULATORY PROTEIN TSC-22 (TGFB STIMULATED CLONE 22 HOMOLOG).//0.17:91:29//GALLUS GALLUS (CHICKEN).//Q91012
F-PLACE1003025//SUPPRESSOR PROTEIN SRP40.//0.0079:214:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
F-PLACE1003027//HYPOTHETICAL 128.6 KD PROTEIN ZK1098.10 IN CHROMOSOME III.//1.3e-49:167:63//CAENORHABDITIS ELEGANS.//P34609
F-PLACE1003044//SPORE COAT PROTEIN D.//0.97:24:45//BACILLUS SUBTILIS.//P07791
F-PLACE1003045
F-PLACE1003092
F-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//3.9e-51:188:57//HOMO SAPIENS (HUMAN).//Q13268
F-PLACE1003108
F-PLACE1003136
F-PLACE1003145//BUTYROPHILIN PRECURSOR (BT).//0.00024:170:24//BOS TAURUS (BOVINE).//P18892
F-PLACE1003153//HUNCHBACK PROTEIN (FRAGMENT).//1.0:32:37//LOCUSTA MIGRATORIA (MIGRATORY LOCUST).//Q01777
F-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//6.3e-05:54:38//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P42743
F-PLACE1003176//HYPOTHETICAL 62.3 KD PROTEIN IN PCS60-ABD1 INTERGENIC REGION.//0.24:74:36//

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SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38319
F-PLACE1003190//SOF1 PROTEIN.//1.0e-52:158:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33750
F-PLACE1003200
F-PLACE1003205//SPERM PROTAMINE P1.//0.074:20:45//CAENOLESTES FULIGINOSUS.//P42131
F-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//0.013:20:55//HOMO SAPIENS (HUMAN).//Q15391
F-PLACE1003249//HYPOTHETICAL PROTEIN KIAA0125.//0.98:48:37//HOMO SAPIENS (HUMAN).//Q14138
F-PLACE1003256//OMEGA-CONOTOXINS GVIA, GVIB AND GVIC PRECURSOR (SHAKER PEPTIDE).//0.84:53:30//CONUS GEOGRAPHUS (GEOGRAPHY CONE).//P01522
F-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN.//4.1e-18:70:47//CAENORHABDITIS ELEGANS.//P21541
F-PLACE1003296//SPECTRIN BETA CHAIN, ERYTHROCYTE.//0.063:160:24//HOMO SAPIENS (HUMAN).//P11277
F-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//9.4e-69:84:94//HOMO SAPIENS (HUMAN).//P51522
F-PLACE1003334//NUCLEOBINDIN PRECURSOR (NUCB1) (BONE 63 KD CALCIUM-BINDING PROTEIN).//0.029:125:24//RATTUS NORVEGICUS (RAT).//Q63083
F-PLACE1003342//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.97:44:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
F-PLACE1003343//GENE 11 PROTEIN.//1.0:37:37//SPIROPLASMA VIRUS SPV1-R8A2 B.//P15902
F-PLACE1003353//SH2/SH3 ADAPTOR CRK (ADAPTER MOLECULE CRK) (CRK2).//6.4e-05:69:40//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P87378
F-PLACE1003361//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//1.6e-23:66:75//HOMO SAPIENS (HUMAN).//P39192
F-PLACE1003366//SMALL PROLINE-RICH PROTEIN 2-1.//0.62:19:57//HOMO SAPIENS (HUMAN).//P35326
F-PLACE1003369//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//4.3e-06:102:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
F-PLACE1003373//PROTEIN Q300.//0.042:29:37//MUS MUSCULUS (MOUSE).//Q02722
F-PLACE1003375//OLFACTORY RECEPTOR 11 (M49) (FRAGMENT).//0.99:46:34//MUS MUSCULUS (MOUSE).//Q60890
F-PLACE1003383
F-PLACE1003394//RAS-RELATED PROTEIN RAB-14.//2.8e-80:166:89//RATTUS NORVEGICUS (RAT).//P35287
F-PLACE1003401
F-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//8.1e-17:138:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40556
F-PLACE1003454
F-PLACE1003478
F-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSOR.//3.4e-11:123:32//HOMO SAPIENS (HUMAN).//Q13201
F-PLACE1003516//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.0e-32:68:76//HOMO SAPIENS (HUMAN).//P08547
F-PLACE1003519//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//9.2e-17:77:50//HOMO SAPIENS (HUMAN).//P39188
F-PLACE1003521//HYPOTHETICAL BAMHI-ORF9 PROTEIN.//1.0:38:42//FOWLPOX VIRUS (ISOLATE HP-438 [MUNICH]).//P14366
F-PLACE1003528//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.96:32:40//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P03931
F-PLACE1003537//CEF PROTEIN.//0.92:47:29//BACTERIOPHAGE T4.//Q01436
F-PLACE1003553
F-PLACE1003566//HYPOTHETICAL BAMHI-ORF9 PROTEIN.//1.0:32:34//FOWLPOX VIRUS (ISOLATE HP-438 [MUNICH]).//P14366
F-PLACE1003575
F-PLACE1003583//PROBABLE E5 PROTEIN.//0.16:64:31//HUMAN PAPILLOMAVIRUS TYPE 35.//P27226
F-PLACE1003584
F-PLACE1003592//EXCISIONASE.//0.26:19:52//BACTERIOPHAGE PHI-80.//P05998
F-PLACE1003593//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:42:30//OVIS ARIES (SHEEP).//

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O78751
F-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.//6.3e-87:238:67// CAENORHABDITIS ELEGANS.//P46975
F-PLACE1003602//HYPOTHETICAL 11.0 KD PROTEIN IN FAA3-MAS3 INTERGENIC REGION.//8.4e-17:98:42// SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40554
F-PLACE1003605//HAP5 TRANSCRIPTIONAL ACTIVATOR.//2.0e-09:82:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q02516
F-PLACE1003611//PANCREATIC SECRETORY TRYPSIN INHIBITOR.//0.99:32:43//CANIS FAMILIARIS (DOG).//P04542
F-PLACE1003618//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.7e-65:229:58//HOMO SAPIENS (HUMAN).//P08547
F-PLACE1003625//30S RIBOSOMAL PROTEIN S20 (FRAGMENT).//1.0:56:26//PROTEUS MIRABILIS.//P42275
F-PLACE1003638//PROTEIN Q300.//0.079:41:39//MUS MUSCULUS (MOUSE).//Q02722
F-PLACE1003669//TRICHOHYALIN.//2.9e-07:180:30//OVIS ARIES (SHEEP).//P22793
F-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//3.3e-16:98:40//HOMO SAPIENS (HUMAN).//Q08170
F-PLACE1003709//HYPOTHETICAL 59.5 KD PROTEIN IN CCT3-CCT8 INTERGENIC REGION.//2.8e-07:128:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47074
F-PLACE1003711//ALPHA/BETA-GLIADIN PRECURSOR (PROLAMIN) (CLASS A-IV).//5.0e-05:88:30//TRITICUM AESTIVUM (WHEAT).//P04724
F-PLACE1003723//TYROSINE-PROTEIN KINASE SRM (EC 2.7.1.112) (PTK70).//6.0e-06:98:36//MUS MUSCULUS (MOUSE).//Q62270
F-PLACE1003738//OOCYTE ZINC FINGER PROTEIN XLCOF6 (FRAGMENT).//2.5e-45:147:46//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18749
F-PLACE1003760//CYTOCHROME B (EC 1.10.2.2).//0.91:49:34//TRYPANOSOMA BRUCEI BRUCEI.//P00164
F-PLACE1003762//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//0.98:28:32//MALUS DOMESTICA (APPLE) (MALUS SYLVESTRIS).//O24058
F-PLACE1003768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//8.5e-19:123:37//HOMO SAPIENS (HUMAN).//P08547
F-PLACE1003771
F-PLACE1003783//SRY-RELATED PROTEIN ADW2 (FRAGMENT).//1.0:29:37//ALLIGATOR MISSISSIPPIENSIS (AMERICAN ALLIGATOR).//P40634
F-PLACE1003784//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC REGION.//1.2e-13:199:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40164
F-PLACE1003795//EC PROTEIN I/II (ZINC-METALLOTHIONEIN CLASS II).//0.67:53:30//TRITICUM AESTIVUM (WHEAT).//P30569
F-PLACE1003833//METHIONYL-TRNA FORMYLTRANSFERASE (EC 2.1.2.9).//0.99:158:28//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P43523
F-PLACE1003850
F-PLACE1003858//HUNCHBACK PROTEIN (FRAGMENT).//0.37:28:42//LITHOBIUS FORFICATUS.//Q02030
F-PLACE1003864//OUTER MEMBRANE LIPOPROTEIN LOLB PRECURSOR.//0.0046:116:31//ACTINOBACILLUS ACTINOMYCETEMCOMITANS (HAEMOPHILUS ACTINOMYCETEMCOMITANS).//O52727
F-PLACE1003870
F-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE) (FRAGMENT).//1.6e-92:166:75//HOMO SAPIENS (HUMAN).//P51003
F-PLACE1003886//IMMEDIATE-EARLY PROTEIN IE180.//0.54:96:34//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675
F-PLACE1003888//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).//8.8e-54:260:46//BOS TAURUS (BOVINE).//P10895
F-PLACE1003892//PROBABLE E5 PROTEIN.//1.0:13:61//HUMAN PAPILLOMAVIRUS TYPE 18.//P06792
F-PLACE1003900//BETA-FRUCTOFURANOSIDASE, SOLUBLE ISOENZYME I (EC 3.2.1.26) (SUCROSE-6-PHOSPHATE HYDROLASE) (INVERTASE) (FRAGMENTS).//0.58:49:36//DAUCUS CAROTA (CARROT).//P80065
F-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE).//3.8e-52:92:85//HOMO SAPIENS (HUMAN).//P17812
F-PLACE1003915//PROBABLE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19) (ARGININE--TRNA LIGASE) (ARGRS).//2.6e-26:202:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q05506

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F-PLACE1003923//HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) (HISTIDINE--TRNA LIGASE) (HISRS).//0.94:65:29//STREPTOCOCCUS EQUISIMILIS.//P30053
F-PLACE1003932//HYPOTHETICAL 17.3 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION.//0.098:79:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53074
F-PLACE1003936
F-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN).//4.7e-68:164:78//RATTUS NORVEGICUS (RAT).//P80385
F-PLACE1004103//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//1.9e-14:60:73//HOMO SAPIENS (HUMAN).//P39192
F-PLACE1004104//EXOCYST COMPLEX COMPONENT SEC5.//0.020:202:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P89102
F-PLACE1004114//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.1e-15:69:60//HOMO SAPIENS (HUMAN).//P39188
F-PLACE1004118//REGULATORY PROTEIN E2.//0.73:58:36//CANINE ORAL PAPILLOMAVIRUS (COPV).//Q89420
F-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA CHAIN 4).//7.7e-62:108:100//MUS MUSCULUS (MOUSE).//P29387
F-PLACE1004149//PROBABLE NUCLEAR ANTIGEN.//0.0011:73:42//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33485
F-PLACE1004156//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//0.00061:39:48//OWENIA FUSIFORMIS.//P21260
F-PLACE1004161//PLASMINOGEN-BINDING PROTEIN PAM PRECURSOR (FRAGMENT).//0.033:108:27//STREPTOCOCCUS PYOGENES.//P49054
F-PLACE1004183//HYPOTHETICAL 64.3 KD PROTEIN IN CDC12-ERP5 INTERGENIC REGION.//4.0e-07:146:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38817
F-PLACE1004197//BUTYROPHILIN PRECURSOR (BT).//5.9e-11:208:27//MUS MUSCULUS (MOUSE).//Q62556
F-PLACE1004203//PROTEIN A39.//8.5e-18:139:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P21062
F-PLACE1004242//PHOTOSYSTEM II REACTION CENTRE J PROTEIN.//1.0:28:42//PISUM SATIVUM (GARDEN PEA).//P13555
F-PLACE1004256//MYOSIN HEAVY CHAIN D (MHC D).//0.73:134:25//CAENORHABDITIS ELEGANS.//P02567
F-PLACE1004257//HYPOTHETICAL PROTEIN HI0490.//0.13:75:29//HAEMOPHILUS INFLUENZAE.//P44006
F-PLACE1004258//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT).//0.027:128:35//HOMO SAPIENS (HUMAN).//P25067
F-PLACE1004270//LARGE TEGUMENT PROTEIN.//1.8e-10:100:44//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03186
F-PLACE1004274//HYPOTHETICAL PROTEIN E-95.//0.44:61:42//HUMAN ADENOVIRUS TYPE 2.//P03286
F-PLACE1004277//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.0013:55:38//BOS TAURUS (BOVINE).//P25508
F-PLACE1004284//7 KD PROTEIN (ORF 4).//1.0:63:23//CHRYSANTHEMUM VIRUS B (CVB).//P37990
F-PLACE1004289//SPERM PROTAMINE P3.//0.00057:22:77//MUS MUSCULUS (MOUSE).//Q62100
F-PLACE1004302//SERINE/THREONINE PROTEIN KINASE AFSK (EC 2.7.1.-).//0.0065:148:29//STREPTOMYCES COELICOLOR.//P54741
F-PLACE1004316//AUTOPHAGY PROTEIN APG5.//8.8e-06:117:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12380
F-PLACE1004336//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.//0.0027:83:36//HOMO SAPIENS (HUMAN).//P53420
F-PLACE1004358//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//2.9e-05:200:33//GALLUS GALLUS (CHICKEN).//P02457
F-PLACE1004376//AXONEME-ASSOCIATED PROTEIN MST101(2).//2.4e-05:179:29//DROSOPHILA HYDEI (FRUIT FLY).//Q08696
F-PLACE1004384//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.6e-28:46:76//HOMO SAPIENS (HUMAN).//P39194
F-PLACE1004388//HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION.//5.7e-34:202:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39722
F-PLACE1004405//NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ (N-ACETYLNEURAMINYLLACTOSE- BINDING FIBRILLAR HEMAGGLUTININ RECEPTOR-BINDING SUBUNIT) (NLBH) (FLAGELLAR SHEATH ADHESIN) (ADHESIN A) (FRAGMENT).//0.93:74:33//HELICOBACTER ACINONYX.//Q47947

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F-PLACE1004425//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.81:70:42//HOMO SAPIENS (HUMAN).// P39195

F-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-).//1.9e-31:203:39//RATTUS NORVEGICUS (RAT).//Q63448

F-PLACE1004437//ISOCITRATE DEHYDROGENASE [NAD], MITOCHONDRIAL SUBUNIT BETA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH) (FRAGMENT).//4.2e-93:140:100// MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//Q28479

F-PLACE1004451//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.00013:40:62//HOMO SAPIENS (HUMAN).// P39188

F-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0066:218:23//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25823

F-PLACE1004467//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//7.8e-10:33:87//HOMO SAPIENS (HUMAN).// P39193

F-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.0e-56:92:58//HOMO SAPIENS (HUMAN).//P51522

F-PLACE1004473//HYPOTHETICAL 54.3 KD PROTEIN C23D3.03C IN CHROMOSOME I.//0.019:136:27// SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09844

F-PLACE1004491//LYSIS PROTEIN.//0.95:53:30//BACTERIOPHAGE FR.//P19903

F-PLACE1004506//AUTOIMMUNOGENIC CANCER/TESTIS ANTIGEN NY-ESO-1 (LAGE-1).//0.58:66:34//HOMO SAPIENS (HUMAN).//P78358

F-PLACE1004510//TRANSCRIPTION INITIATION FACTOR TFIID 150 KD SUBUNIT (TAFII-150) (TAFII150).// 3.0e-07:63:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24325

F-PLACE1004516//HYPOTHETICAL PROTEIN 5' TO ASP-RICH AND HIS-RICH PROTEINS (FRAGMENT).// 0.95:62:29//PLASMODIUM FALCIPARUM (ISOLATE FCM17 / SENEGAL).//P14587

F-PLACE1004518//METALLOTHIONEIN 10-III (MT-10-III).//0.91:28:42//MYTILUS EDULIS (BLUE MUSSEL).// P80248

F-PLACE1004548//DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT.//0.94:75:32//ORYCTOLAGUS CUNICULUS (RABBIT).//P19518

F-PLACE1004550//CUTICLE COLLAGEN 2.//0.90:155:31//CAENORHABDITIS ELEGANS.//P17656

F-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//3.2e-70:121:100//BOS TAURUS (BOVINE).//Q10568

F-PLACE1004629//PROTEIN OS-9 PRECURSOR.//1.7e-10:132:36//HOMO SAPIENS (HUMAN).//Q13438

F-PLACE1004645//TRANSCRIPTION INITIATION FACTOR IIB HOMOLOG (TFIIB).//0.00036:100:30//PYROCOCCUS FURIOSUS.//Q51731

F-PLACE1004646//PROBABLE UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9).//0.91:58:29//KLEBSIELLA PNEUMONIAE.//Q48481

F-PLACE1004658//GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 4 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2D) (NR2D) (NMDAR2D).//0.031:134:32//MUS MUSCULUS (MOUSE).// Q03391

F-PLACE1004664//HYPOTHETICAL 180.2 KD PROTEIN IN FAA4-HOR7 INTERGENIC REGION.//0.025:125:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04781

F-PLACE1004672//HYPOTHETICAL 36.7 KD PROTEIN C2F7:14C IN CHROMOSOME I.//7.6e-52:158:56// SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09704

F-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//1.4e-88:144:93// MUS MUSCULUS (MOUSE).//P12815

F-PLACE1004681//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.0e-34:70:100//MUS MUSCULUS (MOUSE).// Q60809

F-PLACE1004686//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//3.4e-08:48:62//HOMO SAPIENS (HUMAN).// P39192

F-PLACE1004691//METALLOTHIONEIN (MT).//0.064:24:45//ARIANTA ARBUSTORUM.//P55946

F-PLACE1004693

F-PLACE1004716//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:27:37//PAN PANISCUS (PYGMY CHIMPANZEE) (BONOBO).//Q35587

F-PLACE1004722//HYPOTHETICAL 61.5 KD PROTEIN IN CLA4-MID1 INTERGENIC REGION.//0.95:53:33// SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48565

F-PLACE1004736//NEURONAL AXONAL MEMBRANE PROTEIN NAP-22.//0.014:163:30//RATTUS NORVEGICUS (RAT).//Q05175

F-PLACE1004740//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.9e-09:37:70//HOMO SAPIENS (HUMAN).//

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P39194
F-PLACE1004743//HYPOTHETICAL 12.6 KD PROTEIN IN ALGR3 3'REGION.//0.99:72:33//PSEUDOMONAS AERUGINOSA.//P21484
F-PLACE1004751//CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (EC 2.4.99.-) (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALIII) (ALPHA 2,3-ST) (GAL-NAC6S) (STZ) (SIAT4-C) (SAT-3) (ST-4).//2.2e-08:90:38//HOMO SAPIENS (HUMAN).//Q11206
F-PLACE1004773//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//3.2e-25:233:32//HOMO SAPIENS (HUMAN).//P16157
F-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//8.1e-26:210:30//RATTUS NORVEGICUS (RAT).//P30337
F-PLACE1004793//ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36].//0.00062:106:25//MOUSE MAMMARY TUMOR VIRUS (STRAIN BR6).//P10259
F-PLACE1004804
F-PLACE1004813//HYPOTHETICAL PROTEIN UL12.//1.0:22:40//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16777
F-PLACE1004814//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//2.8e-06:136:25//CAENORHABDITIS ELEGANS.//Q09217
F-PLACE1004815
F-PLACE1004824//HYPOTHETICAL 106.7 KD PROTEIN IN MUP1-SPR3 INTERGENIC REGION.//2.3e-09:70:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53236
F-PLACE1004827//HYPOTHETICAL 9.4 KD PROTEIN IN FLAL 3'REGION (ORF3).//0.54:25:56//BACILLUS LICHENIFORMIS.//P22754
F-PLACE1004836//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.0066:12:66//BOS TAURUS (BOVINE).//P20072
F-PLACE1004838
F-PLACE1004840
F-PLACE1004868//MALE STERILITY PROTEIN 2.//4.0e-16:172:30//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q08891
F-PLACE1004885
F-PLACE1004900//MAST CELL DEGRANULATING PEPTIDE PRECURSOR (MCDP) (MCD) (PEPTIDE 401).//1.0:23:47//APIS MELLIFERA (HONEYBEE).//P01499
F-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//7.3e-15:94:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O42643
F-PLACE1004913//HYPOTHETICAL 7.2 KD PROTEIN IN BCSA-DEGR INTERGENIC REGION.//1.0:42:33//BACILLUS SUBTILIS.//P54165
F-PLACE1004918//HYPOTHETICAL 12.4 KD PROTEIN IN RPS21B-MRS3 INTERGENIC REGION.//0.98:50:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47012
F-PLACE1004930//HYPOTHETICAL PROTEIN MJ0562.//0.82:44:36//METHANOCOCCUS JANNASCHII.//Q57982
F-PLACE1004934
F-PLACE1004937//HYPOTHETICAL 67.1 KD TRP-ASP REPEATS CONTAINING PROTEIN C57A10.05C IN CHROMOSOME I.//9.0e-10:87:33//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87053
F-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//4.0e-14:184:25//CAENORHABDITIS ELEGANS.//Q11073
F-PLACE1004972//BROMELAIN INHIBITOR 2 (BI-II) (BROMELAIN INHIBITOR VI) (BI-VI).//1.0:35:37//ANANAS COMOSUS (PINEAPPLE).//P27478
F-PLACE1004979//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//5.3e-30:55:72//HOMO SAPIENS (HUMAN).//P39192
F-PLACE1004982//M PROTEIN, SEROTYPE 12 PRECURSOR (FRAGMENT).//0.00049:124:27//STREPTOCOCCUS PYOGENES.//P19401
F-PLACE1004985//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:26:34//LUMBRICUS TERRESTRIS (COMMON EARTHWORM).//Q34942
F-PLACE1005026//TELOMERE-BINDING PROTEIN HOMOLOG.//0.0011:179:27//EUPLOTES CRASSUS.//Q06183
F-PLACE1005027
F-PLACE1005046//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.082:44:36//BOS TAURUS (BOVINE).//P20072
F-PLACE1005052//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.38:36:44//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645
F-PLACE1005055

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F-PLACE1005066//RING CANAL PROTEIN (KELCH PROTEIN).//2.9e-38:194:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
F-PLACE1005077
F-PLACE1005085//INSECT TOXIN 1 (BOT IT1).//0.85:36:33//BUTHUS OCCITANUS TUNETANUS (COMMON EUROPEAN SCORPION).//P55902
F-PLACE1005086//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//8.5e-38:93:76//HOMO SAPIENS (HUMAN).//P39194
F-PLACE1005101//HYPOTHETICAL PROTEIN ZAP128 (FRAGMENT).//1.6e-11:35:100//HOMO SAPIENS (HUMAN).//P49753
F-PLACE1005102//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).//3.0e-14:110:38//MUS MUSCULUS (MOUSE).//Q60821
F-PLACE1005108//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).//0.41:35:34//BOS TAURUS (BOVINE).//P37359
F-PLACE1005111//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L) (CHARGERIN II).//1.0:29:41//RATTUS NORVEGICUS (RAT).//P11608
F-PLACE1005128//RABPHILIN-3A (FRAGMENT).//5.9e-05:95:36//MUS MUSCULUS (MOUSE).//P47708
F-PLACE1005146//FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 15 (FIN15).//0.17:48:35//MUS MUSCULUS (MOUSE).//Q61075
F-PLACE1005162//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//1.0e-31:60:76//HOMO SAPIENS (HUMAN).//P39189
F-PLACE1005176
F-PLACE1005181//HYPOTHETICAL 7 KD PROTEIN.//1.0:31:45//MEASLES VIRUS (STRAIN HALLE) (SUBACUTE SCLEROSE PANENCEPHALITIS VIRUS).//P06831
F-PLACE1005187//GLUCAN SYNTHASE-1 (EC 2.4.1.34) (1,3-BETA-GLUCAN SYNTHASE) (UDP-GLUCOSE-1,3-BETA-D-GLUCAN GLUCOSYLTRANSFERASE).//0.0025:58:34//NEUROSPORA CRASSA.//P38678
F-PLACE1005206//HYPOTHETICAL 10.7 KD PROTEIN.//0.34:57:42//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20511
F-PLACE1005232//AMELOGENIN, Y ISOFORM PRECURSOR.//0.70:60:35//HOMO SAPIENS (HUMAN).//Q99218
F-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//0.0017:114:27//PHYCOMYCES BLAKESLEEANUS.//Q01577
F-PLACE1005261//HYPOTHETICAL 90.8 KD PROTEIN T05H10.7 IN CHROMOSOME II.//1.2e-38:206:41//CAENORHABDITIS ELEGANS.//Q10003
F-PLACE1005266
F-PLACE1005277//PROTEIN GURKEN PRECURSOR.//0.58:95:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//P42287
F-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.0e-12:211:29//GALLUS GALLUS (CHICKEN).//P53352
F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//1.8e-78:205:78//BOS TAURUS (BOVINE).//P08760
F-PLACE1005308//WOUND-INDUCED BASIC PROTEIN.//0.99:40:40//PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).//Q09020
F-PLACE1005313//HYPOTHETICAL 8.7 KD PROTEIN IN LEUX-FECE INTERGENIC REGION (O67).//0.15:36:41//ESCHERICHIA COLI.//P39355
F-PLACE1005327//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//1.0:19:52//HOMO SAPIENS (HUMAN).//P30808
F-PLACE1005331//BREAKPOINT CLUSTER REGION PROTEIN.//0.00021:98:35//HOMO SAPIENS (HUMAN).//P11274
F-PLACE1005335//IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-3.//0.37:98:33//MUS MUSCULUS (MOUSE).//P81067
F-PLACE1005373//PSEUDOURIDYLATE SYNTHASE 4 (EC 4.2.1.70) (PSEUDOURIDINE SYNTHASE 4) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//0.010:96:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48567
F-PLACE1005374
F-PLACE1005409
F-PLACE1005453//LICHENASE PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3-1,4 GLUCANASE).//1.0:50:32//NICOTIANA PLUMBAGINIFOLIA (LEADWORT-LEAVED TOBACCO).//P07979
F-PLACE1005467//KERATIN, FEATHER (F-KER).//0.0095:42:35//LARUS NOVAE-HOLLANDIAE (SILVER

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GULL).//P02451
F-PLACE1005471//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.23:49:32//PHYTOPHTHORA INFESTANS (POTATO LATE BLIGHT FUNGUS).//Q37598
F-PLACE1005477//HYPOTHETICAL PROTEIN ORF-1137.//9.6e-13:115:38//MUS MUSCULUS (MOUSE).//P11260
F-PLACE1005480//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.97:33:30//HORDEUM VULGARE (BARLEY).//P17991
F-PLACE1005481//HUNCHBACK PROTEIN (FRAGMENT).//0.30:52:38//APIS MELLIFERA (HONEYBEE).//P31504
F-PLACE1005494//TRANSIENT-RECEPTOR-POTENTIAL PROTEIN.//3.9e-05:87:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//P19334
F-PLACE1005502
F-PLACE1005526//IMMEDIATE-EARLY PROTEIN IE180.//4.6e-05:132:32//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479
F-PLACE1005528//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//3.4e-09:31:74//HOMO SAPIENS (HUMAN).//P39195
F-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//9.7e-50:148:58//CAENORHABDITIS ELEGANS.//Q09251
F-PLACE1005550//HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III.//3.0e-21:127:37//CAENORHABDITIS ELEGANS.//P34524
F-PLACE1005554//CYTOCHROME B (EC 1.10.2.2) (FRAGMENT).//0.84:38:31//DIPODOMYS CALIFORNICUS (KANGAROO RAT).//P16359
F-PLACE1005557//60S RIBOSOMAL PROTEIN L27.//4.8e-09:60:48//CRYPTOCOCCUS NEOFORMANS (FILOBASIDIELLA NEOFORMANS).//P46288
F-PLACE1005574//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.89:44:29//BOS TAURUS (BOVINE).//P03929
F-PLACE1005584//MALE SPECIFIC SPERM PROTEIN MST87F.//0.00030:33:48//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175
F-PLACE1005595//IMMEDIATE-EARLY PROTEIN IE180.//0.00048:162:30//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675
F-PLACE1005603//HIGH-MOBILITY-GROUP PROTEIN (NONHISTONE CHROMOSOMAL PROTEIN).//0.00034:83:30//TETRAHYMENA PYRIFORMIS.//P40625
F-PLACE1005611//DNAJ PROTEIN.//8.6e-20:108:48//CLOSTRIDIUM ACETOBUTYLICUM.//P30725
F-PLACE1005623//EXTRACELLULAR SIGNAL-REGULATED KINASE 5 (EC 2.7.1.-) (ERK5) (ERK4) (BMK1 KINASE).//0.80:116:31//HOMO SAPIENS (HUMAN).//Q13164
F-PLACE1005630//INTERLEUKIN-14 PRECURSOR (IL-14) (HIGH MOLECULAR WEIGHT B-CELL GROWTH FACTOR) (HMW-BCGF).//0.0024:74:39//HOMO SAPIENS (HUMAN).//P40222
F-PLACE1005639//EXTRACELLULAR MATRIX PROTEIN 1 (SECRETORY COMPONENT P85) (FRAGMENT).//0.72:18:61//RATTUS NORVEGICUS (RAT).//Q62894
F-PLACE1005646//RNA HELICASE-LIKE PROTEIN DB10.//4.8e-29:172:45//NICOTIANA SYLVESTRIS (WOOD TOBACCO).//P46942
F-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE).//3.7e-64:133:75//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//Q60561
F-PLACE1005666//CHLOROPLAST 50S RIBOSOMAL PROTEIN L28.//0.57:36.41//PORPHYRA PURPUREA.//P51224
F-PLACE1005698//HYPOTHETICAL PROTEIN IN SIGD 3'REGION (ORFC) (FRAGMENT).//0.50:61:29//BACILLUS SUBTILIS.//P40405
F-PLACE1005727//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT).//0.46:27:51//BRASSICA NAPUS (RAPE).//P40603
F-PLACE1005730//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).//0.95:21:52//ORYCTOLAGUS CUNICULUS (RABBIT).//P02456
F-PLACE1005739//INTERFERON-GAMMA INDUCIBLE PROTEIN MG11.//3.4e-46:111:53//MUS MUSCULUS (MOUSE).//Q60710
F-PLACE1005755//HYPOTHETICAL 70.2 KD PROTEIN IN GSH1-CHS6 INTERGENIC REGION.//2.6e-12:66:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42951
F-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//1.5e-26:69:57//RATTUS NORVEGICUS (RAT).//P08635
F-PLACE1005799//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.028:96:32//HOMO

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SAPIENS (HUMAN).//P26371
F-PLACE1005802//PROTEIN PROSPERO.//0.86:64:42//DROSOPHILA MELANOGASTER (FRUIT FLY).// P29617
F-PLACE1005803//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//1.0:95:25//MUS MUSCULUS (MOUSE).//P17564
F-PLACE1005804//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).// 2.8e-73:198:73//MUS MUSCULUS (MOUSE).//P39098
F-PLACE1005813//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION.//0.022:78:38// SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47057
F-PLACE1005828//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.8e-23:56:76//HOMO SAPIENS (HUMAN).// P39195
F-PLACE1005834//LATE CONTROL GENE B PROTEIN (GPB).//0.97:33:39//BACTERIOPHAGE 186.//P08711
F-PLACE1005845
F-PLACE1005850//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//5.5e-28:96:73//HOMO SAPIENS (HUMAN).// P39194
F-PLACE1005851
F-PLACE1005876//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//2.2e-99:155:95//BOS TAURUS (BOVINE).//Q10568
F-PLACE1005884
F-PLACE1005890//BEM46 PROTEIN (FRAGMENT).//1.8e-33:137:49//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P54069
F-PLACE1005898//NADH-UBIQUINONE OXIDOREDUCTASE MLRQ SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-MLRQ) (CI-MLRQ).//0.77:58:34//HOMO SAPIENS (HUMAN).//O00483
F-PLACE1005921//AIG1 PROTEIN.//1.4e-23:165:38//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).// P54120
F-PLACE1005923//HYPOTHETICAL 22.4 KD PROTEIN (ORF16).//0.90:118:28//PARAMECIUM TETRAURELIA.//P15617
F-PLACE1005925//HYPOTHETICAL GENE 30 PROTEIN.//0.94:57:29//HERPESVIRUS SAIMIRI (STRAIN 11).// Q01010
F-PLACE1005932//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).// 0.42:128:32//NICOTIANA TABACUM (COMMON TOBACCO).//P13983
F-PLACE1005934//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6)(RPB1) (FRAGMENT).//0.40:76:35//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414
F-PLACE1005936//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.50:15:66//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CLONE 12) (HIV-1).//P04326
F-PLACE1005951//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).// 0.0025:135:32//NICOTIANA TABACUM (COMMON TOBACCO).//P13983
F-PLACE1005953//HIGH POTENTIAL IRON-SULFUR PROTEIN (HIPIP).//0.64:57:33//RHODOFERAX FERMENTANS.//P80882
F-PLACE1005955//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION.//1.0e-32:110: 50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38821
F-PLACE1005966//TACHYPLESIN II PRECURSOR.//0.97:31:35//TACHYPLEUS TRIDENTATUS (JAPANESE HORSESHOE CRAB).//P14214
F-PLACE1005968//GATA FACTOR SREP.//0.17:52:40//PENICILLIUM CHRYSOGENUM.//Q92259
F-PLACE1005990//CELL PATTERN FORMATION-ASSOCIATED PROTEIN.//0.36:55:36//EMERICELLA NIDULANS (ASPERGILLUS NIDULANS).//P36011
F-PLACE1006002//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//1.5e-36:102:75//HOMO SAPIENS (HUMAN).//P39192
F-PLACE1006003//HYPOTHETICAL 6.8 KD PROTEIN IN COX3-NAD1 INTERGENIC REGION (ORF 61).//1.0: 22:40//MARCHANTIA POLYMORPHA (LIVERWORT).//P38473
F-PLACE1006011//POLY [ADP-RIBOSE] POLYMERASE (EC 2.4.2.30) (PARP) (ADPRT) (NAD(+) ADP- RIBOSYLTRANSFERASE) (POLY[ADP-RIBOSE] SYNTHETASE).//2.8e-21:163:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q11207
F-PLACE1006017//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//1.1e-10:43:67//HOMO SAPIENS (HUMAN).// P39192
F-PLACE1006037//VITELLOGENIN I PRECURSOR (VTG I) [CONTAINS: LIPOVITELLIN 1 (LV1); PHOSVITIN (PV); LIPOVITELLIN 2 (LV2)].//0.00019:123:37//FUNDULUS HETEROCLITUS (KILLIFISH) (MUMMICHOG).// Q90508

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F-PLACE1006040//CAMP-REGULATED PHOSPHOPROTEIN 19 (ARPP-19).//3.2e-40:110:76//HOMO SAPIENS (HUMAN).//P56211
F-PLACE1006076//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR A-II.//0.99:30:40//ARACHIS HYPOGAEA (PEANUT).//P01066
F-PLACE1006119//IMPORTIN BETA-3 SUBUNIT (KARYOPHERIN BETA-3 SUBUNIT) (RAN-BINDING PROTEIN 5).//8.8e-94:218:76//HOMO SAPIENS (HUMAN).//O00410
F-PLACE1006129//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.00092:228:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
F-PLACE1006139//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION.//5.9e-55:128:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43616
F-PLACE1006143//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.4e-25:107:63//HOMO SAPIENS (HUMAN).//P39194
F-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).//1.3e-21:168:32//SUS SCROFA (PIG).//P98110
F-PLACE1006159//COLD SHOCK INDUCED PROTEIN TIR1 PRECURSOR (SERINE-RICH PROTEIN 1).//0.46:98:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P10863
F-PLACE1006164//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0:70:28:42//ARTEMIA SALINA (BRINE SHRIMP).//P19049
F-PLACE1006167//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.9e-05:167:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
F-PLACE1006170//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//1.1e-67:157:88//MUS MUSCULUS (MOUSE).//P17427
F-PLACE1006187//G1/S-SPECIFIC CYCLIN E.//5.6e-75:224:62//HOMO SAPIENS (HUMAN).//P24864
F-PLACE1006195//T-RELATED PROTEIN (TRP) (BRACHYENTERON PROTEIN).//0.99:177:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//P55965
F-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//2.0e-33:183:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09747
F-PLACE1006205
F-PLACE1006223//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.00015:22:50//MUS MUSCULUS (MOUSE).//P15265
F-PLACE1006225//VIRION INFECTIVITY FACTOR (SOR PROTEIN).//1.0:63:34//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18805
F-PLACE1006236
F-PLACE1006239//60S ACIDIC RIBOSOMAL PROTEIN P2 (FRAGMENT).//0.48:23:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P51407
F-PLACE1006246//CMP-SIALIC ACID TRANSPORTER (CMP-SIA-TR).//0.012:84:30//MUS MUSCULUS (MOUSE).//Q61420
F-PLACE1006248//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140).//0.017:203:22//RATTUS NORVEGICUS (RAT).//P41777
F-PLACE1006262//L-FUCULOSE PHOSPHATE ALDOLASE (EC 4.1.2.17).//0.84:25:52//HAEMOPHILUS INFLUENZAE.//P44777
F-PLACE1006288
F-PLACE1006318//CYSTEINE-RICH ANTIFUNGAL PROTEIN 1 (AFP1) (M1).//1.0:29:48//SINAPIS ALBA (WHITE MUSTARD) (BRASSICA HIRTA).//P30231
F-PLACE1006325//CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITOR P57) (P57KIP2).//0.99:97:32//HOMO SAPIENS (HUMAN).//P49918
F-PLACE1006335//PROLINE-RICH PEPTIDE P-B.//0.56:19:52//HOMO SAPIENS (HUMAN).//P02814
F-PLACE1006357
F-PLACE1006360
F-PLACE1006368//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//0.0057:122:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32380
F-PLACE1006371//ARS BINDING PROTEIN 1.//0.00030:142:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P49777
F-PLACE1006382//NEUROTOXIN V.//0.85:28:39//ANDROCTONUS MAURETANICUS MAURETANICUS (SCORPION).//P01482

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F-PLACE1006385//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REGION.//3.1e-35:165:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160
F-PLACE1006412//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.3e-08:40:47//HOMO SAPIENS (HUMAN).//P08547
F-PLACE1006414//FORKHEAD-RELATED TRANSCRIPTION FACTOR 4 (FREAC-4).//3.8e-05:123:39//HOMO SAPIENS (HUMAN).//Q16676
F-PLACE1006438//ZINC FINGER PROTEIN 165.//2.8e-21:76:64//HOMO SAPIENS (HUMAN).//P49910
F-PLACE1006445//SUPPRESSOR OF HAIRY WING PROTEIN.//0.058:99:29//DROSOPHILA VIRILIS (FRUIT FLY).//Q08876
F-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.8e-64:177:50//ESCHERICHIA COLI.//P27550
F-PLACE1006470
F-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//2.0e-47:120:85//GALLUS GALLUS (CHICKEN).//Q90595
F-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.8e-85:173:95//CANIS FAMILIARIS (DOG).//Q00004
F-PLACE1006492//VERY HYPOTHETICAL 11.2 KD PROTEIN C56F8.13 IN CHROMOSOME I.//0.75:32:56//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10261
F-PLACE1006506
F-PLACE1006521
F-PLACE1006531//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.//1.3e-53:167:61//CAENORHABDITIS ELEGANS.//P34681
F-PLACE1006534
F-PLACE1006540
F-PLACE1006552//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//1.3e-07:242:23//HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS).//P39922
F-PLACE1006598//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!//0.17:43:51//HOMO SAPIENS (HUMAN).//P39190
F-PLACE1006615//ACROSIN PRECURSOR (EC 3.4.21.10).//3.6e-05:66:43//ORYCTOLAGUS CUNICULUS (RABBIT).//P48038
F-PLACE1006617//HYPOTHETICAL 14.6 KD PROTEIN (READING FRAME C) (REPUCATION).//1.0:74:29//STAPHYLOCOCCUS AUREUS.//P03861
F-PLACE1006626//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//2.9e-10:73:46//CAENORHABDITIS ELEGANS.//P34529
F-PLACE1006629//HYPOTHETICAL PROTEIN BB0410.//1.0:23:43//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//O51371
F-PLACE1006640
F-PLACE1006673
F-PLACE1006678//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).//1.0:36:41//ORYCTOLAGUS CUNICULUS (RABBIT).//P02456
F-PLACE1006704//BROAD-COMPLEX CORE-TNT1-Q1-Z1 PROTEIN (BRCORE-TNT1-Q1-Z1) [CONTAINS: BROAD-COMPLEX CORE-Q1-Z1
PROTEIN].//0.00062:157:26//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01295
F-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//1.3e-07:127:36//CORYNEBACTERIUM AMMONIAGENES (BREVIBACTERIUM AMMONIAGENES).//Q59263
F-PLACE1006754//CARCINOEMBRYONIC ANTIGEN CGM1 PRECURSOR (CD66D ANTIGEN).//1.9e-19:78:53//HOMO SAPIENS (HUMAN).//P40198
F-PLACE1006760//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.21:107:30//RATTUS NORVEGICUS (RAT).//P13941
F-PLACE1006779//CYTOTOXIN 5 (CTX V).//1.0:20:30//NAJA MOSSAMBICA (MOZAMBIQUE COBRA).//P25517
F-PLACE1006782//ZINC FINGER PROTEIN 1.//0.00052:178:28//CANDIDA ALBICANS (YEAST).//P28875
F-PLACE1006792
F-PLACE1006795//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN SHAW (SHAW2).//1:0:80:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P17972
F-PLACE1006800//HYPOTHETICAL 9.4 KD PROTEIN.//0.99:62:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20569
F-PLACE1006805

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F-PLACE1006815//HYPOTHETICAL PROTEIN UL61.//0.038:146:32//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818
F-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.3e-98:239:76//HOMO SAPIENS (HUMAN).//P08547
F-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//0.061:34:58//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P50102
F-PLACE1006860
F-PLACE1006867
F-PLACE1006878//HYPOTHETICAL 8.2 KD PROTEIN IN MOBL 3'REGION (ORF 3).//0.85:27:37//THIOBACILLUS FERROOXIDANS.//P20087
F-PLACE1006883//VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).//0.78:51:37//MUS MUSCULUS (MOUSE).//P48281
F-PLACE1006901//HYPOTHETICAL 8.1 KD PROTEIN.//0.99:55:23//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20567
F-PLACE1006904//MATING-TYPE LOCUS ALLELE B1 PROTEIN.//0.95:86:26//USTILAGO MAYDIS (SMUT FUNGUS).//P22015
F-PLACE1006917//HYPOTHETICAL 40.9 KD PROTEIN C08B11.5 IN CHROMOSOME II.//6.9e-15:101:45//CAENORHABDITIS ELEGANS.//Q09442
F-PLACE1006932//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//0.089:28:39//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//Q48251
F-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III.//0.93:35:48//CAENORHABDITIS ELEGANS.//Q10000
F-PLACE1006956//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.00079:122:36//HOMO SAPIENS (HUMAN).//O00268
F-PLACE1006958//OSMOTIC STRESS PROTEIN 94 (HEAT SHOCK 70-RELATED PROTEIN APG-1).//8.8e-70:140:98//MUS MUSCULUS (MOUSE).//P48722
F-PLACE1006961
F-PLACE1006962//APOLIPOPROTEIN C-I PRECURSOR (APO-C1).//1.0:25:40//PAPIO HAMADRYAS (HAMADRYAS BABOON).//P34929
F-PLACE1006966//HYPOTHETICAL 49.1 KD PROTEIN IN SSB2-SPX18 INTERGENIC REGION.//1.6e-47:221:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40160
F-PLACE1006989//HYPOTHETICAL 13.1 KD HIT-LIKE PROTEIN IN P37 5'REGION.//0.15:46:32//MYCOPLASMA HYORHINIS.//P32083
F-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12) (DER12).//3.4e-09:120:29//HOMO SAPIENS (HUMAN).//Q14542
F-PLACE1007021//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.00046:42:59//HOMO SAPIENS (HUMAN).//P39188
F-PLACE1007045//HYPOTHETICAL PROTEIN ORF-1137.//8.1e-14:115:35//MUS MUSCULUS (MOUSE).//P11260
F-PLACE1007053//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.038:48:39//HOMO SAPIENS (HUMAN).//P22531
F-PLACE1007068//PROTEIN-LYSINE 6-OXIDASE PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE).//0.0040:113:39//GALLUS GALLUS (CHICKEN).//Q05063
F-PLACE1007097//HYPOTHETICAL 6.8 KD PROTEIN IN HE65-PK2 INTERGENIC REGION.//0.97:47:29//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41663
F-PLACE1007105//HYPOTHETICAL 83.6 KD PROTEIN C15A10.10 IN CHROMOSOME I.//2.9e-33:219:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13730
F-PLACE1007111
F-PLACE1007112//HYPOTHETICAL 9.2 KD PROTEIN.//0.47:75:28//ESCHERICHIA COLI.//P03853
F-PLACE1007132//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.8e-11:56:57//HOMO SAPIENS (HUMAN).//P39188
F-PLACE1007140//GAR2 PROTEIN.//0.72:185:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891
F-PLACE1007178//HYPOTHETICAL 8.5 KD PROTEIN CY274.40C.//0.97:79:30//MYCOBACTERIUM TUBERCULOSIS.//Q10826
F-PLACE1007226//HYPOTHETICAL 42.6 KD PROTEIN IN GSHB-ANSB INTERGENIC REGION (O378).//1.9e-15:123:32//ESCHERICHIA COLI.//P52062

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F-PLACE1007238//MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL).//5.5e-10:98:44//ACANTHAMOEBA CASTELLANII (AMOEBA).//P19706
F-PLACE1007239//TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A).//3.9e-19:96:57//HOMO SAPIENS (HUMAN).//P23193
F-PLACE1007242//GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS FORM B (RALGEF).//1.0:132:30//RATTUS NORVEGICUS (RAT).//Q03386
F-PLACE1007243//HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.//0.041:114:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39981
F-PLACE1007257//DIAPHANOUS PROTEIN.//1.3e-42:205:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48608
F-PLACE1007274//CADMIUM-METALLOTHIONEIN (CD-MT).//0.054:60:30//HELIX POMATIA (ROMAN SNAIL) (EDIBLE SNAIL).//P33187
F-PLACE1007276//BETA-DEFENSIN 1 PRECURSOR (RHBD-1) (DEFENSIN, BETA 1).//1.0:42:28//SUS SCROFA (PIG).//O62697
F-PLACE1007282//OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8].//0.070:126:27//HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN ST. THOMAS 3).//P11200
F-PLACE1007286
F-PLACE1007301//HYPOTHETICAL PROTEIN KIAA0168.//0.042:61:39//HOMO SAPIENS (HUMAN).//P50749
F-PLACE1007317
F-PLACE1007342//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//1.7e-06:77:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13002
F-PLACE1007346//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (KRAB-A INTERACTING PROTEIN) (KRIP-1).//0.0026:147:27//MUS MUSCULUS (MOUSE).//Q62318
F-PLACE1007367//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//1.3e-37:110:76//HOMO SAPIENS (HUMAN).//P39189
F-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13.//4.7e-07:71:39//CAENORHABDITIS ELEGANS.//P27715
F-PLACE1007386//HYPOTHETICAL 7.6 KD PROTEIN IN FLO1-PHO11 INTERGENIC REGION.//0.74:48:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39561
F-PLACE1007402//TRANSCRIPTIONAL REGULATORY PROTEIN ENTR (ENTERICIDIN R).//0.99:63:36//CITROBACTER FREUNDII.//O69280
F-PLACE1007409//WHITE PROTEIN.//7.9e-38:179:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//P10090
F-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP).//0.031:159:23//HOMO SAPIENS (HUMAN).//P27487
F-PLACE1007450//ZINC FINGER PROTEIN 39 (ZINC FINGER PROTEIN KOX27) (FRAGMENT).//0.023:36:50//HOMO SAPIENS (HUMAN).//P17038
F-PLACE1007452//HYPOTHETICAL 22.1 KD PROTEIN IN CCP1-MET1 INTERGENIC REGION.//2.2e-18:85:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36149
F-PLACE1007454//PHOTOSYSTEM II REACTION CENTRE N PROTEIN.//0.66:13:53//CHLAMYDOMONAS REINHARDTII.//Q06480
F-PLACE1007460//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.93:45:33//SUS SCROFA (PIG).//Q35914
F-PLACE1007478//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//5.3e-08:50:56//MUS MUSCULUS (MOUSE).//P11369
F-PLACE1007484//HYPOTHETICAL 6.8 KD PROTEIN IN REPLICATION ORIGIN REGION.//0.87:43:37//ESCHERICHIA COLI.//P03849
F-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN).//1.2e-25:202:31//HOMO SAPIENS (HUMAN).//P98174
F-PLACE1007507//HYPOTHETICAL 16.0 KD PROTEIN IN TAF60-G4P1 INTERGENIC REGION.//0.12:128:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53139
F-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19).//2.1e-45:209:48//BOS TAURUS (BOVINE).//P08728
F-PLACE1007524//HYPOTHETICAL 9.2 KD PROTEIN.//0.74:80:30//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20550
F-PLACE1007525

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F-PLACE1007537//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).//0.045:92:30//MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT).//P80144
F-PLACE1007544//IMMEDIATE-EARLY PROTEIN IE180.//1.5e-07:59:50//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479
F-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//2.5e-16:188:34//CAENORHABDITIS ELEGANS.//P34537
F-PLACE1007557
F-PLACE1007583//PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR (FRAGMENT).//0.98:72:33//DAUCUS CAROTA (CARROT) .//P06600
F-PLACE1007598//ZINC FINGER PROTEIN 92 (ZINC FINGER PROTEIN HTF12) (FRAGMENT).//1.7e-11:88:43//HOMO SAPIENS (HUMAN).//Q03936
F-PLACE1007618//ANION EXCHANGE PROTEIN 2 (NON-ERYTHROID BAND 3-LIKE PROTEIN) (B3RP).//0.19:109:27//MUS MUSCULUS (MOUSE).//P13808
F-PLACE1007621//PHOSPHATE REGULON SENSOR PROTEIN PHOR (EC 2.7.3.-) (FRAGMENT).//0.98:34:41//PSEUDOMONAS AERUGINOSA.//P23621
F-PLACE1007632//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//0.70:110:34//BOS TAURUS (BOVINE).//P02465
F-PLACE1007645//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:20:45//STRUTHIO CAMELUS (OSTRICH).//O21401
F-PLACE1007649//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.1e-06:197:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
F-PLACE1007677//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//1.0:47:46//HOMO SAPIENS (HUMAN).//P39192
F-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//2.7e-06:116:28//AEDES ALBOPICTUS (FOREST DAY MOSQUITO).//Q26457
F-PLACE1007690//SPERM PROTAMINE P1.//0.12:26:50//TACHYGLOSSUS ACULEATUS ACULEATUS (AUSTRALIAN ECHIDNA).//P35311
F-PLACE1007697//SPERM PROTAMINE P1.//0.19:34:52//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM), AND MONODELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM).//P35305
F-PLACE1007705//BIOH PROTEIN.//0.015:97:29//ESCHERICHIA COLI.//P13001
F-PLACE1007706//HYPOTHETICAL 112.2 KD PROTEIN IN TIF35-NPL3 INTERGENIC REGION (ORF1).//5.3e-55:190:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32898
F-PLACE1007725
F-PLACE1007729//PROTEASE (EC 3.4.23.-).//1.8e-21:136:42//MOUSE MAMMARY TUMOR VIRUS (STRAIN BR6).//P10271
F-PLACE1007730//SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).//0.0031:77:40//HOMO SAPIENS (HUMAN).//P81489
F-PLACE1007737//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.78:39:56//HOMO SAPIENS (HUMAN).//P39195
F-PLACE1007743
F-PLACE1007746//RRP5 PROTEIN HOMOLOG (KIAA0185) (FRAGMENT).//0.0066:168:25//HOMO SAPIENS (HUMAN).//Q14690
F-PLACE1007791//KRUEPPEL PROTEIN (FRAGMENT).//0.62:17:41//LITHOBIUS FORFICATUS.//Q01872
F-PLACE1007807//HYPOTHETICAL 6.4 KD PROTEIN IN BLTR-SPOIIIC INTERGENIC REGION.//1.0:40:30//BACILLUS SUBTILIS.//P54446
F-PLACE1007810//ANTHOPLEURIN A (TOXIN AP-A).//0.79:28:46//ANTHOPLEURA XANTHOGRAMMICA (GIANT GREEN SEA ANEMONE).//P01530
F-PLACE1007829//SPORE COAT PROTEIN G.//1.0:65:38//BACILLUS SUBTILIS.//P39801
F-PLACE1007843
F-PLACE1007846//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-32:37:94//HOMO SAPIENS (HUMAN).//P08547
F-PLACE1007852//RHO-RELATED GTP-BINDING PROTEIN RHOH (GTP-BINDING PROTEIN TTF).//8.7e-05:138:30//HOMO SAPIENS (HUMAN).//Q15669
F-PLACE1007858//ANAPHASE SPINDLE ELONGATION PROTEIN.//0.0039:127:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P50275
F-PLACE1007866
F-PLACE1007877

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F-PLACE1007897//CD44 ANTIGEN PRECURSOR (PHAGOCYTIC GLYCOPROTEIN I) (PGP-1) (HUTCH-I) (EXTRACELLULAR MATRIX RECEPTOR-III) (ECMR-III) (GP90 LYMPHOCYTE HOMING/ADHESION RECEPTOR) (HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (HAM1 ANTIGEN).//0.44:128:28//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//Q60522

F-PLACE1007908//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//5.5e-28:61:65//HOMO SAPIENS (HUMAN).//P39192

F-PLACE1007946//HYPOTHETICAL MERCURIC RESISTANCE PROTEIN MERC.//0.84:48:37//PSEUDOMONAS AERUGINOSA.//P04139

F-PLACE1007954//HYPOTHETICAL 45.5 KD PROTEIN IN FIG1-GIP1 INTERGENIC REGION.//0.00070:96:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38226

F-PLACE1007955//HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME II.//0.00027:255:23//CAENORHABDITIS ELEGANS.//Q09625

F-PLACE1007958//HIGH-AFFINITY CAMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE (EC 3.1.4.17).//1.7e-09:127:30//MUS MUSCULUS (MOUSE).//P70453

F-PLACE1007969//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//2.4e-05:104:37//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479

F-PLACE1007990//SPERM PROTAMINE P1.//0.78:36:47//ORNITHORHYNCHUS ANATINUS (DUCKBILL PLATYPUS).//P35307

F-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSYN-110) (SYNAPTIC DENSITY PROTEIN PSD-93).//1.2e-16:128:39//RATTUS NORVEGICUS (RAT).//Q63622

F-PLACE1008002

F-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NUCLEOPORIN) (P105).//3.9e-106:208:93//RATTUS NORVEGICUS (RAT).//P52590

F-PLACE1008045//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//3.9e-09:49:53//BOS TAURUS (BOVINE).//P25508

F-PLACE1008080//RNA REPLICASE POLYPROTEIN (EC 2.7.7.48).//0.00025:100:27//EGGPLANT MOSAIC VIRUS.//P20126

F-PLACE1008095//PROTOPORPHYRINOGEN OXIDASE (EC 1.3.3.4) (PPO).//0.90:74:25//MYCOBACTERIUM TUBERCULOSIS.//O53230

F-PLACE1008111//HYPOTHETICAL PROTEIN MJECS12.//0.30:38:42//METHANOCOCCUS JANNASCHII.//Q60311

F-PLACE1008122//PEA2 PROTEIN (PPF2 PROTEIN).//0.0085:117:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40091

F-PLACE1008129//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS).//1.8e-06:154:36//GALLUS GALLUS (CHICKEN).//P02467

F-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//1.4e-13:227:36//CAENORHABDITIS ELEGANS.//Q09531

F-PLACE1008177//TRICHOHYALIN.//2.7e-10:230:26//OVIS ARIES (SHEEP).//P22793

F-PLACE1008181

F-PLACE1008198//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.00044:121:34//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

F-PLACE1008201//ZINC FINGER PROTEIN ZFMSA12A.//3.0e-05:82:37//MICROPTERUS SALMOIDES (LARGEMOUTH BASS).//P38621

F-PLACE1008209//METALLOTHIONEIN-I (MT-I).//0.95:39:35//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).//P02797

F-PLACE1008231//PROCYCLIC FORM SPECIFIC POLYPEPTIDE B1-ALPHA PRECURSOR (PROCYCLIN) (PARP).//0.028:23:52//TRYPANOSOMA BRUCEI BRUCEI.//P08469

F-PLACE1008244//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//2.2e-23:148:38//PODOSPORA ANSERINA.//Q00808

F-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.1e-97:222:81//BOS TAURUS (BOVINE).//P53620

F-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-).//5.8e-20:161:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P12689

F-PLACE1008280//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.1e-23:124:42//HOMO SAPIENS (HUMAN).//P08547

F-PLACE1008309//HYPOTHETICAL 98.3 KD PROTEIN C9G1.06C IN CHROMOSOME I.//0.47:99:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14302

F-PLACE1008329//PUTATIVE Z PROTEIN.//0.73:52:28//OVIS ARIES (SHEEP).//P08105

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F-PLACE1008330//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//9.0e-37:75:81//HOMO SAPIENS (HUMAN).// P39194
F-PLACE1008331//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.1e-08:70:50//HOMO SAPIENS (HUMAN).// P39188
F-PLACE1008356//FRUIT PROTEIN PKIWI501.//0.0037:148:29//ACTINIDIA CHINENSIS (KIWI) (YANGTAO).// P43393
F-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).//3.5e-18:205:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
F-PLACE1008369
F-PLACE1008392
F-PLACE1008398//GENE 33 POLYPEPTIDE.//1.5e-102:225:84//RATTUS NORVEGICUS (RAT).//P05432
F-PLACE1008401//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//2.9e-08:186:34//MUS MUSCULUS (MOUSE).//P05143
F-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED PROTEIN) (TAP).//9.4e-105:207:98//BOS TAURUS (BOVINE).//P41541
F-PLACE1008405
F-PLACE1008424//PROTEIN UL56.//1.0:65:33//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN HFEM).//P36297
F-PLACE1008426//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//4.4e-05:185:28// DROSOPHILA MELANOGASTER (FRUIT FLY).//Q99323
F-PLACE1008429//NEURONAL AXONAL MEMBRANE PROTEIN NAP-22.//0.00054:172:25//RATTUS NORVEGICUS (RAT).//Q05175
F-PLACE1008437//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.//1.9e-23:226:34// CAENORHABDITIS ELEGANS.//P34681
F-PLACE1008455//DNA-BINDING PROTEIN (AGNOPROTEIN).//0.97:23:52//BUDGERIGAR FLEDGLING DISEASE VIRUS (BFDV).//P13893
F-PLACE1008457//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.1e-12:89:47//HOMO SAPIENS (HUMAN).// P39188
F-PLACE1008465//ZINC FINGER PROTEIN 31 (ZINC FINGER PROTEIN KOX29) (FRAGMENT).//0.00017:23:43//HOMO SAPIENS (HUMAN).//P17040
F-PLACE1008488//HYPOTHETICAL PROTEIN UL61.//9.1e-05:204:30//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818
F-PLACE1008524//HOMEOBOX PROTEIN HLX1 (HOMEOBOX PROTEIN HB24).//0.95:74:36//HOMO SAPIENS (HUMAN).//Q14774
F-PLACE1008531//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//3.1e-05:86:45//HOMO SAPIENS (HUMAN).// P39192
F-PLACE1008532//HYPOTHETICAL 36.4 KD PROTEIN IN SMP1-MBA1 INTERGENIC REGION.//3.9e-21:62:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38298
F-PLACE1008533//HYPOTHETICAL 86.2 KD PROTEIN C4G8.04 IN CHROMOSOME I.//3.5e-06:118:29// SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09830
F-PLACE1008568//NEURONATIN.//0.046:34:52//HOMO SAPIENS (HUMAN).//Q16517
F-PLACE1008584//HUNCHBACK PROTEIN (FRAGMENT).//0.94:30:43//LITHOBIUS FORFICATUS.//Q02030
F-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//3.9e-123:224:96//RATTUS NORVEGICUS (RAT).//P37199
F-PLACE1008621//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//5.0e-05:31:67//HOMO SAPIENS (HUMAN).//P20931
F-PLACE1008625//DISAGREGIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).//0.87:17:52//ORNITHODOROS MOUBATA (SOFT TICK).//P36235
F-PLACE1008626//METALLOTHIONEIN-I (MT-I).//0.77:33:36//SCYLLA SERRATA (MUD CRAB).//P02805
F-PLACE1008627//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF) (GIFB).//0.14:44:31//HOMO SAPIENS (HUMAN).//P25713
F-PLACE1008629
F-PLACE1008630//PROTAMINE Z3 (SCYLLIORHININE Z3).//0.78:33:36//SCYLIORHINUS CANICULA (SPOTTED DOGFISH) (SPOTTED CATSHARK).//P30258
F-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR (ITI HEAVY CHAIN H4) (INTER-ALPHA-TRYPSIN INHIBITOR FAMILY HEAVY CHAIN-RELATED PROTEIN) (PLASMA KALLIKREIN SENSITIVE GLYCOPROTEIN 120) (PK-120).//1.7e-30:220:41//HOMO SAPIENS (HUMAN).//Q14624
F-PLACE1008650//PP1/PP2A PHOSPHATASES PLEIOTROPIC REGULATOR PRL1.//2.5e-10:106:31//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q42384

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F-PLACE1008693//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (MSTI).//1.0:36:38//MEDICAGO SCUTELLATA (SNAIL MEDIC).//P80321
F-PLACE1008696//NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-23KD) (CI-23KD) (TYKY SUBUNIT).//4.8e-14:47:80//HOMO SAPIENS (HUMAN).//O00217
F-PLACE1008715//HYPOTHETICAL 13.4 KD PROTEIN IN ACT5-YCK1 INTERGENIC REGION.//0.66:105:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38834
F-PLACE1008748//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.10:178:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214
F-PLACE1008757//HYPOTHETICAL 10.1 KD PROTEIN IN RHSD-GCL INTERGENIC REGION (ORFD3).//0.60:44:34//ESCHERICHIA COLI.//P33669
F-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBUNIT) (IMPORTIN ALPHA S2).//3.0e-69:191:80//MUS MUSCULUS (MOUSE).//O35345
F-PLACE1008798//BACTERIOCIN LACTOBIN A.//1.0:34:41//LACTOBACILLUS AMYLOVORUS .//P80696
F-PLACE1008807//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.91:77:36//HOMO SAPIENS (HUMAN).//P08547
F-PLACE1008808//REC1 PROTEIN.//0.45:39:30//USTILAGO MAYDIS (SMUT FUNGUS).//P14746
F-PLACE1008813
F-PLACE1008851//VERY HYPOTHETICAL 11.8 KD PROTEIN IN KTR3-DUR1,2 INTERGENIC REGION.//1.0:62:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38309
F-PLACE1008854//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION.//1.0:82:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170
F-PLACE1008867//PATATIN T5 PRECURSOR (POTATO TUBER PROTEIN).//0.65:61:36//SOLANUM TUBEROSUM (POTATO).//P15478
F-PLACE1008887//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-56:180:54//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
F-PLACE1008902
F-PLACE1008920
F-PLACE1008925//HYPOTHETICAL 41.2 KD PROTEIN IN GAPA-RND INTERGENIC REGION.//0.90:77:33//ESCHERICHIA COLI.//P76242
F-PLACE1008934//HYPOTHETICAL PROTEIN IN ADHS 5'REGION (ORF3) (FRAGMENT).//0.14:77:45//GLUCONOBACTER SUBOXYDANS.//O05543
F-PLACE1008941//ZINC FINGER PROTEIN 141.//1.1e-17:45:95//HOMO SAPIENS (HUMAN).//Q15928
F-PLACE1008947//MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B).//4.1e-14:136:39//MUS MUSCULUS (MOUSE).//P27790
F-PLACE1009020//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.74:37:48//BOS TAURUS (BOVINE).//P20072
F-PLACE1009027//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.39:57:36//BALAENOPTERA MUSCULUS (BLUE WHALE).//P41301
F-PLACE1009039
F-PLACE1009045//HYPOTHETICAL 9.5 KD PROTEIN IN SPEA-METK INTERGENIC REGION (F83).//0.48:32:43//ESCHERICHIA COLI.//P46879
F-PLACE1009048
F-PLACE1009050
F-PLACE1009060//HYPOTHETICAL 98.3 KD PROTEIN R10E12.1 IN CHROMOSOME III.//4.9e-23:244:31//CAENORHABDITIS ELEGANS.//P34552
F-PLACE1009090//50S RIBOSOMAL PROTEIN L35.//1.0:27:51//MYCOPLASMA GENITALIUM.//P47439
F-PLACE1009091
F-PLACE1009094//NEL-LIKE PROTEIN (FRAGMENT).//3.6e-15:180:30//HOMO SAPIENS (HUMAN).//Q92832
F-PLACE1009099//ZINC FINGER PROTEIN 27 (ZFP-27) (MKR4 PROTEIN) (FRAGMENT).//1.4e-94:228:71//MUS MUSCULUS (MOUSE).//P10077
F-PLACE1009110//HIRUDIN HV1 (BUFRUDIN).//1.0:49:34//HIRUDINARIA MANILLENSIS (BUFFALO LEECH).//P81492
F-PLACE1009111//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.4e-05:30:83//HOMO SAPIENS (HUMAN).//P39195
F-PLACE1009113//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.032:40:52//BOS TAURUS (BOVINE).//P20072
F-PLACE1009130//HYPOTHETICAL PROTEIN KIAA0032.//3.3e-37:214:38//HOMO SAPIENS (HUMAN).//Q15034
F-PLACE1009150//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.6e-32:56:76//HOMO SAPIENS (HUMAN).//

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P39195
F-PLACE1009155//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.2e-17:101:57//HOMO SAPIENS (HUMAN).//P39194
F-PLACE1009158//HYPOTHETICAL PROTEIN HKRFX (J1I).//0.0058:73:42//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P09711
F-PLACE1009166//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//0.0086:96:30//HOMO SAPIENS (HUMAN).//P49902
F-PLACE1009172//HYPOTHETICAL 8.7 KD PROTEIN IN GAPA-RND INTERGENIC REGION.//1.0:19:52//ESCHERICHIA COLI.//P76246
F-PLACE1009174//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.1e-17:47:82//HOMO SAPIENS (HUMAN).//P39194
F-PLACE1009183
F-PLACE1009186//HYPOTHETICAL 11.4 KD PROTEIN C13G6.04 IN CHROMOSOME I.//0.019:62:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09783
F-PLACE1009190//PALMITOYL-COA HYDROLASE (EC 3.1.2.2) (LONG-CHAIN FATTY-ACYL-COA HYDROLASE) (FRAGMENT).//0.027:53:28//RATTUS NORVEGICUS (RAT).//P80250
F-PLACE1009200//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//5.4e-28:84:71//HOMO SAPIENS (HUMAN).//P39194
F-PLACE1009230//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//2.8e-12:50:74//HOMO SAPIENS (HUMAN).//P39189
F-PLACE1009246//UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PROTEIN (EC 1.10.2.2) (MITOCHONDRIAL HINGE PROTEIN) (CR7).//1.0:17:52//SOLANUM TUBEROSUM (POTATO).//P48504
F-PLACE1009298//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//6.6e-41:177:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P34110
F-PLACE1009308//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.00034:108:33//HOMO SAPIENS (HUMAN).//P26371
F-PLACE1009319//PRESYNAPTIC DENSITY PROTEIN 95 (PSD-95).//5.3e-16:84:50//HOMO SAPIENS (HUMAN).//P78352
F-PLACE1009328//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.9e-82:263:67//HOMO SAPIENS (HUMAN).//P08547
F-PLACE1009335//60S RIBOSOMAL PROTEIN L32.//0.95:71:36//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT).//P02433
F-PLACE1009338//TRANSCRIPTION FACTOR HES-5 (HAIRY AND ENHANCER OF SPLIT 5).//0.90:42:40//MUS MUSCULUS (MOUSE).//P70120
F-PLACE1009368//BASIC PROLINE-RICH PEPTIDE IB-1.//0.013:33:48//HOMO SAPIENS (HUMAN).//P04281
F-PLACE1009375//HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III.//0.0022:135:21//CAENORHABDITIS ELEGANS.//P34492
F-PLACE1009388//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//4.8e-22:73:65//HOMO SAPIENS (HUMAN).//P39195
F-PLACE1009398//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//8.1e-83:223:65//HOMO SAPIENS (HUMAN).//P51523
F-PLACE1009404//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR.//0.047:145:29//TRITICUM AESTIVUM (WHEAT).//P08489
F-PLACE1009410//TOXIN C13S1C1 PRECURSOR.//0.22:21:47//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P18329
F-PLACE1009434//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT K (EC 1.6.5.3) (FRAGMENT).//0.81:61:29//ANTHOCEROS FORMOSAE.//Q31791
F-PLACE1009443//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//9.1e-05:93:32//MUS MUSCULUS (MOUSE).//Q62203
F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//6.4e-15:41:97//HOMO SAPIENS (HUMAN).//P42356
F-PLACE1009459//HYPOTHETICAL 42.3 KD PROTEIN C12G12.11C IN CHROMOSOME I.//0.0011:119:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09874
F-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//4.2e-34:101:75//RATTUS NORVEGICUS (RAT).//P54319
F-PLACE1009476//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.086:21:52//HOMO SAPIENS (HUMAN).//P30808
F-PLACE1009477

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F-PLACE1009493//HYPOTHETICAL 127.3 KD PROTEIN B0416.1 IN CHROMOSOME X.//1.4e-18:138:39// CAENORHABDITIS ELEGANS.//Q11069
F-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FACTOR).//9.4e-80:155:85//HOMO SAPIENS (HUMAN).//Q99418
F-PLACE1009539//GTP-BINDING NUCLEAR PROTEIN RAN/TC4.//1.0:76:26//GIARDIA LAMBLIA (GIARDIA INTESTINALIS).//P38543
F-PLACE1009542//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.00016:31:77//HOMO SAPIENS (HUMAN).// P39188
F-PLACE1009571//ATP SYNTHASE B CHAIN (EC 3.6.1.34) (SUBUNIT I).//0.88:116:29//STREPTOCOCCUS PNEUMONIAE.//Q59952
F-PLACE1009581//50S RIBOSOMAL PROTEIN L32.//0.00023:37:51//RHODOBACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA).//P30788
F-PLACE1009595
F-PLACE1009596//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHROMOSOME III.//2.1e-36:116:49//CAENORHABDITIS ELEGANS.//Q17963
F-PLACE1009607//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.8e-43:73:69//HOMO SAPIENS (HUMAN).// P39188
F-PLACE1009613
F-PLACE1009621//TRANSCRIPTION FACTOR BTF3 HOMOLOG 2.//0.91:29:44//HOMO SAPIENS (HUMAN).// Q13891
F-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.3e-22:132:47//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25159
F-PLACE1009637//HYPOTHETICAL 18.1 KD PROTEIN IN CFXA 3'REGION.//0.30:28:57//BACTEROIDES VULGATUS.//P30905
F-PLACE1009639//LIPASE MODULATOR PRECURSOR (LIPASE HELPER PROTEIN).//0.23:79:31//PSEUDOMONAS AERUGINOSA.//Q04591
F-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (BRAIN PROTEIN H19) (MH19) (FRAGMENT).//3.9e-126:227:96//MUS MUSCULUS (MOUSE).//P28660
F-PLACE1009665//IG KAPPA CHAIN V-I REGION (HAU).//0.52:89:35//HOMO SAPIENS (HUMAN).//P01600
F-PLACE1009670//CYCLOMALTODEXTRIN GLUCANOTRANSFERASE PRECURSOR (EC 2.4.1.19) (CYCLODEXTRIN-GLYCOSYLTRANSFERASE) (CGTASE).//0.16:114:29//PAENIBACILLUS MACERANS (BACILLUS MACERANS).//P31835
F-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN CHROMOSOME I.//9.6e-19:156:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09876
F-PLACE1009721//MSF1 PROTEIN.//7.7e-23:176:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).// P35200
F-PLACE1009731//AIG1 PROTEIN.//1.1e-09:91:43//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).// P54120
F-PLACE1009763//HYPOTHETICAL 48.9 KD PROTEIN C24H6.12C IN CHROMOSOME I.//8.3e-42:171:51// SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09765
F-PLACE1009794//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.99:36:33//HORDEUM VULGARE (BARLEY).//P17991
F-PLACE1009798//HYPOTHETICAL PROTEIN C22F3.14C IN CHROMOSOME I (FRAGMENT).//2.6e-34:191:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09779
F-PLACE1009845//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//2.2e-19:190:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38968
F-PLACE1009861//CATHEPSIN B PRECURSOR (EC 3.4.22.1).//4.4e-20:171:33//BOS TAURUS (BOVINE).// P07688
F-PLACE1009879//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70).//0.99:30:33//ASTASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779
F-PLACE1009886
F-PLACE1009888//NONSTRUCTURAL POLYPROTEIN [CONTAINS: NONSTRUCTURAL PROTEIN NSP4] (FRAGMENT).//1.0:33:42//WESTERN EQUINE ENCEPHALITIS VIRUS.//P13896
F-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN C3F10.16C IN CHROMOSOME I.//3.1e-42:205:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10190
F-PLACE1009921
F-PLACE1009924//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.70:128:29//TRYPANOSOMA BRUCEI BRUCEI.//P24499

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F-PLACE1009925//ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34).//0.99:111:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P30902
F-PLACE1009935//HYPOTHETICAL PROTEIN MJ0258.//0.063:75:32//METHANOCOCCUS JANNASCHII.//Q57706
F-PLACE1009947//NEUROGRANIN (NG) (P17) (B-50 IMMUNOREACTIVE C-KINASE SUBSTRATE) (BICKS) (FRAGMENT).//0.33:51:45//BOS TAURUS (BOVINE).//P35722
F-PLACE1009971//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//0.022:84:27//MUS MUSCULUS (MOUSE).//P28575
F-PLACE1009992//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).//0.00011:35:51//HOMO SAPIENS (HUMAN).//P13497
F-PLACE1009995//TROPOMYOSIN, SMOOTH MUSCLE/FIBROBLAST CTM1.//0.052:185:22//CIONA INTESTINALIS.//Q07068
F-PLACE1009997//TRANSCRIPTION ELONGATION FACTOR S-II (RNA POLYMERASE II ELONGATION FACTOR DMS-II) (TFIIS).//0.68:98:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//P20232
F-PLACE1010023//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III.//6.6e-06:111:32//CAENORHABDITIS ELEGANS.//Q18262
F-PLACE1010031//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//0.0024:72:33//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479
F-PLACE1010053//HYPOTHETICAL PROTEIN HI0593.//0.83:24:45//HAEMOPHILUS INFLUENZAE.//P44022
F-PLACE1010069
F-PLACE1010074//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5.//0.00027:192:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q92331
F-PLACE1010076//HUNCHBACK PROTEIN (FRAGMENT).//0.80:39:30//SCIARA COPROPHILA (FUNGUS GNAT).//Q01790
F-PLACE1010083//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//2.7e-48:177:46//HOMO SAPIENS (HUMAN).//P98171
F-PLACE1010089//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 13) (DEUBIQUITINATING ENZYME 11) (KIAA0055).//7.9e-07:55:43//HOMO SAPIENS (HUMAN).//P40818
F-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.0e-107:232:90//RATTUS NORVEGICUS (RAT).//Q62671
F-PLACE1010102//DNA-DIRECTED RNA POLYMERASE SUBUNIT N (EC 2.7.7.6).//1.0:33:45//METHANOCOCCUS JANNASCHII.//Q57649
F-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-47:200:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
F-PLACE1010106//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//1.2e-14:94:41//MUS MUSCULUS (MOUSE).//P11369
F-PLACE1010134//HYPOTHETICAL 171.5 KD HELICASE IN NUT1-ARO2 INTERGENIC REGION.//4.0e-28:78:76//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53115
F-PLACE1010148//GAR2 PROTEIN.//2.6e-05:180:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891
F-PLACE1010152//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E).//2.1e-59:227:54//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24574
F-PLACE1010181//MALE SPECIFIC SPERM PROTEIN MST87F.//0.39:12:58//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175
F-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//1.4e-07:95:43//GALLUS GALLUS (CHICKEN).//P30352
F-PLACE1010202//TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36).//0.094:109:29//RATTUS NORVEGICUS (RAT).//P47973
F-PLACE1010231//LANTIBIOTIC NISIN A PRECURSOR.//0.99:42:35//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).//P13068
F-PLACE1010261//SEGREGATION DISTORTER PROTEIN.//6.0e-71:201:62//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25722
F-PLACE1010270
F-PLACE1010274//HYPOTHETICAL 16.2 KD PROTEIN C4F8.01 IN CHROMOSOME I.//4.4e-08:100:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14177
F-PLACE1010293//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.9e-26:94:64//HOMO SAPIENS (HUMAN).//P39188

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F-PLACE1010310//SYNAPSINS IA AND IB.//5.7e-09:89:37//RATTUS NORVEGICUS (RAT).//P09951
F-PLACE1010321//IMMEDIATE-EARLY PROTEIN IE180.//0.033:145:31//PSEUDORABIES VIRUS (STRAIN KA-PLAN) (PRV).//P33479
F-PLACE1010324//MAST CELL DEGRANULATING PEPTIDE (MCDP) (MCD).//0.60:25:48//MEGABOMBUS PENNSYLVANICUS (AMERICAN COMMON BUMBLEBEE).//P04567
F-PLACE1010329//TOXIN S5C10.//1.0:39:33//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S MAMBA).//P01419
F-PLACE1010341//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//0.0049:49:55//HOMO SAPIENS (HUMAN).//P39189
F-PLACE1010362//VARIANT-SURFACE-GLYCOPROTEIN PHOSPHOLIPASE C (EC 3.1.4.47) (VSG LIPASE) (GLYCOSYLPHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (GPI-PLC).//0.0034:89:30//TRYPANOSOMA CRUZI.//015886
F-PLACE1010364//NADH-UBIQUINONE OXIDOREDUCTASE B17 SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B17) (CI-B17).//1.0:40:35//SUS SCROFA (PIG).//Q29259
F-PLACE1010383
F-PLACE1010401//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140).//0.10:174:22//RATTUS NORVEGICUS (RAT).//P41777
F-PLACE1010481//HYPOTHETICAL 71.9 KD PROTEIN B0285.5 IN CHROMOSOME III.//1.5e-21:170:35//CAENORHABDITIS ELEGANS.//P46555
F-PLACE1010491//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION.//1.0:31:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40490
F-PLACE1010492//HYPOTHETICAL 42.3 KD PROTEIN C12G12.11C IN CHROMOSOME I.//0.77:97:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09874
F-PLACE1010522//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.74:45:37//HOMO SAPIENS (HUMAN).//P22531
F-PLACE1010529//DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS) [CONTAINS: GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE)].//0.70:58:39//VIGNA ACONITIFOLIA (MOTHBEAN).//P32296
F-PLACE1010547//HYPOTHETICAL 31.0 KD PROTEIN IN BUD9-RME1 INTERGENIC REGION.//0.17:68:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53227
F-PLACE1010562//CHLOROPLAST 50S RIBOSOMAL PROTEIN L33.//0.50:48:29//PORPHYRA PURPUREA.//P51255
F-PLACE1010579//HYPOTHETICAL PROTEIN HI1571.//0.29:37:43//HAEMOPHILUS INFLUENZAE.//P44260
F-PLACE1010580//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//3.3e-38:178:48//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09747
F-PLACE1010599//PEROXISOMAL MEMBRANE PROTEIN PER10 (PEROXIN-14).//4.6e-17:192:31//PICHIA ANGUSTA (YEAST) (HANSENULA POLYMORPHA).//P78723
F-PLACE1010616//HYPOTHETICAL 9.2 KD PROTEIN IN RNPA 3'REGION.//0.44:32:37//PSEUDOMONAS PUTIDA.//P25753
F-PLACE1010622//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//5.0e-06:102:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
F-PLACE1010624//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.00036:134:321/HOMO SAPIENS (HUMAN).//P10162
F-PLACE1010628
F-PLACE1010629//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.7e-12:37:81//HOMO SAPIENS (HUMAN).//P39194
F-PLACE1010630
F-PLACE1010631//WNT-5B PROTEIN (FRAGMENT).//0.49:62:30//EUMECES SKILTONIANUS (WESTERN SKINK).//P28118
F-PLACE1010661//MATERNAL EXUPERANTIA 2 PROTEIN.//1.0:95:30//DROSOPHILA PSEUDOOBSCURA (FRUIT FLY).//Q24617
F-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//3.2e-05:117:24//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q09332
F-PLACE1010702//ZINC FINGER PROTEIN 195.//1.4e-62:117:62//HOMO SAPIENS (HUMAN).//O14628
F-PLACE1010714
F-PLACE1010720//CHROMOSOME ASSEMBLY PROTEIN XCAP-C.//1.1e-64:176:76//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P50532

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F-PLACE1010739//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).//0.97:31:41// HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1).//P04612
F-PLACE1010743//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//3.8e-05:253:30//MUS MUSCULUS (MOUSE).//P05143
F-PLACE1010761//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//1.5e-14:175:25// CAENORHABDITIS ELEGANS.//Q09217
F-PLACE1010771//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP.//1.3e-120:216:89//MUS MUSCULUS (MOUSE).//Q02614
F-PLACE1010786//CENTROSOMIN (ARROW PROTEIN).//0.97:133:24//DROSOPHILA MELANOGASTER (FRUIT FLY).//P54623
F-PLACE1010800//HYPOTHETICAL 31.7 KD PROTEIN IN TRAX-FINO INTERGENIC REGION (ORFC).// 0.0060:111:31//ESCHERICHIA COLI.//Q99390
F-PLACE1010802//UREASE ACCESSORY PROTEIN UREI.//0.82:44:29//BACILLUS SP. (STRAIN TB-90).// Q07415
F-PLACE1010811//CYTOCHROME C-551 (C551).//0.99:42:38//ECTOTHIORHODOSPIRA HALOCHLORIS.// P38587
F-PLACE1010833//CALTRACTIN, ISOFORM 1 (CENTRIN).//2.8e-09:90:34//HOMO SAPIENS (HUMAN).// P41208
F-PLACE1010856//MOLT-INHIBITING HORMONE (MIH).//1.0:32:37//PROCAMBARUS CLARKII (RED SWAMP CRAYFISH).//P55848
F-PLACE1010857//IG ALPHA-1 CHAIN C REGION.//0.49:73:34//GORILLA GORILLA GORILLA (LOWLAND GORILLA).//P20758
F-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.2e-56:173:58//HOMO SAPIENS (HUMAN).//Q05481
F-PLACE1010877//HEAT SHOCK PROTEIN 82.//0.13:130:25//ZEA MAYS (MAIZE).//Q08277
F-PLACE1010891//HYPOTHETICAL 8.2 KD PROTEIN IN BLTR-SPOIIIC INTERGENIC REGION.//0.95:51:27// BACILLUS SUBTILIS.//P54436
F-PLACE1010896//SERINE/THREONINE-PROTEIN KINASE PTK1/STK1 (EC 2.7.1.).//0.98:71:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36002
F-PLACE1010900//HYPOTHETICAL PROTEIN HI0840.//1.0:42:30//HAEMOPHILUS INFLUENZAE.//P44897
F-PLACE1010916//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIB3.//0.060:59:35//OVIS ARIES (SHEEP).// P02444
F-PLACE1010917//E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN) (PEPLOMER PROTEIN).// 0.71:141:24//BOVINE CORONAVIRUS (STRAIN L9).//P25191
F-PLACE1010925//HYPOTHETICAL 8.1 KD PROTEIN.//1.0:17:58//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19285
F-PLACE1010926//HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269.//0.011:51:45//HOMO SAPIENS (HUMAN).//Q92558
F-PLACE1010942//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15).//3.1e-09:64:37//MUS MUSCULUS (MOUSE).//P42567
F-PLACE1010944//GAP JUNCTION ALPHA-3 PROTEIN (CONNEXIN 44) (CX44).//0.17:71:38//BOS TAURUS (BOVINE).//P41987
F-PLACE1010947
F-PLACE1010954//TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE.//0.011:144:26//HOMO SAPIENS (HUMAN).//P09493
F-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//1.1 e-60:136:52//DROSOPHILA MELANOGASTER (FRUIT FLY).//P45890
F-PLACE1010965
F-PLACE1011026//PERIOD CLOCK PROTEIN (FRAGMENT).//1.0:64:31//DROSOPHILA ANANASSAE (FRUIT FLY).//Q03293
F-PLACE1011032//RIBONUCLEASE HI (EC 3.1.26.4) (RNASE HI) (RIBONUCLEASE H) (RNASE H).//1.0:32:37// SALMONELLA TYPHIMURIUM.//P23329
F-PLACE1011041//HOMEOBOX PROTEIN VAB-7.//0.36:65:30//CAENORHABDITIS ELEGANS.//Q93899
F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1 (EC 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PLC-154).//1.3e-22:58:93//RATTUS NORVEGICUS (RAT).//P10687
F-PLACE1011054//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.6e-07:38:73//HOMO SAPIENS (HUMAN).// P39195

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F-PLACE1011056//HISTONE H1.//2.2e-10:109:41//PISUM SATIVUM (GARDEN PEA).//P08283
F-PLACE1011057
F-PLACE1011090//HYPOTHETICAL 33.8 KD PROTEIN IN TWT1-FLO5 INTERGENIC REGION.//1.8e-07:133:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38892
F-PLACE1011109//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//5.4e-25:63:88//RATTUS NORVEGICUS (RAT).//Q07803
F-PLACE1011114//PUTATIVE ATP-DEPENDENT RNA HELICASE C1F7.02C.//8.4e-31:157:45//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09916
F-PLACE1011133//SERUM AMYLOID P-COMPONENT PRECURSOR (SAP) (9.5S ALPHA-1-GLYCOPROTEIN).//0.92:58:31//HOMO SAPIENS (HUMAN).//P02743
F-PLACE1011143//PROBABLE E5 PROTEIN.//0.24:42:35//HUMAN PAPILLOMAVIRUS TYPE31.//P17385
F-PLACE1011160//EARLY NODULIN 55-2 PRECURSOR (N-55-2) (NODULIN-315).//0.88:98:27//GLYCINE MAX (SOYBEAN).//Q02917
F-PLACE1011165//HISTIDINE-RICH PROTEIN.//0.013:13:76//PLASMODIUM FALCIPARUM (ISOLATE FCM17/SENEGAL).//P14586
F-PLACE1011185//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.4e-13:98:50//HOMO SAPIENS (HUMAN).//P39188
F-PLACE1011203
F-PLACE1011214//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:48:27//EQUUS ASINUS (DONKEY).//P92479
F-PLACE1011219//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).//1.9e-15:162:31//STREPTOMYCES ANTIBIOTICUS.//Q03326
F-PLACE1011221//ANTITHROMBIN-III HOMOLOG.//0.84:74:33//FOWLPOX VIRUS (ISOLATE HP-438[MUNICH]).//P14369
F-PLACE1011229//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//3.5e-86:218:68//HOMO SAPIENS (HUMAN).//Q13107
F-PLACE1011263//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//3.0e-07:99:36//HOMO SAPIENS (HUMAN).//Q01485
F-PLACE1011273
F-PLACE1011291//PROTEIN KINASE C SUBSTRATE 80 KD PROTEIN (FRAGMENTS).//0.011:36:50//RATTUS NORVEGICUS (RAT).//P20468
F-PLACE1011296//HOMEOBOX PROTEIN DLX-6.//0.76:55:32//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q98877
F-PLACE1011310//ATP SYNTHASE PROTEIN 9, MITOCHONDRIAL (EC 3.6.1.34) (LIPID-BINDING PROTEIN).//0.46:43:44//PETUNIA SP. (PETUNIA).//Q07060
F-PLACE1011325//HYPOTHETICAL 222.8 KD PROTEIN C1F3.06C IN CHROMOSOME I.//0.00021:171:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10411
F-PLACE1011332//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT101 PRECURSOR.//7.3e-27:113:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q05211
F-PLACE1011340//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.6e-07:40:62//HOMO SAPIENS (HUMAN).//P39188
F-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2).//2.2e-54:227:44//MUS MUSCULUS (MOUSE).//Q61703
F-PLACE1011375//PROBABLE E5 PROTEIN.//0.93:28:57//HUMAN PAPILLOMAVIRUS TYPE 51.//P26553
F-PLACE1011399//HISTONE H2B-IV.//0.19:129:27//VOLVOX CARTERI.//P16868
F-PLACE1011419
F-PLACE1011433//ZINC FINGER PROTEIN GLI3 (FRAGMENT).//3.4e-05:133:24//GALLUS GALLUS (CHICKEN).//P55879
F-PLACE1011452//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.9e-25:76:63//HOMO SAPIENS (HUMAN).//P08547
F-PLACE1011465//ECTODERMAL DYSPLASIA PROTEIN (EDA PROTEIN).//0.97:36:41//HOMO SAPIENS (HUMAN).//Q92838
F-PLACE1011472//METALLOTHIONEIN-1 (CUMT-1).//0.084:55:30//HOMARUS AMERICANUS (AMERICAN LOBSTER).//P29499
F-PLACE1011477//CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1).//0.028:129:34//CLOSTRIDIUM THERMOCELLUM.//Q06852
F-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//

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2.9e-13:147:31//BRASSICA OLERACEA (CAULIFLOWER).//P52178
F-PLACE1011503//PUTATIVE FERREDOXIN-LIKE PROTEIN IN PURL-DPJ INTERGENIC REGION (086).//0.66:32:40//ESCHERICHIA COLI.//P52102
F-PLACE1011520
F-PLACE1011563//LORICRIN.//0.00023:112:39//HOMO SAPIENS (HUMAN).//P23490
F-PLACE1011567//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//9.2e-31:78:76//HOMO SAPIENS (HUMAN).//P39195
F-PLACE1011576//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.5e-32:45:86//HOMO SAPIENS (HUMAN).//Q05481
F-PLACE1011586//N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (OMEGA-CONOTOXIN-SENSITIVE N-TYPE, BRAIN CALCIUM CHANNEL ALPHA-1 SUBUNIT).//0.26:81:37//HOMO SAPIENS (HUMAN).//Q00975
F-PLACE1011635//IMMEDIATE-EARLY PROTEIN IE180.//0.00045:170:30//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER /BECKER) (PRV).//P11675
F-PLACE1011641
F-PLACE1011643//CUTICLE COLLAGEN 40.//1.0:128:32//CAENORHABDITIS ELEGANS.//P34804
F-PLACE1011646//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.1e-15:44:63//HOMO SAPIENS (HUMAN).//P39188
F-PLACE1011649//HYPOTHETICAL PROTEIN F-215.//0.48:106:34//HUMAN ADENOVIRUS TYPE 2.//P03291
F-PLACE1011650
F-PLACE1011664//CROOKED NECK PROTEIN.//1.2e-79:201:68//DROSOPHILA MELANOGASTER (FRUIT FLY).//P17886
F-PLACE1011675//FERREDOXIN.//1.0:44:29//METHANOCOCCUS THERMOLITHOTROPHICUS.//P21305
F-PLACE1011682//HYPOTHETICAL 7.0 KD PROTEIN IN RPS26A-COX4 INTERGENIC REGION.//1.0:40:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53098
F-PLACE1011719//NEUROTOXIN TX2-6.//0.90:31:35//PHONEUTRIA NIGRIVENTER (BRAZILIAN ARMED SPIDER).//P29425
F-PLACE1011725//NUCLEOBINDIN PRECURSOR (NUCB1) (BONE 63 KD CALCIUM-BINDING PROTEIN).//0.0065:125:25//RATTUS NORVEGICUS (RAT).//Q63083
F-PLACE1011729//SRY-RELATED PROTEIN LG27 (FRAGMENT).//0.97:48:39//EUBLEPHARIS MACULARIUS.//P40654
F-PLACE1011749
F-PLACE1011762//D-BINDING PROTEIN (DBP) (ALBUMIN D BOX-BINDING PROTEIN).//0.028:91:39//MUS MUSCULUS (MOUSE).//Q60925
F-PLACE1011778
F-PLACE1011783//EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1).//0.97:48:43//MUS MUSCULUS (MOUSE).//P20863
F-PLACE1011858//COLLAGEN 1(X) CHAIN PRECURSOR.//0.0027:154:33//BOS TAURUS (BOVINE).//P23206
F-PLACE1011874//BACTERIOCHLOROPHYLL A PROTEIN (BCHL A PROTEIN) (BCP).//1.0:60:26//PROSTHECOCHLORIS AESTUARII.//P11741
F-PLACE1011875//HYPOTHETICAL 6.6 KD PROTEIN IN GP54-ALT INTERGENIC REGION.//0.99:34:35//ACTERIOPHAGE T4.//P39495
F-PLACE1011891//SMOOTHELIN.//0.018:122:31//HOMO SAPIENS (HUMAN).//P53814
F-PLACE1011896//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//6.3e-09:203:35//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437
F-PLACE1011922//CRYPTDIN-RELATED PROTEIN 4C-2 PRECURSOR (CRS4C).//0.067:37:48//MUS MUSCULUS (MOUSE).//P50715
F-PLACE1011923//SERINE/THREONINE-PROTEIN KINASE SNK (EC 2.7.1.-) (SERUM INDUCIBLE KINASE).//1.5e-83:175:89//MUS MUSCULUS (MOUSE).//P53351
F-PLACE1011962//MATING-TYPE PHEROMONE BAP1(2) PRECURSOR.//0.50:46:41//SCHIZOPHYLLUM COMMUNE (BRACKET FUNGUS).//Q02593
F-PLACE1011964//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.6e-05:47:51//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
F-PLACE1011982//APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN).//0.98:83:31//PLASMODIUM FRAGILE.//P22622
F-PLACE1011995
F-PLACE1012031//HYPOTHETICAL PROTEIN KIAA0254.//0.032:62:33//HOMO SAPIENS (HUMAN).//Q92543
F-PLACE2000003//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//5.4e-18:63:73//HOMO SAPIENS (HUMAN).//P39193

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F-PLACE2000006//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.14:20:50//BOS TAURUS (BOVINE).//P20072
F-PLACE2000007//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.0045:176:30//MUS MUSCULUS (MOUSE).//P05143
F-PLACE2000011//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.6e-25:57:78//HOMO SAPIENS (HUMAN).//P39194
F-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//0.00013:237:27//CAENORHABDITIS ELEGANS.//Q09475
F-PLACE2000015//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.4e-33:60:80//HOMO SAPIENS (HUMAN).//P39193
F-PLACE2000017//FOLATE RECEPTOR BETA PRECURSOR (FR-BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP).//1.0:83:31//HOMO SAPIENS (HUMAN).//P14207
F-PLACE2000021//EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR CEK8).//0.99:103:26//GALLUS GALLUS (CHICKEN).//Q07496
F-PLACE2000030//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.69:29:44//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01642
F-PLACE2000033//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).//1.1e-05:74:41//STREPTOMYCES ANTIBIOTICUS.//Q03326
F-PLACE2000034//AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) (TRANSIENT AXONAL GLYCOPROTEIN 1).//6.7e-18:191:35//HOMO SAPIENS (HUMAN).//Q02246
F-PLACE2000039//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C).//4.7e-80:163:96//RATTUS NORVEGICUS (RAT).//P38650
F-PLACE2000047//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//6.4e-06:63:49//HOMO SAPIENS (HUMAN).//P39191
F-PLACE2000050//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//3.2e-22:74:64//HOMO SAPIENS (HUMAN).//P39192
F-PLACE2000061
F-PLACE2000062//GLUCOSE STARVATION-INDUCIBLE PROTEIN B (GENERAL STRESS PROTEIN B).//1.9e-06:108:37//BACILLUS SUBTILIS.//P26907
F-PLACE2000072//ZINC FINGER PROTEIN 165.//3.5e-34:175:49//HOMO SAPIENS (HUMAN).//P49910
F-PLACE2000097//RIBONUCLEASE PANCREATIC (EC 3.1.27.5) (RNASE 1) (RNASE A).//0.36:39:38//ONDATRA ZIBETHICUS (MUSKRAT).//P00681
F-PLACE2000100
F-PLACE2000103//TUBULIN ALPHA-4 CHAIN (FRAGMENTS).//0.18:32:37//ZEA MAYS (MAIZE).//P33626
F-PLACE2000111//CMRF35 ANTIGEN PRECURSOR.//0.056:107:27//HOMO SAPIENS (HUMAN).//Q08708
F-PLACE2000115//DIAMINOPIMELATE EPIMERASE (EC 5.1.1.7) (DAP EPIMERASE) (FRAGMENT).//1.0:21:52//CLOSTRIDIUM PERFRINGENS.//Q46185
F-PLACE2000124//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.4e-37:108:68//HOMO SAPIENS (HUMAN).//P39194
F-PLACE2000132//PROBABLE MEMBRANE ANTIGEN GP85.//0.99:133:29//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03224
F-PLACE2000136//VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 2 PRECURSOR (VIP-R-2) (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE III RECEPTOR) (PACAP TYPE III RECEPTOR) (PACAP-R-3).//0.83:65:32//MUS MUSCULUS (MOUSE).//P41588
F-PLACE2000140
F-PLACE2000164//TIPD PROTEIN.//5.7e-12:190:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//O15736
F-PLACE2000170//BACTERIOCIN CARNOBACTERIOCIN BM1 PRECURSOR (CARNOBACTERIOCIN B1).//1.0:30:26//CARNOBACTERIUM PISCICOLA.//P38579
F-PLACE2000172
F-PLACE2000176//HYPOTHETICAL PROTEIN AF0526.//0.76:44:43//ARCHAEOGLOBUS FULGIDUS.//O29724
F-PLACE2000187//EM-LIKE PROTEIN GEA6.//0.84:42:35//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q02973
F-PLACE2000216
F-PLACE2000223//NEUROTOXIN III (LQQ III).//0.99:38:34//LEIURUS QUINQUESTRIATUS QUINQUESTRIATUS (EGYPTIAN SCORPION).//P01487
F-PLACE2000235
F-PLACE2000246//RING CANAL PROTEIN (KELCH PROTEIN).//5.1e-37:121:42//DROSOPHILA MELA-

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NOGASTER (FRUIT FLY).//Q04652
F-PLACE2000264//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!//2.4e-05:77:42//HOMO SAPIENS (HUMAN).//P39191
F-PLACE2000274//DYNEIN BETA CHAIN, CILIARY.//5.3e-46:232:45//TRIPNEUSTES GRATILLA (HAWAIAN SEA URCHIN).//P23098
F-PLACE2000302//TRICHOHYALIN.//1.5e-06:215:29//ORYCTOLAGUS CUNICULUS (RABBIT).//P37709
F-PLACE2000305//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//5.3e-06:33:66//HOMO SAPIENS (HUMAN).//P39188
F-PLACE2000317//TOXIN C13S1C1 PRECURSOR.//0.44:45:33//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P18329
F-PLACE2000335//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//7.9e-08:35:71//HOMO SAPIENS (HUMAN).//P39195
F-PLACE2000341//SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER).//0.014:141:24//ORYCTOLAGUS CUNICULUS (RABBIT).//P11170
F-PLACE2000342//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//5.7e-09:96:38//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479
F-PLACE2000347//ZINC FINGER PROTEIN 177.//5.9e-05:49:53//HOMO SAPIENS (HUMAN).//Q13360
F-PLACE2000359//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//7.5e-10:69:52//HOMO SAPIENS (HUMAN).//P39194
F-PLACE2000366
F-PLACE2000371//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//1.5e-05:216:29//HOMO SAPIENS (HUMAN).//P54259
F-PLACE2000373//MAX BINDING PROTEIN MNT (ROX PROTEIN) (MYC ANTAGONIST MNT).//0.27:63:33//HOMO SAPIENS (HUMAN).//Q99583
F-PLACE2000379//HYPOTHETICAL GENE 1 PROTEIN.//0.72:120:31//EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).//P28978
F-PLACE2000394//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.95:40:42//HOMO SAPIENS (HUMAN).//P02811
F-PLACE2000398//RIBONUCLEASE PRECURSOR (EC 3.1.27.-).//0.88:88:31//AEROMONAS HYDROPHILA.//Q07465
F-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//7.6e-16:180:39//HOMO SAPIENS (HUMAN).//P14209
F-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE-TRNA LIGASE) (LEURS).//1.7e-94:243:64//CAENORHABDITIS ELEGANS.//Q09996
F-PLACE2000411//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PPT) (FRAGMENT).//1.2e-09:78:39//MUS MUSCULUS (MOUSE).//Q60676
F-PLACE2000419//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.6e-20:61:62//HOMO SAPIENS (HUMAN).//P39188
F-PLACE2000425//HYPOTHETICAL 11.9 KD PROTEIN IN MSB2-UGA1 INTERGENIC REGION.//0.98:75:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53211
F-PLACE2000427//INSULIN PRECURSOR.//0.98:55:34//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).//P30407
F-PLACE2000433//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//7.5e-07:65:50//HOMO SAPIENS (HUMAN).//P39188
F-PLACE2000435
F-PLACE2000438//HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III.//4.7e-66:178:47//CAENORHABDITIS ELEGANS.//P34678
F-PLACE2000450//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.1e-23:88:62//HOMO SAPIENS (HUMAN).//P39195
F-PLACE2000455//TOXIN II (TOXIN II.10.9.2) (FRAGMENT).//0.093:18:44//CENTRUROIDES LIMPIDUS LIMPIDUS (MEXICAN SCORPION).//P45630
F-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//3.1e-23:165:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P33450
F-PLACE2000465//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.6e-23:73:63//HOMO SAPIENS (HUMAN).//P39188
F-PLACE2000477//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//4.4e-37:90:78//HOMO SAPIENS (HUMAN).//P39194

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F-PLACE3000004//EYES ABSENT HOMOLOG 3.//1.1e-09:27:100//MUS MUSCULUS (MOUSE).//P97480
F-PLACE3000009//PUTATIVE CUTICLE COLLAGEN C09G5.6.//0.0061:148:34//CAENORHABDITIS ELEGANS.//Q09457
F-PLACE3000020//ADENYLATE CYCLASE, OLFACTIVE TYPE (EC 4.6.1.1) (TYPE III) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//8.8e-93:193:92//RATTUS NORVEGICUS (RAT).//P21932
F-PLACE3000029//50S RIBOSOMAL PROTEIN L31E.//0.15:50:38//METHANOCOCCUS JANNASCHII.//P54009
F-PLACE3000059//TCP1-CHAPERONIN COFACTOR A.//0.96:50:34//BOS TAURUS (BOVINE).//P48427
F-PLACE3000070//HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION.//0.29:22:59//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38898
F-PLACE3000103//LYSIS PROTEIN (E PROTEIN) (GPE).//0.99:53:32//BACTERIOPHAGE ALPHA-3.//P31280
F-PLACE3000119//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//5.4e-41:87:78//HOMO SAPIENS (HUMAN).//P39189
F-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC151/1.0e-07:269:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P22224
F-PLACE3000124//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.2e-29:97:73//HOMO SAPIENS (HUMAN).//P39188
F-PLACE3000136//PARS INTERCEREBRALIS MAJOR PEPTIDE D1 (PMP-D1).//0.77:26:42//LOCUSTA MIGRATORIA (MIGRATORY LOCUST).//P80059
F-PLACE3000142//HYPOTHETICAL 7.1 KD PROTEIN IN NAD2 3'REGION (ORF 63).//0.82:34:41//MARCHANTIA POLYMORPHA (LIVERWORT).//P38468
F-PLACE3000145//TENSIN.//3.5e-91:238:74//GALLUS GALLUS (CHICKEN).//Q04205
F-PLACE3000147//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//4.4e-30:61:65//HOMO SAPIENS (HUMAN).//P39194
F-PLACE3000148//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//1.4e-18:226:34//GIBBON APE LEUKEMIA VIRUS.//P21414
F-PLACE3000155//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.00014:107:33//ZEA MAYS (MAIZE).//P14918
F-PLACE3000156//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//2.7e-19:169:30//BABOON ENDOGENOUS VIRUS (STRAIN M7).//P10272
F-PLACE3000157//PROBABLE SERINE/THREONINE-PROTEIN KINASE CY50.16 (EC 2.7.1.-).//0.0061:92:30//MYCOBACTERIUM TUBERCULOSIS.//Q11053
F-PLACE3000158//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//5.7e-49:56:80//HOMO SAPIENS (HUMAN).//P39189
F-PLACE3000160//DNA TRANSFORMATION PROTEIN TFOX (COMPETENCE ACTIVATOR) (PROTEIN SXY).//0.39:94:34//HAEMOPHILUS INFLUENZAE.//P43779
F-PLACE3000169//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//5.6e-28:99:59//HOMO SAPIENS (HUMAN).//P39193
F-PLACE3000194//PROLINE-RICH PROTEIN LAS17.//0.91:80:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12446
F-PLACE3000197//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//0.24:119:32//GALLUS GALLUS (CHICKEN).//P16053
F-PLACE3000199//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.76:87:37//NICOTIANA TABACUM (COMMON TOBACCO).//P13983
F-PLACE3000207//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.5e-09:32:78//HOMO SAPIENS (HUMAN).//P39188
F-PLACE3000208
F-PLACE3000218//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//7.2e-34:96:70//HOMO SAPIENS (HUMAN).//P39194
F-PLACE3000220//OSTEOCALCIN (GAMMA-CARBOXYGLUTAMIC ACID-CONTAINING PROTEIN) (BONE GLA- PROTEIN) (BGP).//0.46:13:53//CANIS FAMILIARIS (DOG).//P81455
F-PLACE3000221//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.8e-24:178:45//HOMO SAPIENS (HUMAN).//P39188
F-PLACE3000226//30S RIBOSOMAL PROTEIN S18.//0.98:38:34//NEISSERIA GONORRHOEAE.//O07815
F-PLACE3000230//METALLOTHIONEIN (MT).//0.97:25:48//OREOCHROMIS MOSSAMBICUS (MOZAMBIQUE TILAPIA) (TILAPIA MOSSAMBICA).//P52726
F-PLACE3000242//MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN).//8.0e-21:121:39//HOMO SAPIENS (HUMAN).//P43361
F-PLACE3000244//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//2.3e-125:264:87//MUS MUS-

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CULUS (MOUSE).//P53995
F-PLACE3000254//RTOA PROTEIN (RATIO-A).//0.99:142:23//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P54681
F-PLACE3000271//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.2e-12:63:53//HOMO SAPIENS (HUMAN).// P39188
F-PLACE3000276//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN).//1.0:55:38// HOMO SAPIENS (HUMAN).//P27658
F-PLACE3000304//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.0028:31:54//HOMO SAPIENS (HUMAN).//P30808
F-PLACE3000310//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//0.98:82:34// RATTUS NORVEGICUS (RAT).//P54258
F-PLACE3000320
F-PLACE3000322//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1 PRECURSOR.//2.2e-22:61:52// ORYZA SATIVA (RICE).//P25074
F-PLACE3000331//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.32:15:53//HOMO SAPIENS (HUMAN).//P22532
F-PLACE3000339//CHORION PROTEIN S19.//0.34:89:37//DROSOPHILA VIRILIS (FRUIT FLY).//P24516
F-PLACE3000341//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRAGMENT).//1.0:47:38// COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).//P24968
F-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE SULU (EC 2.7.1.-).//3.9e-50:168:60// CAENORHABDITIS ELEGANS .//P46549
F-PLACE3000352//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//7.8e-29:76:71//HOMO SAPIENS (HUMAN).// P39194
F-PLACE3000353//POLYPEPTTOE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1).//3.0e-09:100:41//HOMO SAPIENS (HUMAN).//Q10472
F-PLACE3000362//HYPOTHETICAL PROTEIN TP0064.//1.0:75:26//TREPONEMA PALLIDUM.//O83103
F-PLACE3000363//METALLOTHIONEIN (MT).//0.067:42:33//ASTACUS FLUVIATILIS (BROAD-FINGERED CRAYFISH) (ASTACUS ASTACUS).//P55951
F-PLACE3000365//LYSIS PROTEIN (E PROTEIN) (GPE).//1.0:65:27//BACTERIOPHAGE PHI-K.//Q38040
F-PLACE3000373//RETROVIRUS-RELATED ENV POLYPROTEIN.//1.5e-18:90:47//HOMO SAPIENS (HUMAN).//P10267
F-PLACE3000388
F-PLACE3000399//!!!!ALU SUBFAMILY SP WARNING ENTRY !!!!//6.3e-45:60:75//HOMO SAPIENS (HUMAN).// P39193
F-PLACE3000400
F-PLACE3000401//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.6e-09:46:73//HOMO SAPIENS (HUMAN).// P39188
F-PLACE3000402//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.036:43:44//HOMO SAPIENS (HUMAN).// P39188
F-PLACE3000405//POSTERIOR PITUITARY PEPTIDE.//0.70:25:40//BOS TAURUS (BOVINE).//P01154
F-PLACE3000406//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//4.3e-09:49:67//HOMO SAPIENS (HUMAN).// P39195
F-PLACE3000413//MALE SPECIFIC SPERM PROTEIN MST87F.//0.12:42:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175
F-PLACE3000416//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//0.67:236:21//BOS TAURUS (BOVINE).// P35662
F-PLACE3000425//PROLINE-RICH PEPTIDE P-B.//0.45:19:42//HOMO SAPIENS (HUMAN).//P02814
F-PLACE3000455//AMELOGENIN, CLASS I PRECURSOR.//0.0073:81:43//BOS TAURUS (BOVINE).//P02817
F-PLACE3000475//8.6 KD TRANSGLUTAMINASE SUBSTRATE.//1.0:53:32//TACHYPLEUS TRIDENTATUS (JAPANESE HORSESHOE CRAB).//P81281
F-PLACE3000477//MUSCARINIC TOXIN 7 (MT-7).//0.13:55:32//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P80970
F-PLACE4000009//MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) (FRAGMENT).//7.0e-19:180:27//HOMO SAPIENS (HUMAN).//P35749
F-PLACE4000014//X-LINKED HELICASE II (X-LINKED NUCLEAR PROTEIN) (XNP).//3.2e-15:193:30//HOMO SAPIENS (HUMAN).//P46100
F-PLACE4000034//BRIDE OF SEVENLESS PROTEIN PRECURSOR.//0.0024:97:29//DROSOPHILA MELA-

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NOGASTER (FRUIT FLY).//P22815
F-PLACE4000049//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.8e-32:79:75//HOMO SAPIENS (HUMAN).//P39194
F-PLACE4000052//ATP-BINDING CASSETTE TRANSPORTER 1.//2.2e-99:178:97//MUS MUSCULUS (MOUSE).//P41233
F-PLACE4000063//IMMEDIATE-EARLY PROTEIN.//0.0017:159:25//HERPESVIRUS SAIMIRI (STRAIN 11).//Q01042
F-PLACE4000089
F-PLACE4000093
F-PLACE4000100//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.5e-14:68:60//HOMO SAPIENS (HUMAN).//P39188
F-PLACE4000106//1A PROTEIN [CONTAINS: HELICASE; METHYLTRANSFERASE].//1.0:46:41//BROAD BEAN MOTTLE VIRUS.//Q00020
F-PLACE4000128//HYPOTHETICAL PROTEIN E-115.//0.00020:101:30//HUMAN ADENOVIRUS TYPE 2.//P03290
F-PLACE4000129//CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) (14.9 KD PANCORNULIN).//0.15:57:31//HOMO SAPIENS (HUMAN).//P22528
F-PLACE4000131
F-PLACE4000147//COMPETENCE PHEROMONE PRECURSOR.//1.0:45:24//BACILLUS SUBTILIS.//P45453
F-PLACE4000156//ZINC FINGER PROTEIN 136.//2.1e-88:194:59//HOMO SAPIENS (HUMAN).//P52737
F-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//0.083:148:26//HOMO SAPIENS (HUMAN).//P52746
F-PLACE4000211//CALPHOTIN.//0.20:43:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q02910
F-PLACE4000222//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.1e-05:20:85//HOMO SAPIENS (HUMAN).//P39188
F-PLACE4000230//DIHYDROFOLATE REDUCTASE (EC 1.5.1.3) / THYMIDYLATE SYNTHASE (EC 2.1.1.45) (DHFR-TS).//1.0:96:28//TRYPANOSOMA BRUCEI BRUCEI.//Q27783
F-PLACE4000233
F-PLACE4000247//METALLOTHIONEIN (MT).//1.0e-05:34:41//PLEURONECTES PLATESSA (PLAICE).//P07216
F-PLACE4000250//VPU PROTEIN (ORF-X PROTEIN) (UPX PROTEIN).//0.99:33:42//CAPRINE ARTHRITIS ENCEPHALITIS VIRUS (CAEV).//P31834
F-PLACE4000252//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.42:24:45//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
F-PLACE4000259//PRE-MRNA SPLICING HELICASE BRR2 (EC 3.6.1.-).//3.5e-09:189:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32639
F-PLACE4000261//PEREGRIN (BR140 PROTEIN).//5.0e-11:103:37//HOMO SAPIENS (HUMAN).//P55201
F-PLACE4000269//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.037:181:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25386
F-PLACE4000270//COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21).//1.0:46:39//MUS MUSCULUS (MOUSE).//P70375
F-PLACE4000300//50S RIBOSOMAL PROTEIN L32.//0.81:28:46//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P80339
F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) (RAPAMYCIN TARGET PROTEIN).//1.6e-29:44:93//HOMO SAPIENS (HUMAN).//P42345
F-PLACE4000323
F-PLACE4000326//PARATHYMOSIN.//0.0018:54:48//HOMO SAPIENS (HUMAN).//P20962
F-PLACE4000344//EPIDERMAL GROWTH FACTOR (EGF) (FRAGMENT).//0.97:28:42//SUS SCROFA (PIG).//Q00968
F-PLACE4000367//NEUROTOXIN 1 (TOXIN SHP-I) (SHNA) (NEUROTOXIN SHI).//1.0:33:36//STOICHACTIS HELIANTHUS (CARRIBEAN SEA ANEMONE) (STICHODACTYLA HELIANTHUS).//P19651
F-PLACE4000369//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.071:42:42//SORGHUM VULGARE (SORGHUM).//P24152
F-PLACE4000379//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.4e-16:54:77//HOMO SAPIENS (HUMAN).//P39193
F-PLACE4000387//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR.//0.25:21:52//HORDEUM VULGARE (BARLEY), AND SECALE CEREALE (RYE).//P25877
F-PLACE4000392//FERROCHELATASE (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE)

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(FRAGMENT).//0.91:36:50//YERSINIA PSEUDOTUBERCULOSIS.//Q05338
F-PLACE4000401//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//4.4e-29:96:67//HOMO SAPIENS (HUMAN).//P39194
F-PLACE4000411//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.3e-18:41:73//HOMO SAPIENS (HUMAN).//P39188
F-PLACE4000431//PRE-MRNA SPLICING HELICASE BRR2 (EC 3.6.1.-).//5.4e-21:237:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32639
F-PLACE4000445//HYPOTHETICAL 99.7 KD PROTEIN IN SDL1 5'REGION PRECURSOR.//0.00081:210:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40442
F-PLACE4000450//TRANSCRIPTION FACTOR HBP-1A (HISTONE-SPECIFIC TRANSCRIPTION FACTOR HBP1).//0.020:87:33//TRITICUM AESTIVUM (WHEAT).//P23922
F-PLACE4000465//METALLOTHIONEIN-IL (MT-1L) (MT1X).//0.20:18:38//HOMO SAPIENS (HUMAN).//P80297
F-PLACE4000487//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.5e-19:73:52//HOMO SAPIENS (HUMAN).//P39188
F-PLACE4000489
F-PLACE4000494//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//0.17:130:30//MUS MUSCULUS (MOUSE).//Q03173
F-PLACE4000521//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] (FRAGMENT).//3.0e-05:50:36//MUS MUSCULUS (MOUSE).//P10400
F-PLACE4000522//NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR.//1.8e-45:231:47//RATTUS NORVEGICUS (RAT).//Q07008
F-PLACE4000548//CYTOCHROME C-551 (C551).//0.96:50:34//ECTOTHIORHODOSPIRA HALOPHILA.//P00122
F-PLACE4000558//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE FAF) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF) (DEUBIQUITINATING ENZYME FAF) (FAT FACETS PROTEIN).//1.6e-28:223:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//P55824
F-PLACE000581//P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM) (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).//9.7e-11:166:281/HOMO SAPIENS (HUMAN).//P16109
F-PLACE4000590//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//1.6e-17:134:35//GIBBON APE LEUKEMIA VIRUS.//P21414
F-PLACE4000593//GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R).//1.0:54:29//RATTUS NORVEGICUS (RAT).//P30969
F-PLACE4000612//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30].//2.6e-14:221:32//MOLONEY MURINE SARCOMA VIRUS (STRAIN TS110).//P32594
F-PLACE4000638//HYPOTHETICAL 9.3 KD PROTEIN IN NRDB-INAA INTERGENIC REGION.//0.65:37:40//ESCHERICHIA COLI.//P37910
F-PLACE4000650//ZINC FINGER PROTEIN 16 (ZINC FINGER PROTEIN KOX9) (FRAGMENT).//1.0:33:33//HOMO SAPIENS (HUMAN).//P17020
F-PLACE4000654
F-PLACE4000670//HYPOTHETICAL 44.1 KD PROTEIN IN RPB5-CDC28 INTERGENIC REGION.//1.6e-07:161:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33313
F-SKNMC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//7.4e-15:223:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O60100
F-SKNMC1000013//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (CBF-2) (T-14-6).//0.0013:128:35//GALLUS GALLUS (CHICKEN).//Q98937
F-SKNMC1000046//CUTICLE COLLAGEN 1.//0.0010:154:33//CAENORHABDITIS ELEGANS.//P08124
F-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (M-TYPE).//3.2e-41:87:98//HOMO SAPIENS (HUMAN).//P17655
F-SKNMC1000091//NTAK PROTEIN (NEURAL- AND THYMUS- DERIVED ACTIVATOR FOR ERBB KINASES).//0.0032:154:35//HOMO SAPIENS (HUMAN).//O14511
F-THYRO1000017//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE).//1.6e-23:124:37//CAENORHABDITIS ELEGANS.//Q20939
F-THYRO1000026//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//3.0e-13:54:66//HOMO SAPIENS (HUMAN).//P39192
F-THYRO1000034//HYPOTHETICAL 10.4 KD PROTEIN.//0.16:44:34//HEPATITIS B VIRUS (SUBTYPE AYW).//P03163

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F-THYRO1000035//CAMPATH-1 ANTIGEN PRECURSOR (CD52 ANTIGEN) (CDW52) (CAMBRIDGE PATHOLOGY 1 ANTIGEN).//0.83:59:37//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//P32763
F-THYRO1000040//60S RIBOSOMAL PROTEIN L37 (FRAGMENT).//0.25:23:39//BOS TAURUS (BOVINE).//P79244
F-THYRO1000070//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//2.3e-11:133:36//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//O10341
F-THYRO1000072//C-PROTEIN, SKELETAL MUSCLE SLOW-ISOFORM.//1.5e-14:205:29//HOMO SAPIENS (HUMAN).//Q00872
F-THYRO1000085
F-THYRO1000092//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.063:59:33//HOMO SAPIENS (HUMAN).//P49901
F-THYRO1000107
F-THYRO1000111//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.0e-58:110:67//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
F-THYRO1000121//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//2.6e-06:134:35//MUS MUSCULUS (MOUSE).//Q62203
F-THYRO1000124//TENECIN 3 PRECURSOR.//0.047:76:35//TENEBRIO MOLITOR (YELLOW MEALWORM).//Q27270
F-THYRO1000129//FBROSIN (FRAGMENT).//0.35:43:34/MUS MUSCULUS (MOUSE).//Q60791
F-THYRO1000132//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//8.7e-14:104:42//HOMO SAPIENS (HUMAN).//P39188
F-THYRO1000156
F-THYRO1000163//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//3.7e-20:71:71//HOMO SAPIENS (HUMAN).//P39189
F-THYRO1000173//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//6.7e-88:216:76//MUS MUSCULUS (MOUSE).//P35585
F-THYRO1000186//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//2.9e-24:72:77//HOMO SAPIENS (HUMAN).//P39192
F-THYRO1000187
F-THYRO1000190//PROTEIN TRANSPORT PROTEIN SEC61 BETA 2 SUBUNIT.//0.060:50:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P52871
F-THYRO1000197
F-THYRO1000199//HYPOTHETICAL 49.8 KD PROTEIN D2007.5 IN CHROMOSOME III.//2.0e-06:88:35//CAENORHABDITIS ELEGANS.//34379
F-THYRO1000206
F-THYRO1000221
F-THYRO1000241//HYPOTHETICAL 11.8 KD PROTEIN IN HE65-PK2 INTERGENIC REGION.//1.0:51:35//AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41661
F-THYRO1000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//7.4e-37:137:36//HOMO SAPIENS (HUMAN).//P51523
F-THYRO1000253//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.11:21:52//HOMO SAPIENS (HUMAN).//P30808
F-THYRO1000270//WDNM1 PROTEIN PRECURSOR.//0.40:52:32//MUS MUSCULUS (MOUSE).//Q62477
F-THYRO1000279//BETA CRYSTALLIN A4.//0.97:64:26//BOS TAURUS (BOVINE).//P11842
F-THYRO1000288//POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC ENDOPROTEASE 1) (PPSEP 1).//3.4e-48:142:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10071
F-THYRO1000320//ZINC FINGER PROTEIN 14 (ZFP-14) (KROX-9 PROTEIN) (FRAGMENT).//0.87:35:45//MUS MUSCULUS (MOUSE).//P10755
F-THYRO1000327//HYPOTHETICAL 64.7 KD PROTEIN F26E4.11 IN CHROMOSOME I.//0.00010:75:26//CAENORHABDITIS ELEGANS.//P90859
F-THYRO1000343//CHROMOGRANIN A PRECURSOR (CGA) [CONTAINS: PANCREASTATIN; BETA-GRANIN; WE-14].//0.88:107:26//MUS MUSCULUS (MOUSE).//P26339
F-THYRO1000358//SELENIUM-BINDING LIVER PROTEIN.//4.6e-25:49:81//MUS MUSCULUS (MOUSE).//P17563
F-THYRO1000368//LOCOMOTION-RELATED PROTEIN HIKARU GENKI PRECURSOR.//1.0:136:26//DRO-

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SOPHILA MELANOGASTER (FRUIT FLY).//Q09101
F-THYRO1000381//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10].//0.032:99:35//SIMIAN SARCOMA VIRUS.//P03330
F-THYRO1000387//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.90:46:30//HALICHOERUS GRYPUS (GRAY SEAL).//P38592
F-THYRO1000394//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.00019:48:37//HOMO SAPIENS (HUMAN).//P22531
F-THYRO1000395//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-33:186:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
F-THYRO1000401//50S RIBOSOMAL PROTEIN L7/L12 (FRAGMENT).//0.57:67:31//STAPHYLOCOCCUS AUREUS.//P48860
F-THYRO1000438//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:42:38//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).//P15997
F-THYRO1000452//BACTERIOCIN CARNOBACTERIOCIN A PRECURSOR (PISCICOLIN 61).//0.31:34:44// CARNOBACTERIUM PISCICOLA.//P38578
F-THYRO1000471//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2,1e-31:94:72//HOMO SAPIENS (HUMAN).//P39194
F-THYRO1000484//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//5.9e-08:30:86//HOMO SAPIENS (HUMAN).//P39195
F-THYRO1000488//EARLY NODULIN 55-2 PRECURSOR (N-55-2) (NODULIN-315).//0.93:98:27//GLYCINE MAX (SOYBEAN).//Q02917
F-THYRO1000501//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//2.4e-51:198:50//MUS MUSCULUS (MOUSE).//P15533
F-THYRO1000502//HUNCHBACK PROTEIN (FRAGMENT).//0.84:41:43//APIS MELLIFERA (HONEYBEE).//P31504
F-THYRO1000505//HYPOTHETICAL BHLF1 PROTEIN.//0.99:231:33//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
F-THYRO1000558//ANTITHROMBIN-III PRECURSOR (ATIII) (FRAGMENT).//0.47:58:37//GALLUS GALLUS (CHICKEN).//Q03352
F-THYRO1000569//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.00048:64:42//RATTUS NORVEGICUS (RAT).//P02454
F-THYRO1000570//HYPOTHETICAL 11.6 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION.//0.94:61:32// SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39725
F-THYRO1000585//SPLICING FACTOR, ARGININE/SERINE-RICH 6 (PRE-MRNA SPLICING FACTOR SRP55).//0.050:104:36//HOMO SAPIENS (HUMAN).//Q13247
F-THYRO1000596//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP34.5).//0.99:37:40// HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN MGH-10).//P37319
F-THYRO1000602//EAMZP30-47 PROTEIN (FRAGMENT).//0.88:61:34//EIMERIA ACERVULINA.//P21959
F-THYRO1000605//SUPPRESSOR PROTEIN SRP40.//0.0016:116:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
F-THYRO1000625//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.4e-33:88:78//HOMO SAPIENS (HUMAN).//P39194
F-THYRO1000637//METALLOTHIONEIN A (MT A).//1.0:23:43//SPARUS AURATA (GILTHEAD SEA BREAM).//P52727
F-THYRO1000641//PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN.//0.99:26:46//CYANIDIUM CALDARIUM (GALDIERIA SULPHURARIA).//O19925
F-THYRO1000658//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//1.5e-49:116:69//HOMO SAPIENS (HUMAN).//P39189
F-THYRO1000662//DNA-DAMAGE-INDUCIBLE PROTEIN P.//3.7e-15:119:43//ESCHERICHIA COLI.//Q47155
F-THYRO1000666//KINESIN-LIKE PROTEIN KLP1.//1.0e-44:232:41//CHLAMYDOMONAS REINHARDTII.//P46870
F-THYRO1000676//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//2.1e-15:144:39//HOMO SAPIENS (HUMAN).//P39193
F-THYRO1000684//HYPOTHETICAL 73.5 KD PROTEIN IN SCS3-RPS2 INTERGENIC REGION.//0.00033:84:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53129
F-THYRO1000699//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//0.97:20:85//HOMO SAPIENS (HUMAN).//P39192
F-THYRO1000712//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.2e-10:69:59//HOMO SAPIENS (HUMAN).//

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P39188
F-THYRO1000715//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.6e-10:204:32//HOMO SAPIENS (HUMAN).//P04280
F-THYRO1000734
F-THYRO1000748//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8e-46:130:70//HOMO SAPIENS (HUMAN).//O43295
F-THYRO1000756//ALPHA-N-ACETYLGALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (EC 2.4.99.-) (ST6GALNACIII) (STY).//1.1e-06:95:31//RATTUS NORVEGICUS (RAT).//Q64686
F-THYRO1000777//CUTICLE COLLAGEN 2C (FRAGMENT).//0.0031:119:34//HAEMONCHUS CONTORTUS.// P16252
F-THYRO1000783//MYOSIN IC HEAVY CHAIN.//0.0014:121:37//ACANTHAMOEBA CASTELLANII (AMOEBA).// P10569
F-THYRO1000787//HUNCHBACK PROTEIN (FRAGMENT).//0.54:25:52//PHOLCUS PHALANGIOIDES.// Q02031
F-THYRO1000793//PRE-MRNA SPLICING FACTOR PRP9.//0.91:3 0:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P19736
F-THYRO1000796
F-THYRO1000805//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION.//0.081:31:38//HUMAN ADENOVIRUS TYPE 41.//P23691
F-THYRO1000815//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//6.0e-30:81:70//HOMO SAPIENS (HUMAN).// P39195
F-THYRO1000829//NEUROTOXIN III (BOM III).//0.022:32:34//BUTHUS OCCITANUS MARDOCHEI (MOROCCAN SCORPION).//P13488
F-THYRO1000843//HYPOTHETICAL 7.7 KD PROTEIN IN GENES 5-4 INTERGENIC REGION (ORF 109).//0.98: 25:44//BACTERIOPHAGE P22.//P26750
F-THYRO1000852//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//7.3e-09:83:42//VOLVOX CARTERI.//P21997
F-THYRO1000855//ANTIFREEZE PEPTIDE 4 PRECURSOR.//1.0:54:35//PSEUDOPLEURONECTA AMERICANUS (WINTER FLOUNDER).//P02734
F-THYRO1000865//!!!! ALU SUBFAMILY J WARNING ENTRY!!!!//5.2e-17:66:57//HOMO SAPIENS (HUMAN).// P39188
F-THYRO1000895//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//1.0e-12:58:62//HOMO SAPIENS (HUMAN).// P39189
F-THYRO1000916//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//2.0e-32:101:69//HOMO SAPIENS (HUMAN).//P39189
F-THYRO1000926//NITROGEN FIXATION REGULATORY PROTEIN.//5.5e-05:108:27//KLEBSIELLA OXYTOCA.//P56267
F-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).// 3.9e-50:147:40//HOMO SAPIENS (HUMAN).//P32322
F-THYRO1000951//DIHYDROXYACETONE KINASE (EC 2.7.1.29) (GLYCERONE KINASE).//1.8e-31:136:56// CITROBACTER FREUNDII.//P45510
F-THYRO1000952//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION.//2.4e-05:91: 34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170
F-THYRO1000974//MITOCHONDRIAL ATP-DEPENDENT RNA HELICASE SUV3 PRECURSOR.//1.0:35:40// SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32580
F-THYRO1000975
F-THYRO1000983//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//1.3e-20:96:51// CAENORHABDITIS ELEGANS.//Q11076
F-THYRO1000984//GTP-BINDING ADP-RIBOSYLATION FACTOR HOMOLOG 1 PROTEIN.//0.011:76:34//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25160
F-THYRO1000988
F-THYRO1001003//HYPOTHETICAL 8.1 KD PROTEIN IN MSCL-RPLQ INTERGENIC REGION.//0.97:60:31// ESCHERICHIA COLI.//P36675
F-THYRO1001031//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!//9.5e-18:56:66//HOMO SAPIENS (HUMAN).// P39195
F-THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//5.0e-13:126:35//HOMO SAPIENS (HUMAN).//P31948
F-THYRO1001062//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.1e-35:97:79//HOMO SAPIENS (HUMAN).//

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P39194
F-THYRO1001093//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//6.4e-13:70:57//HOMO SAPIENS (HUMAN).// P39194
F-THYRO1001100//ZINC FINGER X-LINKED PROTEIN ZXDA (FRAGMENT).//4.2e-63:219:63//HOMO SAPIENS (HUMAN).//P98168
F-THYRO1001120//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//0.00068:160:31//HOMO SAPIENS (HUMAN).//Q15427
F-THYRO1001121//VERY HYPOTHETICAL 20.6 KD PROTEIN C56F8.15 IN CHROMOSOME I.//0.37:158:28// SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10263
F-THYRO1001133//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//7.3e-15:59:66//HOMO SAPIENS (HUMAN).// P39188
F-THYRO1001134//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.00088:159:29//HOMO SAPIENS (HUMAN).//P10161
F-THYRO1001142//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.0e-29:81:71//HOMO SAPIENS (HUMAN).// P39194
F-THYRO1001173//CYTOCHROME C OXIDASE POLYPEPTIDE VIIS (EC 1.9.3.1).//0.88:51:35//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P20610
F-THYRO1001177//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//3.0e-24:91:68//HOMO SAPIENS (HUMAN).// P39192
F-THYRO1001189//MKR2 PROTEIN (ZINC FINGER PROTEIN 2).//7.3e-27:165:39//MUS MUSCULUS (MOUSE).//P08043
F-THYRO1001204//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.67:42:42//HOMO SAPIENS (HUMAN).// P02811
F-THYRO1001213//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.9e-16:61:68//HOMO SAPIENS (HUMM).// P39194
F-THYRO1001262//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.4e-36:50:84//HOMO SAPIENS (HUMAN).// P39193
F-THYRO1001271//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.62: 126:30//STREPTOMYCES FRADIAE.//P20186
F-THYRO1001287//HYPOTHETICAL 91.2 KD PROTEIN IN RPS4B-SCH9 INTERGENIC REGION.//1.9e-26:208:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38888
F-THYRO1001290//GIANT HEMOGLOBIN AIV CHAIN (FRAGMENT).//1.0:31:38//LAMELLIBRACHIA SP. (DEEP-SEA GIANT TUBE WORM).//P20413
F-THYRO1001313//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5.//0.00042:105:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q92331
F-THYRO1001320//COLLAGEN ALPHA 1(III) CHAIN.//0.27:57:38//BOS TAURUS (BOVINE).//P04258
F-THYRO1001321//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//5.5e-20:74:64//HOMO SAPIENS (HUMAN).// P39188
F-THYRO1001322//HYPOTHETICAL 7.2 KD PROTEIN.//0.66:49:30//VACCINIA VIRUS (STRAIN COPENHAGEN).//P21123
F-THYRO1001347//TOXIN F-VIII PRECURSOR (TOXIN TA2) (TOXIN DAF8).//0.94:61:36//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P01404
F-THYRO1001363//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.0025:23:73//HOMO SAPIENS (HUMAN).// P39188
F-THYRO1001365//MERSACIDIN PRECURSOR.//0.35:38:42//BACILLUS SP. (STRAIN HIL-Y85/54728).// P43683
F-THYRO1001374//PROTEIN VDLD.//1.6e- 3:140:31//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//O05729
F-THYRO1001401//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//0.047:43:48//HOMO SAPIENS (HUMAN).// P39192
F-THYRO1001403
F-THYRO1001405//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.0068:26:42//HOMO SAPIENS (HUMAN).//P22531
F-THYRO1001406//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).//3.1e-81:97:83//MUS MUSCULUS (MOUSE).//O70503
F-THYRO1001411//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.9e-26:89:74//HOMO SAPIENS (HUMAN).// P39193
F-THYRO1001426//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.4e-09:55:61//HOMO SAPIENS (HUMAN).//

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P39193
F-THYRO1001434//BETA-DEFENSIN 4 PRECURSOR (BNDB-4).//0.68:44:34//BOS TAURUS (BOVINE).//P46162
F-THYRO1001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//3.8e-64:216:62//HOMO SAPIENS (HUMAN).//P35580
F-THYRO1001480//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//9.3e-29:88:75//HOMO SAPIENS (HUMAN).//P39194
F-THYRO1001487//HOMEOBOX PROTEIN HOX-B4 (HOX-2.6).//0.99:59:37//MUS MUSCULUS (MOUSE).//P10284
F-THYRO1001534//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.4e-14:40:82//HOMO SAPIENS (HUMAN).//P39194
F-THYRO1001537//HYPOTHETICAL 33.8 KD PROTEIN IN TWT1-FLO5 INTERGENIC REGION.//2.4e-07:142:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38892
F-THYRO1001541//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.98:26:61//HOMO SAPIENS (HUMAN).//P39195
F-THYRO1001559//PROTEIN Q300.//2.6e-05:20:75//MUS MUSCULUS (MOUSE).//Q02722
F-THYRO1001570
F-THYRO1001573//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.033:71:36//MUS MUSCULUS (MOUSE).//P15265
F-THYRO1001584//SUPPRESSOR PROTEIN SRP40.//2.1e-05:188:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
F-THYRO1001595//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//6.1e-21:35:91//HOMO SAPIENS (HUMAN).//Q15404
F-THYRO1001602//TRK SYSTEM POTASSIUM UPTAKE PROTEIN TRKH.//1.0:57:42//HAEMOPHILUS INFLUENZAE.//P44843
F-THYRO1001605//VENOM BASIC PROTEASE INHIBITORS IX AND VIIIB.//1.0:34:38//BUNGARUS FASCIATUS (BANDED KRAIT).//P25660
F-THYRO1001617//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//7.0e-18:55:81//HOMO SAPIENS (HUMAN).//P39194
F-THYRO1001637//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.00020:25:80//HOMO SAPIENS (HUMAN).//P39195
F-THYRO1001656//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.0091:54:42//MUS MUSCULUS (MOUSE).//P05142
F-THYRO1001661//HYPOTHETICAL 21.1 KD PROTEIN IN SSR-SERA INTERGENIC REGION (O182).//0.033:77:35//ESCHERICHIA COLI.//P09160
F-THYRO1001671//(2'-5')OLIGOADENYLATE SYNTHETASE 1 (EC 2.7.7.-) ((2-5')OLIGO(A) SYNTHETASE 1) (2-5A SYNTHETASE 1) (P46/P41) (E18/E16).//4.3e-34:207:34//HOMO SAPIENS (HUMAN).//P00973
F-THYRO1001673//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.9e-08:49:65//HOMO SAPIENS (HUMAN).//P39194
F-THYRO1001703//HYPOTHETICAL 69.8 KD PROTEIN IN BDF1-SFP1 INTERGENIC REGION.//6.4e-16:134:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06053
F-THYRO1001706
F-THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).//2.7e-27:191:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
F-THYRO1001738//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1) (PROTEIN KINASE A INTERFERENCE PROTEIN).//0.0032:105:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36027
F-THYRO1001745
F-THYRO1001746//GENE 10 PROTEIN.//1.0:55:30//SPIROPLASMA VIRUS SPV1-R8A2 B.//P15901
F-THYRO1001772//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.2e-05:41:63//HOMO SAPIENS (HUMAN).//P39188
F-THYRO1001793//HYPOTHETICAL 21.6 KD PROTEIN F37A4.2 IN CHROMOSOME III.//1.5e-26:161:42//CAENORHABDITIS ELEGANS.//P41880
F-THYRO1001809//LATENCY-RELATED PROTEIN 2.//0.49:74:27//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN F).//P17589
F-THYRO1001828//PROTEINASE INHIBITOR.//0.11:34:50//SOLANUM MELONGENA (EGGPLANT) (AUBERGINE).//P01078
F-THYRO1001854//ACYL-COA-BINDING PROTEIN HOMOLOG (ACBP) (DIAZEPAM BINDING INHIBITOR HOMOLOG) (DBI).//0.63:50:38//RANA RIDIBUNDA (LAUGHING FROG) (MARSH FROG).//P45883

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F-THYRO1001895//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//6.1e-09:72:47//HOMO SAPIENS (HUMAN).//P39188

F-THYRO1001907//TRYPOMASTIGOTE DECAY-ACCELERATING FACTOR (T-DAF) (FRAGMENT).//0.79:36:44//TRYPANOSOMA CRUZI.//Q26327

F-VESEN1000122//HOMEOBOX PROTEIN HB9.//0.57:64:32//HOMO SAPIENS (HUMAN).//P50219

F-Y79AA1000013//METALLOTHIONEIN B (MT-B).//0.034:35:48//SALMO SALAR (ATLANTIC SALMON).//P52720

F-Y79AA1000033//CHOLECYSTOKININ.//0.97:49:30//PSEUDEMYS SCRIPTA (SLIDER TURTLE).//P80345

F-Y79AA1000037//DNA-BINDING PROTEIN BMI-1.//1.4e-23:80:60//HOMO SAPIENS (HUMAN).//P35226

F-Y79AA1000059//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.0075:127:36//STREPTOMYCES FRADIAE.//P20186

F-Y79AA1000065//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.022:135:29//HOMO SAPIENS (HUMAN).//P10162

F-Y79AA1000131//REGULATORY PROTEIN E2.//1.1e-05:175:26//HUMAN PAPILLOMAVIRUS TYPE 24.//P50770

F-Y79AA1000181//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.4e-06:187:29//MUS MUSCULUS (MOUSE).//P05143

F-Y79AA1000202//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//6.2e-09:47:53//OWENIA FUSIFORMIS.//P21260

F-Y79AA1000214//HISTONE H2A VARIANT.//1.7e-50:107:100//GALLUS GALLUS (CHICKEN).//P02272

F-Y79AA1000230//GONADOLIBERIN I PRECURSOR (LHRH I) (LUTEINIZING HORMONE RELEASING HORMONE I) (GONADOTROPIN RELEASING HORMONE I) (GNRH I) (LULIBERIN I).//0.27:64:34//HOMO SAPIENS (HUMAN).//P01148

F-Y79AA1000231//HYPOTHETICAL 47.9 KD PROTEIN M021B04.12.//2.5e-72:277:53//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//O04658

F-Y79AA1000258//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//2.8e-08:174:35//MUS MUSCULUS (MOUSE).//P05142

F-Y79AA1000268//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.00020:176:33//RATTUS NORVEGICUS (RAT).//P13941

F-Y79AA1000313//HYPOTHETICAL 54.0 KD PROTEIN C32A3.1 IN CHROMOSOME III.//0.092:127:21//CAENORHABDITIS ELEGANS.//Q09260

F-Y79AA1000328//SEL-10 PROTEIN.//5.3e-05:129:28//CAENORHABDITIS ELEGANS.//Q93794

F-Y79AA1000342//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//1.0:73:30//OVIS ARIES (SHEEP).//P26372

F-Y79AA1000346//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.8e-95:205:83//BOS TAURUS (BOVINE).//P53620

F-Y79AA1000349//ANTIFREEZE PEPTIDE 4 PRECURSOR.//0.036:37:54//PSEUDOPLEURONECTA AMERICANUS (WINTER FLOUNDER).//P02734

F-Y79AA1000355//HYPOTHETICAL 18.2 KD PROTEIN ZK632.13 IN CHROMOSOME III.//0.0031:106:28//CAENORHABDITIS ELEGANS.//Q10120

F-Y79AA1000368//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.4e-16:208:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25343

F-Y79AA1000405//LIGHT-HARVESTING PROTEIN B-800-850, ALPHA CHAIN C (ANTENNA PIGMENT PROTEIN, ALPHA CHAIN C) (LH II-C ALPHA).//0.98:50:30//RHODOPSEUDOMONAS PALUSTRIS.//P35103

F-Y79AA1000410//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//7.9e-20:62:79//HOMO SAPIENS (HUMAN).//P39 194

F-Y79AA1000420//HYPOTHETICAL 27.7 KD PROTEIN IN UME3-HDA1 INTERGENIC REGION.//1.4e-06:86:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53970

F-Y79AA1000469//HYPOTHETICAL 48.4 KD PROTEIN F44B9.5 IN CHROMOSOME III.//2.8e-34:211:40//CAENORHABDITIS ELEGANS.//P34426

F-Y79AA1000480//HYPOTHETICAL 63.2 KD PROTEIN C1F3.09 IN CHROMOSOME I.//3.9e-15:90:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10414

F-Y79AA1000538//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.37:41:48//HOMO SAPIENS (HUMAN).//P39195

F-Y79AA1000539//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.8e-21:190:37//HOMO SAPIENS (HUMAN).//Q08170

F-Y79AA1000540//SPERM PROTAMINE P1.//0.00045:66:45//DASYURUS VIVERRINUS (SOUTHEASTERN QUOLL), AND DASYURUS HALLUCATUS.//P42135

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F-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//1.6e-79:186:87//MUS MUSCULUS (MOUSE).//P17427

F-Y79AA1000574//AKLAVINONE C-11 HYDROXYLASE (EC 1.-.-.-) (FRAGMENT).//0.010:35:60//STREPTOMYCES PEUCETIUS.//P32009

F-Y79AA1000589//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//4.5e-27:197:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P28320

F-Y79AA1000627//ZINC FINGER PROTEIN 134.//1.6e-34:191:35//HOMO SAPIENS (HUMAN).//P52741

F-Y79AA1000705//HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC REGION.//8.7e-36:250:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P31380

F-Y79AA1000734//PEROXISOMAL MEMBRANE PROTEIN PMP30A (PMP31) (PEROXIN-11A).//0.00037:108:27//CANDIDA BOIDINII (YEAST).//Q00316

F-Y79AA1000748//HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III.//1.0e-23:210:34//CAENORHABDITIS ELEGANS.//Q09316

F-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//1.4e-53:156:68//MUS MUSCULUS (MOUSE).//Q61990

F-Y79AA1000774//HYPOTHETICAL 77.9 KD PROTEIN IN RRN10-MCM2 INTERGENIC REGION.//1.2e-11:231:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38205

F-Y79AA1000782//CUTICLE COLLAGEN 2.//0.012:56:35//CAENORHABDITIS ELEGANS.//P17656

F-Y79AA1000784//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.//1.3e-08:82:39//PLASMODIUM LOPHURAE.//P04929

F-Y79AA1000794//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.043:13:53//HOMO SAPIENS (HUMAN).//P30808

F-Y79AA1000800//PRIA PROTEIN PRECURSOR.//0.031:94:34//LENTINULA EDODES (SHIITAKE MUSHROOM) (LENTINUS EDODES).//Q01200

F-Y79AA1000802//HYPOTHETICAL 67.4 KD PROTEIN IN RPS3-PSD1 INTERGENIC REGION.//0.26:186:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53882

F-Y79AA1000805//AMP DEAMINASE (EC 3.5.4.6) (MYOADENYLATE DEAMINASE).//0.99:78:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P50998

F-Y79AA1000824//HYPOTHETICAL 81.7 KD PROTEIN IN MOL1-NAT2 INTERGENIC REGION.//3.4e-44:111:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48234

F-Y79AA1000827//HYPOTHETICAL BHLF1 PROTEIN.//0.0046:187:33//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-Y79AA1000833//TUBULIN ALPHA-1 CHAIN.//1.0e-75:239:66//CRICETULUS GRISEUS (CHINESE HAMSTER).//P05209

F-Y79AA1000850//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.0078:57:31//HOMO SAPIENS (HUMAN).//P22532

F-Y79AA1000962//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE.//8.5e-11:241:26//GALLUS GALLUS (CHICKEN).//P10587

F-Y79AA1000966//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.69:122:31//TRYPANOSOMA BRUCEI BRUCEI.//P24499

F-Y79AA1000968//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR).//3.3e-102:211:93//RATTUS NORVEGICUS (RAT).//P70541

F-Y79AA1000969//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//1.0:67:38//GALLUS GALLUS (CHICKEN)://P02457

F-Y79AA1000976//INVOLUCRIN.//0.99:66:31//CEBUS ALBIFRONS (WHITE-FRONTED CAPUCHIN).//P24709

F-Y79AA1000985//PERICENTRIN.//1.1e-24:116:59//MUS MUSCULUS (MOUSE).//P48725

F-Y79AA1001023//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION.//0.37:79:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38250

F-Y79AA1001041//SPERMATID-SPECIFIC PROTEIN T1 [CONTAINS: SPERM PROTAMINE SP1].//0.93:43:39//SEPIA OFFICINALIS (COMMON CUTTLEFISH).//P80001

F-Y79AA1001048//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD).//1.5e-51:211:52//BOS TAURUS (BOVINE).//P48818

F-Y79AA1001061//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!.//3.8e-25:85:69//HOMO SAPIENS (HUMAN).//P39194

F-Y79AA1001068//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].//0.0015:207:33//MUS MUSCULUS (MOUSE).//P28481

F-Y79AA1001077//ADULT-SPECIFIC RIGID CUTICULAR PROTEIN 11.9 (ACP 11.9).//0.99:36:41//ARANEUS DI-

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ADEMATUS (SPIDER).//P80515
F-Y79AA1001078//HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III.//1.0e-06:197:23// CAENORHABDITIS ELEGANS .//P34492
F-Y79AA1001105//HOMEOBOX PROTEIN OTX2.//2.9e-62:163:79//MUS MUSCULUS (MOUSE).//P80206
F-Y79AA1001145//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.024:42:59//HOMO SAPIENS (HUMAN).// P39195
F-Y79AA1001167//HYPOTHETICAL 7.1 KD PROTEIN IN IAP2-VLF1 INTERGENIC REGION.//0.96:20:50// AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41471
F-Y79AA1001177//HYPOTHETICAL BHLF1 PROTEIN.//3.9e-05:135:34//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
F-Y79AA1001185//PUTATIVE CUTICLE COLLAGEN C09G5.5.//0.00017:93:38//CAENORHABDITIS ELEGANS.//Q09456
F-Y79AA1001211
F-Y79AA1001216//TENSIN.//0.012:134:32//GALLUS GALLUS (CHICKEN).//Q04205
F-Y79AA1001228//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//0.088:75:34//HOMO SAPIENS (HUMAN).// Q02817
F-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HYDROXYSTEROID DEHYDROGENASE 1).//1.1e-40:139:51//RATTUS NORVEGICUS (RAT).//P51657
F-Y79AA1001236//HYPOTHETICAL 34.7 KD PROTEIN IN ORC2-TIP1 INTERGENIC REGION.//2.0e-22:108:53// SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38238
F-Y79AA1001281
F-Y79AA1001299//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.0022:49:44//MUS MUSCULUS (MOUSE).//P05143
F-Y79AA1001312//50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR.//0.98:117:25//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P92959
F-Y79AA1001323//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).//0.082:44:40//SUS SCROFA (PIG).//P35323
F-Y79AA1001384//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII).//0.99:47:40//MUS MUSCULUS (MOUSE).//P33622
F-Y79AA1001391//HOMEOBOX PROTEIN HOX-A13 (HOX-1J).//9.8e-58:157:62//HOMO SAPIENS (HUMAN).// P31271
F-Y79AA1001394//TRICHOHYALIN.//4.7e-08:121:36//HOMO SAPIENS (HUMAN).//Q07283
F-Y79AA1001402//ETS-DOMAIN TRANSCRIPTION FACTOR ERF.//0.0087:81:33//MUS MUSCULUS (MOUSE).//P70459
F-Y79AA1001493//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//4.5e-21:125:44// CAENORHABDITIS ELEGANS.//Q11076
F-Y79AA1001511//HYPOTHETICAL 86.6 KD PROTEIN IN PFK1-TDS4 INTERGENIC REGION.//2.3e-17:249:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53313
F-Y79AA1001533//DNA-DIRECTED RNA POLYMERASE I49 KD POLYPEPTIDE (EC 2.7.7.6) (A49).//0.0099:155:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q01080
F-Y79AA1001541
F-Y79AA1001548//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//1.1e-17:53:83//HOMO SAPIENS (HUMAN).// P39192
F-Y79AA1001555//MAJOR SURFACE ANTIGEN.//0.046:62:29//HEPATITIS B VIRUS.//P31873
F-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//8.6e-11:144:31//ESCHERICHIA COLI.//P27550
F-Y79AA1001585//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.012:64:40//MUS MUSCULUS (MOUSE).//P15265
F-Y79AA1001594//CORNIFIN BETA.//0.61:88:31//MUS MUSCULUS (MOUSE).//O09116
F-Y79AA1001603//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.024:170:30//HOMO SAPIENS (HUMAN).//O00268
F-Y79AA1001613//ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1).//4.5e-09:136:27//HOMO SAPIENS (HUMAN).//P28698
F-Y79AA1001647//HYPOTHETICAL 23.1 KD PROTEIN CY277.20C.//0.093:94:26//MYCOBACTERIUM TUBERCULOSIS.//P71779
F-Y79AA1001665//HOMEOBOX PROTEIN DLX-2 (HOMEOBOX PROTEIN TES-1).//0.79:90:26//MUS MUSCULUS (MOUSE).//P40764
F-Y79AA1001679//LAMBDA-CRYSTALLIN.//1.6e-95:224:81//ORYCTOLAGUS CUNICULUS (RABBIT).//P14755

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F-Y79AA1001692//GERM CELL-LESS PROTEIN.//3.5e-08:78:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01820
F-Y79AA1001696//INSULIN.//1.0:33:27//ANGUILLA ROSTRATA (AMERICAN EEL).//P42633
F-Y79AA1001705//HYPOTHETICAL BHLF1 PROTEIN.//0.0013:192:33//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
F-Y79AA1001711//PARATHYMOSIN (ZINC-BINDING 11.5 KD PROTEIN).//0.032:38:34//RATTUS NORVEGICUS (RAT).//P04550
F-Y79AA1001781
F-Y79AA1001805//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.0063:128:30//HOMO SAPIENS (HUMAN).//P50552
F-Y79AA1001827//SPERM PROTAMINE P1.//0.015:45:40//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM), AND MONODELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM).//P35305
F-Y79AA1001846//!!!! ALU SUBFAMILY J WARNING ENTRY!!!!//2.4e-09:42:73//HOMO SAPIENS (HUMAN).//P39188
F-Y79AA1001848//KRUEPPEL PROTEIN (FRAGMENT).//1.8e-10:63:44//PSYCHODA CINEREA.//Q02035
F-Y79AA1001866//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).//0.00036:108:37//MUS MUSCULUS (MOUSE).//Q61967
F-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTIVATED GLYCOPROTEIN-1 RECEPTOR) (CD134 ANTIGEN).//3.2e-07:100:35//HOMO SAPIENS (HUMAN).//P43489
F-Y79AA1001875//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.020:25:64//HOMO SAPIENS (HUMAN).//P20931
F-Y79AA1001923//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.016:83:36//HOMO SAPIENS (HUMAN).//P10162
F-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//8.1e-13:94:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O42643
F-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.8e-39:143:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P42743
F-Y79AA1002083//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.036:53:45//HOMO SAPIENS (HUMAN).//P30808
F-Y79AA1002089//HYPOTHETICAL 49.1 KD PROTEIN F02A9.4 IN CHROMOSOME III.//0.12:171:22//CAENORHABDITIS ELEGANS.//P34384
F-Y79AA1002093//MAX PROTEIN.//3.1e-07:111:29//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//P52161
F-Y79AA1002103//SHORT NEUROTOXIN C.//0.040:21:47//AIPYSURUS LAEVIS (OLIVE SEA SNAKE).//P19958
F-Y79AA1002115//HYPOTHETICAL PROTEIN MJ0827.//0.84:68:30//METHANOCOCCUS JANNASCHII.//Q58237
F-Y79AA1002125//HYPOTHETICAL 24.7 KD PROTEIN IN POM152-REC114 INTERGENIC REGION.//3.4e-29:197:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40206
F-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1).//1.9e-19:120:45//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24133
F-Y79AA1002204//TBX6 PROTEIN (T-BOX PROTEIN 6).//0.0011:162:32//MUS MUSCULUS (MOUSE).//P70327
F-Y79AA1002208//ANKYRIN.//2.9e-08:231:29//MUS MUSCULUS (MOUSE).//Q02357
F-Y79AA1002209//TYROSYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (EC 6.1.1.1) (TYROSINE--TRNA LIGASE) (TYRRS).//3.7e-23:170:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48527
F-Y79AA1002210//CORNIFIN A (SMALL PROLINE-RICH PROTEIN IA) (SPR-IA) (SPRK).//0.0061:69:31//HOMO SAPIENS (HUMAN).//P35321
F-Y79AA1002211//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//9.2e-10:43:62//HOMO SAPIENS (HUMAN).//P39193
F-Y79AA1002220
F-Y79AA1002229//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME I.//1.9e-21:147:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10264
F-Y79AA1002234
F-Y79AA1002246//MYOSIN IC HEAVY CHAIN.//0.00066:131:34//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569

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F-Y79AA1002258//HYPOTHETICAL 103.9 KD PROTEIN ZK370.3 IN CHROMOSOME III.//4.3e-45:164:48// CAENORHABDITIS ELEGANS.//Q02328
F-Y79AA1002298//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.0063:99:31//HOMO SAPIENS (HUMAN).//P10161
F-Y79AA1002307
F-Y79AA1002311//HYPOTHETICAL 105.3 KD PROTEIN C01G6.5 IN CHROMOSOME III.//0.75:198:24// CAENORHABDITIS ELEGANS.//P46012
F-Y79AA1002351//CUTICLE COLLAGEN 34.//0.74:128:35//CAENORHABDITIS ELEGANS.//P34687
F-Y79AA1002361//GLC7-INTERACTING PROTEIN 2.//0.050:71:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40036
F-Y79AA1002399//NEUROMODULIN (AXONAL MEMBRANE PROTEIN GAP-43) (PP46) (B-50) (PROTEIN F1) (CALMODULIN-BINDING PROTEIN P-57).//1.0:89:30//CARASSIUS AURATUS (GOLDFISH).//P17691
F-Y79AA1002407//HYPOTHETICAL 31.5 KD PROTEIN IN YGP1-YCK2 INTERGENIC REGION.//3.7e-16:232:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53899
F-Y79AA1002416//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE).//6.7e-72:162:84//HOMO SAPIENS (HUMAN).//P17812
F-Y79AA1002431//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.81:34:41//HOMO SAPIENS (HUMAN).//P22531
F-Y79AA1002433//CELL DIVISION CONTROL PROTEIN 68.//0.00024:85:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32558
F-Y79AA1002472//ZINC FINGER PROTEIN 35 (ZFP-35).//2.3e-60:217:44//MUS MUSCULUS (MOUSE).//P15620
F-Y79AA1002482//ZINC FINGER PROTEIN 141.//2.0e-31:90:55//HOMO SAPIENS (HUMAN).//Q15928
F-Y79AA1002487//HYPOTHETICAL 67.1 KD TRP-ASP REPEATS CONTAINING PROTEIN C57A10.05C IN CHROMOSOME I.//0.18:41:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87053

Homology Search Result Data 2.

[0300] The result of the homology search of the GenBank using the clone sequence of 5'-end except EST and STS.

[0301] Data include

the name of clone,
definition of the top hit data,
the P-value: the length of the compared sequence: identity (%), and
the Accession No. of the top hit data, as in the order separated by *//*.

[0302] Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000005//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds.//3.4e-106:695:86//L16953
F-HEMBA1000012//Caenorhabditis-elegans cosmid C16C10, complete sequence.//1.5e-24:374:66//Z46787
F-HEMBA1000020//Homo sapiens beta 2 gene.//3.5e-112:529:90//X02344
F-HEMBA1000030//Rattus norvegicus G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein (GIT1) mRNA, complete cds.//5.6e-124:743:88//AF085693
F-HEMBA1000042//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-25:529:65//AC004581
F-HEMBA1000046//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 125I3, WORKING DRAFT SEQUENCE.//3.2e-11:330:63//AL033528
F-HEMBA1000050//Homo sapiens DNA sequence from PAC 172K10 on chromosome 6q24. Contains STS, GSS and chromosome 6 fragment, complete sequence.//0.32:407:59//AL022477
F-HEMBA1000076//Homo sapiens full-length insert cDNA clone ZB97G06.//6.2e-135:594:98//AF086182
F-HEMBA1000111//CIT-HSP-2291M18.TF CIT-HSP Homo sapiens genomic clone 2291M18 genomic survey sequence.//2.8e-16:132:79//AQ004134
F-HEMBA1000129//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//8.6e-98:230:93//AC003104
F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds.//2.1e-167:791:98//AB018340
F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 protein, partial cds.//2.2e-44:242:96//AB018331
F-HEMBA1000156//Rattus norvegicus scaffold attachment factor B mRNA, complete cds.//1.1e-10:409:60//AF056324
F-HEMBA1000158//Homo sapiens CAGH44 mRNA, partial cds.//1.6e-35:365:73//U80741

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F-HEMBA1000168//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 321D2, WORKING DRAFT SEQUENCE.//0.99:290:61//AL031033
F-HEMBA1000180//rat u2 small nuclear rna gene and flanks.//3.7e-18:112:98//K00034
F-HEMBA1000185
F-HEMBA1000193//Human FMR1 gene, 5' end.//0.0012:191:67//L19476
F-HEMBA1000201//Human Ini1 mRNA, complete cds.//2.0e-73:440:92//U04847
F-HEMBA1000213//Plasmodium falciparum MAL3P7, complete sequence.//0.90:332:59//AL034559
F-HEMBA1000216//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//4.8e-117:585:83//AF060194
F-HEMBA1000227//H.sapiens CpG island DNA genomic Mse1 fragment, clone 179h6, reverse read cpg179h6.rt1a.//1.9e-14:95:98//Z64921
F-HEMBA1000231//H.sapiens CpG island DNA genomic Mse1 fragment, clone 90a5, reverse read cpg90a5.rt1a.//5.1e-34:186:97//Z56144
F-HEMBA1000243//Human DNA sequence from PAC 440O21 on chromosome X contains ESTs and STS.//4.1e-67:291:82//Z84481
F-HEMBA1000244//M.musculus Ank-1 mRNA for erythroid ankydn.//0.029:316:59//X69065
F-HEMBA1000251//Homo sapiens PAC clone DJ0988L12 from 7q11.23-q21.1, complete sequence.//0.35:467:60//AC004454
F-HEMBA1000264
F-HEMBA1000280//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//8.9e-20:218:78//AC004825
F-HEMBA1000282//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//4.2e-08:134:77//AC004617
F-HEMBA1000288//345L5.TPB CIT978SKA1 Homo sapiens genomic clone A-345L05, genomic survey sequence.//1.1e-06:152:73//B17459
F-HEMBA1000290//Human ornithine decarboxylase gene, complete cds.//3.2e-11:507:62//M33764
F-HEMBA1000302//CIT-HSP-2169N13.TF CIT-HSP Homo sapiens genomic clone 2169N13, genomic survey sequence.//5.4e-06:86:88//B90730
F-HEMBA1000303//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//7.9e-111:701:86//AF030131
F-HEMBA1000304//HS_3006_A1_A09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=17 Row=A, genomic survey sequence.//5.2e-40:240:92//AQ118226
F-HEMBA1000307//Mus musculus mRNA for CDV-1R protein.//7.9e-127:815:84//Y10495
F-HEMBA1000327//HS_3124_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence.//1.4e-11:87:96//AQ187492
F-HEMBA1000333
F-HEMBA1000338//Homo sapiens chromosome X, PAC 671D9, complete sequence.//4.0e-66:271:84//AF031078
F-HEMBA1000351//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence.//0.64:334:60//AC004848
F-HEMBA1000355//Pseudorabies virus serine/threonine kinase (ULPK) gene, partial cds and alkaline nuclease (AN) gene, complete cds.//0.017:313:63//U25056
F-HEMBA1000356//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds.//0.87:198:61//L40178
F-HEMBA1000357//HS_3194_A1_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=G, genomic survey sequence.//6.5e-90:436:98//AQ173748
F-HEMBA1000366//HS_3027_B2_G06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=12 Row=N, genomic survey sequence.//0.0074:192:64//AQ128843
F-HEMBA1000369//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//4.2e-106:133:99//AL031587
F-HEMBA1000376//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.6e-22:659:63//AC006116
F-HEMBA1000387//Homo sapiens chromosome 12p13.3 clone RPCI11-264F23, WORKING DRAFT SEQUENCE, 90 unordered pieces.//3.2e-06:136:75//AC006122
F-HEMBA1000390//Homo sapiens BAC clone RG119C02 from 7p15, complete sequence.//3.5e-111:284:95//AC004520
F-HEMBA1000392//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 173D1, WORKING DRAFT SEQUENCE.//1.8e-39:332:80//AL031984
F-HEMBA1000396//Human Xq13 3' end of PAC 92E23 containing the X inactivation transcipt (XIST) gene, complete sequence.//9.5e-35:364:73//U80460

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F-HEMBA1000411//Human Xp22 contig of 3 PACS (R7-39D12, R7-134G1, R7-185L21) from the Roswell Park Cancer Institute. complete sequence.//8.1e-18:424:64//U96409
F-HEMBA1000418//Drosophila melanogaster Oregon-R mitochondrial A+T region.//0.0026:564:59//U11584
F-HEMBA1000422//Human DNA from chromosome 19 specific cosmid R30292, genomic sequence, complete sequence.//9.2e-14:232:70//AC003112
F-HEMBA1000428//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//3.8e-37:408:69//AC004554
F-HEMBA1000434//Caenorhabditis elegans cosmid Y48E1B, complete sequence.//0.73:454:57//Z93393
F-HEMBA1000442
F-HEMBA1000456//RPCI11-30J5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30J5, genomic survey sequence.//6.3e-06:62:96//B85188
F-HEMBA1000459//Mus musculus hemin-sensitive initiation factor 2 alpha kinase mRNA, complete cds.//6.8e-70:580:79//AF028808
F-HEMBA1000460//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//2.8e-154:746:98//AC004839
F-HEMBA1000464//Homo sapiens, clone hRPK.15_A_1, complete sequence.//4.8e-25:397:72//AC006213
F-HEMBA1000469//CIT-HSP-2167P21.TF CIT-HSP Homo sapiens genomic clone 2167P21, genomic survey sequence.//4.0e-83:406:99//B94160
F-HEMBA1000488//Homo sapiens Chromosome 22q11.2 PAC Clone p_m11 In BCRL2-GGT Region, complete sequence.//4.2e-53:312:93//AC004033
F-HEMBA1000490//Campylobacter jejuni groES, groEL genes.//0.59:451:62//Y13334
F-HEMBA1000491//Murine sarcoma virus (Harvey-strain) H-ras transforming p21 gene.//8.6e-06:338:58//X00740
F-HEMBA1000501//Homo sapiens chromosome 17, clone hRPK.264_B_14, complete sequence.//9.4e-41:591:69//AC005884
F-HEMBA1000504//Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os).//4.0e-07:57:100//D13666
F-HEMBA1000505
F-HEMBA1000508//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0135005; HTGS phase 1, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.035:329:61//AC004661
F-HEMBA1000518//Caenorhabditis elegans cosmid C17H12.//0.96:425:58//AF045642
F-HEMBA1000519//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//1.6e-53:300:89//AC004616
F-HEMBA1000520//Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.7e-10:117:86//AC006006
F-HEMBA1000523
F-HEMBA1000531//Mus musculus Hsp70-related NST-1 (hsr.1) mRNA, complete cds.//3.9e-35:290:80//U08215
F-HEMBA1000534//Homo sapiens chromosome 17, clone hRPK.177_H_5, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.7e-36:328:77//AC005973
F-HEMBA1000540//Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2 (ESSAII project).//0.057:265:63//AL033545
F-HEMBA1000542//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//1.2e-110:572:88//D89340
F-HEMBA1000545//Human DNA from cosmid L27h9, Huntington's Disease Region, chromosome 4p16.3 contains CpG island.//7.5e-130:780:89//Z49237
F-HEMBA1000555//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 134O19, WORKING DRAFT SEQUENCE.//3.2e-175:838:98//AL034555
F-HEMBA1000557//CIT-HSP-2369F15.TF CIT-HSP Homo sapiens genomic clone 2369F15, genomic survey sequence.//2.8e-32:315:78//AQ074611
F-HEMBA1000561//Rattus norvegicus Olf-1/EBF associated Zn finger protein Roaz mRNA, alternatively spliced form, complete cds.//3.4e-69:665:72//U92564
F-HEMBA1000563//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.59:261:61//AC005504
F-HEMBA1000568//HS_3243_B2_A12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3243 Col=24 Row=B, genomic survey sequence.//3.1e-54:323:91//AQ219628
F-HEMBA1000569//M.musculus mRNA for GPI-anchored protein.//1.4e-19:440:61//X89571
F-HEMBA1000575//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0016:557:57//AC005506
F-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//1.7e-11:132:79//AF045573
F-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.3e-43:228:97//AJ007509

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F-HEMBA1000592//Mus musculus clone OST7314, genomic survey sequence.//7.3e-07:68:94//AF046733
F-HEMBA1000594//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//8.7e-71:553:79//Z83822
F-HEMBA1000604//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 237J2, WORKING DRAFT SEQUENCE.//2.9e-21:158:75//AL021394
F-HEMBA1000608//Homo sapiens mRNA for KIAA0456 protein, partial cds.//1.1e-118:561:99//AB007925
F-HEMBA1000622//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//2.2e-28:426:70//AC004382
F-HEMBA1000636//Human CpG island sequence, clone Q2888.//1.0e-15:274:68//D85773
F-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds.//6.7e-137:639:99//AB014590
F-HEMBA1000655//, complete sequence.//5.1e-83:685:80//AC005815
F-HEMBA1000657//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//1.1e-91:597:84//U35776
F-HEMBA1000662//Homo sapiens clone DJ0853H20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.019:695:57//AC004907
F-HEMBA1000673//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 229A8, WORKING DRAFT SEQUENCE.//1.5e-48:325:85//Z86090
F-HEMBA1000682//Homo sapiens (subclone 5_g5 from P1 H25) DNA sequence.//7.7e-61:615:74//L43411
F-HEMBA1000686
F-HEMBA1000702
F-HEMBA1000705//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0037:569:57//AC005507
F-HEMBA1000719//Streptomyces coelicolor cosmid 1C2.//2.0e-09:483:62//AL031124
F-HEMBA1000722//Toxoplasma gondii chloroplast, complete genome.//0.00058:762:57//U87145
F-HEMBA1000726//H.sapiens HLA-DRB1*15 gene.//9.8e-49:189:89//X88791
F-HEMBA1000727//CIT-HSP-387P22.TRB CIT-HSP Homo sapiens genomic clone 387P22, genomic survey sequence.//0.0054:206:67//B60158
F-HEMBA1000747
F-HEMBA1000749//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.3e-05:124:75//AL024509
F-HEMBA1000752//Human Chromosome X, complete sequence.//5.9e-48:502:75//AC004073
F-HEMBA1000769//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.011:179:67//AC005043
F-HEMBA1000773//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y59A8, WORKING DRAFT SEQUENCE.//0.070:231:63//Z98870
F-HEMBA1000774//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//6.2e-40:385:75//AC004953
F-HEMBA1000791
F-HEMBA1000817//Myrmecia pilosula HI87-135 mitochondrion cytochrome b gene, partial cds.//0.99:244:58//U15678
F-HEMBA1000822//Human DNA sequence from PAC 179D3, between markers DXS6791 and DXS8038 on chromosome X contains S10 GTP-binding protein, ESTs and CpG island.//0.033:294:62//Z81370
F-HEMBA1000827//Borrelia burgdorferi (section 50 of 70) of the complete genome.//9.7e-05:463:58//AE001164
F-HEMBA1000843//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//3.0e-153:732:98//AL022394
F-HEMBA1000851//Rattus norvegicus glucocorticoid modulatory element binding protein 2 mRNA, complete cds.//1.6e-31:386:72//AF059273
F-HEMBA1000852//Homo sapiens Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//8.5e-115:455:98//AC005295.
F-HEMBA1000867
F-HEMBA1000869//Human DNA sequence from cosmid J138O17, between markers DXS6791 and DXS8038 on chromosome X contains EST CA repeat and an endogenous retroviral like element.//6.6e-41:424:75//Z72519
F-HEMBA1000870//Gnamptodon pumilio cytochrome oxidase II gene, partial cds; and tRNA-Asp, tRNA-His, and tRNA-Lys genes, complete sequence, mitochondrial genes for mitochondrial products.//0.0049:211:66//AF034598

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F-HEMBA1000872//CIT-HSP-2355D20.TF CIT-HSP Homo sapiens genomic clone 2355D20, genomic survey sequence.//3.7e-33:180:98//AQ059583
F-HEMBA1000876//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 473B4, WORKING DRAFT SEQUENCE.//5.6e-37:262:72//Z83826
F-HEMBA1000908//Triticum aestivum low-affinity cation transporter (LCT1) mRNA, complete cds.//1.0:304:59//AF015523
F-HEMBA1000910//M.musculus necdin mRNA, complete cds.//6.1e-08:256:61//M80840
F-HEMBA1000918//Tetrahymena thermophila micronuclear developmentally eliminated sequence region.//0.13:232:63//U88158
F-HEMBA1000919//Gallus domesticus filamin mRNA, complete cds.//1.0:213:65//U00147
F-HEMBA1000934//CIT-HSP-2053H24.TR CIT-HSP Homo sapiens genomic clone 2053H24, genomic survey sequence.//5.5e-11:275:64//B69224
F-HEMBA1000942//Homo sapiens clone DJ0754G14, WORKING DRAFT SEQUENCE, 15 unordered pieces.//9.7e-05:78:83//AC004878
F-HEMBA1000943//Homo sapiens chromosome 17, clone hRPK.640_I_15, complete sequence.//5.8e-140:661:99//AC005324
F-HEMBA1000946
F-HEMBA1000960//Homo sapiens clone DJ1111F22, WORKING DRAFT SEQUENCE, 12 unordered pieces.//8.3e-16:181:75//AC004967
F-HEMBA1000968//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 69M21, WORKING DRAFT SEQUENCE.//4.4e-117:398:86//AL031735
F-HEMBA1000971//H.sapiens CpG island DNA genomic Mse1 fragment, clone 182f4, forward read cpg182f4ft1a.//1.5e-20:126:96//Z57528
F-HEMBA1000972//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 1/11.//0.34:642:59//AB020858
F-HEMBA1000974//Homo sapiens clone DA0091H08, complete sequence.//5.1e-183:865:98//AC004817
F-HEMBA1000975//Orf virus homologue of retroviral pseudoprotease gene, complete cds.//0.00065:391:62//M30023
F-HEMBA10009851/Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence.//3.4e-05:243:65//Z93929
F-HEMBA1000986//Homo sapiens DNA from chromosome 19-cosmid R31491, genomic sequence.//6.6e-06:508:61//AD000813
F-HEMBA1000991//Homo sapiens mRNA for Hrs, complete cds.//1.2e-22:193:84//D84064 F-HEMBA1001007
F-HEMBA1001008//Human DNA sequence from clone 391O22 on chromosome 6p21.2-21.31 Contains pseudogenes similar to ribosomal protein, ESTs, GSSs, complete sequence.//7.8e-46:532:73//AL031577
F-HEMBA1001009//Human mRNA for IgM heavy chain complete sequence.//0.97:369:59//X17115
F-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds.//4.4e-139:661:98//AB007937
F-HEMBA1001019//Homo sapiens, clone hRPK.15_A_1, complete sequence.//1.6e-16:521:64//AC006213
F-HEMBA1001020//Homo sapiens chromosome 17, clone hRPK.178_C_3, complete sequence.//3.8e-50:367:72//AC005702
F-HEMBA1001022
F-HEMBA1001024//Homo sapiens T-cell receptor alpha delta locus from bases 1 to 250529 (section 1 of 5) of the Complete Nucleotide Sequence.//5.0e-23:378:69//AE000658
F-HEMBA1001026//Homo sapiens DNA sequence from PAC 435D1 on chromosome Xq25. Contains ESTs and STS.//7.6e-19:867:60//Z86064
F-HEMBA1001043//HS_2219_B1_A10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=19 Row=B, genomic survey sequence.//3.0e-15:124:88//AQ301521
F-HEMBA1001051//Human Chromosome X clone bWXD342, complete sequence.//4.8e-79:308:84//AC004072
F-HEMBA1001052//Homo sapiens chromosome 17, clone hRPK.146_P_2, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.53:384:61//AC005341
F-HEMBA1001059//Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 10.//2.8e-26:397:71//U06084
F-HEMBA1001060//Homo sapiens chromosome 17, clone hRPK.855_D_21 complete sequence.//0.98:280:62//AC006079
F-HEMBA1001071//Human mRNA for pro alpha 1 (III) collagen C-terminal propeptide.//1.1e-31:181:96//X01742
F-HEMBA1001077//nuclear protein TIF1 [mice, mRNA, 3951 nt].//3.6e-13:338:65//S78219
F-HEMBA1001080//Streptomyces coelicolor cosmid 1A9.//0.00012:364:63//AL034446

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F-HEMBA1001085//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase IIx genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//8.5e-134:476:96//AC004586
F-HEMBA1001088//Sequence 1 from patent US 5552529.//2.2e-71:303:78//I25863
F-HEMBA1001094//Homo sapiens clone RG491N20, complete sequence.//8.9e-119:609:96//AC005105
F-HEMBA1001099
F-HEMBA1001109//Homo sapiens BAC clone RG318M05 from 7q22-q31.1, complete sequence.//2.4e-58:347:87//AC005250
F-HEMBA1001121//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 90G24, WORKING DRAFT SEQUENCE.//3.4e-21:226:65//AL008723
F-HEMBA1001122//Plasmodium falciparum chromosome 2, section 20 of 73 of the complete sequence.//9.2e-07:732:57//AE001383
F-HEMBA1001123//Homo sapiens full-length insert cDNA clone ZD38E12.//1.1e-11:231:68//AF086247
F-HEMBA1001133//Homo sapiens clone DJ0856O24, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.011:163:69//AC004909
F-HEMBA1001137//Homo sapiens mRNA for KIAA0798 protein, complete cds.//6.9e-72:527:77//AB018341
F-HEMBA1001140//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.3e-120:578:98//AC005077
F-HEMBA1001172//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.010:520:59//AC005507
F-HEMBA1001174//R.norvegicus (Sprague Dawley) ARL5 mRNA for ARF-like protein 5.//1.0e-59:565:73//X78604
F-HEMBA1001197//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0037:151:70//AC004815
F-HEMBA1001208//Human BAC clone RG264L19 from 7p15-p21, complete sequence.//7.4e-35:195:81//AC002410
F-HEMBA1001213//Homo sapiens clone DJ0892G19, complete sequence.//1.9e-171:826:98//AC004917
F-HEMBA1001226//Homo sapiens clone DJ0850101, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.00010:557:57//AC006009
F-HEMBA1001235//Homo sapiens chromosome 17, clone hRPK.601_N_13, complete sequence.//0.0086:372:58//AC005389
F-HEMBA1001247//H.sapiens CpG island DNA genomic Mse1 fragment, clone 11b11, reverse read cpg11b11.rt1a.//2.0e-24:154:93//Z64441
F-HEMBA1001257//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.9e-88:659:81//AF047020
F-HEMBA1001265//Human 18S ribosomal RNA.//1.0e-32:180:97//X03205
F-HEMBA1001281
F-HEMBA1001286//B.taurus mRNA for RF-36-DNA-binding protein.//7.7e-26:236:81//X15543
F-HEMBA1001289//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.//5.5e-28:530:64//AC004131
F-HEMBA1001294//Yeast mitochondrial aapl gene for ATPase subunit 8.//2.8e-15:722:60//X00960
F-HEMBA1001299//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence.//4.2e-24:288:76//AL031003
F-HEMBA1001302//cDNA encoding a human homologue of a mouse novel polypeptide derived from stromal cell.//7.2e-121:439:96//E12260
F-HEMBA1001303//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.011:637:56//AC005505
F-HEMBA1001310//HS_3252_B2_B12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=24 Row=D, genomic survey sequence.//1.2e-16:166:82//AQ217054
F-HEMBA1001319//CIT-HSP-2034J6.TF CIT-HSP Homo sapiens genomic clone 2034J6, genomic survey sequence.//0.33:256:59//B79408
F-HEMBA1001323//Homo sapiens proto-oncogene (Wnt-5a) mRNA, complete cds.//7.8e-30:165:99//L20861
F-HEMBA1001326//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucoronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs(BAC end sequences) and a CA repeat polymorphism, complete sequence.//5.4e-19:347:68//AL021368
F-HEMBA1001327//CIT-HSP-2354E10.TR CIT-HSP Homo sapiens genomic clone 2354E10, genomic survey sequence.//0.012:152:65//AQ075713
F-HEMBA1001330//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-103, com-

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plete sequence.//0.0037:254:62//AL010208
F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//1.1e-103:516:97//AF057358
F-HEMBA1001361//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence.//1.7e-150:706:99//AC006241
F-HEMBA1001375//Streptomyces coelicolor cosmid 1E6.//1.0:375:59//AL033505
F-HEMBA1001377//HS_3020_B1_D12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3020 Col=23 Row=H, genomic survey sequence.//0.00022:63:77//AQ105297
F-HEMBA1001383//Plasmodium falciparum chromosome 2, section 68 of 73 of the complete sequence.//0.00035:317:60//AE001431
F-HEMBA1001387//HS_3039_B1_D01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=1 Row=H, genomic survey sequence.//5.0e-90:437:98//AQ155035
F-HEMBA1001388//Homo sapiens clone RG189J21, WORKING DRAFT SEQUENCE, 15 unordered pieces.//4.2e-47:159:89//AC005073
F-HEMBA1001391//Human DNA sequence from clone 409O10 on chromosome 20q12 Contains CA repeat, GSS, STS, complete sequence.//2.0e-06:495:60//AL031256
F-HEMBA1001398//H.sapiens CpG island DNA genomic Mse1 fragment, clone 70d11, forward read cpg70d11.ft1b.//0.018:46:97//Z62591
F-HEMBA1001405//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.//2.3e-74:623:71//AL034380
F-HEMBA1001407//Mus musculus domesticus Torino (Sry) gene, complete cds.//0.36:363:57//U03645
F-HEMBA1001411//Homo sapiens genomic DNA, 21q region, clone: S39BG29, genomic survey sequence.//8.4e-12:516:60//AG001050
F-HEMBA1001413
F-HEMBA1001415//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 410I8, WORKING DRAFT SEQUENCE.//0.98:177:64//AL031732
F-HEMBA1001432//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.0e-177:859:97//AC006146
F-HEMBA1001433//Homo sapiens clone DJ0892G19, complete sequence.//2.0e-35:376:64//AC004917
F-HEMBA1001435//Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.//1.2e-74:284:84//AC005670
F-HEMBA1001442//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-66, complete sequence.//0.056:194:63//AL010138
F-HEMBA1001446//Homo sapiens chromosome 4 clone B150J4 map 4q25, complete sequence.//0.96:328:61//AC004047
F-HEMBA1001450
F-HEMBA1001454//Human DNA sequence from clone 598A24 on chromosome Xp11.1-11.23 Contains zinc finger X-linked proteins ZXDA, ZXDB, ESTs and STS, complete sequence.//2.0e-47:468:73//AL031115
F-HEMBA1001455//CIT978SK-32J2.TV CIT978SK Homo sapiens genomic clone 32J2, genomic survey sequence.//1.5e-05:223:65//B78859
F-HEMBA1001463//cSRL-69d1-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-69d1, genomic survey sequence.//5.1e-66:564:77//B05652
F-HEMBA1001476//Homo sapiens mRNA for KIAA0572 protein, partial cds.//1.9e-102:489:99//AB011144
F-HEMBA1001478//HS_2228_A2_B03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=6 Row=C, genomic survey sequence.//4.5e-40:275:88//AQ032041
F-HEMBA1001497//Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains ESTs, STSs, GSSs, a putative CpG island and genomic marker D6S1553, complete sequence.//7.7e-47:311:85//AL031133
F-HEMBA1001510//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//2.0e-130:699:93//U89337
F-HEMBA1001515//Homo sapiens chromosome 19, cosmid F24866, complete sequence.//4.1e-114:711:85//AC005794
F-HEMBA1001517//Homo sapiens BAC clone RG459N13 from 7p15, complete sequence.//5.7e-162:769:98//AC004549
F-HEMBA1001522//Caenorhabditis elegans cosmid ZK328.//8.6e-17:498:61//U50193
F-HEMBA1001526//Human DNA sequence from cosmid 444G9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs and CpG islands.//0.31:120:69//Z98258

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F-HEMBA1001533
F-HEMBA1001557//Chionoecetes opilio (clone COP41) DNA microsatellite repeat regions.//7.0e-25:303:72//L49136
F-HEMBA1001566//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//7.2e-18:805:60//AL021026
F-HEMBA1001569//Homo sapiens mRNA for vesicle associated membrane protein 2 (VAMP2).//1.1e-64:338:95//AJ225044
F-HEMBA1001570//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//2.1e-148:698:99//AC004453
F-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.2e-173:678:99//AJ012449
F-HEMBA1001581//Homo sapiens clone DJ1158B01, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.30:484:59//AC004980
F-HEMBA1001585
F-HEMBA1001589//Human BAC clone RG317G18 from 7q31, complete sequence.//0.98:197:63//AC002432
F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds.//8.2e-109:855:78//D50918
F-HEMBA1001608//RPCI11-72E2.TJ RPCI11 Homo sapiens genomic clone R-72E2, genomic survey sequence.//3.8e-05:235:64//AQ267131
F-HEMBA1001620//Oryza sativa RINO1 mRNA for myo-inositol phosphate synthase, complete cds.//3.8e-40:719:64//AB012107
F-HEMBA1001635//HS_3208_A1_D07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3208 Col=13 Row=G, genomic survey sequence.//1.4e-15:120:90//AQ176944
F-HEMBA1001636//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.15:221:64//AC004216
F-HEMBA1001640//HS_3253_B2_D03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3253 Col=6 Row=H, genomic survey sequence.//9.1e-52:278:95//AQ216058
F-HEMBA1001647//H.sapiens gene for plectin.//0.00052:629:61//Z54367
F-HEMBA1001651//Salmo salar DNA for a cryptic repeat.//7.9e-08:270:64//AJ012206
F-HEMBA1001655//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//5.9e-164:802:97//AC005368
F-HEMBA1001658//M.musculus COL3A1 gene for collagen alpha-I.//2.4e-30:742:62//X52046
F-HEMBA1001661//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.2e-144:682:99//AC005740
F-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//6.1e-152:725:98//AF072247
F-HEMBA1001675//RPCI11-54F8.TV RPCI11 Homo sapiens genomic clone R-54F8, genomic survey sequence.//5.3e-75:341:85//AQ082126
F-HEMBA1001678//Homo sapiens Xp22 PAC RPCI1-167A22 (from Roswell Park Cancer Center) complete sequence.//8.4e-54:551:74//AC002349
F-HEMBA1001681
F-HEMBA1001702//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//0.94:676:54//AE001398
F-HEMBA1001709//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 702J19, WORKING DRAFT SEQUENCE.//0.74:659:58//AL033531
F-HEMBA1001711//Lysiphlebus melandriicola NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds.//3.0e-07:413:60//AF069178
F-HEMBA1001712//Homo sapiens BAC clone RG041H04 from 7q21-q22, complete sequence.//0.091:315:61//AC004519
F-HEMBA1001714//Rattus norvegicus mitochondrial ATPase inhibitor gene, complete cds.//1.6e-28:218:75//U12250
F-HEMBA1001718//HS_3056_A2_H08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3056 Col=16 Row=O, genomic survey sequence.//2.0e-79:383:99//AQ106367
F-HEMBA1001723//HS_2188_A2_D02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=4 Row=G, genomic survey sequence.//3.8e-28:174:94//AQ116793
F-HEMBA1001731//HS_3021_A1_A11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3021 Col=21 Row=A, genomic survey sequence.//2.5e-11:420:62//AQ154658

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F-HEMBA1001734//Homo sapiens chromosome Y, clone 264.M.20, complete sequence.//0.00060:392:60// AC004617
F-HEMBA1001744//HS_3194_A1_D05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=G, genomic survey sequence.//5.8e-29:163:97//AQ252295
F-HEMBA1001745//Homo sapiens chromosome 9q34, clone 280C11, complete sequence.//0.66:627:59// AC002102
F-HEMBA1001746//HS_2163_B1_F04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2163 Col=7 Row=L, genomic survey sequence.//1.4e-16:238:70//AQ085995
F-HEMBA1001761//Genomic sequence from Mouse 9, complete sequence.//3.5e-52:198:86//AC002109
F-HEMBA1001781
F-HEMBA1001784//Genomic sequence from Human 9q34, WORKING DRAFT SEQUENCE, 2 unordered-pieces.//5.5e-13:296:65//AC002099
F-HEMBA1001791//Homo sapiens DNA from chromosome 19-cosmids R31158, R31874, and R28125, genomic sequence, complete sequence.//0.18:534:59//AF038458
F-HEMBA1001800//CrT-HFP-2049N5.TF CIT-HSP Homo sapiens genomic clone 2049N5, genomic survey sequence.//2.2e-40:335:80//AQ009222
F-HEMBA1001803//M.musculus (Ba1b/C) P/L01 mRNA.//1.7e-25:286:74//Z31360
F-HEMBA1001804//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.9e-58:358:89//M21977
F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//7.8e-174:809:98// AB007969
F-HEMBA1001809//Bovine herpesvirus 1 complete genome.//9.0e-09:639:57//AJ004801
F-HEMBA1001815
F-HEMBA1001819//HS_3079_B1_E04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079 Col=7 Row=J, genomic survey sequence.//1.4e-79:396:97//AQ186616
F-HEMBA1001820//Homo sapiens BAC clone GS165L15 from 7p15, complete sequence.//0.00026:436:60// AC005013
F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds.//1.2e-40:510:65//AF064243
F-HEMBA1001824//Homo sapiens expanded SCA7 CAG repeat.//6.1e-20:344:68//AF020275
F-HEMBA1001835//Homo sapiens BAC clone RG017K18 from 7q31, complete sequence.//0.0094:553:58// AC005161
F-HEMBA1001844//Homo sapiens chromosome Xp22-135-136 clone GSHB-5671I1, WORKING DRAFT SEQUENCE, 35 unordered pieces.//1.2e-22:316:70//AC005867
F-HEMBA1001847//M.musculus Zfp-29 gene for zinc finger protein.//5.3e-27:397:69//X55126
F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds.//8.8e-184:865:98//AB014517
F-HEMBA1001864//Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence.// 0.38:337:62//AC005395
F-HEMBA1001866//Caenorhabditis elegans cosmid F48E3.//1.4e-10:224:63//U28735
F-HEMBA1001869//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//6.7e-98:288:91// AC005065
F-HEMBA1001888//Human Chromosome 11p15.5 PAC clone pDJ915f1 containing KvLQT1 gene, complete sequence.//4.9e-114:476:84//AC003693
F-HEMBA1001896//Bos taurus pyruvate dehydrogenase phosphatase regulatory subunit precursor, mRNA, complete cds.//2.2e-137:839:86//AF026954
F-HEMBA1001910//Homo sapiens Chromosome 2p13 BAC Clone h173, complete sequence.//0.90:221:63// AC003065
F-HEMBA1001912//HS_2237_A1_C10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=19 Row=E, genomic survey sequence.//9.7e-76:364:100//AQ033732
F-HEMBA1001913//Leishmania major chromosome 3 clone L4625 strain Friedlin, WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.00063:219:65//AC005766
F-HEMBA1001915//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epitherium cancer , segment 5/10.// 0.00011:366:63//AB020873
F-HEMBA1001918//Pneumocystis carinii gene for major surface glycoprotein MSG105, exon1-2, complete cds.// 0.00024:562:58//D82031
F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//2.1e-184: 855:99//AF000145
F-HEMBA1001939//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Aminotransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2)

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pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.1e-42:380:80//AL022310
F-HEMBA1001940//Homo sapiens clone DJ1093I16, WORKING DRAFT SEQUENCE, 5 unordered pieces.//7.5e-175:861:97//AC005629
F-HEMBA1001942//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//0.097:107:71//AC006057
F-HEMBA1001945//Drosophila F family transposable element F12 3' region.//0.94:140:65//X01934
F-HEMBA1001950//H.sapiens CpG island DNA genomic Mse1 fragment, clone 15b5, forward read cpg15b5.ft1q.//1.4e-27:168:95//Z54728
F-HEMBA1001960//Locusta migratoria mRNA for nAChR alpha1 subunit.//0.010:108:71//AJ000390
F-HEMBA1001962//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//9.7e-05:494:60//AC005507
F-HEMBA1001964
F-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs, complete sequence.//9.6e-122:373:99//AL031178
F-HEMBA1001979//HS_3067_B1_A06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3067 Col=11 Row=B, genomic survey sequence.//0.43:193:64//AQ143506
F-HEMBA1001987//Plasmodium falciparum MAL3P6, complete sequence.//1.0:428:56//Z98551
F-HEMBA1001991//HS_2237_A2_G09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=18 Row=M, genomic survey sequence.//4.3e-05:240:64//AQ067283
F-HEMBA1002003//protein phosphatase 2C isoform [rats, liver, mRNA, 1950 nt].//2.7e-33:364:74//S90449
F-HEMBA1002008//WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00032:214:68//AC005948
F-HEMBA1002018
F-HEMBA10020227/Human p37NB mRNA, complete cds.//0.014:58:96//U32907
F-HEMBA1002035//Mouse transcriptional control element.//7.8e-07:200:69//M17284
F-HEMBA1002039//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//0.31:497:58//AL031053
F-HEMBA1002049//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//4.5e-42:532:63//AC005216
F-HEMBA1002084//Homo sapiens chromosome 19 cosmid F15386, genomic sequence, complete sequence.//0.81:435:59//AF025422
F-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//7.2e-130:769:87//U92703
F-HEMBA1002100//Homo sapiens PAC clone DJ0991G20, complete sequence.//1.3e-47:124:96//AC004943
F-HEMBA1002102//Xenopus laevis mRNA for xSox7 protein, complete cds.//2.7e-13:132:71//D83649
F-HEMBA1002113//F.rubripes GSS sequence, clone 063K10bB4, genomic survey sequence.//0.029:142:66//Z88840
F-HEMBA1002119//Human Chromosome 11 pac pDJ1173a5, complete sequence.//1.3e-14:515:62//AC000378
F-HEMBA1002125//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds.//0.98:222:61//AF031815
F-HEMBA1002139//Caenorhabditis elegans cosmid F55C9, complete sequence.//0.0081:371:60//Z81549
F-HEMBA1002144//Saccharomyces cerevisiae mitochondrion transfer RNA-Met (tRNA-Met) gene, oxil gene, and ORF1.//4.9e-06:341:61//L36888
F-HEMBA1002150//Homo sapiens mRNA for KIAA0720 protein, partial cds.//0.00017:353:62//AB018263
F-HEMBA1002151
F-HEMBA1002153//CITBI-E1-2519120.TR CITBI-E1 Homo sapiens genomic clone 2519I20, genomic survey sequence.//8.5e-61:334:94//AQ277613
F-HEMBA1002160//Homo sapiens clone DJ1189D06, complete sequence.//8.5e-44:385:77//AC005232
F-HEMBA1002161//Coturnix coturnix slow myosin heavy chain 2 (qmyhc2) mRNA, partial cds.//2.1e-59:571:74//AF006829
F-HEMBA1002162//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//5.3e-53:698:67//AC006210
F-HEMBA1002166//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//1.2e-50:319:78//AL008712
F-HEMBA1002177//Homo sapiens BAC clone RG293F11 from 7q21-7q22, complete sequence.//2.5e-18:150:88//AC000066
F-HEMBA1002185//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00066:466:59//AC004825

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F-HEMBA1002189//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.3e-23:176:77//AC005015
F-HEMBA1002191//Homo sapiens mRNA for KIAA0689 protein, partial cds.//1.0:382:59//AB014589
F-HEMBA1002199//Homo sapiens chromosome 4 clone B55B24 map 4q25, complete sequence.//1.8e-20:368:66//AC005150
F-HEMBA1002204//HS_2055_A1_H09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=17 Row=O, genomic survey sequence.//1.2e-06:178:65//AQ235350
F-HEMBA1002212//S.cerevisiae chromosome IV reading frame ORF YDL101c.//0.035:345:60//Z74149
F-HEMBA1002215//M.musculus mRNA for testin.//4.6e-80:504:87//X78989
F-HEMBA1002226//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.7e-63:336:74//AC003035
F-HEMBA1002229//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.//2.6e-39:311:81//AC006044
F-HEMBA1002237//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//1.6e-12:397:64//AC004861
F-HEMBA1002241
F-HEMBA1002253
F-HEMBA1002257//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds.//3.5e-151:731:97//AF061936
F-HEMBA1002265//Human DNA sequence from cosmid N28H9 on chromosome 22q11.2-qter contains ESTs, STS and endogenous retrovirus.//1.3e-09:313:62//Z71183
F-HEMBA1002267
F-HEMBA1002270//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//0.069:495:58//AC006210
F-HEMBA1002321//Homo sapiens PAC clone DJ0991O23, complete sequence.//0.019:564:58//AC004944
F-HEMBA1002328//CIT-HSP-2387N15.TF.1 CIT-HSP Homo sapiens genomic clone 2387N15, genomic survey sequence.//1.8e-71:346:99//AQ240836
F-HEMBA1002337//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence.//0.84:547:57//AB020754
F-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds.//2.4e-185:872:98//AB018314
F-HEMBA1002348//CIT-HSP-2372K24.TR CIT-HSP Homo sapiens genomic clone 2372K24, genomic survey sequence.//9.1e-33:230:75//AQ110676
F-HEMBA1002349//Plasmodium falciparum histidine-rich protein II (HRP II) gene, complete cds.//9.4e-06:504:57//U69551
F-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//7.3e-188:872:99//AF092563
F-HEMBA1002381//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11.//2.1e-20:262:72//AB020868
F-HEMBA1002389//D.discoideum spore coat 60 (sp60) gene, 5' flank.//0.010:95:73//M34546
F-HEMBA1002417//Canis familiaris ZO-3 (zo-3) mRNA, complete cds.//6.2e-120:767:85//AF023617
F-HEMBA1002419//HS-1047-A1-F01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=1 Row=K, genomic survey sequence.//7.6e-06:111:76//B38165
F-HEMBA1002430//HS_3137_B2_F10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3137 Col=20 Row=L, genomic survey sequence.//1.6e-56:367:88//AQ148697
F-HEMBA1002439//Dictyostelium discoideum actin 8 gene, 3' UTR.//0.67:129:64//M25216
F-HEMBA1002458//Mus musculus REX-3 mRNA, complete cds.//1.1e-30:274:72//AF051347
F-HEMBA1002460//Homo sapiens clone DJ1137M13, complete sequence.//4.0e-173:822:98//AC005378
F-HEMBA1002462//Sequence 41 from patent US 5708157.//9.8e-51:519:73//I80067
F-HEMBA1002469//Human mRNA for KIAA0122 gene, partial cds.//4.0e-108:603:92//D50912
F-HEMBA1002475//Streptomyces coelicolor cosmid 2H4.//0.0068:626:57//AL031514
F-HEMBA1002477//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//1.5e-40:349:78//AC005034
F-HEMBA1002486
F-HEMBA1002495//HS_3218_B1_A12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=23 Row=B, genomic survey sequence.//1.0:179:67//AQ181410
F-HEMBA1002498//Homo sapiens full-length insert cDNA clone ZD76B01.//1.4e-129:619:98//AF086404
F-HEMBA1002503//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.9e-24:306:68//AC004873

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F-HEMBA1002508//Homo sapiens chromosome 19, cosmid R33516, complete sequence.//2.9e-76:464:83//AC004799
F-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//2.8e-157:738:98//AJ011972
F-HEMBA1002515//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 407F11, WORKING DRAFT SEQUENCE.//2.6e-07:307:64//AL022329
F-HEMBA1002538//HS_2185_B2_B04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2185 Col=8 Row=D, genomic survey sequence.//4.7e-37:339:78//AQ298315
F-HEMBA1002542//HS_3197_B2_B10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=20 Row=D, genomic survey sequence.//3.2e-70:372:95//AQ188792
F-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds.//3.5e-137:655:98//AF016903
F-HEMBA1002552//Human Hep27 protein mRNA, complete cds.//8.8e-07:173:68//U31875
F-HEMBA1002555//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.2e-15:628:60//AC004670
F-HEMBA1002558//Human Xp22 BAC CT-285I15 (from CalTech/Research Genetics) , PAC RPCI1-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//2.3e-41:353:76//AC002366
F-HEMBA1002561//Homo sapiens chromosome 17, clone HRPC29G21, complete sequence.//1.1e-39:538:66//AC003687
F-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds.//1.3e-140:457:99//AF075587
F-HEMBA1002583//CIT-HSP-2321D3.TR CIT-HSP Homo sapiens genomic clone 2321D3, genomic survey sequence.//5.1e-79:385:99//AQ038102
F-HEMBA1002590//Homo sapiens chromosome 17, clone hRPK.167_N_20, complete sequence.//1.9e-35:430:70//AC005940
F-HEMBA1002592//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//4Ae-19:303:71//Z93403
F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds.//4.4e-175:820:99//AB011169
F-HEMBA1002621//Homo sapiens PAC clone DJ0650P09 from 7q21, complete sequence.//0.14:353:58//AC004413
F-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//2.9e-187:632:97//AB018351
F-HEMBA1002628//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.5e-05:792:58//AC004153
F-HEMBA1002629//Streptomyces coelicolor cosmid 1A9.//8.4e-08:576:58//AL034446
F-HEMBA1002645//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 153G14, WORKING DRAFT SEQUENCE.//5.6e-47:222:86//AL031118
F-HEMBA1002651//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//3.8e-182:859:99//AC004839
F-HEMBA1002659//Z.mobilis alcohol dehydrogenase I (adhA) gene, complete cds.//0.97:144:66//M32100
F-HEMBA1002661//Homo sapiens PAC clone DJ0698G21 from 7p21-p22, complete sequence.//1.3e-116:774:84//AC004535
F-HEMBA1002666
F-HEMBA1002678//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1137F22, WORKING DRAFT SEQUENCE.//5.7e-156:750:98//AL034421
F-HEMBA1002679//nbxb0002cC12r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0002F23r, genomic survey sequence.//4.3e-09:517:58//AQ051621
F-HEMBA1002688//Herpes simplex virus type 2 (strain HG52), complete genome.//8.3e-20:651:61//Z86099
F-HEMBA1002696//Mus musculus proteasome regulator PA28 beta subunit gene, complete cds.//7.6e-62:306:81//AF060195
F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete cds.//1.9e-10:327:62//AB007924
F-HEMBA1002712
F-HEMBA1002716//HS_3064_A1_C10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=19 Row=E, genomic survey sequence.//8.4e-97:491:96//AQ142980
F-HEMBA1002728//Homo sapiens chromosome 5, BAC clone 205e20 (LBNL H170), complete sequence.//6.1e-21:217:77//AC004782
F-HEMBA1002730//Human platelet glycoprotein IIIa (GPIIIa) gene, exon 1.//0.57:125:67//M57481
F-HEMBA1002742//RPCI11-39J10.TP RPCI-11 Homo sapiens genomic clone RPCI-11-39J10, genomic survey sequence.//1.1e-86:414:99//AQ029102

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F-HEMBA1002746//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//7.1e-70:303:82//AC003694
F-HEMBA1002748//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 410I8, WORKING DRAFT SEQUENCE.//0.096:212:62//AL031732
F-HEMBA1002750//Homo sapiens chromosome 5, PAC clone 170m10 (LBNL H89), complete sequence.//6.7e-40:232:70//AC004622
F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds.//9.0e-177:834:98//AB011126
F-HEMBA1002770//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.3e-140:840:88//E12829
F-HEMBA1002777//F.rubripes GSS sequence, clone 189C06dB12, genomic survey sequence.//1.1e-28:263:77//AL007965
F-HEMBA1002779//CIT-HSP-2333I1.TF CIT-HSP Homo sapiens genomic clone 2333I1, genomic survey sequence.//1.8e-32:180:98//AQ036891
F-HEMBA1002780//Homo sapiens PAC clone DJ0244J05 from 5q31, complete sequence.//7.0e-06:199:67//AC004592
F-HEMBA1002794//H.sapiens mRNA for protein kinase C mu.//0.00015:244:67//X75756
F-HEMBA1002801//Plasmodium falciparum MAL3P2, complete sequence.//0.0010:534:57//AL034558
F-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//1.1e-167:820:97//AF071185
F-HEMBA1002816//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.1e-113:254:90//AC005043
F-HEMBA1002818//Cricetulus griseus H411 precursor (H411) mRNA, complete cds.//1.2e-122:760:86//AF046870
F-HEMBA1002826//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//0.0055:235:65//AL022153
F-HEMBA1002833//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence.//1.4e-170:744:99//AC004707
F-HEMBA1002850//Ephedrus persicae NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds.//1.3e-05:334:59//AF069186
F-HEMBA1002863//CIT-HSP-2323A16.TF CIT-HSP Homo sapiens genomic clone 2323A16, genomic survey sequence.//2.9e-140:750:93//AQ028419
F-HEMBA1002876//HS_2270_B1_H03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=5 Row=P, genomic survey sequence.//0.44:163:64//AQ164031
F-HEMBA1002886
F-HEMBA1002896//Homo sapiens chromosome 5, P1 clone 793C5 (LBNL H58), complete sequence.//0.00015:277:61//AC005195
F-HEMBA1002921
F-HEMBA1002924//CIT-HSP-2171H4.TR CIT-HSP Homo sapiens genomic clone 2171H4, genomic survey sequence.//0.0016:175:66//B89715
F-HEMBA1002934//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE.//1.2e-169:797:98//AL031681
F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds.//4.9e-173:803:99//AB011148
F-HEMBA1002937//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 702J19, WORKING DRAFT SEQUENCE.//1.2e-163:411:99//AL033531
F-HEMBA1002939//RPCI11-74O14.TJ RPCI11 Homo sapiens genomic clone R-74O14, genomic survey sequence.//1.7e-41:215:99//AQ266676
F-HEMBA1002944//RPCI11-55C2.TV RPCI11 Homo sapiens genomic clone R-55C2, genomic survey sequence.//1.7e-37:375:74//AQ082240
F-HEMBA1002951//Homo sapiens chromosome 19, cosmid F20887, complete sequence.//0.00074:683:58//AC005578
F-HEMBA1002954//RPCI11-79F7.TV RPCI11 Homo sapiens genomic clone R-79F7, genomic survey sequence.//6.1e-24:250:78//AQ284146
F-HEMBA1002968//HS_2262_B2_G04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2262 Col=8 Row=N, genomic survey sequence.//0.99:270:60//AQ217059
F-HEMBA1002970//RPCI11-5L24.TV RPCI-11 Homo sapiens genomic clone RPCI-11-5L24, genomic survey sequence.//1.4e-10:189:71//B49289
F-HEMBA1002971//CIT-HSP-2363L16.TF CIT-HSP Homo sapiens genomic clone 2363L16, genomic survey sequence.//4.3e-21:181:80//AQ080538
F-HEMBA1002973//Rattus norvegicus Wistar 3',5'-cyclic AMP phosphodiesterase (PDE4-10) gene, exon 10.//2.5e-40:257:89//U01290

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F-HEMBA1002997//CIT-HSP-2387H15.TF.1 CIT-HSP Homo sapiens genomic clone 2387H15, genomic survey sequence.//9.5e-17:128:92//AQ240797
F-HEMBA1002999//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//3.1e-62:713:73//U20286
F-HEMBA1003021//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.5e-50:331:85//AC005484
F-HEMBA1003033//Drosophila melanogaster, chromosome 3L, region 62A10-62B5, P1 clones DS02777, DS03222, DS02345, and DS04808, complete sequence.//2.6e-20:357:66//AC005557
F-HEMBA1003034//Human DNA sequence from 4PTEL, Huntington's Disease Region, chromosome 4p16.3.//4.5e-60:415:73//Z95704
F-HEMBA1003035//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//2.3e-05:591:57//AC004617
F-HEMBA1003037//RPCI11-88F2.TJ RPCI11 Homo sapiens genomic clone R-88F2, genomic survey sequence.//0.68:230:60//AQ286677
F-HEMBA1003041//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//8.1e-128:550:94//AC004983
F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds.//1.0e-164:777:98//AF054182
F-HEMBA1003064//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.5e-07:744:59//AC005505
F-HEMBA1003067//Rat dynorphin gene, exon 3.//1.0:140:63//M32783
F-HEMBA1003071//Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds.//1.5e-20:595:65//U72648
F-HEMBA1003077//CIT-HSP-2366J21.TF CIT-HSP Homo sapiens genomic clone 2366J21, genomic survey sequence.//4.4e-33:176:99//AQ080257
F-HEMBA1003078//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceeded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//9.4e-43:478:70//Z99297
F-HEMBA1003079//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//0.96:57:85//AC004673
F-HEMBA1003083//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//8.0e-74:359:81//AC004548
F-HEMBA1003086//Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.//3.6e-11:734:58//AF001550
F-HEMBA1003096//Sequence 4 from patent US 5440017.//5.7e-56:594:71//I13750
F-HEMBA1003098//Human DNA sequence from cosmid SRL11M20, chromosome region 11p13. Contains EST and STS.//1.9e-09:230:69//Z83308
F-HEMBA1003117//Mouse TIS11 primary response gene, complete cds.//0.00054:480:60//M58564
F-HEMBA1003129//HS_3139_B2_F05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3139 Col=10 Row=L, genomic survey sequence.//2.3e-100:510:97//AQ187635
F-HEMBA1003133//Mouse BAC CitbCJ7 219m7, genomic sequence, complete sequence.//1.3e-78:370:90//AC005259
F-HEMBA1003136
F-HEMBA1003142//Homo sapiens full-length insert cDNA clone ZC39B06.//6.9e-121:563:100//AF086197
F-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//6.7e-183:850:99//AJ005670
F-HEMBA1003166//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 ~complete genomic sequence, complete sequence.//3.8e-27:229:76//AC002302
F-HEMBA1003175//Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, WORKING DRAFT SEQUENCE.//9.4e-09:837:58//AB000882
F-HEMBA1003179//Homo sapiens DNA sequence from Fosmid 27C3 on chromosome 22q11.2-qter. Contains two possibly alternatively spliced unknown genes, one with homology to a worm protein. Contains ESTs, complete sequence.//5.4e-115:174:98//AL022325
F-HEMBA1003197//Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence.//1.1e-05:473:59//AC005824
F-HEMBA1003199//Rattus norvegicus Sprague-Dawley thyroid hormone receptor alpha gene, exon 1.//1.6e-05:367:61//U09302
F-HEMBA1003202//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//9.0e-23:247:73//AC004003

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F-HEMBA1003204//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 409J21, WORKING DRAFT SEQUENCE.//4.7e-26:141:83//Z83824
F-HEMBA1003212//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.//1.9e-31:158:86//AC002037
F-HEMBA1003220//Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.4e-24:284:75//AC004150
F-HEMBA1003222//RPCI11-47P17.TJ RPCI11 Homo sapiens genomic clone R-47P17, genomic survey sequence.//8.7e-39:202:99//AQ202885
F-HEMBA1003229//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence.//0.86:227:62//AB019230
F-HEMBA1003235//Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence.//8.6e-05:372:61//AE001373
F-HEMBA1003250//HS-1063-A1-H02-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 796 Col=3 Row=O, genomic survey sequence.//0.00032:57:96//B46142
F-HEMBA1003257//H.sapiens mRNA for RDC-1 POU domain containing protein.//2.2e-08:531:59//X64624
F-HEMBA1003273//H.sapiens flow-sorted chromosome 6 HindIII-fragment, SC6pA19H4.//0.070:267:64//Z78949
F-HEMBA1003276//CIT-HSP-2301B4.TF CIT-HSP Homo sapiens genomic clone 2301B4, genomic survey sequence.//5.2e-08:295:63//AQ015073
F-HEMBA1003278//HS_3075_A1_G09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=17 Row=M, genomic survey sequence.//0.98:399:58//AQ120599
F-HEMBA1003281//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//4.8e-101:277:97//AC005840
F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1,4-galactosyltransferase mRNA, complete cds.//9.0e-145:539:97//AF038662
F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//5.0e-166:799:98//AB011109
F-HEMBA1003296//CITBI-E1-2507M8.TR CITBI-E1 Homo sapiens genomic clone 2507M8, genomic survey sequence.//1.9e-05:388:63//AQ262551
F-HEMBA1003304//Budworm mitochondrial partial transfer RNA-Met (tRNA-Met) gene, and partial 12S ribosomal RNA (12S rRNA) gene.//8.0e-05:388:62//L17343
F-HEMBA1003309//Crassostrea gigas clone CN20 microsatellite sequence.//0.0017:210:64//AF051177
F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds.//4.6e-188:865:99//AB001872
F-HEMBA1003322//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 169I5, WORKING DRAFT SEQUENCE.//2.4e-54:316:87//Z93015
F-HEMBA1003327//CIT-HSP-2024C24.TRB CIT-HSP Homo sapiens genomic clone 2024C24, genomic survey sequence.//8.4e-12:166:76//B67147
F-HEMBA1003328//HS_2230_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2230 Col=16 Row=P, genomic survey sequence.//0.026:128:71//AQ153313
F-HEMBA1003330//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//4.0e-160:745:99//AF045555
F-HEMBA1003348//HS_3194_A1_G05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=M, genomic survey sequence.//5.0e-79:381:99//AQ173779
F-HEMBA1003369//H.vulgare GAA-satellite DNA.//0.12:89:71//Z50100
F-HEMBA1003370//Homo sapiens cosmid 123E15, complete sequence.//3.5e-32:199:80//AF024533
F-HEMBA1003373//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SEQUENCE.//0.019:117:71//AL034405
F-HEMBA1003376//Human clone HS4.66 Alu-Ya5 sequence.//4.2e-30:196:85//U67229
F-HEMBA1003380//Homo sapiens DNA sequence from clone 394P21 on chromosome 1p36.12-36.13. Contains the PAX7 gene, locus D1S2644, ESTs and STSs, complete sequence.//4.6e-22:206:81//AL021528
F-HEMBA1003384//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00094:72:90//AC006026
F-HEMBA1003395//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//0.00041:826:57//AL031744
F-HEMBA1003402//CIT-HSP-2339K16.TR CIT-HSP Homo sapiens genomic clone 2339K16, genomic survey sequence.//2.4e-05:265:64//AQ056234
F-HEMBA1003403//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//4.3e-135:780:90//AC004066
F-HEMBA1003408

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F-HEMBA1003417//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//1.9e-41:239:95//AL031321
F-HEMBA1003418//Rattus norvegicus Wistar polymeric immunoglobulin receptor (PIGR) gene, 3'UTR and trinucleotide repeat microsatellites.//2.2e-06:247:64//U08273
F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds.//1.4e-149:697:99//AF051334
F-HEMBA1003447//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//1.7e-77:461:90//AC004066
F-HEMBA1003461//Rhodobacter sphaeroides FliH (fliH) gene, partial cds, F1il (flil) and FliJ (fliJ) genes, complete cds.//8.6e-08:752:58//U31090
F-HEMBA1003463//Homo sapiens chromosome 17, clone HCIT305D20, complete sequence.//0.089:172:68//AC004098
F-HEMBA1003480//Homo sapiens clone NH0523H20, complete sequence.//4.5e-150:562:97//AC005041
F-HEMBA1003528//Streptomyces fradiae gene for trypsinogen precursor, complete cds.//4.7e-09:433:60//D16687
F-HEMBA1003531//Homo sapiens PAC clone DJ1185I07 from 7q11.23-q21, complete sequence.//2.3e-48:297:90//AC004990
F-HEMBA1003538//Human complement C1r mRNA, complete cds.//4.3e-22:474:63//M14058
F-HEMBA1003545//Rattus norvegicus (clone 1.6kB) islet-2 mRNA, complete cds.//3.5e-143:805:91//L35571
F-HEMBA1003548
F-HEMBA1003555//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 447E6, WORKING DRAFT SEQUENCE.//3.4e-58:331:83//AL031724
F-HEMBA1003556//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete sequence.//6.0e-99:703:84//AC005913
F-HEMBA1003560//Bovine GTP-binding regulatory protein gamma-6 subunit mRNA, complete cds.//1.3e-99:587:89//J05071
F-HEMBA1003568//HS_3149_A1_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3149 Col=7 Row=E, genomic survey sequence.//4.1e-05:389:57//AQ166810
F-HEMBA1003569//Homo sapiens BAC clone NH0335J18 from 2, complete sequence.//1.6e-102:669:85//AC005539
F-HEMBA1003571//Dictyostelium discoideum RegA (regA) gene, complete cds.//0.00033:649:58//U60170
F-HEMBA1003579//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//0.00034:623:56//AL031744
F-HEMBA1003581//Mouse mRNA for talin.//3.3e-41:181:86//X56123
F-HEMBA1003591//Homo sapiens chromosome 16, BAC clone RPCI-11_192K18, complete sequence.//4.4e-70:273:94//AC006075
F-HEMBA1003595//Plasmodium falciparum chromosome 2, section 32 of 73 of the complete sequence.//6.0e-17:768:58//AE001395
F-HEMBA1003597//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//4.0e-09:777:56//AE001398
F-HEMBA1003598//Homo sapiens PAC clone DJ0537P09 from 7p11.2-p12, complete sequence.//1.3e-146:692:98//AC005153
F-HEMBA1003615//HS_2010_A2_A07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2010 Col=14 Row=A, genomic survey sequence.//1.1e-22:137:97//AQ226592
F-HEMBA1003617//Homo sapiens HRIHFB2157 mRNA, partial cds.//2.4e-169:501:97//AB015344
F-HEMBA1003621//Mus musculus PIAS3 mRNA, complete cds.//4.7e-37:165:92//AF034080
F-HEMBA1003622//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0024:514:58//AC005139
F-HEMBA1003630//CIT-HSP-2168N15.TR CIT-HSP Homo sapiens genomic clone 2168N15, genomic survey sequence.//6.5e-15:358:63//B92984
F-HEMBA1003637//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.0e-21:238:76//AC005077
F-HEMBA1003640//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 112K5, WORKING DRAFT SEQUENCE.//2.3e-15:371:63//Z85987
F-HEMBA1003645//A.thaliana 81kb genomic sequence.//1.0:529:57//X98130
F-HEMBA1003646
F-HEMBA1003656
F-HEMBA1003662//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence.//1.6e-175:824:98//AC005746
F-HEMBA1003667//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered piec-

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es.//1.1e-24:190:87//AC004765
F-HEMBA1003679//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//1.7e-162:579:99//AC005065
F-HEMBA1003680//H.sapiens DNA sequence.//7.3e-22:172:87//Z22322
F-HEMBA1003684//H.sapiens mRNA for Miz-1 protein.//0.0054:146:70//Y09723
F-HEMBA1003690//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//2.9e-72:606:77//AF039691
F-HEMBA1003692
F-HEMBA1003711//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//0.55:450:60//AC003101
F-HEMBA1003714
F-HEMBA1003715//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//3.0e-16:316:68//AL023575
F-HEMBA1003720//Homo sapiens chromosome 4 clone B227H22 map 4q25, complete sequence.//1.3e-41:483:73//AC004056
F-HEMBA1003725//CIT-HSP-2351H9.TF CIT-HSP Homo sapiens genomic clone 2351H9, genomic survey sequence./1.1e-112:532:99//AQ079348
F-HEMBA1003729//HS_3043_A1_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3043 Col=13 Row=I, genomic survey sequence.//1.6e-12:87:98//AQ129345
F-HEMBA1003733//Homo sapiens, clone hRPK.15_A_1, complete sequence.//4.7e-104:761:82//AC006213
F-HEMBA1003742//HS_3027_A2_B02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=4 Row=C, genomic survey sequence.//3.4e-08:67:97//AQ154731
F-HEMBA1003758//CIT-HSP-2379D18.TR CIT-HSP Homo sapiens genomic clone 2379D18, genomic survey sequence.//2.9e-10:310:63//AQ113513
F-HEMBA1003760//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//6.4e-114:714:86//AF060194
F-HEMBA1003773//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.078:378:58//AC005139
F-HEMBA1003783//Human DNA sequence from PAC 509L4 on chromosome 6q22.1-6q22.33. Contains SSX3 like pseudogene, EST, STS.//9.0e-135:804:89//Z99496
F-HEMBA1003784//Caenorhabditis elegans cosmid C55B6.//0.054:463:58//U88181
F-HEMBA1003799//Homo sapiens Chromosome 22q11.2 Cosmid Clone 105a In DGCR Region, complete sequence.//1.9e-44:425:76//AC000070
F-HEMBA1003803//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds.//0.95:198:62//L40178
F-HEMBA1003804//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence.//1.2e-138:275:99//AC004596
F-HEMBA1003805//Mus musculus quaking type I (QKI) mRNA, complete cds.//6.6e-148:753:95//U44940
F-HEMBA1003807//HS-1068-B1-G06-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 278 Col=11 Row=N, genomic survey sequence.//6.7e-07:241:67//B47212
F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cds.//1.0e-83:586:87//AB014516
F-HEMBA1003836//S.cerevisiae chromosome IX cosmid 9150.//5.1e-16:368:63//Z38125
F-HEMBA1003838//CIT-HSP-384J15.TR CIT-HSP Homo sapiens genomic clone 384J15, genomic survey sequence.//1.4e-45:180:90//B54810
F-HEMBA1003856//Homo sapiens chromosome 10 clone CIT9875K-1188B12 map 10p12.1, complete sequence.//0.0014:574:58//AC005875
F-HEMBA1003864//, complete sequence.//2.1e-91:234:95//AC005300
F-HEMBA1003866//Mus musculus semaphorin VIa mRNA, complete cds.//5.9e-81:853:71//AF030430
F-HEMBA1003879//H.sapiens CBP80 mRNA.//2.0e-08:87:95//X80030
F-HEMBA1003880//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//1.7e-180:853:98//AP000036
F-HEMBA1003885//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//4.5e-39:376:67//AC004079
F-HEMBA1003893//H.sapiens CpG island DNA genomic Mse1 fragment, clone 11b6, forward read cpg11b6.ft1a.//3.6e-32:173:99//Z59012
F-HEMBA1003902//RPCI11-26M20.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-26M20, genomic survey sequence.//8.2e-12:422:61//AQ003455
F-HEMBA1003908//Plasmodium falciparum chromosome 2, section 38 of 73 of the complete sequence.//0.0063:468:58//AE001401
F-HEMBA1003926//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 310O13, WORKING

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DRAFT SEQUENCE.//3.6e-27:278:76//AL031658
F-HEMBA1003937//Homo sapiens chromosome 3 subtelomeric region.//1.4e-55:315:81//AF109718
F-HEMBA1003939//HS-1047-A1-G04-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=7 Row=M, genomic survey sequence.//6.1e-09:413:63//B38195
F-HEMBA1003942//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.42:205:65//AC005140
F-HEMBA1003950//M.capricolum DNA for CONTIG MC072.//0.029:458:58//Z33058
F-HEMBA1003953//HS_2268_A1_B04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=7 Row=C, genomic survey sequence.//9.0e-07:239:64//AQ085098
F-HEMBA1003958//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence.//2.8e-57:424:74//AC004894
F-HEMBA1003959//RPCI11-78E8.TV RPCI11 Homo sapiens genomic clone R-78E8, genomic survey sequence.//4.3e-86:441:9611AQ285498
F-HEMBA1003976//HS_3146_A1_H09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3146 Col=17 Row=O, genomic survey sequence.//6.3e-10:129:80//AQ141146
F-HEMBA1003978
F-HEMBA1003985//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y105C5, WORKING DRAFT SEQUENCE.//1.0:258:60//Z98855
F-HEMBA1003987
F-HEMBA1003989//Streptomyces coelicolor cosmid 1A9.//0.40:238:61//AL034446
F-HEMBA1004000//Rattus norvegicus satellite sequence d0Mco2.//2.0e-07:116:70//U19354
F-HEMBA1004011//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.098:286:60//AC004710
F-HEMBA1004012//Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.//2.8e-185:896:97//AC005670
F-HEMBA1004015//Homo sapiens chromosome 17, clone hRPK.721_K_1, complete sequence.//6.3e-68:417:80//AC005411
F-HEMBA1004024//Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) complete sequence.//2.0e-47:418:77//AC005859
F-HEMBA1004038//Homo sapiens genomic DNA, chromosome 21q11.1, segment 23/28, WORKING DRAFT SEQUENCE.//1.6e-51:564:74//AP000052
F-HEMBA1004042//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//1.2e-05:636:55//AE001398
F-HEMBA1004045//Homo sapiens (subclone 1_g7 from BAC H76) DNA sequence, complete sequence.//1.9e-31:373:76//AC002252
F-HEMBA1004048//Homo sapiens DNA for P35-related protein, exon 2.//0.039:234:63//D63393
F-HEMBA1004049//Homo sapiens Xp22 GS-524I1 (Genome Systems Human BAC library), complete sequence.//4.8e-135:780:89//AC003106
F-HEMBA1004055//Human chromosome 3p21.1 gene sequence.//4.7e-09:457:58//L13435
F-HEMBA1004056//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 447C4, WORKING DRAFT SEQUENCE.//3.3e-25:246 :77//AL021977
F-HEMBA1004074//CIT-HSP-2053J5.TF CIT-HSP Homo sapiens genomic clone 2053J5, genomic survey sequence.//7.8e-24:233:76//B68555
F-HEMBA1004086//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//4.5e-08:614:59//U49822
F-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//5.9e-121:502:85//AF091234
F-HEMBA1004111//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0481P14; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.0e-36:317:80//AC006160
F-HEMBA1004131//Mus musculus clone OST2067, genomic survey sequence.//8.7e-24:320:71//AF046393
F-HEMBA1004132//HS_3226_B1_D10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3226 Col=19 Row=H, genomic survey sequence.//9.7e-13:232:71//AQ182017
F-HEMBA1004133
F-HEMBA1004138//HS_3036_B1_G11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=21 Row=N, genomic survey sequence.//0.0035:165:64//AQ294763
F-HEMBA1004143
F-HEMBA1004146

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F-HEMBA1004150//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.// 0.00011:618:60//Z96811
F-HEMBA1004164//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//2.9e-30:454:68//AC005913
F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//4.5e-133:649:97//AF067855
F-HEMBA1004199
F-HEMBA1004200//HS_2015_A1_B05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2015 Col=9 Row=C, genomic survey sequence.//8.5e-34:236:87//AQ247957
F-HEMBA1004202//Mus musculus chromosome 11, clone mCIT.268_P_23, complete sequence.//7.8e-59:216: 83//AC004807
F-HEMBA1004203//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.// 6.3e-98:173:98//AC005488
F-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//3.2e-166:791:98// U50748
F-HEMBA1004225//Plasmodium falciparum chromosome 2, section 61 of 73 of the complete sequence.//6.5e-08: 584:60//AE001424
F-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//8.0e-115:713:86// AF095927
F-HEMBA1004238
F-HEMBA1004241//CIC5B11.1 check: 4870 from: 1 to: 167234, complete sequence.//0.57:552:58//AC004708
F-HEMBA1004246//Human DNA sequence from clone 422F24 on chromosome 6q24.1-25.2. Contains a novel gene similar to C. elegans C02C2.5. Contains ESTs, STSs and GSSs, complete sequence.//6.1e-21:254:77// AL031010
F-HEMBA1004248//Rattus rattus insulin-induced growth-respons protein (CL-6) mRNA, complete cds.//1.7e-30: 315 :74//L13619
F-HEMBA1004264//Homo sapiens cosmid clone LUCA20 from 3p21.3, complete sequence.//4.4e-07:674:60// AC004693
F-HEMBA1004267//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence.//3.1e-78:335: 87//AC004707
F-HEMBA1004272//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.4e-176:856:97//AC005831
F-HEMBA1004274//HS_3064_B2_A04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-28:153:100//AQ136993
F-HEMBA1004275//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 501A4, WORKING DRAFT SEQUENCE.//5.2e-17:109:99//Z98051
F-HEMBA1004276//CIT-HSP-2387K6.TF.1 CIT-HSP Homo sapiens genomic clone 2387K6, genomic survey sequence.//5.0e-07:63:98//AQ240477
F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.//2.1e-185:868: 99//AF022795
F-HEMBA1004289//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence.// 1.0:387:59//AB013395
F-HEMBA1004295//Homo sapiens DNA, anonymous heat-stable fragment RP11-3A.//7.8e-06:92:89//AB012254
F-HEMBA1004306//Homo sapiens clone DJ0811N16, complete sequence.//0.00037:413:59//AC004897
F-HEMBA1004312//Rickettsia prowazekii strain Madrid E, complete genome; segment 2/4.//0.28:522:57// AJ235271
F-HEMBA1004321//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//7.1e-136:548:92// AC006130
F-HEMBA1004323//Human DNA sequence from PAC 450C20 on chromosome X.//1.3e-32:320:65//Z84720
F-HEMBA1004327//Homo sapiens mRNA for KIAA0522 protein, partial cds.//0.93:222:62//AB011094
F-HEMBA1004330//Homo sapiens clone DJ1196H06, WORKING DRAFT SEQUENCE, 4 unordered pieces.// 7.0e-168:895:93//AC004995
F-HEMBA1004334//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//4.6e-73:713:75//AC002980
F-HEMBA1004335//Human DNA-sequence *** SEQUENCING IN PROGRESS *** from clone 417M14, WORKING DRAFT SEQUENCE.//1.3e-25:121:85//AL024498
F-HEMBA1004341
F-HEMBA1004353//***ALU WARNING: Human Alu-Sc subfamily consensus sequence.//6.4e-38:278:85//U14571
F-HEMBA1004354//Human clone C3 CHL1 protein (CHLR1) mRNA, alternatively spliced, complete cds.//4.1e-45:

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190:92//U75968
F-HEMBA1004356
F-HEMBA1004366//P.falciparum complete gene map of plastid-like DNA (IR-A).//2.2e-07:736:57//X95275
F-HEMBA1004372//H.sapiens dystrophin gene intron 44.//1.0:129:62//X77644
F-HEMBA1004389//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//4.7e-42:237:94//M21977
F-HEMBA1004394//Plasmodium falciparum chromosome 2, section 39 of 73 of the complete sequence.//5.2e-05:519:59//AE001402
F-HEMBA1004396//Human BAC clone RG302F04 from 7q31, complete sequence.//4.0e-32:261:76//AC002463
F-HEMBA1004405//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.4e-07:693 :58//AC005507
F-HEMBA1004408//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-69:195:100//AC005037
F-HEMBA1004429//HS_3193_A1_B06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3193 Col=11 Row=C, genomic survey sequence.//5.1e-67:386:91//AQ172942
F-HEMBA1004433//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//3.2e-27:242:82//AC002554
F-HEMBA1004460//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.7e-75:590:81//AC004846
F-HEMBA1004461//Human DNA sequence from clone 657J8 on chromosome Xq26.1-26.3 Contains GSS, complete sequence.//0.045:215:66//AL034407
F-HEMBA1004479//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//5.2e-43:364:79//AF060194
F-HEMBA1004482//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//6.8e-17:791:59//AC005505
F-HEMBA1004499//Homo sapiens chromosome 17, clone hRPC.1073_F_15, complete sequence.//4.4e-125:251:94//AC004686
F-HEMBA1004502//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.012:635:57//AC004709
F-HEMBA1004506//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//2.8e-127:766:88//AC004453
F-HEMBA1004507
F-HEMBA1004509//Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14 (ESSAII project).//1.0e-13:244:67//AL021712
F-HEMBA1004534//Human mRNA for actin-binding protein (filamin) (ABP-280).//1.6e-72:678:74//X53416
F-HEMBA1004538//Sequence 1 from patent US 5612190.//0.00015:416:59//I36871
F-HEMBA1004542//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.95:202:64//AC005038
F-HEMBA1004554//Arabidopsis thaliana BAC T26D22.//0.45:624:56//AFO58826
F-HEMBA1004560//Human mRNA for KIAA0281 gene, complete cds.//9.1e-10:173:70//D87457
F-HEMBA1004573//Human BAC clone RG114A06 from 7q31, complete sequence.//6.1e-23:134:73//AC002542
F-HEMBA1004577//Homo sapiens Chromosome 16 BAC clone CIT987SK-582J2, complete sequence.//1.6e-15:190:77//AC004525
F-HEMBA1004586//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.1e-31:388:76//AC004895
F-HEMBA1004596//RPCI11-81O21.TJ RPCI11 Homo sapiens genomic clone R-81O21, genomic survey sequence.//2.2e-90:458:90//AQ285136
F-HEMBA1004604//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//8.6e-105:699:84//AF071316
F-HEMBA1004610//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//5.4e-20:267:72//AC004983
F-HEMBA1004617//CIT-HSP-2319H15.TF CIT-HSP Homo sapiens genomic clone 2319H15, genomic survey sequence.//6.2e-26:147:99//AQ034944
F-HEMBA1004629//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.6e-06:766:56//AC005504
F-HEMBA1004631//Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs, CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) like gene and STSs.//4.7e-73:412:92//Z83843
F-HEMBA1004632//Canine herpesvirus DNA for gene homolog of HSV1 UL16, EHV1 ORF 46, VZV ORF 44.//0.92:181:61//X90418

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F-HEMBA1004637//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//7.8e-47:784:65//X74904
F-HEMBA1004638//Rattus norvegicus homeodomain protein Nkx6.1 (nkx6.1) mRNA, complete cds.//6.4e-06:458:61//AF004431
F-HEMBA1004666//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y47D3, WORKING DRAFT SEQUENCE.//0.30:733:55//Z98865
F-HEMBA1004669//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence.//7.5e-136:521:98//AL031432
F-HEMBA1004670//Homo sapiens Chromosome 22q12 Cosmid Clone p90g5, complete sequence.//0.43:365:59//AC000045
F-HEMBA1004672
F-HEMBA1004693//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.096:651:54//AC005308
F-HEMBA1004697//CIT-HSP-2326C13.TR CIT-HSP Homo sapiens genomic clone 2326C13, genomic survey sequence.//0.23:238:65//AQ040642
F-HEMBA1004705//Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore X library) and PAC RPCI1-93D11 (from Roswell Park Cancer Center) complete sequence.//2.1e-27:375:72//AC002357
F-HEMBA1004709//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.6e-36:191:91//AC006210
F-HEMBA1004711//Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.//1.1e-133:639:99//AC005562
F-HEMBA1004725//RPCI11-75013.TJ RPCI11 Homo sapiens genomic clone R-75O13, genomic survey sequence.//6.2e-32:169:100//AQ266512
F-HEMBA1004730//Human BAC clone RG035E18 from 7q31, complete sequence.//8.0e-68:732:72//AC004029
F-HEMBA1004733//CIT-HSP-2305M23.TF CIT-HSP Homo sapiens genomic clone 2305M23, genomic survey sequence.//4.9e-18:209:69//AQ017556
F-HEMBA1004734//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds.//1.8e-13:451:62//AF028340
F-HEMBA1004736//Human DNA Sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs. complete sequence.//5.0e-87:646:78//Z94056
F-HEMBA1004748//Human BAC clone RG204I16 from 7q31, complete sequence.//0.24:526:57//AC002461
F-HEMBA1004751//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.4e-25:268:76//AC004913
F-HEMBA1004752//R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).//1.1e-07:503:61//X83546
F-HEMBA1004753//Homo sapiens Chromosome 12 Cosmid Clone 6e5, complete sequence.//4.5e-38:314:81//AC000028
F-HEMBA1004756//Homo sapiens, complete sequence.//1.4e-111:326:84//AC005854
F-HEMBA1004758//Sequence 29 from patent US 5534410.//3.9e-135:769:91//I23472
F-HEMBA1004763//Homo sapiens apoptosis inhibitor survivin gene, complete cds.//3.6e-47:404:79//U75285
F-HEMBA1004768//Homo sapiens PAC clone DJ0979P20 from 7q33-q35, complete sequence.//6.7e-107:890:78//AC004941
F-HEMBA1004770//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.9e-09:806:59//AC004709
F-HEMBA1004771//G.muris ribosomal RNA operon DNA encoding 16S, 23S and 5.8S ribosomal RNA.//0.69:239:61//X65063
F-HEMBA1004776
F-HEMBA1004778
F-HEMBA1004795//Drosophila melanogaster A-kinase anchor protein DAKAP550 mRNA, partial cds.//3.4e-46:778:64//AF003622
F-HEMBA1004803//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//4.3e-82:580:82//AC004617
F-HEMBA1004806//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//5.4e-07:642:59//AC005083
F-HEMBA1004807//Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3.//1.4e-46:171:92//L01042
F-HEMBA1004816//Homo sapiens calpastatin (CAST) gene, exons 10-14.//3.5e-31:546:66//M86257
F-HEMBA1004820//C.botulinum progenitor toxin complex genes.//0.0014:343:62//X87972

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F-HEMBA1004847//Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).//1.5e-85:512:88//X53744
F-HEMBA1004850//Homo sapiens TGF-beta type I receptor (TGFBR1) gene, exon 1.//0.0065:284:61//AF054590
F-HEMBA1004863//Genomic sequence from Mouse 11, complete sequence.//0.92:250:59//AC000400
F-HEMBA1004864
F-HEMBA1004865//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//3.6e-12:214:72//AL031120
F-HEMBA1004880//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//1.1e-08:255:69//AC004020
F-HEMBA1004889//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds.//0.062:155:69//U32943
F-HEMBA1004900//Plasmodium falciparum unidentified mRNA sequence.//0.00055:323:60//L12043
F-HEMBA1004909//Homo sapiens chromosome 17, clone 289A8, complete sequence.//9.6e-16:166:80//AC003051
F-HEMBA1004918//Turritella communis mitochondrial 16S ribosomal RNA gene, partial.//0.81:146:65//M94003
F-HEMBA1004923//Human DNA from overlapping chromosome 19-specific cosmids R32543,, and F15613 containing ZNF gene family member, genomic sequence, complete sequence.//1.4e-36:338:78//AC003006
F-HEMBA1004929//CIT-HSP-2373I16.TR CIT-HSP Homo sapiens genomic clone 2373I16, genomic survey sequence.//2.4e-86:443:96//AQ108676
F-HEMBA1004930//Homo sapiens PAC clone DJ0608H12 from 7q21, complete sequence.//4.6e-20:219:73//AC004109
F-HEMBA1004933//HS-1003-A1-E10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 497 Col=19 Row=I, genomic survey sequence.//1.4e-28:216:85//B30726
F-HEMBA1004934//Homo sapiens chromosome 21q22.3 PAC 267O10, complete sequence.//0.53:222:61//AF042091
F-HEMBA1004944//Homo sapiens clone DJ0736H05, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.2e-58:509:78//AC005482
F-HEMBA1004954//HS_2033_A2_A08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=16 Row=A, genomic survey sequence.//3.7e-47:243:99//AQ229758
F-HEMBA1004956//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.048:421:58//X95276
F-HEMBA1004960//Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 8.//0.89:333:58//Z97343
F-HEMBA1004972
F-HEMBA1004973//RPCI11-66P8.TK RPCI11 Homo sapiens genomic clone R-66P8, genomic survey sequence.//3.5e-22:245:77//AQ238471
F-HEMBA1004977//Homo sapiens full-length insert cDNA clone YZ83B08.//9.0e-11:84:98//AF086080
F-HEMBA1004978//CIT-HSP-2354E10.TR CIT-HSP Homo sapiens genomic clone 2354E10, genomic survey sequence.//0.0021:152:66//AQ075713
F-HEMBA1004980//HS_3018_A2_E04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=8 Row=I, genomic survey sequence.//1.9e-77:392:97//AQ071873
F-HEMBA1004983//Albinaria corrugata isolate cor. Prn1.1 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence.//0.0030:276:61//AF031680
F-HEMBA1004995//Homo sapiens chromosome 16, cosmid bridge clone 306E6 (LANL), complete sequence.//4.2e-138:640:99//AC005590
F-HEMBA1005008//Human mariner1 transposase gene, complete consensus sequence.//6.8e-20:160:88//U52077
F-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//2.0e-144:668:99//AF041474
F-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds.//1.4e-146:693:98//AB014548
F-HEMBA1005029//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence.//2.2e-115:668:90//AL009179
F-HEMBA1005035//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence.//4.6e-138:591:98//AC004596
F-HEMBA1005039//CIT-HSP-2338L5.TR CIT-HSP Homo sapiens genomic clone 2338L5, genomic survey sequence.//3.7e-61:271:88//AQ055486
F-HEMBA1005047//Mus musculus mRNA for Rab24 protein.//3.8e-17:218:73//Z22819
F-HEMBA1005050//Human Tis11d gene, complete cds.//0.079:251:63//U07802

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F-HEMBA1005062//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.018:560:56//AC004688
F-HEMBA1005066//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 774G10, WORKING DRAFT SEQUENCE.//3.4e-97:432:84//AL034410
F-HEMBA1005075//H.sapiens DNA 3' flanking simple sequence region clone wg2c3.//6.9e-07:176:68//X76589
F-HEMBA1005079//CIT-HSP-2325M21.TRB CIT-HSP Homo sapiens genomic clone 2325M21, genomic survey sequence.//2.1e-48:274:93//AQ038720
F-HEMBA1005083//HS_2248_B1_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2248 Col=9 Row=H, genomic survey sequence.//3.4e-06:230:64//AQ129575
F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//1.3e-161:762:98//AF080561
F-HEMBA1005113//L.esculentum microsatellite repeat DNA region.//0.0038:742:57//X90770
F-HEMBA1005123//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//9.6e-83:479:78//AC004854
F-HEMBA1005133//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//3.9e-24:576:64//AL023808
F-HEMBA1005149//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//4.7e-36:283:80//AC004542
F-HEMBA1005152//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.//5.0e-10:332:64//AC004469
F-HEMBA1005159//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE.//4.0e-10:734:58//AP000023
F-HEMBA1005185//H.sapiens CpG island DNA genomic Mse1 fragment, clone 91b2, forward read cpg91b2.ft1a.//12.2e-14:93:100//Z63847
F-HEMBA1005201//Drosophila melanogaster cosmid 152A3.//4.7e-35:679:64//AL009194
F-HEMBA1005202//Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).//6.7e-138:778:90//X53744
F-HEMBA1005206//Drosophila melanogaster Su(P) and anon-73B1 genes and partial o25 gene and Pros26 gene.//7.1e-12:376:62//AJ011320
F-HEMBA1005219//Homo sapiens mRNA for KIAA0445 protein, complete cds.//7.1e-05:411:60//AB007914
F-HEMBA1005223//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//3.5e-06:212:66//AC004542
F-HEMBA1005232//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.7e-07:625:57//AC005308
F-HEMBA1005241//Homo sapiens PAC clone DJ0777O23 from 7p14-p15, complete sequence.//8.7e-45:567:72//AC005154
F-HEMBA1005244//Homo sapiens chromosome X clone U177G4, U152H5, U168D5, 174A6, U172D6, and U186B3 from Xp22, complete sequence.//0.96:298:62//AC002365
F-HEMBA1005251
F-HEMBA1005252//Homo sapiens chromosome 17, clone hRPK.318_A_15, complete sequence.//4.5e-160:392:99//AC005837
F-HEMBA1005274//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence.//2.3e-05:496:60//AF069291
F-HEMBA1005275//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence.//5.7e-05:220:64//AL033521
F-HEMBA1005293//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//2.4e-20:338:65//U97018
F-HEMBA1005296
F-HEMBA1005304//Human DNA sequence from clone 364I22 on chromosome Xq21.31-22.3. Contains an STS and GSSs, complete sequence.//1.6e-51:381:78//AL031012
F-HEMBA1005311
F-HEMBA1005314//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE.//0.94:226:63//AP000031
F-HEMBA1005315//Homo sapiens BAC810, complete sequence.//9.5e-15:684:62//U85198
F-HEMBA1005318//Human DNA sequence from PAC 394F12 on chromosome X contains EST, STS, CpG island clone.//2.6e-05:472:59//Z83823
F-HEMBA1005331//Homo sapiens chromosome 17, clone hRPK.214_C_8, complete sequence.//3.3e-90:300:90//AC005803

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F-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial.//1.4e-151:740:97//AJ007581
F-HEMBA1005353//CIT-HSP-2310N10.TR CIT-HSP Homo sapiens genomic clone 2310N10, genomic survey sequence.//2.1e-86:438:97//AQ016145
F-HEMBA1005359//Human zinc finger protein ZNF137 mRNA, complete cds.//1.8e-98:500:88//U09414
F-HEMBA1005367//Mus musculus melastatin mRNA, complete cds.//8.3e-72:577:73//AF047714
F-HEMBA1005372//Human DNA sequence from PAC 293E14 contains ESTs, STS.//1.3e-07:274:66//Z82900
F-HEMBA1005374//Homo sapiens clone 277F10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.9e-48:611:69//AC004813
F-HEMBA1005382//HS_3063_B2_F11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3063 Col=22 Row=L, genomic survey sequence.//1.6e-27:154:98//AQ103204
F-HEMBA1005389//Plasmodium falciparum telomere nucleotide sequence.//4.0e-07:443:61//M23175
F-HEMBA1005394//CIT-HSP-2368B11.TR CIT-HSP Homo sapiens genomic clone 2368B11, genomic survey sequence.//7.6e-17:225:71//AQ076749
F-HEMBA1005403//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//4.5e-131:278:98//AL034379
F-HEMBA1005408//HS_3007_B2_G04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=8 Row=N, genomic survey sequence.//8.0e-06:218:66//AQ294366
F-HEMBA1005410//Human DNA sequence from cosmid cU120E2, on chromosome X contains Lowe oculocerebrorenal syndrome (OCRL) ESTs and STS.//1.5e-41:432:76//Z73496
F-HEMBA1005411
F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.//1.0e-169:537:99//AF041248
F-HEMBA1005426
F-HEMBA1005443//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//7.1e-37:260:76//AC006130
F-HEMBA1005447//CIT-HSP-2173N7.TR CIT-HSP Homo sapiens genomic clone 2173N7, genomic survey sequence.//5.0e-133:631:98//B93234
F-HEMBA1005468//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence.//1.5e-118:868:83//AL022576
F-HEMBA1005469//Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence.//1.2e-179:838:99//AC005212
F-HEMBA1005472//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING DRAFT SEQUENCE.//3.4e-20:187:74//AL031985
F-HEMBA1005474//Homo sapiens genomic DNA, chromosome 21q11.1, segment 12/28, WORKING DRAFT SEQUENCE.//4.1e-22:445:65//AP000041
F-HEMBA1005475//CIT-HSP-2322D14.TR CIT-HSP Homo sapiens genomic clone 2322D14, genomic survey sequence.//6.7e-51:269:97//AQ026941
F-HEMBA1005497//HS_3097_A2_G05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3097 Col=10 Row=M, genomic survey sequence.//1.4e-66:345:96//AQ103810
F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21, complete sequence.//5.4e-178:818:98//AC004957
F-HEMBA1005506//Mus musculus (clone 0EBF17) early B-cell factor (EBF) mRNA, complete cds.//2.6e-06:73:98//L12147
F-HEMBA1005508//Homo sapiens clone hRPK.1_A_1, complete sequence.//0.00012:455:60//AC006196
F-HEMBA1005511//Homo sapiens MHC class 1 region.//3.3e-43:421:77//AF055066
F-HEMBA1005513//Drosophila melanogaster males-absent on the first (mof) gene, complete cds.//2.3e-20:352:69//U71219
F-HEMBA1005517//Homo sapiens DNA for (CGG)n trinucleotide repeat region, isolate E7.//2.5e-08:431:62//AJ001216
F-HEMBA1005518//M.musculus mRNA for paladin gene.//8.2e-90:651:81//X99384
F-HEMBA1005520//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.8e-167:755:99//AC004913
F-HEMBA1005526//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence.//2.4e-42:475:73//AC006241
F-HEMBA1005528//Mus musculus mCAF1 protein mRNA, complete cds.//1.2e-94:512:92//U21855
F-HEMBA1005530
F-HEMBA1005548//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 970A17, WORKING

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DRAFT SEQUENCE.//9.4e-87:422:99//AL034431
F-HEMBA1005552//Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence.//6.1e-41:486:68//AC004743
F-HEMBA1005558//Drosophila melanogaster DNA sequence (P1 DS00837 (D87)), complete sequence.//2.9e-19:306:68//AC004377
F-HEMBA1005568//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0093:345:60//AC004153
F-HEMBA1005570//Plasmodium falciparum chromosome 2, section 44 of 73 of the complete sequence.//4.2e-09:592:59//AE001407
F-HEMBA1005576//Homo sapiens mRNA for KIAA0463 protein, partial cds.//5.9e-127:610:98//AB007932
F-HEMBA1005577//HS-1004-A1-E11 -MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 498 Col=21 Row=I, genomic survey sequence.//0.00034:254:64//B30971
F-HEMBA1005581//Rattus norvegicus mRNA for MEGF5, complete cds.//4.0e-57:826:65//AB011531
F-HEMBA1005582//HS_3242_A1_B07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=13 Row=C, genomic survey sequence.//1.1e-13:91:98//AQ211275
F-HEMBA1005583
F-HEMBA1005588//Homo sapiens PAC clone DJ1188N21 from 7q11.23-q21.1, complete sequence.//8.7e-31:283:75//AC006025
F-HEMBA1005593//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence.//8.3e-158:748:99//AC005746
F-HEMBA1005595//CIT-HSP-2309F14.TF CIT-HSP Homo sapiens genomic clone 2309F14, genomic survey sequence.//6.4e-30:194:91//AQ016527
F-HEMBA1005606//CIT-HSP-2326I6.TR CIT-HSP Homo sapiens genomic clone 2326I6, genomic survey sequence.//0.0014:132:70//AQ041484
F-HEMBA1005609//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.9e-33:249:85//AC005089
F-HEMBA1005616//Homo sapiens DNA sequence from PAC 43C13 on chromosome Xq21.1-Xq21.3. rab proteins geranylgeranyltransferase component A 1 (rab escort protein 1) (REP-1) (choroideraemia protein) (TCD protein).//6.5e-29:279:69//AL009175
F-HEMBA1005621//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 330012, WORKING DRAFT SEQUENCE.//6.4e-90:158:87//AL031731
F-HEMBA1005627//RPCI11-34P9 TJ RPCI-11 Homo sapiens genomic clone RPCI-11-34P9, genomic survey sequence.//0.014:168:67//AQ045110
F-HEMBA1005631//Homo sapiens PAC clone DJ1086D14, complete sequence.//1.0e-149:736:93//AC004460
F-HEMBA1005632
F-HEMBA1005634//Human DNA sequence from PAC 187N21 on chromosome 6p21.2-6p21.33. Contains ESTs.//6.6e-38:452:67//Z98036
F-HEMBA1005666
F-HEMBA1005670//Homo sapiens PAC clone DJ0665C04 from 7p14-p13, complete sequence.//5.1e-59:687:74//AC004850
F-HEMBA1005679//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.0e-47:357:85//AC005478
F-HEMBA1005680
F-HEMBA1005685//RPCI11-23D19.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-23D19, genomic survey sequence.//0.99:228:63//AQ013742
F-HEMBA1005699//Human ligand for eph-related receptor tyrosine kinases (EPLG8) mRNA, complete cds.//1.4e-72:406:92//U57001
F-HEMBA1005705//Human (D21S172) DNA segment containing (CA) repeat.//0.00040:190:66//X56513
F-HEMBA1005717//Plasmodium falciparum MAL3P1, complete sequence.//0.0099:260:63//Z97348
F-HEMBA1005732//Human mRNA for KIAA0003 gene, complete cds.//8.1e-19:151:88//D14697
F-HEMBA1005737//Homo sapiens PAC clone DJ1099C19 from 7q21-q22, complete sequence.//5.6e-15:157:79//AC005156
F-HEMBA1005746//RPCI11-63N8.TK RPCI11 Homo sapiens genomic clone R-63N8, genomic survey sequence.//1.3e-18:113:100//AQ238535
F-HEMBA1005755//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//3.6e-56:764:70//Z97181
F-HEMBA1005765//Human DNA sequence from PAC 288L1 on chromosome 22q12-qter contains ESTs and polymorphic CA repeat (D22S1152).//1.1e-30:275:77//Z82196

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F-HEMBA1005780//RPCI11-74E19.TJ RPCI11 Homo sapiens genomic clone R-74E19, genomic survey sequence.//0.0011:283:62//AQ268432
F-HEMBA1005813//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//0.14:326:61//AC004079
F-HEMBA1005815//M.musculus mRNA for skeletal muscle-specific calpain.//6.3e-10:706:59//X92523
F-HEMBA1005822//Mouse Bac 291G16, WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.87:417:56//AC003020
F-HEMBA1005829//Homo sapiens Chromosome 22q11.2 Fosmid Clone f39e1 In DGCR Region, complete sequence.//8.8e-42:370:79//AC000094
F-HEMBA1005834//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-42:690:67//AL022577
F-HEMBA1005852//F.rubripes GSS sequence, clone 163A22aE9, genomic survey sequence.//4.3e-07:253:59//AL018749
F-HEMBA1005853//CIT-HSP-2289L23.TR CIT-HSP Homo sapiens genomic clone-2289L23, genomic survey sequence.//2.2e-68:333:99//B98952
F-HEMBA1005884//Homo sapiens chromosome 5, BAC clone 78c6 (LBNL H191), complete sequence.//1.9e-57:331:87//AC005351
F-HEMBA1005891//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//5.1e-182:864:98//AC004945
F-HEMBA1005894//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//3.0e-44:340:80//AC004086
F-HEMBA1005909//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//8.3e-12:828:57//AL021026
F-HEMBA1005911//Human DNA sequence from clone 1158E12 on chromosome Xp11.23-11.4 Contains EST, STS, GSS, CpG island, complete sequence.//1.0e-44:328:77//AL031584
F-HEMBA1005921//Homo sapiens chromosome 17, clone hRPK.112_H_10, complete sequence.//1.3e-41:431:77//AC005666
F-HEMBA1005931//Homo sapiens chromosome 12p13.3 clone RPCI4-761J14, WORKING DRAFT SEQUENCE, 60 unordered pieces.//1.1e-29:394:70//AC006086
F-HEMBA1005934//Homo sapiens PAC clone DJ1140G11 from 14q24.3, complete sequence.//8.1e-06:115:80//AC004974
F-HEMBA1005962//RPCI11-17O15.TV RPCI-11 Homo sapiens genomic clone RPCI-11-17015, genomic survey sequence.//9.5e-36:315:84//B82821
F-HEMBA1005963//HS_3055_A1_E08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=15 Row=I, genomic survey sequence.//9.3e-73:372:97//AQ147357
F-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//1.3e-149:697:99//AF082516
F-HEMBA1005991//Plasmodium falciparum chromosome 2, section 45 of 73 of the complete sequence.//6.3e-07:423:60//AE001408
F-HEMBA1005999//Homo sapiens chromosome 4 clone C0026P05 map 4P16, complete sequence.//3.8e-09:360:64//AC005599
F-HEMBA1006002
F-HEMBA1006005//Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds.//4.5e-83:495:90//AF036405
F-HEMBA1006031
F-HEMBA1006035
F-HEMBA1006036//Human (lambda) DNA for immunogloblin light chain.//2.4e-59:652:74//D87009
F-HEMBA1006042//Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10q25, complete sequence.//2.1e-43:330:7011AC005386
F-HEMBA1006067//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.11:433:59//AC004153
F-HEMBA1006081
F-HEMBA1006090//, complete sequence.//4.5e-139:748:92//AC005500
F-HEMBA1006091//Homo sapiens gene encoding telethonin, exons 1 to 2, partial.//0.0091:346:62//AJ011098

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F-HEMBA1006100//Homo sapiens chromosome 10 clone CIT987SK-1143A11 map 10q25, complete sequence.// 2.8e-18:180:78//AC005880
F-HEMBA1006108//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte-Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.26:84: 71//AL031177
F-HEMBA1006121//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 691N24, WORKING DRAFT SEQUENCE.//5.2e-18:147:87//AL031672
F-HEMBA1006124//CIT-HSP-2355B17.TF CIT-HSP Homo sapiens genomic clone 2355B17, genomic survey sequence.//0.044:225:61//AQ058966
F-HEMBA1006130//CIT-HSP-386A20.TF CIT-HSP Homo sapiens genomic clone 386A20, genomic survey sequence.//8.8e-07:173:69//B55085
F-HEMBA1006138//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//7.5e-22:164:75//AL022162
F-HEMBA1006142//, complete sequence.//7.9e-125:586:99//AC005500
F-HEMBA1006155//H.sapiens CpG island DNA genomic Mse1 fragment, clone 119b6, forward read cpg119b6.ft1a.//1.0:85:72//Z64428
F-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//1.1e-185: 852:99//AF048693
F-HEMBA1006173//striatum enriched phosphatase=protein-tyrosine-phosphatase [rat, striata, mRNA, 2815 nt].// 8.4e-50:642:73//S49400
F-HEMBA1006182//Homo sapiens Chromosome 15q26.1 PAC clone pDJ105i19, complete sequence.//1.4e-22: 194:74//AC005318
F-HEMBA1006198
F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//2.6e-175:836:98//AF070557
F-HEMBA1006248//Pinctada fucata mRNA for insoluble protein, complete cds.//8.2e-05:359:61//D86074
F-HEMBA1006252//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 531H16, WORKING DRAFT SEQUENCE.//0.98:397:58//AL031664
F-HEMBA1006253
F-HEMBA1006259//HS_2231_A1_D10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2231 Col=19 Row=G, genomic survey sequence.//1.2e-11:233:68//AQ152722
F-HEMBA1006268//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//5.2e-27:156:85//AC004673
F-HEMBA1006272//Human endogenous retrovirus gag mRNA.//8.1e-115:847:80//X72791
F-HEMBA1006278//Mus musculus poly(A) polymerase VI mRNA, complete cds.//2.1e-57:665:70//U58134
F-HEMBA1006283
F-HEMBA1006284//Streptomyces fradiae tylactone synthase, starter module and modules 1-7, (tylG) gene, complete cds.//9.6e-06:623:60//U78289
F-HEMBA1006291//HS_2208_A1_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=5 Row=E, genomic survey sequence.//1.2e-13:105:92//AQ091804
F-HEMBA1006293//Sequence 8 from patent US 5721351.//5.6e-77:580:75//I89415
F-HEMBA1006309//Caenorhabditis elegans cosmid F01F1.//1.1e-21:420:63//U13070
F-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//6.8e-120:748:85//AF076183
F-HEMBA1006328//Homo sapiens fragile X mental retardation protein (FMR-1) gene (6 alternative splices), complete cds.//1.5e-46:485:73//L29074
F-HEMBA1006334//HS-1051-B2-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 773 Col=2 Row=L, genomic survey sequence.//0.0032:61:91//B40563
F-HEMBA1006344//HS-1009-A2-B02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 331 Col=4 Row=C, genomic survey sequence.//3.3e-09:218:66//B31420
F-HEMBA1006347//Drosophila melanogaster males-absent on the first (mof) gene, complete cds.//1.6e-31:484: 68//U71219
F-HEMBA1006349//HS-1054-A1-G06-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 776 Col=11 Row=M, genomic survey sequence.//5.4e-15:95:100//B41671
F-HEMBA1006359//Human ZNF43 mRNA.//1.4e-115:823:81//X59244
F-HEMBA1006364//Mouse mRNA for transforming growth factor-beta2.//2.7e-10:247:71//X57413

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F-HEMBA1006377//Mus musculus chromosome 7, clone 19K5, complete sequence.//3.0e-57:401:81//AC002327
F-HEMBA1006380//CIT-HSP-2172K18.TF CIT-HSP Homo sapiens genomic clone 2172K18, genomic survey sequence.//1.3e-110:525:99//B92570
F-HEMBA1006381//HS-1045-B2-F10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 828 Col=20 Row=L, genomic survey sequence.//4.4e-05:163:70//B37813
F-HEMBA1006398//Homo sapiens 12q24.2 BAC RPCI11-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//3.8e-62:370:86//AC004806
F-HEMBA1006416//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence.//3.7e-15:157:78//AC005179
F-HEMBA1006419//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055, complete sequence.//1.2e-39:752:63//AL022165
F-HEMBA1006421//Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown genes.//2.4e-41:438:76//AF107885
F-HEMBA1006424//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//0.027:293:64//AL031781
F-HEMBA1006426//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 292E10, WORKING DRAFT SEQUENCE.//1.7e-50:310:80//Z93930
F-HEMBA1006438//Liverwort Marchantia polymorpha chloroplast genome DNA.//0.051:440:59//X04465
F-HEMBA1006445//Felis catus ras p21 (H-ras) mRNA, partial cds.//1.0:238:59//U62088
F-HEMBA1006446//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P6, WORKING DRAFT SEQUENCE.//2.4e-05:702:58//AL031749
F-HEMBA1006461//Homo sapiens chromosome 19, cosmid R30676, complete sequence.//8.6e-55:409:83//AC004560
F-HEMBA1006467//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//1.0:293:59//AC006120
F-HEMBA1006471//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.4e-05:731:59//AC004709
F-HEMBA1006474//CIT-HSP-2017H3.TF CIT-HSP Homo sapiens genomic clone 2017H3, genomic survey sequence.//5.2e-60:435:83//B54247
F-HEMBA1006483//Homo sapiens chromosome 5, BAC clone 8e5 (LBNL H167), complete sequence.//2.9e-48:286:84//AC004752
F-HEMBA1006485//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence.//0.96:283:59//AC006031
F-HEMBA1006486//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.8e-14:259:67//AL022577
F-HEMBA1006489//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 467K16, WORKING DRAFT SEQUENCE.//6.6e-11:595:61//AL031283
F-HEMBA1006492//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.//6.0e-122:337:100//AC005828
F-HEMBA1006494//Homo sapiens chromosome 7qtelo BAC E3, complete sequence.//3.8e-23:459:68//AF093117
F-HEMBA1006497//HS_3023_B2_H03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=6 Row=P, genomic survey sequence.//2.3e-81:433:95//AQ093846
F-HEMBA1006502//H.sapiens 7SL repeat (clones 2-19b).//1.6e-13:86:87//X62364
F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds.//2.3e-139:470:98//AB014566
F-HEMBA1006521//Human BAC clone RG167B05 from 7q21, complete sequence.//4.3e-27:406:71//AC003991
F-HEMBA1006530//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE.//2.9e-27:408:65//AL031650
F-HEMBA1006535//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.028:599:60//AL034557
F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds.//1.4e-171:654:98//AF093419

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F-HEMBA1006546//Human DNA sequence from cosmid 232L22, between markers DXS366 and DXS87 on chromosome X contains ESTs glycerol kinase pseudogene.//3.8e-104:811:80//Z73986
F-HEMBA1006559//Mus musculus PRAJA1 (Praja1) mRNA, complete cds.//4.8e-99:386:82//U06944
F-HEMBA1006562//Human fructose-1,6-biphosphatase (FBP1) gene, exon 1.//0.012:322:60//U21925
F-HEMBA1006566//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0026:580:58//AC005504
F-HEMBA1006569//Ovis aries beta actin mRNA, complete cds.//6.3e-08:231:70//U39357
F-HEMBA1006579//CIT-HSP-2380A22.TR CIT-HSP Homo sapiens genomic clone 2380A22, genomic survey sequence.//0.036:250:62//AQ197107
F-HEMBA1006583//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.//1.0:225:63//AL021841
F-HEMBA1006595//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30A23, WORKING DRAFT SEQUENCE.//3.6e-50:689:69//AL022156
F-HEMBA1006597//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.9e-42:253:84//AC004166
F-HEMBA1006612//RPCI11-88F20.TJ RPCI11 Homo sapiens genomic clone R-88F20, genomic survey sequence.//1.1e-51:266:98//AQ286726
F-HEMBA1006617//HS_2193_B2_H07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=14 Row=P, genomic survey sequence.//1.1e-59:413:85//AQ299685
F-HEMBA1006624//Human DNA sequence from clone 406A7 on chromosome 6q23-24. Contains three pseudogenes similar to Elongation Factor 1-Alpha (EF-1-ALPHA, Statin S1), 60S Acidic Ribosomal Protein P1 and NADH-Ubiquinone Oxidoreductase 15 kDa subunit, and part of the Microtuble Associated Protein E-MAP-115 gene. Contains ESTs, STSs and GSSs, complete sequence.//1.4e-35:257:89//AL023284
F-HEMBA1006631//Homo sapiens Chromosome 11q23 PAC clone pDJ356d6, complete sequence.//9.6e-112:800:83//AC002036
F-HEMBA1006635//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P2, WORKING DRAFT SEQUENCE.//0.15:393:58//AL031745
F-HEMBA1006639//Petromyzon marinus polyadenylate binding protein (PABP) mRNA, complete cds.//9.6e-15:318:68//AF032896
F-HEMBA1006643//Homo sapiens clone DJ0902E20, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.58:254:65//AC006148
F-HEMBA1006648//Mus musculus integrin binding protein kinase mRNA, complete cds.//1.5e-37:108:88//U94479
F-HEMBA1006652//Homo sapiens chromosome 5, BAC clone 343g16 (LBNL H180), complete sequence.//1.3e-154:671:96//AC005601
F-HEMBA1006653
F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//5.2e-110:254:93//AC005189
F-HEMBA1006665//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//1.4e-14:177:76//AC004554
F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56.//5.5e-15:122:90//Y12065
F-HEMBA1006676//Homo sapiens chromosome 19, fosmid 37502, complete sequence.//0.098:218:63//AC004755
F-HEMBA1006682//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 668J24, WORKING DRAFT SEQUENCE.//1.4e-05:719:57//AL034346
F-HEMBA1006695//Homo sapiens clone DJ0935K16, complete sequence.//3.1e-22:151:78//AC006011
F-HEMBA1006696//CITBI-E1-2522D16.TF CITBI-E1 Homo sapiens genomic clone 2522D16, genomic survey sequence.//5.6e-17:324:66//AQ280738
F-HEMBA1006708
F-HEMBA1006709
F-HEMBA1006717//Homo sapiens clone GS308H05, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.3e-08:136:79//AC005537
F-HEMBA1006737//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.//5.8e-162:497:98//AC005828
F-HEMBA1006744//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//7.4e-48:320:87//AC004796
F-HEMBA1006754//Human DNA sequence from PAC 82J11 and cosmid U134E6 on chromosome Xq22. Contains NIK like and Thyroxin-binding globulin precursor (T4-binding globulin, TBG) genes, ESTs and STSs.//4.1e-129:804:85//Z83850

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F-HEMBA1006758//Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.//2.2e-162:766:99//AC005752
F-HEMBA1006767//Human Xq28 cosmid U247A3 from LLOXNC01 X chromosome library, complete sequence.//1.2e-19:326:69//U73465
F-HEMBA1006779//Human DNA sequence from clone 80I19 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence.//1.4e-103:355:87//AL022727
F-HEMBA1006780//CIT-HSP-2359P7.TR CIT-HSP Homo sapiens genomic clone 2359P7, genomic survey sequence.//0.072:147:68//AQ077208
F-HEMBA1006789//nbxb0037I13r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0037I13r, genomic survey sequence.//0.00011:288:63//AQ290474
F-HEMBA1006795//CIT-HSP-2307E3.TF CIT-HSP Homo sapiens genomic clone 2307E3, genomic survey sequence.//5.1e-80:420:96//AQ020511
F-HEMBA1006796//Human clone 23803 mRNA, partial cds.//4.5e-06:202:68//U79298
F-HEMBA1006807//Homo sapiens mRNA for SPOP.//1.2e-66:651:73//AJ000644
F-HEMBA1006821//Homo sapiens chromosome 17, clone hRPC.62_O_9, complete sequence.//6.0e-116:541:99//AC004797
F-HEMBA1006824//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//0.40:159:66//AC004262
F-HEMBA1006832//Homo sapiens (subclone 3_g8 from P1 H25) DNA sequence, complete sequence.//1.8e-24:323:71//AC002196
F-HEMBA1006849//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epitherium cancer, segment 4/10.//0.15:403:60//AB020872
F-HEMBA1006865//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence.//0.20:472:57//AE001369
F-HEMBA1006877//Mus musculus clone OST9241, genomic survey sequence.//3.4e-79:641:76//AF046757
F-HEMBA1006885//HS_2208_B2_G06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=12 Row=N, genomic survey sequence.//4.9e-18:206:76//AQ089246
F-HEMBA1006900//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//5.4e-07:298:65//AL031321
F-HEMBA1006914//S.pombe chromosome II cosmid c16H5.//0.00040:194:66//AL022104
F-HEMBA1006921//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//1.1e-174:813:99//AC006027
F-HEMBA1006926//Caenorhabditis elegans cosmid ZK185.//0.0075:183:65//AF036704
F-HEMBA1006929//P.falciparum complete gene map of plastid-like DNA (IR-A).//4.0e-06:739:57//X95275
F-HEMBA1006936
F-HEMBA1006938//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P4, WORKING DRAFT SEQUENCE.//1.1e-05:733:57//AL031747
F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.//1.3e-90:437:98//AJ010841
F-HEMBA1006949//Human DNA sequence from PAC 363L9 on chromosome X. contains STS and polymorphic CA repeat.//0.67:217:62//Z82205
F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.6e-143:740:94//AF004828
F-HEMBA1006976//cDNA encoding alpha 2 to 3 sialyltransferase.//2.8e-101:338:89//E06058
F-HEMBA1006993//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//7.1e-31:536:66//AC003071
F-HEMBA1006996//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//9.5e-07:285:60//Z82209
F-HEMBA1007002//Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence.//0.99:388:58//AC002328
F-HEMBA1007017//Sequence 3 from Patent WO9416067.//0.96:220:62//A39358
F-HEMBA1007018//G.gallus mRNA for dynein light chain-A.//1.3e-124:838:83//X79088
F-HEMBA1007045
F-HEMBA1007051//Caenorhabditis elegans cosmid Y57G11C, complete sequence.//0.17:343:60//Z99281
F-HEMBA1007052//Homo sapiens FSHD-associated repeat DNA, proximal region.//4.3e-67:659:74//U85056
F-HEMBA1007062//Tubulin gene.//1.0:113:67//A18572
F-HEMBA1007066//HS_3116_A2_A03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3116 Col=6 Row=A, genomic survey sequence.//0.80:214:62//AQ140467
F-HEMBA1007073//Homo sapiens 12q13 PAC RPCI1-316M24 (Roswell Park Cancer Institute Human PAC library)

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complete sequence.//9.3e-54:519:68//AC004242
F-HEMBA1007078//CIT-HSP-2318N6.TF CIT-HSP Homo sapiens genomic clone 2318N6, genomic survey sequence.//8.7e-80:387:98//AQ044076
F-HEMBA1007080
F-HEMBA1007085//Streptomyces coelicolor cosmid 7A1.//3.5e-06:496:59//AL034447
F-HEMBA1007087//Plasmodium falciparum MAL3P6, complete sequence.//7.4e-07:553:56//Z98551
F-HEMBA1007112//HS_2171_A1_B01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=1 Row=C, genomic survey sequence.//1.0:172:61//AQ091865
F-HEMBA1007113//Human DNA sequence from clone 1044O17 on chromosome Xp11.3-11.4 Contains GSS and STS, complete sequence.//0.54:502:56//AL023875
F-HEMBA1007121//Caenorhabditis elegans cosmid ZK430.//1.4e-08:265:64//U42833
F-HEMBA1007129//CITBI-E1-2504A5.TF CITBI-E1 Homo sapiens genomic clone 2504A5, genomic survey sequence.//0.97:267:62//AQ264035
F-HEMBA1007147//HS_3208_A2_C04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3208 Col=8 Row=E, genomic survey sequence.//9.1e-90:466:95//AQ176696
F-HEMBA1007149//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//6.0e-138:524:98//AC005239
F-HEMBA1007151//CITBI-E1-2522H6.TF CITBI-E1 Homo sapiens genomic clone 2522H6, genomic survey sequence.//2.0e-20:157:87//AQ280780
F-HEMBA1007174//Homo sapiens epsin 2a mRNA, complete cds.//2.0e-62:318:97//AF062085
F-HEMBA1007178//Homo sapiens chromosome 12p13.3 clone RPCI11-372B4, WORKING DRAFT SEQUENCE, 129 ordered pieces.//1.6e-21:205:80//AC005911
F-HEMBA1007194//HS_3124_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence.//1.3e-11:87:96//AQ187492
F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds.//1.7e-156:478:98//D86987
F-HEMBA1007206//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//0.024:342:63//AC004223
F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds.//5.0e-176:839:98//AB018340
F-HEMBA1007243//Chinese hamster hprt mRNA, complete cds.//4.3e-58:687:68//J00060
F-HEMBA1007251//Rabbit troponin T messenger fragment (aa 49 to 129).//0.084:177:62//V00899
F-HEMBA1007256//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 328E19, WORKING DRAFT SEQUENCE.//1.3e-75:490:88//AL022240
F-HEMBA1007267//HS_3218_A1_F07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=13 Row=K, genomic survey sequence.//2.9e-62:393:87//AQ181128
F-HEMBA1007273//CIT-HSP-2171B10.TF CIT-HSP Homo sapiens genomic clone 2171B10, genomic survey sequence.//1.1e-63:314:99//B95401
F-HEMBA1007279//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.//3.1e-31:401:72//AC004638
F-HEMBA1007281//HS_3115_A1_A11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3115 Col=21 Row=A, genomic survey sequence.//5.0e-70:372:96//AQ186691
F-HEMBA1007288//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence.//1.2e-152:727:98//AL031003
F-HEMBA1007300//Canis familiaris PDE5 mRNA for 3',5'-Cyclic GMP Phosphodiesterase, complete cds.//2.1e-21:542:63//AB008467
F-HEMBA1007301//COL1A1=type I collagen pro alpha 1(I) chain propeptide {3' region} [human, fetal cells 86-237, 86-146, 88-251, mRNA Partial Mutant, 855 nt].//1.7e-08:388:61//S64596
F-HEMBA1007319//Genomic sequence from Mouse 9, complete sequence.//6.0e-84:390:75//AC000399
F-HEMBA1007320
F-HEMBA1007322//Homo sapiens BAC clone RG118E13 from 7p15-p21, complete sequence.//0.091:260:64//AC004485
F-HEMBA1007327//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.12:472:59//AC005140
F-HEMBA1007341//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//1.5e-18:408:64//AC006120
F-HEMBA1007342//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//8.7e-25:500:62//AC005377
F-HEMBA1007347//Homo sapiens chromosome 5, BAC clone 7g12 (LBNL H126), complete sequence.//0.75:269:61//AC005738

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F-HEMBB1000005//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//5.0e-05:441:60//AC004617
F-HEMBB1000008//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//1.0e-44:417:77//AC004491
F-HEMBB1000018//HS_2179_B2_E04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=8 Row=J, genomic survey sequence.//0.012:87:77//AQ023250
F-HEMBB1000024//Human DNA sequence from PAC 106I20 on chromosome 22q12-qter contains NADH pseudogene, ESTs, STS.//8.1e-11:461:61//Z81369
F-HEMBB1000025//CIT-HSP-2348F3.TR CIT-HSP Homo sapiens genomic clone 2348F3, genomic survey sequence.//0.96:198:62//AQ062938
F-HEMBB1000030//Homo sapiens DNA sequence from PAC 32F7 on chromosome X. Contains NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 3, ESTs.//0.00049:276:64//AL009173
F-HEMBB1000036//H.sapiens chromosome 22 CpG island DNA genomic Mse1 fragment, clone 302e2, reverse read 302e2.r.//0.0057:66:81//Z79857
F-HEMBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//1.9e-100:450:98//AF084928
F-HEMBB1000039//HS_2167_B1_F12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2167 Col=23 Row=L, genomic survey sequence.//0.022:108:69//AQ092404
F-HEMBB1000044//Borrelia burgdorferi (section 50 of 70) of the complete genome.//1.0e-07:486:61//AE001164
F-HEMBB1000048//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//5.3e-05:585:58//AC005507
F-HEMBB1000050//Homo sapiens DNA sequence from clone 501N12 on chromosome 6p22.1-22.3 Contains a gene almost identical to four genes of unknown function, a pseudogene, three (pseudo?) genes similar to genes of unknown function, an unknown gene similar to a rat EST, a PX19 LIKE pseudogene and another unknown gene. Contains ESTs, STSs and GSSs, complete sequence.//5.8e-38:549:67//AL022170
F-HEMBB1000054//Homo sapiens Xp22 PAC RPCI1-167A22 (from Roswell Park Cancer Center) complete sequence.//7.0e-98:328:83//AC002349
F-HEMBB1000055//Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, cosmid clone: TY2F10, WORKING DRAFT SEQUENCE.//3.7e-05:600:58//AB000880
F-HEMBB1000059//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//1.3e-48:472:78//AC005096
F-HEMBB1000083
F-HEMBB1000089//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//0.0036:679:56//AL031744
F-HEMBB1000099//Homo sapiens chromosome 18 BAC RPCI11-128D14 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.1e-15:312:68//AC005909
F-HEMBB1000103//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.0e-37:316:74//AC006210
F-HEMBB1000113//Homo sapiens chromosome 21q22.3 cosmid Q11M15, complete sequence.//3.1e-25:259:76//AF045450
F-HEMBB1000119//Homo sapiens ASMTL gene.//1.2e-137:654:98//Y15521
F-HEMBB1000136//Mycobacterium tuberculosis H37Rv complete genome; segment 127/162.//0.59:217:66//Z74697
F-HEMBB1000141//Homo sapiens DNA from choromosome 19q13.1 cosmid f14121 containing ATP4A and GADPH-2 genes, genomic sequence.//8.4e-31:113:88//AD000090
F-HEMBB1000144//Human BAC clone RG114A06 from 7q31, complete sequence.//4.4e-58:339:87//AC002542
F-HEMBB1000173//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//9.4e-160:562:93//AC002996
F-HEMBB1000175
F-HEMBB1000198//HS_3071_A2_A10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=20 Row=A, genomic survey sequence.//0.99:261:61//AQ137388
F-HEMBB1000215//Homo sapiens chromosome 17, clone hRPK.481_C_4, complete sequence.//6.7e-17:138:86//AC005839
F-HEMBB1000217//Arabidopsis thaliana ubiquitin activating enzyme (UBA1) gene, complete cds.//0.00083:287:60//U80808
F-HEMBB1000218//Caenorhabditis elegans cosmid C52A11, complete sequence.//0.90:337:56//Z46792
F-HEMBB1000226//Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island.//1.7e-90:175:92//Z69890

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F-HEMBB1000240//Human G-protein-coupled inwardly rectifying potassium channel (KCNJ3) gene, polymorphic repeat sequence.//0.16:171:62//U07918
F-HEMBB1000244//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.// 4.8e-08:355:63//AC005522
F-HEMBB1000250//Homo sapiens protein associated with Myc mRNA, complete cds.//6.6e-155:735:98// AF075587
F-HEMBB1000258//Human adenosine monophosphate deaminase 1 (AMPD1) gene, exons 1-16.//0.58:396:59// M98818
F-HEMBB1000264//Human clone C3 CHL1 protein (CHLR1) mRNA, alternatively spliced, complete cds.//4.4e-32: 100:100//U75968
F-HEMBB1000266//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence.//3.8e-16:176:78//AC004470
F-HEMBB1000272//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence.//0.011:379: 58//AE001369
F-HEMBB1000274//Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSAII project).//0.92:272:61// AL022580
F-HEMBB1000284//Human Xp22 BAC CT-285I15 (from CalTech/Research Genetics) , PAC RPCI1-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//0.00071:568: 57//AC002366
F-HEMBB1000307//Human DNA sequence from PAC 29K1 on chromosome 6p21.3-22.2. Contains glutathione peroxidase-like; zinc finger, ESTs, mRNA, STS, tRNAs, olfactory receptor pseudogene.//3.0e-13:439:65//Z98745
F-HEMBB1000312//Homo sapiens clone GS051M12, complete sequence.//0.031:252:65//AC005007
F-HEMBB1000317//Fugu rubripes GSS sequence, clone 060J22aE10, genomic survey sequence.//0.00033:173: 65//AL026242
F-HEMBB1000318//HS_3244_B2_H10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=20 Row=P, genomic survey sequence.//3.9e-85:438:95//AQ252951
F-HEMBB1000335//Homo sapiens chromosome 18, clone hRPK.24_A_23, complete sequence.//0.63:285:61// AC005968
F-HEMBB1000336
F-HEMBB1000337//Homo sapiens chromosome 4 clone B208G5 map 4q25, complete sequence.//0.0014:309: 64//AC004051
F-HEMBB1000338//HS_3108_A2_F07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=14 Row=K, genomic survey sequence.//3.8e-09:331:63//AQ140356
F-HEMBB1000339//Homo sapiens 12q24 PAC RPCI1-46F2 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.2e-52:295:77//AC002351
F-HEMBB1000341
F-HEMBB1000343//Plasmodium falciparum MAL3P3, complete sequence.//0.00081:397:61//Z98547
F-HEMBB1000354//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//9.1e-34:596:66//AL020989
F-HEMBB1000369//Genomic sequence from Human 17, complete sequence.//0.012:298:60//AC002090
F-HEMBB1000374//Human Xp22 contig of 3 PACS (R7-39D12, R7-134G1, R7-185L21) from the Roswell Park Cancer Institute, complete sequence.//9.3e-69:294:89//U96409
F-HEMBB1000376//Human DNA sequence from clone 751H9 on chromosome 6q13. Contains part of an unknown gene, ESTs, STSs and GSSs, complete sequence.//3.5e-54:352:88//AL034377
F-HEMBB1000391//Trichothecium roseum internal transcribed spacer 1, 5.8S ribosomal RNA gene; and internal transcribed spacer 2, complete sequence.//0.011:168:67//U51982
F-HEMBB1000399//Homo sapiens Rad17-like protein (RAD17) mRNA, complete cds.//2.6e-163:762:98// AF076838
F-HEMBB1000402//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//7.7e-15:466:63//AC002368
F-HEMBB1000404//Homo sapiens mRNA for myosin-IXA.//3.5e-65:324:98//AJ001714
F-HEMBB1000420//244Kb Contig from Human Chromsome 11p15.5 spanning D11S1 through D11S25, complete sequence.//0.013:399:62//AC001228
F-HEMBB1000434//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//6.1e-83:571:84//AC004263
F-HEMBB1000438//RPCI11-21E14.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21E14, genomic survey sequence.//0.0030:295:63//B83110
F-HEMBB1000441//Homo sapiens Chromosome 22q12 Cosmid Clone II47g11, complete sequence.//2.5e-33:372: 72//AC000035

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F-HEMBB1000449//Human DNA sequence from PAC 296K21 on chromosome X contains cytokeratin exon, delta-aminolevulinate synthase (erythroid); 5-aminolevulinic acid synthase.(EC 2.3.1.37). 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//1.3e-51:534:72//Z83821
F-HEMBB1000455//Saccharomyces cerevisiae mitochondrion origin of replication (ori6) and oli1 gene, complete cds.//0.016:522:58//L36899
F-HEMBB1000472
F-HEMBB1000480
F-HEMBB1000487//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 128O3, WORKING DRAFT SEQUENCE.//0.00013:314:64//Z98742
F-HEMBB1000490//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE.//4.1e-110:529:98//AL034423
F-HEMBB1000491//Plasmodium falciparum chromosome 2, section 25 of 73 of the complete sequence.//0.10:187:65//AE001388
F-HEMBB1000493//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.7e-06:637:58//AL022577
F-HEMBB1000510//Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence.//3.1e-96:737:81//AC005553
F-HEMBB1000518//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.00014:163:68//AC004676
F-HEMBB1000523//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-105, complete sequence.//0.41:349:56//AL010212
F-HEMBB1000530//H.sapiens mRNA for extracellular matrix protein collagen type XIV, C-terminus.//6.6e-37:138:96//Y11710
F-HEMBB1000550//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11.//3.9e-56:683:71//AB020860
F-HEMBB1000554//Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRAFT SEQUENCE.//2.2e-51:282:84//AJ011929
F-HEMBB1000556//Homo sapiens mRNA for KIAA0750 protein, complete cds.//6.1e-32:537:65//AB018293
F-HEMBB1000564
F-HEMBB1000573//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//8.2e-33:268:73//AC005077
F-HEMBB1000575//Human DNA sequence from clone 323M22 on chromosome 22q13.1-13.2. Contains the 5' part of the human ortholog of chicken P52 and mouse H74, and a novel gene coding for a protein similar to KIAA0173 and worm Tubulin Tyrosine Ligase. Contains ESTs, STSs, GSSs, genomic marker D22S418 and putative CpG islands, complete sequence.//5.8e-47:734:66//AL022476
F-HEMBB1000586//H.sapiens highly polymorphic microsatellite DNA.//0.030:147:67//X79883
F-HEMBB1000589//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//6.3e-41:278:83//AC002300
F-HEMBB1000591//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//1.1e-182:871:98//AC005184
F-HEMBB1000592//Hepatitis C virus genomic RNA, 3' nonstranslated region, partial sequence. clone #19.//0.012:185:64//AF009074
F-HEMBB1000593//Homo sapiens chromosome 7q22 sequence, complete sequence.//1.2e-131:353:93//AF053356
F-HEMBB1000598//Homo sapiens 12p13.3 BAC RPCI3-488H23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//9.1e-58:600:72//AC006207
F-HEMBB1000623//cDNA encoding Coliolus manganese peroxidase.//0.89:284:62//E12284
F-HEMBB1000630//Mus musculus clone NSAT47 nonsatellite RNA sequence.//1.9e-15:129:87//U26231
F-HEMBB1000631//Sequence 26 from patent US 5708157.//3.2e-27:180:88//I80057
F-HEMBB1000632//Human mRNA for KIAA0351 gene, complete cds.//1.6e-48:811:65//AB002349
F-HEMBB1000637//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.1e-58:649:73//AC005478
F-HEMBB1000638//HS_3051_A1_G01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=M, genomic survey sequence.//0.0032:497:56//AQ155234
F-HEMBB1000643//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.4e-50:791:68//AC005077

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F-HEMBB1000649//Homo sapiens Chromosome 16 BAC clone CIT987-SK502C10, complete sequence.//5.2e-64:775:69//AC003009
F-HEMBB1000652//Homo sapiens chromosome 10 clone CRI-JC2048 map 10q22.1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.7e-52:334:89//AC006186
F-HEMBB1000665//Human DNA sequence from clone 452M16 on chromosome Xq21.1-21.33 Contains capping protein alpha subunit isoform 1 pseudogene, STS, GSS, and CA repeat, complete sequence.//0.0062:426:60//AL024493
F-HEMBB1000671//Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG island.//9.6e-95:399:78//Z84488
F-HEMBB1000673//HS_3039_A2_C08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=16 Row=E, genomic survey sequence.//3.8e-50:293:92//AQ155121
F-HEMBB1000684//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 222E13, WORKING DRAFT SEQUENCE.//8.0e-65 :282:83//Z93241
F-HEMBB1000693//Homo sapiens neuroan1 mRNA, complete cds.//1.6e-118:575:97//AF040723
F-HEMBB1000705//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//8.6e-07:251:61//AC005507
F-HEMBB1000706//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 153G14, WORKING DRAFT SEQUENCE.//2.9e-20:434:64//AL031118
F-HEMBB1000709//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 994L9, WORKING DRAFT SEQUENCE.//0.26:184:65//AL034554
F-HEMBB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//1.8e-129:692:93//U53475
F-HEMBB1000726//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//2.7e-40:304:80//U91321
F-HEMBB1000738//Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence.//8.9e-35:582:63//AF011889
F-HEMBB1000749//Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE, 9 unordered pieces.//6.2e-46:262:89//AC005849
F-HEMBB1000763//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SEQUENCE.//1.6e-99:316:98//AL034405
F-HEMBB1000770//Human DNA sequence from clone 80I19 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence.//0.044:325:60//AL022727
F-HEMBB1000774
F-HEMBB1000781//Sequence 3 from patent US 5753446.//1.2e-92:599:86//AR008277
F-HEMBB1000789//Homo sapiens mRNA for KIAA0677 protein, complete cds.//9.3e-64:672:71//AB014577
F-HEMBB1000790//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.4e-41:460:74//AC004801
F-HEMBB1000794//HS_3034_B2_D12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3034 Col=24 Row=H, genomic survey sequence.//1.8e-74:378:97//AQ117099
F-HEMBB1000807//H.sapiens CpG island DNA genomic Mse1 fragment, clone 39d7, reverse read cpg39d7.rt1a.//8.5e-14:95:97//Z58412
F-HEMBB1000810//H.sapiens chromosome 22 CpG island DNA genomic Mse1 fragment, clone 303a8, complete read.//3.2e-05:138:71//Z79983
F-HEMBB1000821//HS_2168_B1_A12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=23 Row=B, genomic survey sequence.//0.85 :208:60//AQ086361
F-HEMBB1000822//Human BAC clone GS113H23 from 5p15.2, complete sequence.//3.0e-06:361:60//AC003015
F-HEMBB1000826//Human BAC clone RG180F08 from 7q31, complete sequence.//1.1e-27:360:69//AC002431
F-HEMBB1000827
F-HEMBB1000831
F-HEMBB1000835//Human DNA sequence from clone 45I4 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//0.00098:234:63//AL023581
F-HEMBB1000840//Human Chromosome 11 Cosmid cSRL97a6, complete sequence.//4.5e-61:328:79//U73649
F-HEMBB1000848//Homo sapiens DNA sequence from PAC 206D15 on chromosome 1q24. Contains a Reduced Folate Carrier protein (RFC) LIKE gene, a mitochondrial ATP Synthetase protein 8 (ATP8, MTATP8) LIKE pseudogene, an unknown gene and the last exon of the JEM1 gene coding for the Basic-Leucine Zipper nuclear factor JEM-1. Contains ESTs, an STS and a BAC end sequence (GSS), complete sequence.//9.7e-144:809:87//AL021068
F-HEMBB1000852//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING

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DRAFT SEQUENCE, 9 unordered pieces.//0.12:492:58//AC004157
F-HEMBB1000870//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0024:212:67//AC004157
F-HEMBB1000876//Homo sapiens ELISC-1 mRNA, partial cds.//1.5e-32:200:94//AF085351
F-HEMBB1000883//HS_3065_B2_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3065 Col=8 Row=F, genomic survey sequence.//0.0017:152:66//AQ137687
F-HEMBB1000887
F-HEMBB1000888//CIT-HSP-2329A10.TR CIT-HSP Homo sapiens genomic clone 2329A10, genomic survey sequence.//1.5e-31:172:98//AQ044369
F-HEMBB1000890
F-HEMBB1000893//Plasmodium falciparum MAL3P2, complete sequence.//9.5e-06:768:56//AL034558
F-HEMBB1000908//Homo sapiens clone DJ1119N05, complete sequence.//4.5e-21:199:82//AC004968
F-HEMBB1000910//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.72:366:59//AL034557
F-HEMBB1000913//HS_3078_B1_C02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=3 Row=F, genomic survey sequence.//9.9e-12:221:63//AQ144507
F-HEMBB1000915//Homo sapiens DNA for (CGG)n trinucleotide repeat region, isolate P4.//1.2e-49:252:99//AJ001215
F-HEMBB1000917//Homo sapiens chromosome 5, P1 clone 254f11 (LBNL H62), complete sequence.//2.3e-42:316:76//AC006077
F-HEMBB1000927//Human BDR-2 mRNA for hippocalcin, complete cds.//3.6e-30:528:65/D16593
F-HEMBB1000947//CpG0856B CpIOWAgDNA1 Cryptosporidium parvum genomic, genomic survey sequence.//0.81:262:62//AQ254493
F-HEMBB1000959//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 346O6, WORKING DRAFT SEQUENCE.//1.2e-43:454:75//Z84487
F-HEMBB1000973//Mus musculus schlafen2 (Slfn2) mRNA, complete cds.//8.3e-42:458:72//AF099973
F-HEMBB1000975//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence.//0.98:196:63//AB005234
F-HEMBB1000981
F-HEMBB1000985//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//2.9e-06:566:57//AC004476
F-HEMBB1000991//Human DNA sequence from PAC 238J17 on chromosome 6q22. Contains EST and STS.//0.099:391:57//Z98753
F-HEMBB1000996//Human DNA sequence from BAC 999D10 on chromosome 22q13.3. Contains two BAC end-sequences (GSSs).//6.2e-33:227:80//Z94802
F-HEMBB1001004
F-HEMBB1001008//Human Chromosome 16 BAC clone CIT987SK-A-951C11, complete sequence.//4.0e-13:164:79//AC002551
F-HEMBB1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.//7.5e-13:229:69//AC002310
F-HEMBB1001014//Homo sapiens chromosome 16, BAC clone 375G12 (LANL), complete sequence.//0.32:474:58//AC005751
F-HEMBB1001020//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence.//2.6e-39:218:80//AF069291
F-HEMBB1001024//Homo sapiens BAC clone 393I22 from 8q21, complete sequence.//5.3e-05:656:59//AF070717
F-HEMBB1001037//CIT-HSP-2358K16.TF CIT-HSP Homo sapiens genomic clone 2358K16, genomic survey sequence.//6.6e-05:228:64//AQ080539
F-HEMBB1001047//Homo sapiens cosmids Qc14E2, Qc12H12, Qc11F9, Qc10G9, LA1733 and Qc17B8 from Xq28, complete sequence.//4.0e-27:385:71//U82671
F-HEMBB1001051//H.sapiens mRNA for FAN protein.//1.2e-27:160:98//X96586
F-HEMBB1001056//Homo sapiens clone DJ0953A04, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.3e-89:180:91//AC006014
F-HEMBB1001058//Homo sapiens 3p22-8 PAC RPCI4-736H12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.2e-41:468:74//AC006060
F-HEMBB1001060//Human Tigger1 transposable element, complete consensus sequence.//4.3e-122:785:86//U49973
F-HEMBB1001063//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 523G1, WORKING DRAFT SEQUENCE.//7.1e-162:770:99//AL034375

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F-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//3.1e-146:736:95//AF034803
F-HEMBB1001096//Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene, partial cds.//0.00088:690:57//AF008210
F-HEMBB1001102//Homo sapiens huntingtin interacting protein HYPH mRNA, partial cds.//2.1e-76:368:99//AF049612
F-HEMBB1001105//CIT-HSP-2185N1.TR CIT-HSP Homo sapiens genomic clone 2185N1, genomic survey sequence.//1.0e-09:136:76//AQ002987
F-HEMBB1001112//Rattus rattus sec61 homologue mRNA, complete cds.//1.0e-108:909:76//M96630
F-HEMBB1001114//Homo sapiens chromosome 17, clone hRPK.795_F_17, complete sequence.//7.2e-07:459:59//AC005284
F-HEMBB1001117//HS_2178_B1_E12_MR CIT Approved-Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=23 Row=J, genomic survey sequence.//7.8e-50:331:86//AQ068244
F-HEMBB1001119//Human collagen type XII alpha-1 precursor (COL12A1) mRNA, complete cds.//1.6e-25:150:98//U73778
F-HEMBB1001126
F-HEMBB1001133//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//2.8e-24:228:80//AC004673
F-HEMBB1001137
F-HEMBB1001142//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//1.0e-40:231:76//AC004617
F-HEMBB1001151//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//2.9e-47:640:67//AF015264
F-HEMBB1001153//CIT-HSP-2359K11.TR CIT-HSP Homo sapiens genomic clone 2359K11, genomic survey sequence.//0.76:136:67//AQ075724
F-HEMBB1001169//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//9.9e-63:259:79//AL008712
F-HEMBB1001175//Human mRNA for ankyrin motif, complete cds.//2.2e-34:509:66//D78334
F-HEMBB1001177//CIT-HSP-2321I17.TR CIT-HSP Homo sapiens genomic clone 2321I17, genomic survey sequence.//5.9e-27:320:75//AQ036473
F-HEMBB1001182//RPCI11-30J5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30J5, genomic survey sequence.//5.7e-06:62:96//B85188
F-HEMBB1001199
F-HEMBB1001208//HS_2026_B1_C07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=13 Row=F, genomic survey sequence.//0.00018:134:70//AQ229237
F-HEMBB1001209//CITBI-E1-2521F23.TF CITBI-E1 Homo sapiens genomic clone 2521F23, genomic survey sequence.//1.4e-95:464:98//AQ278357
F-HEMBB1001210//HS_3102_A2_F09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3102 Col=18 Row=K, genomic survey sequence.//2.6e-90:446:98//AQ119196
F-HEMBB1001218//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796F18, WORKING DRAFT SEQUENCE.//1.0e-31:315:72//AL031291
F-HEMBB1001221//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.7e-17:770:59//AC005504
F-HEMBB1001234//H.sapiens CpG island DNA genomic Mse1 fragment, clone 39f9, forward read cpg39f9.ft1e//4.0e-30:171:97//Z65435
F-HEMBB1001242//Homo sapiens mRNA for LAK-1, complete cds.//3.8e-30:458:67//AB005754
F-HEMBB1001249//CIT-HSP-2375N19.TF CIT-HSP Homo sapiens genomic clone 2375N19, genomic survey sequence.//0.0076:250:63//AQ109087
F-HEMBB1001253//Homo sapiens genomic DNA, chromosome 21q11.1, segment 3/28, WORKING DRAFT SEQUENCE.//0.0097:89:80//AP000032
F-HEMBB1001254//CIT-HSP-2320E5.TF CIT-HSP Homo sapiens genomic clone 2320E5, genomic survey sequence.//3.7e-54:284:97//AQ037173
F-HEMBB1001267//Homo sapiens chromosome 17, clone hRPK.488_L_1, complete sequence.//3.5e-30:236:78//AC005303
F-HEMBB1001271//HS_3011_A1_G02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3011 Col=3 Row=M, genomic survey sequence.//5.2e-07:364:62//AQ214217
F-HEMBB1001282//CIT-HSP-2356J20.TF CIT-HSP Homo sapiens genomic clone 2356J20; genomic survey sequence.//1.8e-16:109:97//AQ060969

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F-HEMBB1001288//R.norvegicus mRNA for gephyrin.//3.4e-18:194:77//X66366
F-HEMBB1001289//Genomic sequence from Human 9q34, complete sequence.//4.8e-66:434:74//AC000387
F-HEMBB1001294//HS_3039_B1_D01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=1 Row=H, genomic survey sequence.//2.0e-90:437:99//AQ155035
F-HEMBB1001302
F-HEMBB1001304//CIT-HSP-2053E15.TF CIT-HSP Homo sapiens genomic clone 2053E15, genomic survey sequence.//2.2e-07:370:61//B69144
F-HEMBB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//5.7e-116:663:85//U92703
F-HEMBB1001315//Homo sapiens chromosome 10 clone LA10NC01_40_G_3 map 10q26.1-10q26.2, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.5e-33:328:77//AC006096
F-HEMBB1001317//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.4e-122:680:91//AC006210
F-HEMBB1001326//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence.//2.8e-09:518:60//AC004129
F-HEMBB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//3.7e-56:458:79//D63850
F-HEMBB1001335//HS_3055_A1_H10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=19 Row=O, genomic survey sequence.//1.0:222:63//AQ147384
F-HEMBB1001337//Human PAC clone DJ0093I03 from Xq23, complete sequence.//1.0e-74:319:85//AC003983
F-HEMBB1001339//Homo sapiens FSHD-associated repeat DNA, proximal region.//4.0e-135:856:87//U85056
F-HEMBB1001346//Human familial Alzheimer's disease (STM2) gene, complete cds.//3.3e-44:481:74//U50871
F-HEMBB1001348//Homo sapiens BAC clone NH0491B03 from 7p21-p15, complete sequence.//1.8e-17:210:73//AC006041
F-HEMBB1001356//Homo sapiens clone RG252P22, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:386:59//AC005079
F-HEMBB1001364//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//0.97:349:61//AC004662
F-HEMBB1001366//Homo sapiens chromosome 10 clone CIT987SK-1188I5 map 10p11.2-10p12.1, complete sequence.//5.5e-161:766:98//AC005876
F-HEMBB1001367//Homo sapiens chromosome 17, clone hRPC.906_A_24, complete sequence.//3.0e-55:510:76//AC004408
F-HEMBB1001369//Homo sapiens BAC clone RG163K11 from 7q31, complete sequence.//0.048:244:64//AC005192
F-HEMBB1001380//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence.//2.5e-26:257:78//AC006204
F-HEMBB1001384//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//5.1e-99:571:89//AF071314
F-HEMBB1001387//Leishmania tarentolae mitochondrial 12S ribosomal RNA gene.//7.1e-05:546:58//X02354
F-HEMBB1001394//Homo sapiens BAC clone GS421I03 from Xq25-q26, complete sequence.//4.0e-129:788:88//AC005023
F-HEMBB1001410//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//4.8e-11:632:59//AF045555
F-HEMBB1001424//Mus musculus Chromosome 4 BAC clone BacB6, complete sequence.//0.0012:435:59//AC003019
F-HEMBB1001426//Homo sapiens clone DJ0736H05, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.8e-17:360:64//AC005482
F-HEMBB1001429//leucine aminopeptidase [cattle, kidney, mRNA, 2056 nt].//4.1e-114:668:88//S65367
F-HEMBB1001436//Homo sapiens FUT2 gene, intron 1, complete sequence.//2.3e-37:438:74//AB000931
F-HEMBB1001443//Bos taurus pyruvate dehydrogenase phosphatase mRNA, complete cds.//9.1e-92:550:88//L18966
F-HEMBB1001449//Homo sapiens chromosome 5, PAC clone 228g9 (LBNL H142), complete sequence.//0.00024:385:62//AC004768
F-HEMBB1001454//Homo sapiens chromosome 19, cosmid R34169, complete sequence.//0.84:577:57//AC005790
F-HEMBB1001458//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//8.0e-40:377:78//AC000382
F-HEMBB1001463//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//0.011:482:

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59//AF001549
F-HEMBB1001464//Human chromosome 16p13 BAC clone CIT987SK-3H8 complete sequence.//0.019:263:61//U91320
F-HEMBB1001482//Rattus norvegicus Olf-1/EBF associated Zn finger protein Roaz mRNA, alternatively spliced form, complete cds.//1.0e-30:521:66//U92564
F-HEMBB1001500//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.3e-31:479:71//AC004873
F-HEMBB1001521//Homo sapiens clone RG269P13, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.7e-51:680:70//AC005080
F-HEMBB1001527
F-HEMBB1001531//Homo sapiens Chromosome 22q11.2 Cosmid Clone 89h In DGCR Region, complete sequence.//1.3e-79:696:79//AC000089
F-HEMBB1001535//0.aries DNA for polymorphic marker 'OVINRA01' (339 bp).//0.00034:217:62//X89268
F-HEMBB1001536//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//0.54:266:60//AC004548
F-HEMBB1001537//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//4.6e-25:784:61//AC004262
F-HEMBB1001555//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//6.9e-50:213:80//AC004605
F-HEMBB1001562//Homo sapiens clone NH0523H20, complete sequence.//0.46:269:60//AC005041
F-HEMBB1001564//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//1.7e-107:620:83//AL020989
F-HEMBB1001565//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//2.4e-50:734:67//AC004003
F-HEMBB1001585//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//1.4e-166:816:97//AL031677
F-HEMBB1001586
F-HEMBB1001588//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.6e-21:419:65//AC005261
F-HEMBB1001603
F-HEMBB1001618//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence.//4.5e-29:422:72//Z99289
F-HEMBB1001619//HS_3079_B1_A04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079 Col=7 Row=B, genomic survey sequence.//0.0010:77:79//AQ123388
F-HEMBB1001630//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-12:667:59//AC005089
F-HEMBB1001635//Plasmodium falciparum MAL3P7, complete sequence.//3.8e-05:475:57//AL034559
F-HEMBB1001637//Homo sapiens DNA sequence from PAC 934G17 on chromosome 1p36.21. Contains the alternatively spliced CLCN6 gene for chloride chanel proteins CLC-6A (KIAA0046) -B, -C and -D, the alternatively spliced NPPA gene coding for Atrial Natriuretic Factor ANF precursor (Atrial Natriuretic peptide ANP, Prepronatriodilatin), the NPPB gene for Brain Natriuretic Protein BNP, and a pseudogene similar to SBF1 (and other Myotubularin-related protein genes). Contains ESTs, STSs and the genomic marker D1S2740, complete sequence.//9.2e-13:168:76//AL021155
F-HEMBB1001641//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence.//0.00097:721:58//AB006702
F-HEMBB1001653//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//0.15:276:63//AC002038
F-HEMBB1001665//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.43:393:61//L14320
F-HEMBB1001668//F16C15-T7 IGF Arabidopsis thaliana genomic clone F16C15, genomic survey sequence.//0.040:275:60//B12308
F-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//7.2e-171:803:98//AB014546
F-HEMBB1001684//Sequence 1 from patent US 5700927.//7.5e-124:883:81//I86429
F-HEMBB1001685//CIT-HSP-2287O9.TF CIT-HSP Homo sapiens genomic clone 2287O9, genomic survey sequence.//2.3e-34:191:97//B99261
F-HEMBB1001695//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding

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exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STss, GSSs, and a putative CpG island, complete sequence.//0.0091:334:63//AL009178

F-HEMBB1001704//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//1.2e-17:144:87//AL023575

F-HEMBB1001706

F-HEMBB1001707//Guinea pig CD19 mRNA, complete cds.//0.57:232:62//M62543

F-HEMBB1001717//Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & amp; tRNA-Met genes.//1.1e-13:723:58//AJ223323

F-HEMBB1001735//Human PAC clone DJ0596O09 from 7p15, complete sequence.//1.3e-36:427:73//AC003074

F-HEMBB1001736//S.pombe chromosome II cosmid c4B4.//0.0085:479:57//AL023706

F-HEMBB1001747//Homo sapiens PAC clone DJ1002N02 from 7p21-p22, complete sequence.//4.0e-112:532:84//AC005376

F-HEMBB1001749//Homo sapiens chromosome 17, clone hRPK.259_G_18, complete sequence.//1.3e-98:395:82//AC005829

F-HEMBB1001753//S.maximus repeat region, 342bp.//4.2e-11:69:85//Z78099

F-HEMBB1001756//Homo sapiens full-length insert cDNA clone ZD86A11.//0.0015:302:62//AF088064

F-HEMBB1001760//P.falciparum complete gene map of plastid-like DNA (IR-A).//0.011:615:56//X95275

F-HEMBB1001762//CIT-HSP-2290J16.TF CIT-HSP Homo sapiens genomic clone 2290J16, genomic survey sequence.//0.84:208:64//AQ005184

F-HEMBB1001785//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P3, WORKING DRAFT SEQUENCE.//0.0019:469:60//AL031746

F-HEMBB1001797//Human heterogenous nuclear RNA W16W.//0.00012:83:86//X17272

F-HEMBB1001802//Plasmodium falciparum MAL3P7, complete sequence.//1.8e-11:538:60//AL034559

F-HEMBB1001812//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 356B8, WORKING DRAFT SEQUENCE.//1.0e-56:304:84//Z98882

F-HEMBB1001816//Homo sapiens chromosome 19, cosmid F24083, complete sequence.//3.6e-75:300:87//AC005204

F-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//2.3e-162:763:98//AF056209

F-HEMBB1001834//CIT-HSP-2291012.TF CIT-HSP Homo sapiens genomic clone 2291O12, genomic survey sequence.//7.6e-08:73:94//AQ004168

F-HEMBB1001836//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.7e-30:297:79//AC004801

F-HEMBB1001839//Human Chromosome X, complete sequence.//0.016:293:63//AC004073

F-HEMBB1001850//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0027:812:58//AC005504

F-HEMBB1001863//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.3e-43:520:72//AC004581

F-HEMBB1001867//Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.//1.7e-56:399:86//U07563

F-HEMBB1001868//Rattus norvegicus clone 923 polymeric immunoglobulin receptor mRNA 3' untranslated region, GA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats.//6.1e-08:234:67//U01145

F-HEMBB1001869//Homo sapiens full-length insert cDNA clone YT86F01.//7.4e-87:432:97//AF085974

F-HEMBB1001872

F-HEMBB1001874//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.4e-14:631:61//AC005000

F-HEMBB1001875//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//0.93:415:57//Z82209

F-HEMBB1001880//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//1.0e-18:729:60//Z93403

F-HEMBB1001899//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-10, complete sequence.//0.0038:425:58//AL010216

F-HEMBB1001905//S.pombe chromosome III cosmid c330.//1.1e-23:520:62//AL031603

F-HEMBB1001906

F-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds.//3.7e-82:672:81//U47742

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F-HEMBB1001910//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0033:566:55//AC005505
F-HEMBB1001911//Arabidopsis thaliana chromosome II BAC F26C24 genomic sequence, complete sequence.// 1.0:581:58//AC004705
F-HEMBB1001915//Caenorhabditis elegans cosmid T05H10, complete sequence.//1.2e-16:283:67//Z47812
F-HEMBB1001921//Homo sapiens chromosome 17, clone hCIT.123_J_14, complete sequence.//3.4e-07:803:58// AC003950
F-HEMBB1001922//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence.//5.0e-06: 756:56///AE001391
F-HEMBB1001925//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat,.//3.1e-45:609:73//AL009181
F-HEMBB1001930//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 10/11.//3.2e-158:745:99//AB020867
F-HEMBB1001944//, complete sequence.//4.1e-60:638:73//AC005815
F-HEMBB1001945//HS_3185_B1_G05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=9 Row=N, genomic survey sequence.//1.0:280:58//AQ188882
F-HEMBB1001947//Human mRNA for KIAA0392 gene, partial cds.//5.6e-20:333:66//AB002390
F-HEMBB1001950//Human lipocortin (LIP) 2 gene, upstream region.//0.0094:180:63//M62899
F-HEMBB1001952//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 101A4, WORKING DRAFT SEQUENCE.//5.4e-19:329:70//Z93341
F-HEMBB1001953//Homo sapiens chromosome 17, clone hRPK.795_F_17, complete sequence.//0.11:589:58// AC005284
F-HEMBB1001957//Human DNA sequence from PAC 204E5 on chromosome 12. Contains exon similar to Wilms' Tumour-related protein QM-like P2X-like receptor, ATP ligand gated ion channel, ESTs, CpG island.//9.8e-25:446: 67//Z98941
F-HEMBB1001962//Homo sapiens chromosome 16, BAC clone 462G18 (LANL), complete sequence.//2.8e-147: 727:97//AC005736
F-HEMBB1001967//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces.// 3.2e-56:650:71//AC004963
F-HEMBB1001973//Homo sapiens chromosome 12p13.3-clone RPCI11-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.//1.2e-42:327:84//AC005844
F-HEMBB1001983//CIT-HSP-2315M4.TF CIT-HSP Homo sapiens genomic clone 2315M4, genomic survey sequence.//8.8e-35:198:96//AQ028071
F-HEMBB1001988//D.polychroa microsatellite sequence (clone Dp 1C e12).//4.5e-07:337:62//X92189
F-HEMBB1001990//HS_3234_A1_G08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3234 Col=15 Row=M, genomic survey sequence.//0.039:279:59//AQ204689
F-HEMBB1001996//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191J18, WORKING DRAFT SEQUENCE.//0.18:392:58//AL024507
F-HEMBB1001997//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.3e-43:446:71//AC005069
F-HEMBB1002002//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.077:444:58//AC004153
F-HEMBB1002005//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 963K23, WORKING DRAFT SEQUENCE.//3.4e-16:173:78//AL031685
F-HEMBB1002009//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00033:790:56//AC005506
F-HEMBB1002015//Homo sapiens genomic DNA, chromosome 21q11.1, segment 27/28, WORKING DRAFT SEQUENCE.//6.7e-05 :126:76//AP000056
F-HEMBB1002042//Oncorhynchus mykiss cytochrome P450 (CYP4V1) mRNA, partial cds.//6.4e-33:402:69// AF046012
F-HEMBB1002043
F-HEMBB1002044//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//3.0e-167:809:97//AC005740
F-HEMBB1002045
F-HEMBB1002049//Homo sapiens chromosome 17, clone hRPC.161_P_9, complete sequence.//0.87:177:65// AC006237
F-HEMBB1002050//Streptomyces coelicolor cosmid D78.//8.5e-08:644:58//AL034355
F-HEMBB1002068//Homo sapiens mRNA for KIAA0612 protein, partial cds.//2.5e-05:402:61//AB014512

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F-HEMBB1002069
F-HEMBB1002092//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B331O8; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//7.8e-104:550:83//AC004064
F-HEMBB1002094//Homo sapiens genomic DNA, 21q region, clone: 125H6N2, genomic survey sequence.//2.9e-49:302:83//AG001476
F-HEMBB1002115//Homo sapiens chromosome 16, cosmid clone 378E2 (LANL), complete sequence.//0.00023:542:61//AC004035
F-HEMBB1002134//Human h-neuro-d4 protein mRNA, complete cds.//7.3e-43:533:70//U43843
F-HEMBB1002139//HS-1048-A2-B02-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 831 Col=4 Row=C, genomic survey sequence.//0.055:228:66//B38714
F-HEMBB1002142//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P5, WORKING DRAFT SEQUENCE.//0.0095:276:64//AL031748
F-HEMBB1002152//Human Chromosome X, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.055:520:57//AC002421
F-HEMBB1002189//Homo sapiens cosmid ICRFc104I0935Q8 from Xq28, complete sequence.//2.6e-05:311:63//AF002998
F-HEMBB1002190//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//5.4e-05:647:59//AC005140
F-HEMBB1002193//Sequence 5 from patent US 5709858.//1.8e-34:179:100//I80846
F-HEMBB1002217//Homo sapiens mRNA for zinc finger protein 10.//1.2e-23:405:67//X52332
F-HEMBB1002218//HS_2056_B1_C09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=17 Row=F, genomic survey sequence.//3.3e-45:245:97//AQ244711
F-HEMBB1002232//Human chromosome 11 72g7 cosmid, complete sequence.//1.9e-21:314:70//U73648
F-HEMBB1002247
F-HEMBB1002249//Homo sapiens DNA sequence from BAC 3418 on chromosome 6p21.3-22.1. Contains ZNF184 gene coding for Kruppel related Zinc Finger protein 184, a hnRNP core protein A1 (mouse Fli-2, rat helix destabilizing protein, mouse Topoisomerase-inhibitor suppressed gene TIS) LIKE pseudogene, a HB15 (CD83 antigen precursor) LIKE pseudogene, Ser-tRNA, Glu-tRNA and Met-tRNA (Met-tRNA-i gene 1) genes. Contains ESTs, STSs and GSSs, complete sequence.//4.1e-45:327:83//AL021918
F-HEMBB1002254//Human chromosome 16 BAC clone LANL cosmid-440E5, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.8e-40:315:82//AC002506
F-HEMBB1002255//Plasmodium falciparum MAL3P3, complete sequence.//0.0035:312:62//Z98547
F-HEMBB1002266//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.013:469:59//AC005504
F-HEMBB1002280//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-259H10, complete sequence.//5.3e-18:527:61//AC004682
F-HEMBB1002300//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//8.6e-139:818:88//U73642
F-HEMBB1002306//HS_3109_A2_H01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3109 Col=2 Row=O, genomic survey sequence.//1.3e-75:371:98//AQ148164
F-HEMBB1002327//HS_3235_B2_G10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=20 Row=N, genomic survey sequence.//3.3e-83:418:97//AQ209752
F-HEMBB1002329//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//3.3e-31:220:88//AQ263402
F-HEMBB1002340
F-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.//4.1e-154:724:98//AJ010841
F-HEMBB1002358//Human thymidylate kinase (CDC8) mRNA, complete cds.//3.3e-36:192:98//L16991
F-HEMBB1002359//Human Rev interacting protein Rip-1 mRNA, complete cds.//1.8e-13:96:96//U55766
F-HEMBB1002364//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 376D21, WORKING DRAFT SEQUENCE.//7.5e-24:202:71//Z98946
F-HEMBB1002371//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.9e-06:674:56//AC004153
F-HEMBB1002381//Homo sapiens chromosome 16, cosmid clone RT163 (LANL), complete sequence.//0.34:238:61//AC005222
F-HEMBB1002383
F-HEMBB1002387//CIT-HSP-2173E20.TR CIT-HSP Homo sapiens genomic clone 2173E20, genomic survey sequence.//5.2e-17:434:66//B91052
F-HEMBB1002409//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3

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precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//1.2e-56:324:88//AL008712
F-HEMBB1002415//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 364I1, WORKING DRAFT SEQUENCE.//8.9e-35:334:75//AL031319
F-HEMBB1002425//Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence.//1.0e-36:317:76//U62317
F-HEMBB1002442//Rattus norvegicus lin-10 protein homolog (lin-10) mRNA, complete cds.//4.3e-88:296:92//U92010
F-HEMBB1002453//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 86D1, WORKING DRAFT SEQUENCE.//2.7e-43:419:78//AL034349
F-HEMBB1002457//Homo sapiens clone DJ0982E09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.3e-27:542:68//AC005534
F-HEMBB1002458//HS_3246_A2_G05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3246 Col=10 Row=M, genomic survey sequence.//3.2e-51:257:99//AQ217993
F-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds.//1.9e-87:493:92//U43885
F-HEMBB1002489
F-HEMBB1002492//Arabidopsis thaliana BAC T15B16.//0.028:516:57//AF104919
F-HEMBB1002495//Homo sapiens chromosome 17, clone hRPK.421_E_14, complete sequence.//1.1e-16:297:68//AC006141
F-HEMBB1002502//Homo sapiens clone DJ1163L11, complete sequence.//1.1e-91:675:82//AC005230
F-HEMBB1002509//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//2.7e-11:648:60//AC004605
F-HEMBB1002510//HS_3236_B1_H11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3236 Col=21 Row=P, genomic survey sequence.//1.2e-06:67:94//AQ205992
F-HEMBB1002520//Homo sapiens BAC clone NH0004N07 from Y, complete sequence.//1.2e-70:580:72//AC006152
F-HEMBB1002522//Homo sapiens Xp22 bin 150 clone GSHB-223P11 (Genome Systems Human BAC library) complete sequence.//5.6e-22:516:64//AC004553 F-HEMBB1002531
F-HEMBB1002534//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 668J24, WORKING DRAFT SEQUENCE.//6.9e-62:265:87//AL034346
F-HEMBB1002545//Human BAC clone RG128M16 from 7q21-7q22, complete sequence.//2.7e-44:200:82//AC000059
F-HEMBB1002550//Homo sapiens PAC clone DJ0910I17 from 7q11.21-q11.23, complete sequence.//0.22:161:68//AC004927
F-HEMBB1002556//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//7.5e-43:306:77//AC004861
F-HEMBB1002579
F-HEMBB1002582//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 349A12, WORKING DRAFT SEQUENCE.//0.00018:431:61//AL033520
F-HEMBB1002590//Yeast (S.cerevisiae) mitochondrial apocytochrome b gene, 3' flank.//0.78:147:64//J01471
F-HEMBB1002596//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 9E21, WORKING DRAFT SEQUENCE.//3.6e-50:692:69//AL008639
F-HEMBB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds.//9.1e-151:710:98//AF089749
F-HEMBB1002601//Human BAC clone RG020D02 from 7q22, complete sequence.//1.5e-07:416:60//AC002381
F-HEMBB1002603//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//0.40:341:60//AC002454
F-HEMBB1002607//Mus musculus homeobox containing nuclear transcriptional factor Hmx1 (Hmx1) gene, complete cds.//0.0042:460:60//AF009614
F-HEMBB1002610//Homo sapiens Chromosome 12q24 PAC RPCI3-462E2 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.3e-23:559:63//AC003029
F-HEMBB1002613//Homo sapiens Chromosome 22q12 BAC Clone 566c1, complete sequence.//4.2e-17:441:63//AC000025
F-HEMBB1002614//Plasmodium falciparum chromosome 2, section 54 of 73 of the complete sequence.//0.013:324:56//AE001417
F-HEMBB1002617//Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.//2.1e-07:441:60//AF001550
F-HEMBB1002623//C.hyalina microsatellite marker DNA (id ATCC4).//0.57:106:66//Z95304
F-HEMBB1002635//Human JNK3 alpha2 protein kinase (JNK3A2) mRNA, complete cds.//4.8e-22:127:100//U34819
F-HEMBB1002664//HS_2265_A1_H06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

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nomic clone Plate=2265 Col=11 Row=O, genomic survey sequence.//0.54:115:67//AQ101557
F-HEMBB1002677//Homo sapiens (subclone 3_d1 from P1 H25) DNA sequence, complete sequence.//2.2e-49:784:68//L81774
F-HEMBB1002683//Homo sapiens type IV collagen 5a chain (COL4A5) gene, exon 23.//1.0:112:63//U04492
F-HEMBB1002684//HS-1050-A2-G06-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 772 Col=12 Row=M, genomic survey sequence.//4.4e-07:86:84//B39748
F-HEMBB1002686//HS-1023-B2-F10-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 802 Col=20 Row=L, genomic survey sequence.//0.98:183:61//B34077
F-HEMBB1002692//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1108H3, WORKING DRAFT SEQUENCE.//0.00039:408:60//AL033525
F-HEMBB1002697//Homo sapiens clone DJ1087M19, WORKING DRAFT SEQUENCE, 7 unordered pieces.//7.3e-35:323:74//AC004955
F-HEMBB1002699//Mus musculus D6MM5e protein (D6Mm5e) and DOK protein (Dok) genes, complete cds; and LOR2 protein (Lor2) gene, partial cds.//0.031:325:62//AF084363
F-HEMBB1002702//HS-1025-A2-D01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 804 Col=2 Row=G, genomic survey sequence.//1.8e-25:158:95//B34720
F-HEMBB1002705//Homo sapiens DNA, chromosome 21q22.2, PAC clone 25P16 complete sequence, encoding carbonyl reductase and carbonyl reductase 3 (complete cds).//1.7e-137:534:96//AB003151
F-HEMBB1002712//Human DNA sequence from cosmid cU115G11, between markers DXS6791 and DXS8038 on chromosome X contains ESTs and STS.//0.0019:612:58//Z71187
F-MAMMA1000009//Human chromosome 1 BAC 308G1 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//6.1e-43:354:81//AC003117
F-MAMMA1000019
F-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FMO5).//2.0e-40:185:97//Z47553
F-MAMMA1000025//Homo sapiens PAC clone DJ0806A17 from 7p13-p14, complete sequence.//1.0:211:65//AC005483
F-MAMMA1000043//Human angiotensin I-converting enzyme (ACE) gene, intron 12.//0.075:204:65//M73275
F-MAMMA1000045//Human DNA sequence from clone 142F18 on chromosome Xq26.3-27.2 Contains part of a gene similar to melanoma-associated antigen, EST, GSS and an inverted repeat, complete sequence.//4.1e-122:495:79//AL031073
F-MAMMA1000055//M.musculus mRNA for testin.//2.1e-35:559:66//X78989
F-MAMMA1000057//Homo sapiens chromosome 17, clone hRPK.259_G_18, complete sequence.//5.5e-121:703:89//AC005829
F-MAMMA1000069//Homo sapiens minisatellite ceb1 repeat region.//0.00013:329:60//AF048727
F-MAMMA1000084//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//2.1e-53:445:79//Z93023
F-MAMMA1000085//Caenorhabditis elegans cosmid Y23H5A.//0.0017:164:64//AF077541
F-MAMMA1000092//Homo sapiens BAC clone GS465N13 from 7p15-p21, complete sequence.//1.2e-70:598:78//AC004744
F-MAMMA1000103//Homo sapiens chromosome 17, clone hCIT.91_J_4, complete sequence.//1.1e-156:857:92//AC003976
F-MAMMA1000117//HS_3223_B2_D08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=16 Row=H, genomic survey sequence.//5.4e-100:527:94//AQ221160
F-MAMMA1000129//ryanodine receptor.//0.055 :492:59//A20359
F-MAMMA1000133
F-MAMMA1000134//HS_3078_B1_C02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=3 Row=F, genomic survey sequence.//2.1e-93:462:97//AQ144362
F-MAMMA1000139//Homo sapiens Xp22 PAC RPCI1-5G11 (from Roswell Park Cancer Center) complete sequence.//3.3e-14:322:65//AC002369
F-MAMMA1000143//Homo sapiens mRNA for KIAA0685 protein, complete cds.//6.9e-25:148:97//AB014585
F-MAMMA1000155//Homo sapiens homeobox transcription factor barx2 (BARX2) mRNA, complete cds.//1.0e-29:219:87//AF031924
F-MAMMA1000163
F-MAMMA1000171//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence.//6.3e-14:92:88//AC005393
F-MAMMA1000173//Mus musculus SH3-containing protein SH3P7 mRNA, complete cds. similar to Human Drebrin.//2.2e-114:698:87//U58884
F-MAMMA1000175//HS_3050_B1_B03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

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nomic clone Plate=3050 Col=5 Row=D, genomic survey sequence.//6.2e-73:357:99//AQ102678
F-MAMMA1000183//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//4.6e-94:904:73//AL023808
F-MAMMA1000198//Z.diploperennis repetitive DNA (clone ZEAR 266).//0.18:152:70//X53610
F-MAMMA1000221//Human Chromosome 15q11-q13 PAC clone pDJ778a2, complete sequence.//0.017:99:75//AC004583
F-MAMMA1000227//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 467K16, WORKING DRAFT SEQUENCE.//0.36:312:62//AL031283
F-MAMMA1000241//HS_3217_B1_B02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3217 Col=3 Row=D, genomic survey sequence.//1.9e-94:456:98//AQ193401
F-MAMMA1000251//Homo sapiens NF2 gene.//0.00092:270:64//Y18000
F-MAMMA1000254//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0034:777:57//AC005140
F-MAMMA1000257//Homo sapiens DNA sequence from PAC 201D7 on chromosome 6p22.1-22.3. Contains EST and STS.//0.00036:230:65//AL022717
F-MAMMA1000264//Homo sapiens (subclone 9_f5 from P1 H17) DNA sequence, complete sequence.//1.5e-30:499:68//L81612
F-MAMMA1000266//Bacillus lynceorum strain pMEL12 Bag320 satellite DNA.//0.28:218:64//AF034430
F-MAMMA1000270//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//1 .4e-157:788:96//AF001549
F-MAMMA1000277//Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.//0.70:320:61//AL021897
F-MAMMA1000278//Sequence 23 from patent US 5708157.//9.3e-103:540:95//I80055
F-MAMMA1000279//Human DNA sequence from clone 769D20 on chromosome Xp21.1-21.3 Contains EST, STS, GSS, complete sequence.//2.4e-49:262:77//AL031643
F-MAMMA1000284//cSRL-165E12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-165E12, genomic survey sequence.//1.1e-30:324:75//B03004
F-MAMMA1000287//Homo sapiens, clone hRPK.15_A_1, complete sequence.//2.7e-54:401:83//AC006213
F-MAMMA1000302//Drosophila melanogaster complete mitochondrial genome.//0.0051:307:61//U37541
F-MAMMA1000307//Homo sapiens chromosome 12p13.3 clone RPCI5-1154L15, WORKING DRAFT SEQUENCE, 67 unordered pieces.//0.15:449:59//AC006205
F-MAMMA1000309//cDNA coding human apolipoprotein E3.//0.00010:691:58//E00359
F-MAMMA1000312//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 798A17, WORKING DRAFT SEQUENCE.//0.27:301:60//AL031274
F-MAMMA1000313
F-MAMMA1000331//Human Chromosome 16 BAC clone CIT987SK-A-735G6, complete sequence.//9.8e-06:151:71//AC002400
F-MAMMA1000339
F-MAMMA1000340//HS_2181_B2_F07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2181 Col=14 Row=L, genomic survey sequence.//4.3e-05:181:68//AQ024288
F-MAMMA1000348//Homo sapiens chromosome 17, clone HRPC843B9, complete sequence.//5.3e-30:575:66//AC004139
F-MAMMA1000356//Homo sapiens clone RG038K21, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-52:264:76//AC005052
F-MAMMA1000360//Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence.//6.5e-91:569:88//AC004879
F-MAMMA1000361//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//1.4e-42:315:83//Z98950
F-MAMMA1000372//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//2.9e-114:516:89//AL022345
F-MAMMA1000385//CITBI-E1-2517E13.TF CITBI-E1 Homo sapiens genomic clone 2517E13, genomic survey sequence.//6.9e-26:377:71//AQ279944
F-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds.//3.7e-148:710:98//AB015132
F-MAMMA1000395
F-MAMMA1000402//Homo sapiens clone DJ0718N17, complete sequence.//4.0e-115:845:85//AC005999
F-MAMMA1000410//HS_3245_A1_C02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3245 Col=3 Row=E, genomic survey sequence.//9.6e-42:350:80//AQ205768

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F-MAMMA1000413//HS_3223_B2_F01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=2 Row=L, genomic survey sequence.//1.6e-48:318:89//AQ188456
F-MAMMA1000414//HS_2027_B2_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=8 Row=F, genomic survey sequence.//1.4e-46:286:92//AQ231369
F-MAMMA1000416//Drosophila melanogaster DNA sequence (P1s DS07528 (D169) and DS06665 (D220)), complete sequence.//9.4e-33:310:72//AC004640
F-MAMMA1000421//Homo sapiens clone DJ1129D05, complete sequence.//3.3e-29:223:84//AC005630
F-MAMMA1000422
F-MAMMA1000423//Drosophila yakuba mitochondrial DNA molecule.//2.2e-10:639:57//X03240
F-MAMMA1000424//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.6e-47:556:68//AC003973
F-MAMMA1000429//Mus musculus SDP8 mRNA, complete cds.//8.0e-99:545:92//AF062484
F-MAMMA1000431//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.8e-41:289:79//AC005283
F-MAMMA1000444//Human DNA sequence from clone 714B7 on chromosome 22q12.2-13.2 Contains CYTOCHROME C OXIDASE VIIB precursor like pseudogene and ESTs, complete sequence.//2.3e-34:291:80//Z99755
F-MAMMA1000446
F-MAMMA1000458//Mus musculus clone OST9003, genomic survey sequence.//5.0e-53:231:84//AF046620
F-MAMMA1000468//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 291J10, WORKING DRAFT SEQUENCE.//0.75:303:60//Z93017
F-MAMMA1000472//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 414D7, WORKING DRAFT SEQUENCE.//4.0e-41:403:77//AL033543
F-MAMMA1000478//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//9.5e-54:369:77//AC005081
F-MAMMA1000483//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//3.6e-34:332:77//AC004381
F-MAMMA1000490//Homo sapiens 12q13.1 PAC RPCI1-90J4 (Roswell Park Cancer Institute Human PAC library) complete sequence.//8.9e-128:822:87//AC003686
F-MAMMA1000500//CIT-HSP-231905.TF CIT-HSP Homo sapiens genomic clone 2319O5, genomic survey sequence.//4.8e-29:175:94//AQ044812
F-MAMMA1000501//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//5.7e-45:334:82//AL022336
F-MAMMA1000516//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATPSG1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.9e-43:529:69//Z92545
F-MAMMA1000522//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence.//2.0e-14:380:63//AL022576
F-MAMMA1000524//Homo sapiens chromosome 10 clone CIT-HSP-1338F24 map 10p11.2-10p12.1, complete sequence.//1.4e-22:420:66//AC006101
F-MAMMA1000559//Human HepG2 3' region cDNA, clone hmd3f08.//5.4e-29:168:97//D16922
F-MAMMA1000565//RPCI11-61K6.TJ RPCI11 Homo sapiens genomic clone R-61K6, genomic survey sequence.//1.7e-120:561:100//AQ194238
F-MAMMA1000567//Human DNA sequence from PAC 179D3, between markers DXS6791 and DXS8038 on chromosome X contains S10 GTP-binding protein, ESTs and CpG island.//3.1e-43:387:80//Z81370
F-MAMMA1000576//Homo sapiens BAC clone RG442F18 from 2, complete sequence.//1.2e-30:237:75//AC005104
F-MAMMA1000583//RPCI11-60M22.TJ RPCI11 Homo sapiens genomic clone R-60M22, genomic survey sequence.//9.6e-102:487:99//AQ198091
F-MAMMA1000585//Homo sapiens clone UWGC:djs14 from 7p14-15, complete sequence.//5.2e-39:370:78//AC006195
F-MAMMA1000594//Homo sapiens chromosome 19, cosmid R31646, complete sequence.//3.9e-43:328:83//AC005338
F-MAMMA1000597//Homo sapiens chromosome 17, clone hRPK.481_C_4, complete sequence.//1.5e-32:259:82//AC005839
F-MAMMA1000605//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//2.4e-59:318:83//AL031297

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F-MAMMA1000612//HS_2188_A2_D02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=4 Row=G, genomic survey sequence.//4.8e-30:171:96//AQ116793
F-MAMMA1000616//HS_3176_A1_E06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3176 Col=11 Row=I, genomic survey sequence.//4.7e-28:287:79//AQ300310
F-MAMMA1000621//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 273F20, WORKING DRAFT SEQUENCE.//0.015:478:58//AL034371
F-MAMMA1000623
F-MAMMA1000625//DNA encoding Hepatitis C virus antigen.//0.93:196:61//E06898
F-MAMMA1000643//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds.//0.95:365:59//AF023674
F-MAMMA1000664//HS_3096_B1_C02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3096 Col=3 Row=F, genomic survey sequence.//2.7e-51:257:99//AQ145137
F-MAMMA1000669//Homo sapiens chromosome 19, cosmid R26908, complete sequence.//2.0e-66:586:67//AC004785
F-MAMMA1000670//HS_2243_B2_A08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2243 Col=16 Row=B, genomic survey sequence.//8.7e-05:94:80//AQ153650
F-MAMMA1000672//Mus musculus clone OST8270, genomic survey sequence.//3.9e-64:471:81//AF046705
F-MAMMA1000684//Suid herpesvirus 1 Rsp40 mRNA, partial cds.//1.2e-07:186:67//U27489
F-MAMMA1000696//Human oligodendrocyte myelin glycoprotein (OMG) exons 1-2; neurofibromatosis 1 (NF1) exons 28-49; ecotropic viral integration site 2B (EVI2B) exons 1-2; ecotropic viral integration site 2A (EVI2A) exons 1-2; adenylate kinase (AK3) exons 1-2.//3.0e-53:653:70//L05367
F-MAMMA1000707//CIT-HSP-2302019.TR CIT-HSP Homo sapiens genomic clone 2302O19, genomic survey sequence.//1.8e-08:131:77//AQ017947
F-MAMMA1000713//Rattus norvegicus clonel polymeric immunoglobulin receptor mRNA 3' untranslated region, GA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats.//0.062:134:67//U00762
F-MAMMA1000714//Chicken hsp90 gene for 90 kDa-heat shock protein 5'-end.//1.0:266:61//X15028
F-MAMMA1000718//CIT-HSP-2171B10.TF CIT-HSP Homo sapiens genomic clone 2171B10, genomic survey sequence.//3.6e-05:289:60//B95401
F-MAMMA1000720//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//4.4e-184:842:98//AC005781
F-MAMMA1000723//Homo sapiens clone DJ0892G19, complete sequence.//8.8e-05:430:60//AC004917
F-MAMMA1000731//Drosophila melanogaster DNA sequence (P1 DS07049 (D133)), complete sequence.//3.8e-55:796:66//AC004274
F-MAMMA1000732//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.//6.6e-77:555:74//AF064859
F-MAMMA1000733//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P6, WORKING DRAFT SEQUENCE.//0.98:479:58//AL031749
F-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//7.3e-168:802:98//AF100141
F-MAMMA1000738//S.cerevisiae chromosome XIV reading frame ORF YNL132w.//8.6e-31:626:63//Z71408
F-MAMMA1000744//Gorilla Alu-repetitive sequence in beta-globin gene cluster.//2.7e-54:410:82//X06123
F-MAMMA1000746//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-10F4, complete sequence.//3.7e-109:779:83//AC004158
F-MAMMA1000752//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.2e-20:444:63//AC005075
F-MAMMA1000760//Homo sapiens clone RG015P03, complete sequence.//1.5e-44:403:79//AC005048
F-MAMMA1000761//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.3e-22:159:81//AC004166
F-MAMMA1000775//Homo sapiens chromosome 17, clone hRPK.849_N_15, complete sequence.//1.3e-51:789:68//AC005703
F-MAMMA1000776//Human DNA sequence from BAC 57G9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS.//5.7e-40:238:78//Z95116
F-MAMMA1000778//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 153G14, WORKING DRAFT SEQUENCE.//7.6e-29:222:84//AL031118
F-MAMMA1000782//Human 2,4-dienoyl-CoA reductase gene, exon 9.//0.90:137:62//U94987
F-MAMMA1000798//*** SEQUENCING IN PROGRESS *** EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//0.00058:163:71//AC003656
F-MAMMA1000802//Homo sapiens chromosome 19, cosmid R33729, complete sequence.//6.3e-151:714:99//

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AC005339
F-MAMMA1000824//Homo sapiens 12p13.3 BAC RPCI11-543P15 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//4.2e-104:503:99//AC005912
F-MAMMA1000831//Homo sapiens clone UWGC:g1211a139, complete sequence.//0.76:302:58//AC005502
F-MAMMA1000839//Human BAC clone RG013L03 from 7q21, complete sequence.//1.9e-54:322:68//AC002456
F-MAMMA1000841//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//6.7e-140:647:92//AL023755
F-MAMMA1000842//, complete sequence.//0.0068:499:59//AC005817
F-MAMMA1000843//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.13:439:59//AC004710
F-MAMMA1000845//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//2.2e-05:208:64//AL034557
F-MAMMA1000851//Gallus domesticus filamin gene 5' region, partial cds.//0.86:193:63//U00146
F-MAMMA1000855//Human minisatellite region detected by myoglobin 33-repeat probe, clone lambda 33.10.//0.081:229:62//M30549
F-MAMMA1000856//B.taurus microsatellite marker ETH8 (D6S3) DNA.//0.0024:253:60//Z22747
F-MAMMA1000859//Sequence 6 from Patent WO9722695.//2.3e-79:533:82//A63553
F-MAMMA1000862
F-MAMMA1000863//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//1.0e-28:439:64//AP000050
F-MAMMA1000865
F-MAMMA1000867//CIT-HSP-2385J8.TR.1 CIT-HSP Homo sapiens genomic clone 2385J8, genomic survey sequence.//0.00017:158:70//AQ240906
F-MAMMA1000875//Homo sapiens DNA sequence from PAC 232G24 on chromosome Xq27.1-q27.3. Contains two exons similar to MAGE gene family, EST, CA repeat, STS, complete sequence.//1.0:121:68//AL022152
F-MAMMA1000876//Homo sapiens clone HS19.6 Alu-Ya5 sequence.//8.4e-41:185:90//AF015152
F-MAMMA1000877//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//8.3e-57:522:75//AL022336
F-MAMMA1000880//Homo sapiens full-length insert cDNA clone ZD54A10.//5.2e-26:143:100//AF086327
F-MAMMA1000883//Human DNA sequence from clone 786D3 on chromosome 22q13.31-33 Contains GSS, complete sequence.//0.99:225:63//AL023801
F-MAMMA1000897//R.norvegicus mRNA for plasma protein.//4.8e-07:479:58//Y11283
F-MAMMA1000905//F26L5TRB IGF Arabidopsis thaliana genomic clone F26L5, genomic survey sequence.//0.94:115:66//B61433
F-MAMMA1000906//HS_3110_B2_A11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3110 Col=22 Row=B, genomic survey sequence.//2.5e-63:548:78//AQ182819
F-MAMMA1000908//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27K12, WORKING DRAFT SEQUENCE.//5.2e-80:480:90//AL033397
F-MAMMA1000914//Plasmodium falciparum MAL3P8, complete sequence.//7.6e-09:596:58//AL034560
F-MAMMA1000921//CIT-HSP-2171D8.TR CIT-HSP Homo sapiens genomic clone 2171D8, genomic survey sequence.//6.6e-07:249:66//889575
F-MAMMA1000931//Homo sapiens clone DJ0892G19, complete sequence.//2.9e-43:415:66//AC004917
F-MAMMA1000940//HS-1056-A2-E02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 778 Col=4 Row=I, genomic survey sequence.//6.1e-44:235:78//B47296
F-MAMMA1000941//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 complete genomic sequence, complete sequence.//9.4e-48:443:75//AC002299
F-MAMMA1000942//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//1.8e-14:175:76//AL031117
F-MAMMA1000943//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0082:684:56//AC005308
F-MAMMA1000956//Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence.//3.3e-30:530:67//AC004643
F-MAMMA1000957//HS_3039_A2_C08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=16 Row=E, genomic survey sequence.//1.3e-72:390:94//AQ155121
F-MAMMA1000962//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-58:318:86//AC006001
F-MAMMA1000968//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the

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TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//1.4e-18:396:65//AL022394

F-MAMMA1000975//Human DNA sequence from clone 344I7 on chromosome Xp11.21-11.3. Contains a Keratin, Type II Cytoskeletal 8 (Cytokeratin 8, CYK8, KRT8) pseudogene, ESTs and a GSS, complete sequence.//1.4e-79:690:77//AL024458

F-MAMMA1000979//Homo sapiens PAC clone DJ1186C01 from 7q21.2-q31.1, complete sequence.//0.089:214:66//AC004991

F-MAMMA1000987//Human PAC clone DJ527C21 from Xq23, complete sequence.//1.1e-58:458:82//AC000114

F-MAMMA1000998//Human DNA sequence from PAC 997K18 on chromosome 20p12. Contains ESTs and CA repeat.//1.1e-05:439:62//AL021406

F-MAMMA1001003//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains ESTs and an STS, complete sequence.//0.24:166:68//AL022401

F-MAMMA1001008//Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRAFT SEQUENCE.//1.6e-103:139:99//AJ011929

F-MAMMA1001021//Homo sapiens clone 24544 beta-dystrobrevin mRNA, partial cds.//6.5e-48:465:76//AF070567

F-MAMMA1001024//CITBI-E1-2501L21.TF.1 CITBI-E1 Homo sapiens genomic clone 2501L21, genomic survey sequence.//1.0:175:62//AQ241701

F-MAMMA1001030//Homo sapiens G protein-coupled receptor LGR5 (LGR5) mRNA, complete cds.//1.1e-30:753:6//1AF061444

F-MAMMA1001035//Human Chromosome 16 BAC clone CIT987SK-A-1000D7, complete sequence.//7.9e-24:256:76//AC002990

F-MAMMA1001038//CIT-HSP-2284N21.TF CIT-HSP Homo sapiens genomic clone 2284N21, genomic survey sequence.//0.96:78:75//AQ000903

F-MAMMA1001041//chicken mRNA for alpha-actinin, complete cds.//2.8e-09:355:63//D26597

F-MAMMA1001050//Homo sapiens BAC clone RG060P12 from 7q21, complete sequence.//2.6e-40:378:76//AC002457

F-MAMMA1001059//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//4.8e-97:661:83//L25125

F-MAMMA1001067//Homo sapiens genomic intron breakpoint sequence of MLL rearrangement, 285 bp.//2.8e-18:110:100//AJ000169

F-MAMMA1001073//HS_3046_A2_G08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3046 Col=16 Row=M, genomic survey sequence.//1.0:142:68//AQ098420

F-MAMMA1001074//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 455J7, WORKING DRAFT SEQUENCE.//1.2e-23:386:70//AL031733

F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA sequence.//1.1e-27:559:65//L09749

F-MAMMA1001078//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//2.0e-22:334:69//AC006120

F-MAMMA1001080//Human immunoglobulin heavy chain variable region (VH III family) from IgM rheumatoid factor.//6.4e-58:327:92//L29155

F-MAMMA1001082//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//3.8e-87:695:77//AC004087

F-MAMMA1001091//Homo sapiens chromosome 19, cosmid F21967, complete sequence.//7.0e-05 :594:60//AC005256

F-MAMMA1001092//Human DNA sequence from PAC 49C23 on chromosome X contains malate dehydrogenase pseudogene and STS.//1.6e-91:174:87//Z93019

F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds.//6.4e-23:507:66//AF016045

F-MAMMA1001110//Homo sapiens chromosome 19, cosmid F16815, complete sequence.//0.77:316:60//AC004637

F-MAMMA1001126//Homo sapiens PAC 50H2 in the CUTL1 locus, complete sequence.//3.3e-21:237:73//AF047825

F-MAMMA1001133//Human DNA sequence from BAC 57G9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS.//0.97:202:63//Z95116

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F-MAMMA1001139//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].//1.6e-84:406:82//S70011
F-MAMMA1001143//Homo sapiens DNA sequence from cosmid N75B3 on chromosome 22 Contains EST, exon trap, complete sequence.//1.3e-14:182:76//AL022339
F-MAMMA1001145//Human DNA sequence from cosmid cU115G11, between markers DXS6791 and DXS8038 on chromosome X contains ESTs and STS.//5.2e-87:714:78//Z71187
F-MAMMA1001154//CIT-HSP-2341D13.TF CIT-HSP Homo sapiens genomic clone 2341D13 genomic survey sequence.//0.00051:249:61//AQ055735
F-MAMMA1001161//Homo sapiens chromosome 14, BAC CITB-135H17 containing the RAD51L1 gene, complete sequence.//2.2e-30:410:70//AC004518
F-MAMMA1001162//Homo sapiens full-length insert cDNA clone ZA79C01.//2.4e-13:87:100//AF086123
F-MAMMA1001181//Mus musculus C2C12 unknown mRNA, partial cds.//9.3e-15:432:60//U31629
F-MAMMA1001186//Homo sapiens chromosome 17, clone hRPK.74_E_22, complete sequence.//6.8e-57:670:72//AC005696
F-MAMMA1001191
F-MAMMA1001198//Mus musculus eps15R mRNA, complete cds.//1.5e-117:759:84//U29156
F-MAMMA1001202
F-MAMMA1001203//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.5e-161:764:98//AC005412
F-MAMMA1001206//Homo sapiens chromosome 17, clone HCIT421K24, complete sequence.//5:1e-30:535:65//AC004099
F-MAMMA1001215//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence.//8.4e-182:860:98//AC005393
F-MAMMA1001220//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//7.7e-58:690:70//AC004875
F-MAMMA1001222//Mouse loricrin mRNA, complete cds.//2.7e-07:624:58//M34398
F-MAMMA1001243//Homo sapiens chromosome 17, clone hRPK.192_H_23, complete sequence.//0.91:177:66//AC005726
F-MAMMA1001244
F-MAMMA1001249//Human 28S ribosomal RNA psuedogenes and alu repeat region sequence.//6.7e-09:502:58//U67616
F-MAMMA1001256//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//5.0e-37:342:80//Z99495
F-MAMMA1001259
F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds.//8.7e-40:659:64//AB014561
F-MAMMA1001268//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//4.9e-43:265:81//AC004453
F-MAMMA1001271//Salmo salar DNA for a cryptic repeat.//2.6e-06:311:63//AJ012206
F-MAMMA1001274//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//6.6e-70:327:83//AC004840
F-MAMMA1001280//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0e-05 :276:66//AC003035
F-MAMMA1001292//Human DNA sequence from clone 1170K4 on chromosome 22q12.2-13.1. Contains three novel genes, one of which codes for a Trypsin family protein with class A LDL receptor domains, and the IL2RB gene for Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen). Contains a putative CpG island, ESTs, and GSSs, complete sequence.//3.6e-98:199:98//AL022314
F-MAMMA1001296//RPCI11-38B4.TV RPCI-11 Homo sapiens genomic clone RPCI-11-38B4, genomic survey sequence.//4.7e-33:292:71//AQ030084
F-MAMMA1001298//Homo sapiens chromosome 17, clone hRPK.849_N_15, complete sequence.//1.6e-182:860:98//AC005703
F-MAMMA1001305//Human DNA sequence from clone 116F5 on chromosome 22q13. Contains part of an unknown gene and part of a RhoGAP (CDC42 GTPAse Activating Protein) LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D22S1168 and a CA repeat polymorphism, complete sequence.//1.9e-70:163:97//Z93244
F-MAMMA1001322//Human DNA sequence from clone 774I24 on chromosome 1q24.1-24.3 Contains protein similar to pregnancy-associated plasma protein A precursor neuronal migration protein astrotactin, ESTs, STS and GSS, complete sequence.//2.6e-19:379:68//AL031290
F-MAMMA1001324//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 197L1, WORKING DRAFT SEQUENCE.//4.5e-131:751:90//AL031390
F-MAMMA1001330

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F-MAMMA1001341//Sus scrofa.//1.6e-36:420:73//Z46906
F-MAMMA1001343//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//1.1e-05:818:58//AL031744
F-MAMMA1001346
F-MAMMA1001383//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//2.0e-44:505:74//AC004086
F-MAMMA1001388//Human IGF binding protein complex acid-labile subunit a mRNA, complete cds.//1.5e-07:415:58//M86826
F-MAMMA1001397//Human DNA sequence from clone 462D8 on chromosome 22q11.21-12.1 Contains EST, STS and GSS, complete sequence.//1.6e-23 :209:75//AL022332
F-MAMMA1001408//HS_3242_A1_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=21 Row=O, genomic survey sequence.//2.7e-07:181:69//AQ207300
F-MAMMA1001411//Homo sapiens autosomal dominant polycystic kidney disease type II protein (PKD2) gene, exon 14.//0.98:120:68//AF004872
F-MAMMA1001419//HS_2053_B1_F12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2053 Col=23 Row=L, genomic survey sequence.//1.9e-75 :424:93//AQ244585
F-MAMMA1001420//Homo sapiens chromosome 4 clone B203C23 map 4q25, complete sequence.//2.4e-09:199:70//AC004049
F-MAMMA1001435//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-2011O4, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-42:558:69//AC004529 F-MAMMA1001442//Plasmodium falciparum chromosome 2, section 37 of 73 of the complete sequence.//0.0019:516:56//AE001400
F-MAMMA1001446//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//3.6e-42:486:70//AC003684
F-MAMMA1001452//RPCI11-48022.TJ RPCI11 Homo sapiens genomic clone R-48O22, genomic survey sequence.//5.3e-87:423:98//AQ199294
F-MAMMA1001465//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 414D7, WORKING DRAFT SEQUENCE.//0.00038:114:75//AL033543
F-MAMMA1001476//Mus musculus uridine kinase mRNA, partial cds.//4.1e-99:604:87//L31783
F-MAMMA1001487//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.0e-13:158:77//AC005486
F-MAMMA1001501//Human mRNA for calcium activated neutral protease large subunit (muCANP, calpain, EC 3.4.22.17).//9.6e-52:438:81//X04366
F-MAMMA1001502//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 356B7, WORKING DRAFT SEQUENCE.//3.7e-152:720:99//AL031714
F-MAMMA1001510//Human PAC clone DJ438O4 from 22q12.1-qter, complete sequence.//1.1e-05:371:61//AC002378
F-MAMMA1001522
F-MAMMA1001547
F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 protein, partial cds.//2.3e-128:614:98//AB007931
F-MAMMA1001575//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//0.97:154:68//AF001548
F-MAMMA1001576//Human gamma-tubulin mRNA, complete cds.//1.8e-95:529:91//M61764
F-MAMMA1001590//Human DNA sequence from clone 125H2 on chromosome 22q11-12 Contains part of myosin heavy chain gene, EST, CA repeat, STS, GSS, complete sequence.//1.8e-07:104:84//Z98949
F-MAMMA1001600//HS_3022_A2_H01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022 Col=2 Row=O, genomic survey sequence.//1.6e-66:405:90//AQ163791
F-MAMMA1001604//Human DNA sequence from clone 1114G22 on chromosome 1q24-25 Contains EST, CA repeat, Ninenin like sequence, complete sequence.//0.00043:715:58//AL008626
F-MAMMA1001606//jd114 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 2G6, genomic survey sequence.//0.19:266:62//B13685
F-MAMMA1001620//Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds.//9.7e-54:442:69//AF053630
F-MAMMA1001627//X.borealis ribosomal spacer DNA, with a DNaseI-hypersensitive site.//0.14:221:62//M29833
F-MAMMA1001630//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//2.0e-47:611:71//AC005412
F-MAMMA1001633//Human zinc finger protein (LD5-1) mRNA, complete cds.//1.1e-42:611:67//U57796
F-MAMMA1001635//Human BAC clone RG072E11 from 7q21-7q22, complete sequence.//4.0e-35:407:70//AC000118

BNSDOCID: <EP___1074617A2_I_>

F-MAMMA1001649//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.44:245:63//AL022577
F-MAMMA1001654//Mouse transcriptional control element.//0.0025:189:63//M17284
F-MAMMA1001663//CIT-HSP-2165E16.TR CIT-HSP Homo sapiens genomic clone 2165E16, genomic survey sequence.//9.7e-05:146:66//B95491
F-MAMMA1001670//HS_3136_A1_G06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3136 Col=11 Row=M, genomic survey sequence.//3.1e-28:237:85//AQ148779
F-MAMMA1001671//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//3.3e-181:863:98//AC005614
F-MAMMA1001679//HS_3054_A1_H11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=21 Row=O, genomic survey sequence.//1.0:89:70//AQ106118
F-MAMMA1001683//Spermatozopsis similis mRNA for 90 kD basal apparatus-protein.//8.3e-07:480:62//AJ224970
F-MAMMA1001686//HS_3219_B1_A03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=5 Row=B, genomic survey sequence.//0.00072:180:65//AQ180345
F-MAMMA1001692//HS_3047_B1_B10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=19 Row=D, genomic survey sequence.//2.5e-94:459:98//AQ134228
F-MAMMA1001711//Homo sapiens clone DJ0635O05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-42:316:82//AC004845
F-MAMMA1001715//CIT-HSP-2347A14.TF CIT-HSP Homo sapiens genomic clone 2347A14, genomic survey sequence.//1.1e-60:413:87//AQ059125
F-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.//1.8e-133:646:97//AF095687
F-MAMMA1001735//chicken brain tubulin beta chain mrna.//3.5e-110:740:84//J00913
F-MAMMA1001740//Human DNA sequence from PAC 136017 on chromosome X contains ESTs and STS.//0.98:416:57//Z72001
F-MAMMA1001743//Homo sapiens clone DJ0981O07, complete sequence.//3.2e-16:194:75//AC006017
F-MAMMA1001744//Homo sapiens DNA sequence from clone 46618 on chromosome Xq11.1-13.2. Contains an unknown gene similar to Coagulation Factor V (Activated Protein C Cofactor), Coagulation Factor VIII (Procoagulant Component) and Ceruloplasmin (EC 1.16.3.1, Ferroxidase). Contains ESTs and an STS, complete sequence.//0.0036:181:66//AL030998
F-MAMMA1001745//Homo sapiens BAC clone 529F11 from 8q21, complete sequence.//1.2e-60:822:68//AF070718
F-MAMMA1001751//Human potassium channel KCNO1 mRNA, complete cds.//1.2e-35:583:65//U90065
F-MAMMA1001754//Bos taurus vacuolar proton pump subunit SFD alpha isoform (SFD) mRNA, complete cds.//8.4e-102:627:87//AF041338
F-MAMMA1001757//HS_2058_B2_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=8 Row=F, genomic survey sequence.//1.7e-24:173:88//AQ243865
F-MAMMA1001760//Human DNA sequence from clone 354N19 on chromosome 6q22. Contains the 3' part of the gene for Mannosyl-Oligosaccharide Alpha-1,2-Mannosidase (Man(9)-alpha-mannosidase, EC 3.2.1.113), a Cytochrome C Oxidase Polypeptide I (EC 1.9.3.1) pseudogene and a pseudogene similar to 60S Ribosomal Protein L13A. Contains genomic markers D6S287 and D6S1696, ESTs, STSs, GSSs and two CA repeat polymorphisms, complete sequence.//6.6e-76:349:87//AL022722
F-MAMMA1001764//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//0.23:633:57//M97514
F-MAMMA1001768//Bovine herpesvirus 1 complete genome.//2.3e-11:547:60//AJ004801
F-MAMMA1001769//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.1e-76:509:78//AC004801
F-MAMMA1001771//M.musculus mRNA for semaphorin B.//2.7e-106:744:82//X85991
F-MAMMA1001783//Human PAC clone 127H14 from 12q, complete sequence.//6.0e-20:228:75//AC002563
F-MAMMA1001785
F-MAMMA1001788//Human DNA sequence from clone 425C14 on chromosome 6q22 Contains the HSF2 gene for Heat Shock Factor 2 (Heat Shock Transcription Factor 2, HSTF 2) and an unknown gene similar to the placental protein DIFF33 gene. Contains ESTs, STSs and GSSs, complete sequence.//5.0e-05:152:74//Z99129
F-MAMMA1001790//Homo sapiens chromosome 12p13.3 clone RPCI3-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces.//4.5e-53:318:80//AC005845

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F-MAMMA1001806//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//1.0:131:67//AC004262
F-MAMMA1001812//Human Chromosome X clone bWXD187, complete sequence.//3.0e-34:257:83//AC004383
F-MAMMA1001815//Homo sapiens PAC clone DJ0850G01 from 7q21.2-q22, complete sequence.//5.2e-61:516:79//AC004128
F-MAMMA1001817//Homo sapiens 12q24 PAC RPCI1-261P5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.1e-32:295:78//AC004031
F-MAMMA1001818//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1.333303.//0.71:179:67//AJ011930
F-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene.//3.0e-91:726:79//Y13148
F-MAMMA1001824//HS_3108_A1_G12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=23 Row=M, genomic survey sequence.//3.4e-05:119:74//AQ107508
F-MAMMA1001836//Homo sapiens chromosome 18, clone hRPK.537_E_1, complete sequence.//3.4e-45:312:85//AC006211
F-MAMMA1001837//Rattus norvegicus zinc finger protein Y1 (RLZF-Y) mRNA, complete cds.//4.5e-51:480:75//AF052042
F-MAMMA1001848//CITBI-E1-2516P17.TF CITBI-E1 Homo sapiens genomic clone 2516P17, genomic survey sequence.//1.0e-100:486:98//AQ279620
F-MAMMA1001851//Human DNA from overlapping chromosome 19-specific cosmids R30072 and R28588, genomic sequence, complete sequence.//5.1e-07:197:67//AC002390
F-MAMMA1001854
F-MAMMA1001858//RPCI11-11L22.TP RPCI-11 Homo sapiens genomic clone RPCI-11-11L22, genomic survey sequence.//0.091:161:65//B75631
F-MAMMA1001864//Human PAC clone DJ0205E24 from Xq23, complete sequence.//2.6e-09:397:61//AC003013
F-MAMMA1001868//HS_2196_B2_A12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196 Col=24 Row=B, genomic survey sequence.//5.8e-13:86:100//AQ032455
F-MAMMA1001874//H.sapiens CpG island DNA genomic Mse1 fragment, clone 63h5, reverse read cpg63h5.rtla.//1.0:127:63//Z62129
F-MAMMA1001878//Human DNA sequence from BAC 999D10 on chromosome 22q13.3. Contains two BAC end-sequences (GSSs).//1.7e-19:372:67//Z94802
F-MAMMA1001880//RPCI11-90K3.TJ RPCI11 Homo sapiens genomic clone R-90K3, genomic survey sequence.//6.6e-11:362:62//AQ283465
F-MAMMA1001890//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 508I15, WORKING DRAFT SEQUENCE.//1.8e-45:317:86//AL021707
F-MAMMA1001907//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//2.7e-23:255:77//Z82207
F-MAMMA1001908//HS_2225_A1_A03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2225 Col=5 Row=A, genomic survey sequence.//5.4e-08:264:62//AQ301597
F-MAMMA1001931//HS_3049_B2_D09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3049 Col=18 Row=H, genomic survey sequence.//1.7e-47:295:90//AQ100157
F-MAMMA1001956//H.sapiens DNA sequence.//0.056:233:66//Z22493
F-MAMMA1001963//Homo sapiens adenylosuccinate lyase gene, complete cds.//0.99:173:68//AF106656
F-MAMMA1001969//Human DNA sequence from cosmid 232L22, between markers DXS366 and DXS87 on chromosome X contains ESTs glycerol kinase pseudogene.//5.3e-63:479:78//Z73986
F-MAMMA1001970//Homo Sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.4e-126:699:93//AC003071
F-MAMMA1001992//HS_3078_A1_A09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=17 Row=A, genomic survey sequence.//3.3e-08:257:65//AQ143646
F-MAMMA1002009//Homo sapiens chromosome 17, clone hRPK.214_O_I, complete sequence.//1.5e-07:244:62//AC005224
F-MAMMA1002011//HS_3252_B1_B05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=9 Row=D, genomic survey sequence.//1.3e-07:170:69//AQ304711
F-MAMMA1002032//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 37 unordered pieces.//2.1e-34:315:79//AC004803
F-MAMMA1002033//HS_3023_A2_G04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=8 Row=M, genomic survey sequence.//4.3e-69:366:94//AQ105493
F-MAMMA1002041//Genomic sequence from Human 9q34, complete sequence.//5.3e-85:439:82//AC001227
F-MAMMA1002042//Homo sapiens chromosome 3, clone hRPK.165_I_16, complete sequence.//1.4e-20:314:70//

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AC005669
F-MAMMA1002047//Homo sapiens 12p13.3 BAC RPCII1-429A20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//6.8e-14:526:62//AC005906
F-MAMMA1002056//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//1.1e-47:648:71//AL030996
F-MAMMA1002058//Homo sapiens PAC clone DJ0732C22 from 7p11.2-p13, complete sequence.//2.4e-19:256:74//AC004869
F-MAMMA1002068//Homo sapiens, clone hRPK.2_A_1, complete sequence.//5.4e-41:407:78//AC006197
F-MAMMA1002078//Human DNA sequence from PAC 106I20 on chromosome 22q12 Contains ESTs and STS, complete sequence.//0.021:333:64//Z81313
F-MAMMA1002082
F-MAMMA1002084//Caenorhabditis elegans cosmid F28C12, complete sequence.//0.032:469:58//Z93380
F-MAMMA1002093//HS_3050_B1_F06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=11 Row=L, genomic survey sequence.//1.0:77:71//AQ105997
F-MAMMA1002108//Homo sapiens anion exchanger 3 gene, exons 1 and 2 and complete 5'UTR.//8.3e-10:464:60//AF017308
F-MAMMA1002118
F-MAMMA1002125//Homo sapiens chromosome 17, clone HCIT217L10, complete sequence.//1.0e-35:619:68//AC003962
F-MAMMA1002132//RPCI11-78F11.TJ RPCI11 Homo sapiens genomic clone R-78F11, genomic survey sequence.//1.0e-90:357:97//AQ286460
F-MAMMA1002140//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-45:583:64//AC004216
F-MAMMA1002143//Human serum constituent protein (MSE55) mRNA, complete cds.//6.0e-11:192:70//M88338
F-MAMMA1002145//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 102D24, WORKING DRAFT SEQUENCE.//0.0028:570:59//AL021391
F-MAMMA1002153//HS_3005_A1_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=7 Row=G, genomic survey sequence.//4.9e-41:213:99//AQ132213
F-MAMMA1002155//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 462O23, WORKING DRAFT SEQUENCE.//1.2e-45:303:78//AL031431
F-MAMMA1002156
F-MAMMA1002158//CITBI-E1-2508P18.TR CITBI-E1 Homo sapiens genomic clone 2508P18, genomic survey sequence.//7.1e-42:255:92//AQ266165
F-MAMMA1002170//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//2.0e-81:604:81//AC004448
F-MAMMA1002174//Homo sapiens clone UWGC:y67c126 from 6p21, complete sequence.//3.2e-43:333:83//AC004212
F-MAMMA1002198//H.sapiens thiol-specific antioxidant protein mRNA.//1.0e-34:121:98//Z22548
F-MAMMA1002209//HS_2197_B1_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2197 Col=13 Row=J, genomic survey sequence.//9.6e-18:163:84//AQ210058
F-MAMMA1002215//Homo sapiens anion exchanger 3 gene, exons 1 and 2 and complete 5'UTR.//6.3e-08:435:60//AF017308
F-MAMMA1002219//Rattus norvegicus rexo70 mRNA, complete cds.//1.8e-124:752:87//AF032667
F-MAMMA1002230//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.67:356:59//AC004710
F-MAMMA1002236//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//9.3e-140:836:87//U38253
F-MAMMA1002243//Homo sapiens chromosome 17, clone hRPK.112_H_10, complete sequence.//1.4e-145:691:98//AC005666
F-MAMMA1002250//Homo sapiens chromosome 16, P1 clone 109-9G (LANL), complete sequence.//6.0e-138:660:98//AC005600
F-MAMMA1002267//Homo sapiens chromosome 2, P1 clone 777H5 (LBNL H27), complete sequence.//0.066:333:60//AC003676
F-MAMMA1002268//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//1.1e-39:404:74//AF068748
F-MAMMA1002269//HS_3163_B1_D03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

BNSDOCID: <EP___1074617A2_I_>

nomic clone Plate=3163 Col=5 Row=H, genomic survey sequence.//1.0:150:63//AQ171576
F-MAMMA1002282//Human Chromosome 16 BAC clone CIT987SK-327O24, complete sequence.//1.5e-22:315:67//AC003108
F-MAMMA1002292//B.garinii (strain Tls1) p83/100 gene (partial).//0.73:200:64//X81533
F-MAMMA1002293//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//1.6e-56:408:75//AC006023
F-MAMMA1002294//Sequence 2 from Patent WO9516779.//1.8e-06:401:62//A45258
F-MAMMA1002297
F-MAMMA1002298//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//0.0056:525:61//AC004221
F-MAMMA1002299//CIT-HSP-2345B2.TR CIT-HSP Homo sapiens genomic clone 2345B2, genomic survey sequence.//1.2e-90:446:98//AQ053994
F-MAMMA1002308//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 850H21, WORKING DRAFT SEQUENCE.//1.3e-35:329:78//AL031680
F-MAMMA1002310//Human gastric ($H^+ + K^+$)-ATPase gene, complete cds.//0.0060:301:60//J05451
F-MAMMA1002311//Human Chromosome 15q11-q13 clone pDJ276c12 from the Prader-Willi/Angelman syndrome region, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.6e-50:327:69//AC004737
F-MAMMA1002312//Homo sapiens DNA sequence from PAC 435D1 on chromosome Xq25. Contains ESTs and STS.//1.3e-09:741:58//Z86064
F-MAMMA1002317
F-MAMMA1002319//Homo sapiens chromosome 19, fosmid 39347, complete sequence.//1.9e-158:746:99//AC005756
F-MAMMA1002322//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//5.3e-52:617:70//AC004796
F-MAMMA1002329//Homo sapiens RaP2 interacting protein 8 (RPIP8) mRNA, complete cds.//0.22:143:67//U93871
F-MAMMA1002332//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30G7, WORKING DRAFT SEQUENCE.//1.6e-31:287:74//AL034402
F-MAMMA1002333//Mycobacterium tuberculosis H37Rv complete genome; segment 148/162.//2.5e-09:674:59//AL022022
F-MAMMA1002339//Homo sapiens chromosome 21q22.3, cosmid clone Q4H9 complete sequence bases 1.41604.//2.1e-57:522:77//AJ011932
F-MAMMA1002347//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence.//2.0e-14:258:69//AC004129
F-MAMMA1002351//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1059H15, WORKING DRAFT SEQUENCE.//7.8e-132:723:91//AL022100
F-MAMMA1002352//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 128O3, WORKING DRAFT SEQUENCE.//5.8e-17:326:70//Z98742
F-MAMMA1002353//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.1e-14:399:63//AC004825
F-MAMMA1002355//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 109G6, WORKING DRAFT SEQUENCE.//3.7e-43:420:75//AL023879
F-MAMMA1002356//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0022:534:59//AC004153
F-MAMMA1002359//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.3e-18:156:75//AC005831
F-MAMMA1002360//Human DNA sequence from cosmid L21F12B, Huntington's Disease Region, chromosome 4p16.3, contains EST.//4.9e-43:353:69//Z68885
F-MAMMA1002361//Human DNA sequence from clone 342B11 on chromosome 22q12.1-12.3. Contains ESTs and a GSS, complete sequence.//1.8e-22:282:74//AL008719
F-MAMMA1002362//Platemys spixii CR1-like LINE, partial sequence.//0.00058:83:79//D82938
F-MAMMA1002380//CIT-HSP-2383K24.TF CIT-HSP Homo sapiens genomic clone 2383K24, genomic survey sequence.//4.4e-10:85:92//AQ196889
F-MAMMA1002384//RPCI11-80J20.TV RPCI11 Homo sapiens genomic clone R-80J20, genomic survey sequence.//2.7e-56:286:98//AQ284134
F-MAMMA1002385//CIT-HSP-2328G13.TF CIT-HSP Homo sapiens genomic clone 2328G13, genomic survey sequence.//5.5e-46:335:84//AQ043985
F-MAMMA1002392//Homo sapiens PAC clone DJ0797C05 from 7q31, complete sequence.//8.5e-29:273:78//

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AC004888
F-MAMMA1002411//Human DNA sequence from clone 1044017 on chromosome Xp11.3-11.4 Contains GSS and STS, complete sequence.//8.2e-09:287:63//AL023 875
F-MAMMA1002413//Plasmodium falciparum (strain Dd2) variant-specific surface protein (var1) gene, complete cds.//9.6e-08:730:57//L40608
F-MAMMA1002417//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30G7, WORKING DRAFT SEQUENCE.//4.1e-06:181:72//AL034402
F-MAMMA1002427//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//1.3e-51:593:72//AC004604
F-MAMMA1002428
F-MAMMA1002434//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//7.3e-56:388:81//Z93023
F-MAMMA1002446//CIT-HSP-2324O22.TR CIT-HSP Homo sapiens genomic clone 2324O22, genomic survey sequence.//2.3e-56:302:95//AQ027479
F-MAMMA1002454//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.1e-54:190:94//AC005229
F-MAMMA1002461//Rattus norvegicus calcium channel alpha-1 subunit gene, partial cds.//0.00045:457:60//U14005
F-MAMMA1002470//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//9.7e-33:709:60//U10556
F-MAMMA1002475//Homo sapiens 12p13.3 PAC RPCI3-340I3 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.092:506:58//AC004671
F-MAMMA1002480//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2-unordered pieces.//0.025:100:76//AC005077
F-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//2.9e-118:560:98//AF055460
F-MAMMA1002494//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//1.5e-22:297:73//AC005913
F-MAMMA1002498//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//7.2e-10:330:64//AC002477
F-MAMMA1002524//Homo sapiens huntingtin gene, partial exon.//0.0080:124:72//L49359
F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.//1.4e-160:775:97//AF065214
F-MAMMA1002545//Homo sapiens chromosome 17, clone hRPK.74_E_22 complete sequence.//1.9e-41:345:80//AC005696
F-MAMMA1002554
F-MAMMA1002556
F-MAMMA1002566
F-MAMMA1002571//CIT-HSP-2296N17.TR CIT-HSP Homo sapiens genomic clone 2296N17, genomic survey sequence.//1.7e-07:76:90//AQ006579
F-MAMMA1002573//Homo sapiens DNA, trinucleotide repeats region, clone GAA C27.//2.7e-08:195:70//AB018507
F-MAMMA1002585
F-MAMMA1002590//Homo sapiens BAC clone GS250A16 from 7p21-p22, complete sequence.//2.1e-26:361:69//AC005019
F-MAMMA1002597//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1103G7, WORKING DRAFT SEQUENCE.//1.3e-34:550:69//AL034548
F-MAMMA1002598//H.sapiens mRNA for ribosomal protein L7.//1.1e-21:123:100//X57958
F-MAMMA1002603//Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence.//0.0018:358:61//AC005220
F-MAMMA1002612//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//2.1e-13:336:63//AC004861
F-MAMMA1002617//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.14:229:64//AC005486
F-MAMMA1002618
F-MAMMA1002619//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2.//9.5e-71:319:85//AJ010598
F-MAMMA1002622//Homo sapiens advillin mRNA, complete cds.//1.5e-20:157:90//AF041449
F-MAMMA1002623//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//8.3e-06:137:72//AE000660
F-MAMMA1002625//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1056L3, WORKING

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DRAFT SEQUENCE.//1.9e-171:819:98//AL031727
F-MAMMA1002629//Human BAC clone RG385F02 from 7p15, complete sequence.//4.8e-85:478:78//AC003093
F-MAMMA1002636//Human POU daomain factor (Brn-3a) gene, exon 2, complete cds.//5.6e-09:499:62//U10063
F-MAMMA1002637//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//3.6e-115:785:82//AF055666
F-MAMMA1002646//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//1.5e-45:291:90//AC002038
F-MAMMA1002650//Homo sapiens candidate tumor suppressor HIC-1 (HIC-1) gene, complete cds.//6.6e-06:661:59//L41919
F-MAMMA1002655//HS_2003_A2_A11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2003 Col=22 Row=A, genomic survey sequence.//9.0e-15:198:74//AQ224233
F-MAMMA1002662
F-MAMMA1002665//Homo sapiens BAC clone GS588G18 from 7p12-p14, complete sequence.//1.4e-37:235:84//AC005029
F-MAMMA1002671//Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.//0.00027:272:64//U22398
F-MAMMA1002673
F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds.//3.7e-161:752:99//D86987
F-MAMMA1002685//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 394I7, WORKING DRAFT SEQUENCE.//6.2e-45:510:70//AL023585
F-MAMMA1002698//HS_3024_B1_C06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3024 Col=11 Row=F, genomic survey sequence.//1.7e-10:155:75//AQ072214
F-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//5.9e-75:509:83//AF018261
F-MAMMA1002701//Homo sapiens gene for AF-6, complete cds.//1.2e-159:749:99//AB011399
F-MAMMA1002708//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//3.0e-57:347:79//AL031053
F-MAMMA1002711//Homo sapiens BAC clone GS589P19 from 7p13-p14, complete sequence.//3.4e-31:484:69//AC005030
F-MAMMA1002721//CIT-HSP-2350M5.TR CIT-HSP Homo sapiens genomic clone 2350M5, genomic survey sequence.//1.4e-06:265:63//AQ061245
F-MAMMA1002727//Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVEP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs and an AAAT repeat polymorphism, complete sequence.//0.18:386:58//AL023584
F-MAMMA1002728//Human DNA sequence from PAC 296K21 on chromosome X contains cytokeratin exon, delta-aminolevulinate synthase (erythroid); 5-aminolevulinic acid synthase.(EC 2.3.1.37). 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//3.2e-05:362:63//Z83821
F-MAMMA1002744//Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence.//0.00010:535:58//AE001368
F-MAMMA1002746//Homo sapiens chromosome 17, clone hRPK.136_H_19, complete sequence.//1.2e-182:880:97//AC005856
F-MAMMA1002748//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.7e-175:829:98//AC006055
F-MAMMA1002754//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.1e-31:372:75//AC004676
F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partial cds.//3.3e-26:151:98//AB007902
F-MAMMA1002764//Human Chromosome 11 Cosmid cSRL166a1, complete sequence.//5.2e-49:355:81//U73636
F-MAMMA1002765//RPCI11-20A22.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-20A22, genomic survey sequence.//6.7e-13:155:76//B92153
F-MAMMA1002769//CIT-HSP-2323G1.TF CIT-HSP Homo sapiens genomic clone 2323G1, genomic survey sequence.//9.7e-21:151:90//AQ028244
F-MAMMA1002775//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//5.6e-105:179:99//U07561
F-MAMMA1002780//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-08, complete sequence.//0.071:277:58//Z98546
F-MAMMA1002782//HS_3213_B2_B08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=16 Row=D; genomic survey sequence.//0.00018:219:63//AQ175845
F-MAMMA1002796
F-MAMMA1002807//Human Chromosome X PAC RPCI1-290C9 from the Pieter de Jong Human PAC library; complete sequence.//6.9e-22:332:69//AC002404

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F-MAMMA1002820//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.9e-11:483:62//AC003035
F-MAMMA1002830//Homo sapiens chromosome 17, clone hCIT529I10, complete sequence.//1.0e-64:320:83//AC002553
F-MAMMA1002833//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//2.8e-47:413:80//AC004875
F-MAMMA1002835
F-MAMMA1002838//A-916H10.TP CIT978SK Homo sapiens genomic clone A-916H10, genomic survey sequence.//1.1e-39:164:83//B14462
F-MAMMA1002842//Mus musculus c-Cbl associated protein CAP mRNA, complete cds.//1.9e-62:373:81//U58883
F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 protein, partial cds.//1.7e-135:635:99//AB018353
F-MAMMA1002844//F1707-T7 IGF Arabidopsis thaliana genomic clone F17O7, genomic survey sequence.//6.7e-17:383:66//B11616
F-MAMMA1002858
F-MAMMA1002868//RPCI11-54F9.TJ RPCI11 Homo sapiens genomic clone R-54F9, genomic survey sequence.//8.3e-81:392:99//AQ081566
F-MAMMA1002869//Sequence 1 from patent US 5552529.//2.2e-86:696:78//I25863
F-MAMMA1002871//Lupinus angustifolius nodulin-45 gene, complete cds.//0.029:370:59//L12388
F-MAMMA1002880//RPCI11-23M23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-23M23, genomic survey sequence.//1.8e-20:271:74//B86518
F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete cds.//1.2e-28:680:61//D45027
F-MAMMA1002886//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 380A1, WORKING DRAFT SEQUENCE.//0.00040:505:57//Z97653
F-MAMMA1002887//HS_3238_B2_G08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=16 Row=N, genomic survey sequence.//5.5e-79:401:97//AQ219814
F-MAMMA1002890//Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70t, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes.//4.6e-35:136:73//AF109906
F-MAMMA1002892//Mouse Cosmid ma66a100 from 14D1-D2, complete sequence.//5.7e-14:450:60//AC004096
F-MAMMA1002895//H.sapiens CpG island DNA genomic Mse1 fragment, clone 46b6, forward read cpg46b6.ft1a.//3.7e-36:190:100//Z58616
F-MAMMA1002908//Penaeus monodon microsatellite locus Pmo27.//1.1e-05:195:62//AF068828
F-MAMMA1002909//Human Chromosome 11 pac pDJ205d23, complete sequence.//1.0e-13:457:61//AC002402
F-MAMMA1002930//Homo sapiens Xp22 BAC GSHB-512P14 (Genome Systems Human BAC library) complete sequence.//0.25:260:62//AC004467
F-MAMMA1002937//H.sapiens ZNF74-1 mRNA.//6.3e-13:577:59//X71623
F-MAMMA1002938//Homo sapiens mRNA for KIAA0698 protein, complete cds.//5.1e-193:910:98//AB014598
F-MAMMA1002941//Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 In BCRL2-GGT Region, complete sequence.//2.7e-23:174:77//AC004032
F-MAMMA1002947//Rhodobacter capsulatus strain SB1003, partial genome.//1.3e-09:475:61//AF010496
F-MAMMA1002964//Human thiopurine methyltransferase (TPMT) gene, exon 5.//0.0029:314:60//AF019366
F-MAMMA1002970//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs. complete sequence.//4.0e-10:194:71//Z94056
F-MAMMA1002972//H.sapiens CpG island DNA genomic Mse1 fragment, clone 2g10, forward read cpg2g10.ft1aa.//0.38:156:66//Z55272
F-MAMMA1002973//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence.//2.9e-41:234:79//AC005919
F-MAMMA1002982//Homo sapiens DNA sequence from PAC 510L9 on chromosome 6p24.1-p25.3.//1.7e-05:322:63//AL022098
F-MAMMA1002987//CITBI-E1-2514J12.TR CITBI-E1 Homo sapiens genomic clone 2514J12, genomic survey sequence.//0.0064:135:66//AQ275871
F-MAMMA1003003//cSRL-145D12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-145D12, genomic survey sequence.//2.8e-31:201:89//B01998
F-MAMMA1003004//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y237C10, WORKING DRAFT SEQUENCE.//1.6e-10:180:73//AL031601
F-MAMMA1003007//Homo sapiens (clone cosmid c11q-8D1) tetranucleotide repeat polymorphism at the D11S488 locus.//3.5e-12:435:61//L04732

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F-MAMMA1003011//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//2.3e-50:734:67//U79139
F-MAMMA1003013//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//1.2e-86:341:79//AC003694
F-MAMMA1003015//Homo sapiens Chromosome 16 BAC clone CIT987SK-591M7, complete sequence.//2.6e-13:443:61//AC003661
F-MAMMA1003019//HS_3221_A1_A01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=1 Row=A, genomic survey sequence.//2.8e-51:299:92//AQ184271
F-MAMMA1003026
F-MAMMA1003031//Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.//0.0037:134:73//AC005214
F-MAMMA1003035//RPCI11-11P4.TP RPCI-11 Homo sapiens genomic clone RPCI-11-11P4, genomic survey sequence.//1.1e-07:66:100//B74936
F-MAMMA1003039//Homo sapiens 12p13.3 PAC RPCI3-340I3 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.1e-19:220:76//AC004671
F-MAMMA1003040//Human DNA sequence from PAC 340N1 on chromosome 1p35-36.2. Contains ESTs, polymorphic CA repeat, trna and endogenous retrovirus.//9.5e-91:469:78//Z98257
F-MAMMA1003044//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//0.21:289:61//AL031321
F-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds.//1.7e-139:663:98//AF077952
F-MAMMA1003049
F-MAMMA1003055//HS_3014_B2_F10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3014 Col=20 Row=L, genomic survey sequence.//4.2e-05:215:64//AQ164940
F-MAMMA1003056//HS_3221_B2_D12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=24 Row=H, genomic survey sequence.//1.4e-16:206:74//AQ302772
F-MAMMA1003057//M.domesticus MD6 mRNA.//8.5e-128:654:94//X54352
F-MAMMA1003066//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 273F20, WORKING DRAFT SEQUENCE.//1.0:142:71//AL034371
F-MAMMA1003089//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//1.7e-42:373:78//AC004796
F-MAMMA1003099//Homo sapiens beta-filamin mRNA, complete cds.//2.6e-42:288:88//AF042166
F-MAMMA1003104//Mus musculus rostral cerebellar malformation protein (rcm) mRNA, complete cds.//1.6e-12:477:64//U72634
F-MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//3.4e-121:789:85//AF071316
F-MAMMA1003127//R.norvegicus MYR1 mRNA for myosin I heavy chain.//9.4e-58:423:83//X68199
F-MAMMA1003135//Mus musculus dentin sialophosphoprotein precursor (DSPP) mRNA, complete cds.//0.62:676:58//U67916
F-MAMMA1003140
F-MAMMA1003146//Homo sapiens mRNA for GalT3 protein.//2.2e-80:397:97//Y15062
F-MAMMA1003150//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 598F2, WORKING DRAFT SEQUENCE.//7.3e-123:266:88//AL021579
F-MAMMA1003166//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 250D10, WORKING DRAFT SEQUENCE.//1.6e-33:143:82//Z99716
F-NT2RM1000001//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs, complete sequence.//0.50:216:61//Z95400
F-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds.//4.8e-65:385:92//D31886
F-NT2RM1000032
F-NT2RM1000035//Cricetulus griseus SREBP cleavage activating protein (SCAP) mRNA, complete cds.//6.3e-135:565:84//U67060
F-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds.//1.1 e-106:542:95//AB014590
F-NT2RM1000039//Mouse genetic suppressor element mRNA.//0.080:239:60//L27155
F-NT2RM1000055//Rattus norvegicus mRNA for TIP120, complete cds.//8.4e-96:535:91//D87671
F-NT2RM1000059//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
F-NT2RM1000062//Nephila clavipes dragline silk protein spidroin 1 gene, partial cds.//0.54:306:63//U37520
F-NT2RM1000080//Sequence 2 from patent US 5763589.//1.5e-115:566:97//AR012692
F-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds.//1.8e-114:550:97//AB014561

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F-NT2RM1000092//Homo sapiens chromosome 19, cosmid R26894, complete sequence.//0.63:180:65//AC005594
F-NT2RM1000118//Homo sapiens clone 23763 unknown mRNA, partial cds.//0.027:126:70//AF007155
F-NT2RM1000119//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 466N1, WORKING DRAFT SEQUENCE.//0.022:644:58//Z97630
F-NT2RM1000127//RPCI11-44E5.TJ RPCI11 Homo sapiens genomic clone R-44E5, genomic survey sequence.//1.6e-45:254:94//AQ195884
F-NT2RM1000131//Homo sapiens mRNA for KIAA0792 protein, complete cds.//5.5e-153:778:95//AB018335
F-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUFS6 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.1e-90:448:97//AF044959
F-NT2RM1000153//Human NotI linking clone 924A081D, genomic survey sequence.//5.9e-07:66:96//U49890
F-NT2RM1000186//Homo sapiens clone 23763 unknown mRNA, partial cds.//0.025:126:70//AF007155
F-NT2RM1000187//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//1.1e-05:56:98//AQ261184
F-NT2RM1000199//Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.//1.6e-38:711:65//D64009
F-NT2RM1000242
F-NT2RM1000244//HS_2229_A1_C04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2229 Col=7 Row=E, genomic survey sequence.//2.0e-13:95:95//AQ298474
F-NT2RM1000252//Homo sapiens chromosome 17, clone hRPK.206_C_20, complete sequence.//0.023:225:61//AC006070
F-NT2RM1000256//Caenorhabditis elegans cosmid F22B3, complete sequence.//8.5e-24:473:64//Z68336
F-NT2RM1000257//Homo sapiens MAGOH mRNA, complete cds.//6.4e-69:455:85//AF035940
F-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds.//6.5e-57:460:80//D50920
F-NT2RM1000271
F-NT2RM1000272
F-NT2RM1000280//Bos gaurus vacuolar H-ATPase subunit D (VATD) mRNA, complete cds.//6.7e-97:430:92//U11927
F-NT2RM1000300//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 92N15, WORKING DRAFT SEQUENCE.//2.1e-96:170:100//Z93097
F-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds.//8.1e-127:708:92//D63880
F-NT2RM1000318//Homo sapiens mRNA for ribosomal protein L39, complete cds.//5.7e-34:182:99//D79205
F-NT2RM1000341//Homo sapiens full-length insert cDNA clone YP11F06.//1.3e-100:504:97//AF085879
F-NT2RM1000354//HS_2001_B1_E06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=11 Row=J, genomic survey sequence.//1.6e-11:201:73//AQ218494
F-NT2RM1000355//Mus musculus E25B protein mRNA, complete cds.//1.8e-77:578:82//U76253
F-NT2RM1000365//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUENCE, 5 unordered pieces.//9.4e-113:367:97//AC004821
F-NT2RM1000377//H.sapiens mRNA for MAP kinase phosphatase 4.//6.1e-14:362:62//Y08302
F-NT2RM1000388//Azospirillum brasilense lateral flagellin (laf1) gene, complete cds.//1.0:482:58//U26679
F-NT2RM1000394//M.musculus mRNA for histone H3.3A.//1.7e-94:549:89//Z85979
F-NT2RM1000399
F-NT2RM1000421//HS_2213_B1_E01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=1 Row=J, genomic survey sequence.//3.6e-08:195:72//AQ032737
F-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//3.7e-84:418:97//AF084928
F-NT2RM1000499//Human mRNA for KIAA0167 gene, complete cds.//1.3e-35:525:69//D79989
F-NT2RM1000539//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence.//4.6e-73:533:83//AC004993
F-NT2RM1000553
F-NT2RM1000555//Homo sapiens clone 24514 unknown mRNA.//2.3e-110:555:97//AF070542
F-NT2RM1000563//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.3e-123:477:100//AC004873
F-NT2RM1000623//HS_2213_B1_E01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=1 Row=J, genomic survey sequence.//8.2e-06:75:89//AQ032737
F-NT2RM1000648//Halobium cutirubrum L11, L1, L10 and L12 equivalent ribosomal protein gene cluster.//1.3e-06:414:61//X15078
F-NT2RM1000661//Homo sapiens cap-binding protein 4EHP mRNA, complete cds.//9.3e-54:275:97//AF047695

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F-NT2RM1000666//HS_2016_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=16 Row=P, genomic survey sequence.//5.7e-13:199:73//AQ227865
F-NT2RM1000669//Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains ESTs, STSs, GSSs, a putative CpG island and genomic marker D6S1553, complete sequence.//2.7e-94:499:94//AL031133
F-NT2RM1000672
F-NT2RM1000691//Homo sapiens HRIHFB2060 mRNA, partial cds.//2.2e-119:582:98//AB015348
F-NT2RM1000699//Caenorhabditis elegans cosmid Y41C4A, complete sequence.//0.95:284:61//AL032627
F-NT2RM1000702//HS_3005_A1_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=3 Row=A, genomic survey sequence.//0.073:290:58//AQ089514
F-NT2RM1000725//Homo sapiens mRNA for neuropathy target esterase.//4.8e-65:435:85//AJ004832
F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cds.//8.0e-126:690:92//AB011139
F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds.//2.5e-66:524:83//AF027208
F-NT2RM1000746//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.//0.92:395:58//AJ011930
F-NT2RM1000770//Homo sapiens inosine monophosphate dehydrogenase type II gene, complete cds.//2.1e-70:407:92//L39210
F-NT2RM1000772//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.6e-36:98:93//AC000380
F-NT2RM1000780//Human DNA for 5' terminal region of LINE-1 transposable element clone CGL1-4.//9.3e-22:126:99//X52233
F-NT2RM1000781//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.1e-09:540:59//AC004153
F-NT2RM1000800//Mus musculus mRNA for B-IND1 protein.//4.0e-81:497:88//Z97207
F-NT2RM1000802
F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds.//3.7e-63:490:84//AF027208
F-NT2RM1000826//Homo sapiens clone 24514 unknown mRNA.//7.2e-153:749:96//AF070542
F-NT2RM1000829//HS_3047_A1_A05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=A, genomic survey sequence.//0.74:215:67//AQ099134
F-NT2RM1000833//Canis familiaris sec61 homologue mRNA, complete cds.//5.1e-114:683:88//M96629
F-NT2RM1000850//F.rubripes GSS sequence, clone 163A22aF11, genomic survey sequence.//1.1e-26:279:74//AL018762
F-NT2RM1000852//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//9.3e-148:726:97//AJ010840
F-NT2RM1000857//Rattus norvegicus gene for cytochrome P450/6 beta B, exon 2.//0.97:124:65//AB008378
F-NT2RM1000867//H.sapiens DNA sequence surrounding NotI site, clone NRLA143D.//1.2e-31:172:98//K95834
F-NT2RM1000874//Homo sapiens KE05 protein mRNA, complete cds.//2.8e-131:632:97//AF064605
F-NT2RM1000882//Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.//1.2e-98:214:99//AC004228
F-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//2.7e-156:762:97//AF082516
F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 protein, complete cds.//2.0e-17:310:67//AB014561
F-NT2RM1000894//Mus musculus second largest subunit of RNA polymerase I (RPA2) mRNA, complete cds.//3.2e-95:469:83//U58280
F-NT2RM1000898
F-NT2RM1000905//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 466N1, WORKING DRAFT SEQUENCE.//1.8e-74:188:98//Z97630
F-NT2RM1000924//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.7e-148:601:98//AC004873
F-NT2RM1000927//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//0.071:392:60//AC004846
F-NT2RM1000962//H.sapiens CpG island DNA genomic Mse1 fragment, clone 140d1, forward read cpg140d1.ft1a.//4.1e-35:187:99//Z56803
F-NT2RM1000978//Homo sapiens Chromosome 15q22.3-23 PAC 88m3, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.1e-23:266:77//AC005959
F-NT2RM1001003//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//4.0e-160:760:98//U97067
F-NT2RM1001008//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//1.7e-11:602:61//U52064

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F-NT2RM1001043//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monoamine oxidase B (MAOB), ESTs and polymorphic CA repeats.//3.9e-93:645:86//Z95125
F-NT2RM1001044//S.pombe chromosome III cosmid c320.//0.90:128:66//AL022245
F-NT2RM1001059//Homo sapiens chromosome 5, Bac clone 58g14 (LBNL H76), complete sequence.//3.8e-53:261:80//AC005915
F-NT2RM1001066//CIT-HSP-2172N17.TF CIT-HSP Homo sapiens genomic clone 2172N17, genomic survey sequence.//0.64:285:59//B94391
F-NT2RM1001072//HS_3115_B1_D07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3115 Col=13 Row=H, genomic survey sequence.//7.3e-23:140:95//AQ147905
F-NT2RM1001074//Homo sapiens chromosome 19, cosmid F20489, complete sequence.//5.0e-50:186:98//AC005263
F-NT2RM1001082//Sequence 1 from Patent WO9718303.//2.1e-144:736:95//A62731
F-NT2RM1001085//CIT-HSP-2310F21.TR CIT-HSP Homo sapiens genomic clone 2310F21, genomic survey sequence.//8.8e-45:235:97//AQ020757
F-NT2RM1001092//HS_3055_B1_G05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=9 Row=N, genomic survey sequence.//1.1e-89:471:95//AQ155489
F-NT2RM1001102//Human HEM45 mRNA, complete cds.//1.2e-28:482:63//U88964
F-NT2RM1001105//Homo sapiens hRED1 gene, exon 1 (5'UTR).//0.0014:349:61//Z95973
F-NT2RM1001112//Homo sapiens chromosome 19, cosmid R34094, complete sequence.//0.060:429:58//AC004678
F-NT2RM1001115//Plasmodium falciparum merozoite surface protein 3 (MSP-3) gene, partial cds.//0.93:156:62//AF024624
F-NT2RM1001139//Homo sapiens chromosome 19, fosmid 37502, complete sequence.//1.2e-10:466:59//AC004755
F-NT2RM2000006//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796F18, WORKING DRAFT SEQUENCE.//5.3e-150:724:98//AL031291
F-NT2RM2000013//D.melanogaster DmRP128 gene for RNA polymerase III second-largest subunit.//1.5e-58:749:69//X58826
F-NT2RM2000030//Homo sapiens clone DJ0708P22, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.1e-97:270:77//AC004863
F-NT2RM2000032//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//1.9e-25:172:76//AL034379
F-NT2RM2000042//Human DNA sequence from cosmid U55E4, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//5.0e-05:325:65//Z73418
F-NT2RM2000092//Homo sapiens (D8S321 locus) DNA sequence, tetranucleotide repeat polymorphism.//0.63:117:68//L12269
F-NT2RM2000093//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//0.38:312:62//AF109905
F-NT2RM2000101
F-NT2RM2000124//Mouse cAMP-dependent protein kinase catalytic subunit mRNA, complete cds.//3.8e-58:297:97//M12303
F-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A2 (PDE9A) mRNA, complete cds.//3.8e-138:653:98//AF067224
F-NT2RM2000192//CIT-HSP-2172B3.TF CIT-HSP Homo sapiens genomic clone 2172B3, genomic survey sequence.//2.2e-33:191:95//B93289
F-NT2RM2000239//F rubripes GSS sequence, clone 156P04aG12, genomic survey sequence.//8.9e-44:445:69//AL018549
F-nnnnnnnnnnn//Homo sapiens fibroblast growth factor 18 (FGF18) mRNA, complete cds.//0.00020:380:61//AF075292
F-NT2RM2000250//Homo sapiens mRNA for KIAA0590 protein, complete cds.//3.1e-128:615:98//AB011162
F-NT2RM2000259//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 310O13, WORKING DRAFT SEQUENCE.//0.0013:305:63//AL031658
F-NT2RM2000260//Mus musculus WW domain binding protein 15 mRNA, partial sequence.//3.0e-14:645:61//AF073934
F-NT2RM2000287//*** SEQUENCING IN PROGRESS *** EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SE-

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QUENCE, 50 unordered pieces.//1.3e-11:96:86//AC003656
F-NT2RM2000322//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//8.5e-115:233:97//AL031864
F-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds.//8.8e-175:805:99//AB011132
F-NT2RM2000363//RPCI11-90B10.TJ RPCI11 Homo sapiens genomic clone R-90B10, genomic survey sequence.//6.7e-15:96:98//AQ285300
F-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//1.2e-94:599:86//U48251
F-NT2RM2000371//RPCI11-57I4.TJ RPCI11 Homo sapiens genomic clone R-57I4, genomic survey sequence.//1.1e-52:312:91//AQ083343
F-NT2RM2000374//M. musculus nodal gene, a TGF-beta-like gene.//6.7e-31:196:91//X70514
F-NT2RM2000395//Leishmania major chromosome 1, complete sequence.//0.99:345:58//AE001274
F-NT2RM2000402//Arabidopsis thaliana BAC T19D16 genomic sequence.//2.1e-23:414:63//U95973
F-NT2RM2000407//Mus musculus semaphorin VIa mRNA, complete cds.//1.4e-131:439:88//AF030430
F-NT2RM2000420//HS_3063_B2_F11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3063 Col=22 Row=L, genomic survey sequence.//3.2e-25:154:95//AQ103204
F-NT2RM2000422//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.//1.7e-128:782:86//L22022
F-NT2RM2000452//HS_3009_B2_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=10 Row=H, genomic survey sequence.//1.2e-16:122:90//AQ130794
F-NT2RM2000469//HS_2019_A1_G02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2019 Col=3 Row=M, genomic survey sequence.//9.6e-22:176:85//AQ229041
F-NT2RM2000490//Homo sapiens mRNA for KIAA0747 protein, partial cds.//7.5e-15:386:63//AB018290
F-NT2RM2000502
F-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//5.1e-171:824:97//AF061243
F-NT2RM2000522
F-NT2RM2000540
F-NT2RM2000556//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.9e-42:344:82//AC004466
F-NT2RM2000566//Homo sapiens integrin alpha-7 mRNA, complete cds.//2.8e-154:751:97//AF072132
F-NT2RM2000567//Pseudomonas aeruginosa enoyl-CoA hydratase gene, partial cds; pilin biosynthetic protein (fimL) gene, complete cds; and unknown gene.//3.0e-06:664:58//AF083252
F-NT2RM2000569//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE.//1.3e-15:348:67//AL031681
F-NT2RM2000577//RPCI11-43G22.TJ RPCI11 Homo sapiens genomic clone R-43G22, genomic survey sequence.//1.6e-14:155:80//AQ199391
F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds.//5.4e-174:820:98//D86987
F-NT2RM2000588//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.1e-60:344:82//AC004466
F-NT2RM2000594//Mus musculus DNA cytosine-5 methyltransferase 3B1 (Dnmt3b) mRNA, alternatively spliced, complete cds.//4.9e-118:761:85//AF068626
F-NT2RM2000599//O.sativa osr40g3 gene.//0.30:585:56//Y08988
F-NT2RM2000609
F-NT2RM2000612//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//7.8e-102:709:83//U35776
F-NT2RM2000623//Homo sapiens chromosome 19, cosmid F19847, complete sequence.//3.4e-17:450:65//AC005952
F-NT2RM2000624
2.9e-06:231:64//Z82061
F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds.//6.3e-142:664:98//AB018272
F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds.//7.4e-138:664:98//AB014558
F-NT2RM2000639//RPCI11-69E5.TJ RPCI11 Homo sapiens genomic clone R-69E5, genomic survey sequence.//3.7e-14:97:97//AQ267491
F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds.//1.1e-167:518:99//AB014576
F-NT2RM2000669
F-NT2RM2000691//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//1.1e-106:748:82//AC002038
F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds.//6.8e-49:748:64//D86984

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F-NT2RM2000718//Homo sapiens HRIHFB2436 mRNA, partial cds.//2.4e-124:594:98//AB015342
F-NT2RM2000735//Human ZNF43 mRNA.//8.4e-111:756:82//X59244
F-NT2RM2000740//Mus musculus lymphocyte specific helicase mRNA, complete cds.//1.3e-141:815:89//U25691
F-NT2RM2000795//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 439F8, WORKING DRAFT SEQUENCE.//1.0e-78:723:76//AL021392
F-NT2RM2000821//Rat mRNA for beta COP.//2.0e-150:879:88//X57228
F-NT2RM2000837//Homo sapiens BAC clone GS214N13 from 7p14-p15, complete sequence.//1.1e-05:361:62//AC005017
F-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//8.7e-184:847:99//AB015046
F-NT2RM2000952
F-NT2RM2000984//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; sm-RNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//7.6e-41:239:76//AF109905
F-NT2RM2001004//CIT-HSP-2333N18.TR CIT-HSP Homo sapiens genomic clone 2333N18, genomic survey sequence.//1.1e-11:298:66//AQ035862
F-NT2RM2001035//Mus musculus mCAF1 protein mRNA, complete cds.//1.4e-120:627:91//U21855
F-NT2RM2001065//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//6.8e-118:690:88//AF071314
F-NT2RM2001100//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.3e-145:614:99//AC004873
F-NT2RM2001105//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50O24, WORKING DRAFT SEQUENCE.//2.7e-95:461:99//AL034380
F-NT2RM2001131//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//7.2e-24:726:62//U52064
F-NT2RM2001141
F-NT2RM2001152//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains ESTs and an STS, complete sequence.//0.98:300:62//AL022401
F-NT2RM2001177//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//1.2e-147:741:96//AC005488
F-NT2RM2001194//Suid herpesvirus 1 UL5 gene, partial cds, UL6 and UL7 genes, complete cds, UL8 gene, partial cds.//0.026:408:59//U66829
F-NT2RM2001196//Homo sapiens clone DJ1173I20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.2e-135:627:98//AC004987
F-NT2RM2001201//Mus musculus clone OST431, genomic survey sequence.//6.1e-80:503:86//AF046700
F-NT2RM2001221//Chimpanzee (P.paniscus) involucrin, complete cds.//0.53:670:55//M26514
F-NT2RM2001238//Rat glutaminase mRNA, complete cds.//3.4e-128:719:90//M65150
F-NT2RM2001243
F-NT2RM2001247//CITBI-E1-2521M18.TR CITBI-E1 Homo sapiens genomic clone 2521M18, genomic survey sequence.//0.0011:274:59//AQ276184
F-NT2RM2001256//M.musculus mRNA for 200 kD protein.//2.3e-129:742:90//X80169
F-NT2RM2001291//CIT-HSP-2010I15.TR CIT-HSP Homo sapiens genomic clone 2010I15, genomic survey sequence.//4.6e-09:156:72//B57734
F-NT2RM2001306//RPCI11-28I5.TP RPCI-11 Homo sapiens genomic clone RPCI-11-28I5, genomic survey sequence.//0.069:234:64//B84850
F-NT2RM2001312//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence.//1.1e-22:111:81//AC005919
F-NT2RM2001319//Borrelia burgdorferi (section 4 of 70) of the complete genome.//0.99:340:58//AE001118
F-NT2RM2001324//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 209H1, WORKING DRAFT SEQUENCE.//3.7e-44:340:85//Z84465
F-NT2RM2001345//HS_3005_A1_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=3 Row=A, genomic survey sequence.//0.042:290:58//AQ089514
F-NT2RM2001360//Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.//5.0e-60:365:87//U56429
F-NT2RM2001370//Homo sapiens PAC clone DJ0815D20 from 7p11-p13, complete sequence.//0.98:415:58//AC004899
F-NT2RM2001393//Homo sapiens Chromosome 22q11.2 PAC Clone p_m11 In BCRL2-GGT Region, complete

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sequence.//4.0e-54:394:75//AC004033
F-NT2RM2001420//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 349A12, WORKING DRAFT SEQUENCE.//2.8e-169:789:99//AL033520
F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.1e-96:453:99//AJ007509
F-NT2RM2001499//Rattus norvegicus mRNA for cationic amino acid transporter 3, complete cds.//7.1e-91:601:83//AB000113
F-NT2RM2001504//Homo sapiens chromosome 19, cosmid R30017, complete sequence.//0.81:200:69//AC005624
F-NT2RM2001524//Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No. 2.//3.8e-16:316:65//Z99708
F-NT2RM2001544
F-NT2RM2001547//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//3.3e-24:318:67//AL032657
F-NT2RM2001575//Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.//2.1e-26:582:64//M34551
F-NT2RM2001582//M.musculus red-1 gene.//1.4e-102:581:90//X92750
F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds.//7.0e-10:282:65//AB007902
F-NT2RM2001592//Rattus norvegicus rexo70 mRNA, complete cds.//9.6e-131:736:90//AF032667
F-NT2RM2001605//RBP2=retinoblastoma binding protein 2 [human, Nalm-6 pre-B cell leukemia, mRNA, 6455 nt].//2.3e-85:749:75//S66431
F-NT2RM2001613//Rattus rattus sec61 homologue mRNA, complete cds.//8.6e-118:779:85//M96630
F-NT2RM2001632//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//1.5e-50:561:71//AC004691
F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds.//9.2e-153:740:98//AB014518
F-NT2RM2001637//F.rubripes GSS sequence, clone 155D22bD8, genomic survey sequence.//2.5e-13:224:64//Z91020
F-NT2RM2001641//CIT-HSP-2347F23.TF CIT-HSP Homo sapiens genomic clone 2347F23, genomic survey sequence.//1.3e-67:340:98//AQ060913
F-NT2RM2001648//Canis familiaris sec61 homologue mRNA, complete cds.//1.4e-110:459:89//M96629
F-NT2RM2001652//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//1.2e-153:807:93//AF023451
F-NT2RM2001659//nbxb0002cE07f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0002J13f, genomic survey sequence.//1.0:485:56//AQ051653
F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//3.7e-172:802:99//AF044195
F-NT2RM2001668
F-NT2RM2001670//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//3.2e-18:279:70//AJ003147
F-NT2RM2001671//Oryctolagus cuniculus sarcolemmal associated protein-3 mRNA; complete cds.//1.6e-137:683:94//U21157
F-NT2RM2001675//RPCI11-51J16.TJ RPCI11 Homo sapiens genomic clone R-51J16, genomic survey sequence.//1.0:394:58//AQ053677
F-NT2RM2001681//Arabidopsis thaliana DNA chromosome 4, BAC clone T8O5 (ESSAII project).//0.87:220:61//AL021890
F-NT2RM2001688//B.parapertussis bvg locus (transcription regulators of virulence factors) with bvgA and bvgS genes.//1.0:286:62//X52948
F-NT2RM2001695//CIT-HSP-345H13.TVB CIT-HSP Homo sapiens genomic clone 345H13, genomic survey sequence.//3.2e-53:241:82//B59854
F-NT2RM2001696//Mouse DNA with homology to EBV IR3 repeat, segment 2, clone Mu2.//1.2e-05:306:58//M10668
F-NT2RM2001698//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//6.0e-06:548:59//AL021920
F-NT2RM2001699//HS_3195_8B2_DO1_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3195 Col=2 Row=H, genomic survey sequence.//2.7e-07:322:61//AQ189056
F-NT2RM2001700//Mycobacterium tuberculosis H37Rv complete genome; segment 109/162.//7.8e-05:354:58//Z95556
F-NT2RM2001706//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.//7.5e-42:335:81//AC004469
F-NT2RM2001716

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F-NT2RM2001718//Drosophila melanogaster DNA sequence (P1 DS04106 (D172)), complete sequence.//4.2e-08:536:58//AC004290
F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence.//1.4e-26:163:95//AF052123
F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds.//6.2e-111:530:98//AB007931
F-NT2RM2001730//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2.//3.1e-102:248:95//AJ010598
F-NT2RM2001743
F-NT2RM2001753//Caenorhabditis elegans cosmid F45E6, complete sequence.//0.11:138:66//Z68117
F-NT2RM2001760//Canis familiaris sec61 homologue mRNA, complete cds.//9.4e100:418:88//M96629
F-NT2RM2001768//HS_3064_B2_A04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-28:153:100//AQ136993
F-NT2RM2001771//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.3e-66:680:72//AC006116
F-NT2RM2001782
F-NT2RM2001784//Bovine herpesvirus type 1 (Cooper) DNA (30 kb).//0.027:384:60//Z48053
F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.//1.6e-18:229:65//AC004770
F-NT2RM2001797//HS_3045_AT_D01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3045 Col=1 Row=G, genomic survey sequence.//1.4e-74:381:97//AQ129456
F-NT2RM2001800
F-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//8.3e-178:827:99//AF044195
F-NT2RM2001805//Malus domestica leucine-rich receptor-like protein kinase (LRPKm1) gene, 5' flanking region and 5' UTR.//1.0:290:58//AF053126
F-NT2RM2001813//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence.//3.3e-16:109:95//B89870
F-NT2RM2001823//Drosophila melanogaster DNA sequence (P1 DS07049 (D133)), complete sequence.//5.8e-62:819:68//AC004274
F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds.//3.6e-131:738:90//AF013759
F-NT2RM2001840//Homo sapiens chromosome 17, clone 297N7, complete sequence.//1.1e-57:422:79//AC002347
F-NT2RM2001855//HS_3224_A1_H07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3224 Col=13 Row=O, genomic survey sequence.//0.00012:68:91//AQ205285
F-NT2RM2001867//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.068:102:70//AL031177
F-NT2RM2001879//Human DNA sequence from cosmid cU72E5, between markers DXS366 and DXS87 on chromosome X.//0.0029:500:59//Z68328
F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds.//1.9e-187:866:97//AB014610
F-NT2RM2001896//S.cerevisiae chromosome III complete DNA sequence.//8.6e-30:613:63//X59720
F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds.//2.9e-176:859:97//AB007931
F-NT2RM2001930//M.musculus mRNA for semaphorin G.//4.7e-117:730:85//X97818
F-NT2RM2001935//Sequence 11 from Patent WO9610637.//1.0:356:60//A50028
F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequence.//6.9e-138:653:98//AF091080
F-NT2RM2001950//RPCI11-24L12.TP RPCI-11 Homo sapiens genomic clone RPCI-11-24L12, genomic survey sequence.//2.7e-19:188:81//B86700
F-NT2RM2001982//Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence.//0.42:179:65//AC005825
F-NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.//3.8e-20:123:98//AF089816
F-NT2RM2001989//Sequence 3 from patent US 5747317.//1.9e-167:786:98//AR004981
F-NT2RM2001997//Human HepG2 partial cDNA, clone hmd1b08m5.//9.6e-25:160:95//D16955
F-NT2RM2001998//Homo sapiens DNA, chromosome 21q22.2, PAC clone 25P16 complete sequence, encoding carbonyl reductase and carbonyl reductase 3 (complete cds).//0.88:380:60//AB003151
F-NT2RM2002004//Human Chromosome X, complete sequence.//5.0e-88:831:77//AC002407
F-NT2RM2002014
F-NT2RM2002030//Mus musculus glutamine:fructose-6-phosphate amidotransferase mRNA, complete cds.//

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1.5e-89:822:74//U00932
F-NT2RM2002049//Bovine elastin mRNA, partial cds.//8.8e-11:125:81//M26132
F-NT2RM2002055
F-NT2RM2002088//Mus musculus WW domain binding protein 17 mRNA, partial sequence.//1.4e-15:421:63//AF073936
F-NT2RM2002091//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50O24, WORKING DRAFT SEQUENCE.//4.6e-160:771:98//AL034380
F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//7.7e-164:776:98//AJ010840
F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//2.4e-143:684:98//AF030435
F-NT2RM2002128//Mesocricetus auratus guanine nucleotide-binding protein beta 5 (Gnb5) mRNA, complete cds.//7.0e-27:330:73//U13152
F-NT2RM2002142//Danio rerio gastrulation specific (G12) mRNA, complete cds.//6.3e-10:135:80//U27121
F-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//4.2e-143:800:92//AF084928
F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 protein, partial cds.//5.2e-164:787:97//AB007936
F-NT2RM2002580//Drosophila melanogaster DNA sequence (P1 DS02110 (D147)), complete sequence.//7.4e-13:337:62//AC004423
F-NT2RM4000024//D.melanogaster DmRP128 gene for RNA polymerase III second-largest subunit.//1.2e-62:801:70//X58826
F-NT2RM4000027//Caenorhabditis elegans cosmid F09E5.//0.36:336:60//U37429
F-NT2RM4000030//H.sapiens CpG island DNA genomic Mse1 fragment, clone 56h10, forward read cpg56h10.ft1a.//9.3e-22:127:100//Z55685
F-NT2RM4000046//Curcurbita maxima 25S - 18S rDNA intergenic spacer.//4.1e-05:386:60//X13059
F-NT2RM4000061
F-NT2RM4000085//B.taurus mRNA for nuclear DNA helicase II.//1.9e-10:485:59//X82829
F-NT2RM4000086
F-NT2RM4000104//Homo sapiens chromosome 16 zinc finger protein ZNF210 (ZNF210) mRNA, complete cds.//4.2e-23:345:69//AF060865
F-NT2RM4000139//R.norvegicus trg mRNA.//1.4e-56:708:69//X68101
F-NT2RM4000155//CIT-HSP-2282N15.TR CIT-HSP Homo sapiens genomic clone 2282N15, genomic survey sequence.//3.0e-09:88:90//AQ000070
F-NT2RM4000156//H.sapiens HPBRII-7 gene.//2.0e-21:586:60//X67336
F-NT2RM4000167//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//2.7e-143:810:90//D12646
F-NT2RM4000169//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0054:746:57//AC004157
F-NT2RM4000191//Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.//0.00018:468:60//AF051726
F-NT2RM4000197
F-NT2RM4000199//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 620E11, WORKING DRAFT SEQUENCE.//0.67:461:60//AL031667
F-NT2RM4000200
F-NT2RM4000202//H.sapiens CpG island DNA genomic Mse1 fragment, clone 34c2, forward read cpg34c2.ft1a.//1.7e-27:190:90//Z65361
F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//1.4e-182:856:98//AB018255
F-NT2RM4000215//S.cerevisiae MAK16 protein gene, complete cds, and LTE1 protein gene, 3' end.//3.1e-31:731:62//J03852
F-NT2RM4000229//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//4.6e-102:233:94//AC005383
F-NT2RM4000233//Mus musculus semaphorin VIa mRNA, complete cds.//1.6e-135:835:86//AF030430
F-NT2RM4000244//RPCI11-24P15.TV RPCI-11 Homo sapiens genomic clone RPCI-11-24P15, genomic survey sequence.//5.5e-08:422:62//B86757
F-NT2RM4000251//Mus musculus clone UWGC:mbac92 from 14D1-D2 (T-Cell Receptor Alpha Locus), complete sequence.//0.98:207:60//AC005855
F-NT2RM4000265//Homo sapiens Chromosome 11q12.2 PAC clone pDJ1081b4 containing human mRNA for T-cell glycoprotein CD6, complete sequence.//5.2e-41:707:65//AC003689
F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//7.9e-153:609:93//

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M99438
F-NT2RM4000324
F-NT2RM4000327//Rattus norvegicus guanine nucleotide binding protein beta 4 subunit mRNA, partial cds.//3.9e-44:727:68//AF022085
F-NT2RM4000344//Mus musculus ATP-dependent metalloprotease FtsH1 mRNA, complete cds.//1.0e-143:801:90//AF090430
F-NT2RM4000349//Mus musculus clone OST431, genomic survey sequence.//6.1e-80:503:86//AF046700
F-NT2RM4000354//HS_2221_A2_C07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2221 Col=14 Row=E, genomic survey sequence.//1.0e-20:180:83//AQ253449
F-NT2RM4000356
F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds.//1.6e-133:628:99//AB014542
F-NT2RM4000368//RPCI11-91B5.TJ RPCI11 Homo sapiens genomic clone R-91B5, genomic survey sequence.//5.0e-12:431:61//AQ283217
F-NT2RM4000386//Mus musculus DOC4 (Doc4) mRNA, complete cds.//7.4e-86:845:72//AF059485
F-NT2RM4000395//Saccharomyces cerevisiae chromosome VI cosmid 9965.//2.5e-34:767:61//D44597
F-NT2RM4000414//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//1.5e-15:114:94//AB015046
F-NT2RM4000421
F-NT2RM4000425//Homo sapiens chromosome 17, clone hRPK.294_J_22, complete sequence.//1.5e-37:295:82//AC005921
F-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.//3.9e-94:740:78//AF062476
F-NT2RM4000457//CIT-HSP-2346B17.TR CIT-HSP Homo sapiens genomic clone 2346B17, genomic survey sequence.//1.5e-22:149:92//AQ062111
F-NT2RM4000471//Homo sapiens mRNA for putative tRNA splicing protein, partial.//1.3e-76:386:97//AJ010952
F-NT2RM4000486//Homo sapiens mRNA, complete cds, clone:RES4-22A, //1.1e-22:356:67//AB000459
F-NT2RM4000496//Homo sapiens 12p13.3 BAC RPCI11-476M19 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.53:198:70//AC005908
F-NT2RM4000511
F-NT2RM4000514
F-NT2RM4000515//CIT-HSP-2285L3.TR CIT-HSP Homo sapiens genomic clone 2285L3, genomic survey sequence.//0.0012:200:66//AQ000113
F-NT2RM4000520
F-NT2RM4000531//Human zinc finger protein 42 (MZF-1) mRNA, complete cds.//2.9e-31:732:64//M58297
F-NT2RM4000532//HS_3231_B1_C05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3231 Col=9 Row=F, genomic survey sequence.//1.3e-59:362:90//AQ192093
F-NT2RM4000534
F-NT2RM4000585//CITBI-E1-2508I18.TR CITBI-E1 Homo sapiens genomic clone 2508I18, genomic survey sequence.//1.1e-34:208:93//AQ260706
F-NT2RM4000590//CIT-HSP-2291M14.TF CIT-HSP Homo sapiens genomic clone 2291M14, genomic survey sequence.//8.3e-34:180:99//AQ004125
F-NT2RM4000595//Homo sapiens chromosome 17, clone hCIT.131_K_11, complete sequence.//1.2e-09:203:66//AC005288
F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds.//5.3e-14:305:68//AB002390
F-NT2RM4000611//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence.//8.4e-16:109:94//B89870
F-NT2RM4000616//D.melanogaster mRNA for acetyl-CoA synthetase.//2.3e-59:721:68//Z46786
F-NT2RM4000674
F-NT2RM4000689//CIT-HSP-2381O13.TF CIT-HSP Homo sapiens genomic clone 2381O13, genomic survey sequence.//2.6e-31:174:97//AQ110303
F-NT2RM4000698
F-NT2RM4000700
F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.//1.1e-89:744:77//AF022789
F-NT2RM4000717
F-NT2RM4000733//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//2.1e-140:299:99//AL034379
F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds.//3.8e-158:743:98//AB018303
F-NT2RM4000741

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F-NT2RM4000751//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//7.1e-95:754:77//M99593
F-NT2RM4000764
F-NT2RM4000778//Caenorhabditis elegans cosmid F36H12.//0.30:523:60//AF078790
F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds.//5.5e-172:810:98//AB007920
F-NT2RM4000787//Human DNA sequence from PAC 370M22 on chromosome 22q12-qter, contains GRB2 ADAPTOR LIKE PROTEIN, UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT PRECURSOR (UQCRFS1) exon, ESTs, STS, CA repeat and CpG island.//0.0057:163:69//Z82206
F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216, complete sequence.//6.9e-39:237:94//AC005306
F-NT2RM4000795//Rattus norvegicus neuroligin 3 mRNA, complete cds.//5.9e-97:857:74//U41663
F-NT2RM4000796//HS_3214_B1_F11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3214 Col=21 Row=L, genomic survey sequence.//1.1e-14:254:68//AQ175988
F-NT2RM4000798//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//6.2e-78:816:72//AF023451
F-NT2RM4000813//Leishmania major glycoprotein 96-92 (GP 96-92) gene, partial cds.//0.33:276:63//M63109
F-NT2RM4000820//, complete sequence.//2.6e-142:450:97//AC005406
F-NT2RM4000833//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//1.9e-52:501:71//AC004373
F-NT2RM4000848//Homo sapiens chromosome 17, clone hRPK.167_N_20, complete sequence.//1.0:477:56//AC005940
F-NT2RM4000852
F-NT2RM4000855//Homo sapiens chromosome 17, clone hCIT.457_L_16, complete sequence.//3.4e-29:229:83//AC003957
F-NT2RM4000887
F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosamine pyrophosphorylase, complete cds.//2.1e-20:407:64//AB011004
F-NT2RM4000950//Homo sapiens clone DJ0917G04, WORKING DRAFT SEQUENCE, 35 unordered pieces.//0.41:311:64//AC004929
F-NT2RM4000971//RPCI11-53H3.TJ RPCI11 Homo sapiens genomic clone R-53H3, genomic survey sequence.//1.0:208:64//AQ053735
F-NT2RM4000979//Homo sapiens chromosome 17, clone hRPK.642_C_21, complete sequence.//1.3e-19:207:78//AC005245
F-NT2RM4000996//CITBI-E1-2506B10.TF CITBI-E1 Homo sapiens genomic clone 2506B10, genomic survey sequence.//1.4e-73:361:98//AQ263651
F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds.//5.1e-170:803:98//AB018272
F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds.//3.3e-125:584:99//AB014539
F-NT2RM4001032//Gallus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds.//0.00034:777:58//U47276
F-NT2RM4001047//MO25 gene [mice, embryos, mRNA, 2322 nt].//2.5e-92:776:74//S51858
F-NT2RM4001054//Canis familiaris sec61 homologue mRNA, complete cds.//3.1e-102:859:76//M96629
F-NT2RM4001084//CIT-HSP-2330F9.TR CIT-HSP Homo sapiens genomic clone 2330F9, genomic survey sequence.//4.6e-78:379:99//AQ044479
F-NT2RM4001092//cSRL-71b1-u cSRL flow sorted Chromosome 11 specific cosmid Homosapiens genomic clone cSRL-71b1, genomic survey sequence.//1.1e-12:152:75//B05776
F-NT2RM4001116
F-NT2RM4001140//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.//1.9e-136:717:93//AC004593
F-NT2RM4001151//Streptomyces antibioticus ATP-binding protein and membrane protein (oleC-ORF1, oleC-ORF2, oleC-ORF3, oleC-ORF4, and oleC-PRF5) genes, complete cds; 3427 base-pairs.//0.0083:368:60//L06249
F-NT2RM4001155//Bos taurus 50 kDa protein (adp50) mRNA, complete cds.//3.9e-120:764:85//U04706
F-NT2RM4001160
F-NT2RM4001187
F-NT2RM4001191//CIT-HSP-2010E7.TF CIT-HSP Homo sapiens genomic clone 2010E7, genomic survey sequence.//6.2e-12:181:72//B53378
F-NT2RM4001200//H.sapiens HZF10 mRNA for zinc finger protein.//1.3e-66:799:69//X78933
F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//4.2e-152:707:99//AF004828
F-NT2RM4001204

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F-NT2RM4001217//Homo sapiens ectoderm-neural cortex-1 protein (ENC-1) mRNA, complete cds.//1.6e-62:715:70//AF005381
F-NT2RM4001256//Human NotI linking clone 924A058R, genomic survey sequence.//7.6e-14:109:90//U49884
F-NT2RM4001258//HS_3171_B2_G09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3171 Col=18 Row=N, genomic survey sequence.//2.5e-18:215:77//AQ149676
F-NT2RM4001309//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//4.9e-28:526:66//AL022163
F-NT2RM4001313//H.sapiens mRNA for phosphatidylinositol 3-kinase.//2.5e-77:474:89//Z46973
F-NT2RM4001316//Caenorhabditis elegans cosmid K09H11.//1.2e-16:230:73//U97002
F-NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds.//1.1e-41:642:66//D89016
F-NT2RM4001340//EP(3)0614 Drosophila melanogaster EP line Drosophila melanogaster genomic Sequence recovered from 5' end of P element, genomic survey sequence.//0.0040:141:68//AQ025127
F-NT2RM4001344//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y1E3, WORKING DRAFT SEQUENCE.//5.5e-06:469:60//AL021388
F-NT2RM4001347
F-NT2RM4001371//Arabidopsis thaliana chromosome II BAC T20K9 genomic sequence, complete sequence.//0.10:400:61//AC004786
F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//2.2e-167:790:98//AF098799
F-NT2RM4001384//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence.//0.99:255:59//AL021393
F-NT2RM4001410//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE.//0.027:336:58//AP000023
F-NT2RM4001411//Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA, complete cds.//5.9e-124:783:85//AF020526
F-NT2RM4001412//Rattus norvegicus GTPase activating protein SynGAP-c mRNA, complete cds.//2.2e-34:418:71//AF050183
F-NT2RM4001414//Homo sapiens full-length insert cDNA clone ZE16C11.//9.1e-76:363:100//AF086563
F-NT2RM4001437//Homo sapiens chromosome 5, BAC clone 313n8 (LBNL H146), complete sequence.//2.0e-47:623:69//AC004226
F-NT2RM4001444//Streptococcus pneumoniae penicillin-binding protein 2b (pbp2b), RecM (recM), D-Ala-D-Ala ligase (ddl), D-Ala-D-Ala adding enzyme (murF), MutT (mutT), cell division protein FtsA (ftsA), cell division protein FtsZ (ftsZ), YlmE (ylmE), YlmF (ylmF), YlmG (ylmG), YlmH (ylmH), cell division protein DivIVA (divIVA), and isoleucine-tRNA synthetase (ileS) genes, complete cds; and unknown gene.//3.6e-09:566:58//AF068901
F-NT2RM4001454
F-NT2RM4001455
F-NT2RM4001483//Human zinc finger protein ZNF136.//3.2e-36:329:78//U09367
F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds.//1.2e-155:724:99//AB014585
F-NT2RM4001519//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.00019:418:59//AC004688
F-NT2RM4001522//Human HepG2 3' region MboI cDNA, clone hmd6a08m3.//1.4e-16:130:88//D17274
F-NT2RM4001557
F-NT2RM4001565
F-NT2RM4001566
F-NT2RM4001569//HS_2050_B1_C08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2050 Col=15 Row=F, genomic survey sequence.//2.7e-09:109:84//AQ234720
F-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//1.2e-127:740:89//AF071317
F-NT2RM4001592//M.musculus mRNA of enhancer-trap-locus 1.//7.3e-117:710:88//X69942
F-NT2RM4001594//Homo sapiens chromosome 9q34, clone 107G20, WORKING DRAFT SEQUENCE, 2 ordered pieces.//0.34:388:59//AC002355
F-NT2RM4001597//M.musculus red-1 gene.//6.2e-139:788:90//X92750
F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds.//3.3e-162:750:99//AB018334
F-NT2RM4001611//Synechocystis sp. PCC6803 complete genome, 12/27, 1430419-1576592.//2.5e-05:490:58//D90910
F-NT2RM4001629//Mus musculus palmytoylated protein p55 mRNA, complete cds.//0.65:186:64//U38196
F-NT2RM4001650//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0435P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//0.99:422:59//AC004689

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F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds.//2.6e-81:449:93//AB002320
F-NT2RM4001666
F-NT2RM4001682//Mus musculus clone OST9187, genomic survey sequence.//3.2e-35:240:87//AF046699
F-NT2RM4001710//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE.//1.9e-151:564:97//AL031447
F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds.//7.0e-85:748:74//D86957
F-NT2RM4001715//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//1.2e-91:488:94//AL034430
F-NT2RM4001731//Orang-utan in volucrin gene, complete cds.//0.40:530:59//M25312
F-NT2RM4001741//Mouse mRNA for talin.//1.1e-129:737:90//X56123
F-NT2RM4001746//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 316G12, WORKING DRAFT SEQUENCE.//2.3e-49:320:89//AL031709
F-NT2RM4001754//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//6.3e-64:379:76//AC005831
F-NT2RM4001758//R.norvegicus mRNA for serine/threonine kinase MARK1.//3.7e-146:871:87//Z83868
F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds.//2.3e-173:803:99//AB018270
F-NT2RM4001783//Homo sapiens clone DJ0981007, complete sequence.//2.0e-165:593:99//AC006017
F-NT2RM4001810
F-NT2RM4001813//Homo sapiens BAC clone NH0364H22 from 2, complete sequence.//7.1e-31:176:84//AC005036
F-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds.//4.4e-34:195:95//M37712
F-NT2RM4001823//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//3.3e-51:490:75//U49046
F-NT2RM4001828//Human zinc finger containing protein ZNF157 (ZNF157) mRNA, complete cds.//5.6e-74:688:72//U28687
F-NT2RM4001836//Homo sapiens Chromosome 22q11.2 Cosmid Clone 2h In DGCR Region, complete sequence.//1.0:406:60//AC000076
F-NT2RM4001841//Mus musculus A kinase anchor protein (AKAP-KL) mRNA, alternatively spliced isoform 2, complete cds.//1.6e-131:831:86//AF033275
F-NT2RM4001842//HS_3163_A2_G10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=20 Row=M, genomic survey sequence.//1.5e-05:355:60//AQ168513
F-NT2RM4001856//Caenorhabditis elegans cosmid K08F11.//4.0e-23:823:60//U70855
F-NT2RM4001858//Notophthalmus viridescens NvTbox1 mRNA, partial cds.//6.4e-11:266:66//U64433
F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//6.9e-149:704:98//Y17711
F-NT2RM4001876//F.rubripes GSS sequence, clone 060E22bA4, genomic survey sequence.//5.7e-48:600:68//Z88651
F-NT2RM4001880//CIT-HSP-2348J1.TF CIT-HSP Homo sapiens genomic clone 2348J1, genomic survey sequence.//0.0025:61:88//AQ060809
F-NT2RM4001905//R.norvegicus CYP3A1 gene, 5' flanking region.//2.5e-29:535:67//X98335
F-NT2RM4001922//HS_2237_A1_C10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=19 Row=E, genomic survey sequence.//2.2e-73:364:98//AQ033732
F-NT2RM4001930//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI10, complete sequence.//4.9e-10:269:63//AB005248
F-NT2RM4001938//Homo sapiens chromosome 17, clone hRPC.1081_P_3, complete sequence.//7.6e-152:311:100//AC005207
F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//1.1e-170:808:98//AF098162
F-NT2RM4001953//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B13E4; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.7e-45:310:86//AC004046
F-NT2RM4001965//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11.//1.6e-107:622:90//AB020868
F-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//3.9e-24:221:76//X99330
F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds.//1.0e-61:527:76//AB018341
F-NT2RM4001984//Human DNA sequence from cosmid U151E3, between markers on chromosome X.//5.8e-07:502:60//Z82253
F-NT2RM4001987//RPCI11-49L11.TJ RPCI11 Homo sapiens genomic clone R-49L11, genomic survey sequence.//2.6e-33:177:99//AQ051701
F-NT2RM4002013//Homo sapiens chromosome 17, clone hRPK.294_J_22, complete sequence.//0.019:65:90//AC005921

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F-NT2RM4002018//Human high molecular weight B cell growth factor mRNA sequence.///1.0:527:57//L15344
F-NT2RM4002034//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//0.11:322:60//AL008712
F-NT2RM4002044//Homo sapiens SS-A/Ro autoantigen 52 kda component gene, complete cds.//0.015:513:61//U01882
F-NT2RM4002054//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.0e-44:473;76//AC005283
F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds.//1.0e-171:803:98//AB014540
F-NT2RM4002062//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0031:298:59//AC005122
F-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//1.1e-147:705:98//U82267
F-NT2RM4002066//Human mRNA for KIAA0192 gene, partial cds.//3.4e-73:889:69//D83783
F-NT2RM4002067//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//1.1e-53:295:76//AC005216
F-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//7.8e-25:277:75//AF072758
F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//9.0e-23:588:61//AF059569
F-NT2RM4002093//Rat PYBP1 mRNA for pyrimidine binding protein 1.//3.1e-68:544:69//X60789
F-NT2RM4002109//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//2.0e-121:762:86//D12646
F-NT2RM4002128//HS_3084_A1_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=7 Row=G, genomic survey sequence.//7.7e-18:117:95//AQ186312
F-NT2RM4002140
F-NT2RM4002145//Homo sapiens chromosome 19, fosmid 37308, complete sequence.//1.8e-49:736:65//AC004152
F-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.5e-70:454:85//AF035940
F-NT2RM4002161//Homo sapiens mRNA for LAFPTPase, isoform 1, partial.//4.2e-151:763:96//AJ130763
F-NT2RM4002174//Helicobacter pylori 26695 section 18 of 134 of the complete genome.//2.1e-16:580:60//AE000540
F-NT2RM4002189//Homo sapiens DNA sequence from BAC 722E9 on chromosome 22q13.2-13.33. Contains ESTs.//1.0e-07:792:61//AL008636
F-NT2RM4002194//Mus musculus semaphorin VIa mRNA, complete cds.//3.2e-132:782:87//AF030430
F-NT2RM4002205//Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.//1.5e-40:292: 84//L14684
F-NT2RM4002213
F-NT2RM4002226//Mus musculus p190-B gene, complete cds.//0.099:350:59//U67160
F-NT2RM4002251//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//1.0:428:58//AC004448
F-NT2RM4002256//Mouse genomic DNA, chromosome 17, clone cosmid 49.1, genomic survey sequence.//9.4e-60:294:81//AB005959
F-NT2RM4002266//Fugu rubripes GSS sequence, clone 006l18aG12, genomic survey sequence.//3.3e-12:217:67//AL024779
F-NT2RM4002278//HS_3089_A1_E05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3089 Col=9 Row=I, genomic survey sequence.//1.9e-64:381:92//AQ121653
F-NT2RM4002281
F-NT2RM4002287//CIT-HSP-2327E14.TF CIT-HSP Homo sapiens genomic clone 2327E14, genomic survey sequence.//9.0e-49:336:86//AQ042515
F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds.//2.1e-48:511:72//D87457
F-NT2RM4002301//Human NotI linking clone 924A053D, genomic survey sequence.//8.9e-05:62:91//U49881
F-NT2RM4002323//Human DNA sequence from clone 59B16 on chromosome 6p22.1-22.3. Contains a pseudogene similar to GPISG20 and other exonucleases). Contains ESTs, STSs, GSSs, genomic markers D6S1691 and D6S299 and a ca repeat polymorphism, complete sequence.//4.9e-115:729:87//AL032822
F-NT2RM4002339//Homo sapiens PAC clone DJ0728D04, complete sequence.//1.1e-97:457:93//AC004865
F-NT2RM4002344//Caenorhabditis elegans cosmid K04A8.//2.2e-06:190:69//U64849
F-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds.//2.8e-149:708:98//AB014549
F-NT2RM4002374//Homo sapiens 12q24 PAC P336P3 (Research Park Cancer Institute Human Genome PAC library) complete sequence.//0.00040:312:63//AC002978

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F-NT2RM4002383//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469D22, WORKING DRAFT SEQUENCE.//6.8e-29:378:66//AL031284
F-NT2RM4002390
F-NT2RM4002398//CIT-HSP-2288N22.TR CIT-HSP Homo sapiens genomic clone 2288N22, genomic survey sequence.//3.4e-35:184:100//AQ001110
F-NT2RM4002409//Archaeoglobus fulgidus section 15 of 172 of the complete genome.//2.0e-16:468:59//AE001092
F-NT2RM4002438//Human HLA class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gene, receptor for advanced glycosylation end products (RAGE) gene, complete cds, and 6 unidentified cds, complete sequence.//1.6e-16:123:91//U89336
F-NT2RM4002446//Human DNA sequence from cosmid 443D9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs, STS and CpG islands.//9.6e-64:467:84//Z92845
F-NT2RM4002452
F-NT2RM4002457//Human DNA sequence from PAC 151B14 on chromosome 22, complete sequence.//2.2e-24:201:86//Z85988
F-NT2RM4002460//Homo sapiens PAC clone DJ0630C24 from 7q31-q32, complete sequence.//1.3e-45:487:70//AC004690
F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds.//2.7e-163:777:98//AF083255
F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds.//2.3e-93:464:97//AB014591
F-NT2RM4002493
F-NT2RM4002499//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-41:442:75//AC005484
F-NT2RM4002504//Human DNA sequence from clone 391O22 on chromosome 6p21.2-21.31 Contains pseudogenes similar to ribosomal protein, ESTs, GSSs, complete sequence.//3.8e-31:233:87//AL031577
F-NT2RM4002527//Fugu rubripes GSS sequence, clone 096G17aC8, genomic survey sequence.//7.7e-08:274:62//AL027162
F-NT2RM4002532
F-NT2RM4002534
F-NT2RM4002558//Mus musculus fatty acid transport protein 4 mRNA, partial cds.//3.8e-53:394:81//AF072759
F-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//6.4e-160:902:89//AF022962
F-NT2RM4002567//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//8.5e-31:220:88//AQ263402
F-NT2RM4002571//Rattus norvegicus UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase T5 mRNA, complete cds.//5.2e-05:199:65//AF049344
F-NT2RM4002593//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//0.89:275:61//AC004875
F-NT2RM4002594//Drosophila melanogaster, chromosome 2R, region 31C1-31D6, P1 clone DS08879, complete sequence.//3.7e-44:768:64//AC005454
F-NT2RM4002623//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.8e-34:574:65//AC005122
F-NT2RP1000018//Homo sapiens mRNA for NIK, partial cds.//3.9e-111:582:95//AB013385
F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//1.1e-153:747:96//AJ012449
F-NT2RP1000040//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE.//1.6e-125:243:88//AP000047
F-NT2RP1000063//Caenorhabditis elegans cosmid F31C3, complete sequence.//9.6e-09:414:59//Z92784
F-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsal2.//2.8e-183:548:91//X98834
F-NT2RP1000101//H.sapiens CpG island DNA genomic Mse1 fragment, clone 28b4, forward read cpg28b4.ft1a.//6.0e-27:163:95//Z60555
F-NT2RP1000111//CIT-HSP-2307O14.TR CIT-HSP Homo sapiens genomic clone 2307O14, genomic survey sequence.//1.2e-11:128:81//AQ016069
F-NT2RP1000112//Human kinase (TTK) mRNA, complete cds.//1.0e-38:324:81//M86699
F-NT2RP1000124//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.59:476:59//AL034557
F-NT2RP1000130//DNA encoding human Hepatoma-derived Growth Factor.//2.7e-35:535:681/E08546
F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//6.7e-05:77:90//AF011792
F-NT2RP1000170//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//

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1.9e-20:431:64//AC006030
F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence.//2.5e-138:679:97//AF070535
F-NT2RP1000191
F-NT2RP1000202//Porcine mRNA for M130 of smooth muscle myosin phosphatase, partial cds.//5.3e-05:220:61//D89496
F-NT2RP1000243//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//4.7e-51:508:69//AC004373
F-NT2RP1000259
F-NT2RP1000272//Mus musculus TLS-associated protein with SR repeats mRNA, complete cds.//7.8e-142:866:88//AF042383
F-NT2RP1000324//RPCI11-81O21.TJ RPCI11 Homo sapiens genomic clone R-81O21, genomic survey sequence.//2.8e-29:182:92//AQ285136
F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//4.2e-147:693:98//AF053551
F-NT2RP1000333//Caenorhabditis elegans cosmid C03D6, complete sequence.//1.4e-08:281:61//Z75525
F-NT2RP1000348//H.sapiens CpG island DNA genomic Mse1 fragment, clone 12f1, reverse read cpg12f1.rt1c.//1.7e-09:71:100//Z56610
F-NT2RP1000357
F-NT2RP1000358 5.7e-16:403:61//AC005456
F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds.//9.8e-125:497:86//AB014538
F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete cds.//1.8e-176:877:96//AF064594
F-NT2RP1000409//Homo sapiens repetitive sequences, alphoid DNA, 2482bp.//4.6e-106:700:84//AJ001558
F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds.//9.4e-178:710:98//AB011159
F-NT2RP1000416
F-NT2RP1000418//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds.//1.0:198:60//L40178
F-NT2RP1000439//HS_2182_A1_D06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=11 Row=G, genomic survey sequence.//2.1e-68:441:87//AQ024305
F-NT2RP1000443//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE.//3.8e-57:185:88//AP000047
F-NT2RP1000460//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//2.7e-132:204:99//AC004453
F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence, complete sequence.//4.9e-80:196:95//AC002985
F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds.//1.9e-55:440:80//U47634
F-NT2RP1000481//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceeded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//2.6e-92:562:88//Z99297
F-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds.//2.0e-130:622:98//D87686
F-NT2RP1000513//Xanthomonas campestris campestris xpsD, xpsM, and xpsN genes, complete cds's.//0.11:360:58//M81648
F-NT2RP1000522//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//4.9e-34:209:93//AC004895
F-NT2RP1000547//Cricetulus griseus COP-coated vesicle membrane protein CHOp24 mRNA, partial cds.//1.2e-08:331:63//U26264
F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partial cds.//4.4e-81:295:92//AF017418
F-NT2RP1000577//HS_2228_B2_C05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=10 Row=F, genomic survey sequence.//1.9e-31:179:75//AQ185128
F-NT2RP1000581//Pan troglodytes von Willebrand factor (vWF) gene, partial cds.//4.7e-34:223:90//U31620
F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.//1.6e-18:229:65//AC004770
F-NT2RP1000629//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//9.3e-89:584:84//M62419
F-NT2RP1000630//Human DNA sequence from PAC 151B14 on chromosome 22 Contains EST, complete sequence.//1.0:203:63//Z85989
F-NT2RP1000677//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//0.0034:350:61//AC005943

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F-NT2RP1000688//H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form).//5.2e-10:120:80//X69907
F-NT2RP1000695
F-NT2RP1000701//Sequence 1 from patent US 5580968.//2.4e-99:624:86//I30536
F-NT2RP1000721//Homo sapiens clone DJ0943F02, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-19:188:81//AC004932
F-NT2RP1000730
F-NT2RP1000733//Human chromosome 16p13-1 BAC clone CIT987SK-551G9 complete sequence.//1.3e-30:315:75//U95742
F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds.//8.0e-122:604:96//AF101434
F-NT2RP1000746//HS_3084_A1_H03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=5 Row=O, genomic survey sequence.//1.5e-83:466:92//AQ186344
F-NT2RP1000767//Homo sapiens full-length insert cDNA clone ZD81B04.//2.8e-21:144:91//AF086442
F-NT2RP1000782//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//2.1e-121:591:97//AF054840
F-NT2RP1000796//T.thermophilus phosphofructokinase 1 (PFK1) gene, complete cds.//0.76:263:64//M71213
F-NT2RP1000825//Human DNA sequence from clone 116F5 on chromosome 22q13. Contains part of an unknown gene and part of a RhoGAP (CDC42 GTPAse Activating Protein) LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D22S1168 and a CA repeat polymorphism, complete sequence.//1.5e-77:163:96//Z93244
F-NT2RP1000833//Homo sapiens cGMP-specific phosphodiesterase (PDE9A2) mRNA, complete cds.//1.3e-147:424:96//AF048837
F-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.9e-89:702:79//AF047020
F-NT2RP1000836//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//8.7e-169:842:96//AL022398
F-NT2RP1000846//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//3.3e-15:196:76//U96629
F-NT2RP1000851//Homo sapiens PAC clone 267D11 from 12, complete sequence.//1.6e-144:724:96//AC004812
F-NT2RP1000856//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//2.1e-121:591:97//AF054840
F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds.//6.7e-106:551:95//AF064094
F-NT2RP1000902//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 316D5, WORKING DRAFT SEQUENCE.//0.0097:55:100//Z82199
F-NT2RP1000915//H.sapiens genomic DNA fragment (clone J32A032R).//1.3e-30:174:97//Z94761
F-NT2RP1000916
F-NT2RP1000943//Hylobates lar huntingtin gene, partial exon.//0.19:103:72//L49362
F-NT2RP1000944//HS_2179_B2_C12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=24 Row=F, genomic survey sequence.//0.032:140:63//AQ065269
F-NT2RP1000947//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//3.7e-53:461:78//U62483
F-NT2RP1000954//cSRL-143G4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-143G4, genomic survey sequence.//0.030:89:78//B01950
F-NT2RP1000958//Caenorhabditis elegans cosmid K01C8, complete sequence.//3.9e-11:445:61//Z49068
F-NT2RP1000959//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//3.3e-57:326:92//AC004263
F-NT2RP1000966//Human nucleolin gene, complete cds.//3.4e-64:197:981/M60858
F-NT2RP1000980//CIT-HSP-2314B10.TF CIT-HSP Homo sapiens genomic clone 2314B10, genomic survey sequence.//0.32:137:68//AQ017126
F-NT2RP1000988//Human chromosome 3p21.1 gene sequence.//8.0e-72:665:80//L13435
F-NT2RP1001011//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds.//1.3e-31:497:65//U34925
F-NT2RP1001013//HS_3068_B1_809_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3068 Col=17 Row=D, genomic survey sequence.//1.0e-24:414:66//AQ127667
F-NT2RP1001014//HS_3252_B1_B05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=9 Row=D, genomic survey sequence.//0.00052:83:81//AQ304711
F-NT2RP1001033//Homo sapiens chromosome 17, clone hRPC-1073_F_15, complete sequence.//1.3e-134:241:99//AC004686

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F-NT2RP1001073//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence.//2.5e-59:451:83//AC004993
F-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//4.5e-93:476:96//U82267
F-NT2RP1001080//Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.//6.6e-54:217:89//AC004938
F-NT2RP1001113
F-NT2RP1001173
F-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//8.1e-26:373:681/U79139
F-NT2RP1001185//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-32:388:73//AC006039
F-NT2RP1001199
F-NT2RP1001247//Homo sapiens signaling molecule LEFTY-A gene, exon 1.//2.0e-29:166:96//AF081508
F-NT2RP1001248//Homo sapiens Chromosome 11q23 PAC clone pDJ356d6, complete sequence.//7.3e-50:128 : 99//AC002036
F-NT2RP1001253//Homo sapiens oscillin (hLn) mRNA, complete cds.//4-3e-91:344:93//AF029914
F-NT2RP1001286//Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's-//0.54:292:63//L44140
F-NT2RP1001294
F-NT2RP1001302
F-NT2RP1001310//Rabbit skeletal muscle mRNA for ryanodine receptor.//1.5e-07:335:64//X15750
F-NT2RP1001311//RPCI11-67O14.TK RPCI11 Homo sapiens genomic clone R-67O14, genomic survey sequence.//0.26:80:75//AQ239291
F-NT2RP1001313//Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.//8.8e-75:304:98//AC004228
F-NT2RP1001361//B.taurus CI-B14.5b mRNA for NADH dehydrogenase (ubiquinone).//2.7e-57:412:84//X68647
F-NT2RP1001385
F-NT2RP1001395//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//1.4e-72:535:83//AF071316
F-NT2RP1001410//Homo sapiens DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D),TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.//5.8e-105:570:94//AL021878

F-NT2RP1001424
F-NT2RP1001432
F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence.//1.7e-84:422:97//AF052149
F-NT2RP1001457//Xenopus laevis notchless (nle) mRNA, complete cds.//1.3e-47:471:73//AF069737
F-NT2RP1001466//HS_3006_A2_D08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=16 Row=G, genomic survey sequence.//0.56:289:60//AQ154336
F-NT2RP1001475//H.sapiens genomic DNA fragment (clone NLMA194R).//0.00011:91:79//Z95375
F-NT2RP1001482//Mouse oncogene (ect2) mRNA, complete cds.1/4-0e-87:563:85//L11316
F-NT2RP1001494
F-NT2RP10015431/Drosophila melanogaster DNA sequence (P1 DS01142 (D148)), complete sequence.//1.9e-27:387:67//AC004280
F-NT2RP1001546//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//8.0e-63:314:98//AF054840
F-NT2RP1001569//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//1.2e-68:514:81//U17343
F-NT2RP100T616//Human clone 23665 mRNA sequence.//7.6e-40:496:74//U90913
F-NT2RP1001665//CIT-HSP-2059N5.TF CIT-HSP Homo sapiens genomic clone 2059N5, genomic survey sequence.//2.4e-45:305:88//B69912
F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence.//1.5e-135:685:96//AF091081
F-NT2RP2000006//HS_3061_B2_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3061 Col=6 Row=F, genomic survey sequence.//1.9e-17:394:67//AQ178856
F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds.//3.5e-14:241:68//AB002390
F-NT2RP2000008//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 257E24, WORKING DRAFT SEQUENCE.//1.7e-34:147:99//AL034424
F-NT2RP2000027//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//1.4e-32:345:75//

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AC005066
F-NT2RP2000032//F.rubripes GSS sequence, clone 060E22aG10, genomic survey sequence.//5.0e-41:445:72//Z88655
F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds.//1.9e-76:383:97//AB018290
F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//2.4e-95:467:97//AF061749
F-NT2RP2000054//CIT-HSP-2328J24.TF CIT-HSP Homo sapiens genomic clone 2328J24, genomic survey sequence.//3.3e-39:236:91//AQ043092
F-NT2RP2000056//Rat mRNA for protein tyrosine phosphatase epsilon C, partial cds.//3.2e-50:311:90//D78610
F-NT2RP2000067//Mus musculus DOC4 (Doc4) mRNA, complete cds.//3.0e-55:766:66//AF059485
F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//2.0e-118:597:95//AC005754
F-NT2RP2000076//Homo sapiens clone NH0263G22, complete sequence.//0.0017:423:60//AC006037
F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds.//2.1e-77:278:97//AF050079
F-NT2RP2000079//H.sapiens CpG island DNA genomic Mse1 fragment, clone 40c2, forward read cpg40c2.ft1k.//3.2e-33:197:95//Z55440
F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//2.2e-158:752:98//AB018338
F-NT2RP2000091//HS_2228_A2_B02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=4 Row=C, genomic survey sequence.//0.26:55:90//AQ146363
F-NT2RP2000097
F-NT2RP2000098//Homo sapiens clone DJ1098J04, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.5e-05:482:60//AC004961
F-NT2RP2000108//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.0e-22:274:69//AC003973
F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//4.9e-114:551:97//AB018356
F-NT2RP2000120//HS_3000_B1_E03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=5 Row=J, genomic survey sequence.//1.8e-21:129:97//AQ090365
F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//4.2e-119:607:96//AF054177
F-NT2RP2000133//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.3e-07:339:63//AC004827
F-NT2RP2000147//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//9.0e-101:638:85//M62419
F-NT2RP2000153//Human DNA sequence from clone 218J18 on chromosome Xp11.3-11.4. Contains the NDP (Norrie Disease (Pseudoglioma)) gene and a CC1.3 Splicing Factor pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.45:377:58//AL034370
F-NT2RP2000157//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//4.0e-73:317:87//AC005924
F-NT2RP2000161//CIT-HSP-2353L5.TF.1 CIT-HSP Homo sapiens genomic clone 2353L5, genomic survey sequence.//3.0e-14:123:90//AQ263431
F-NT2RP2000173
F-NT2RP2000175
F-NT2RP2000183//F.rubripes GSS sequence, clone 168M02aC2, genomic survey sequence.//3.7e-06:152:66//AL007295
F-NT2RP2000195//Human DNA sequence from clone 451 4 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//7.6e-62:170:99//AL023581
F-NT2RP2000205
F-NT2RP2000208//Homo sapiens chromosome 19, overlapping cosmids R29828 and F25496, complete sequence.//7.2e-80:170:90//AC003030
F-NT2RP2000224//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//5.5e-64:400:85//AC004382
F-NT2RP2000232//Human DNA sequence from PAC 196E23 on chromosome Xq26.1-27.2. Contains the TAT-SF1 (HIV-1 transcriptional elongation factor TAT cofactor TAT-SF1) gene, the BRS3 (Bombesin Receptor subtype-3 (Uterine Bombesin Receptor, BRS-3) gene, an unknown gene coding for two isoforms, a predicted CpG island, ESTs and STSs.//2.2e-07:280:66//Z97632
F-NT2RP2000233//Mus musculus tumor metastasis associated gene product (MAG) mRNA, complete cds.//8.8e-30:508:67//U88401
F-NT2RP2000239//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//4.0e-79:504:

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87//AC004066
F-NT2RP2000248
F-NT2RP2000257//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y1E3, WORKING DRAFT SEQUENCE.//0.0078:286:60//AL021388
F-NT2RP2000258//CIT-HSP-2349P21.TF CIT-HSP Homo sapiens genomic clone 2349P21, genomic survey sequence.//5.7e-82:416:97//AQ059184
F-NT2RP2000270//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//4.5e-29:310:73//AC006116
F-NT2RP2000274
F-NT2RP2000283//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//6.3e-20:260:73//X74904
F-NT2RP2000288
F-NT2RP2000289
F-NT2RP2000297//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and - 9.//4.6e-69:744:70//M27877
F-NT2RP2000298//Streptomyces coelicolor cosmid 2E9.//4.4e-05:502:59//AL021530
F-NT2RP2000310//WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.1e-13:173:76//AC006082
F-NT2RP2000327//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//8.3e-144:731:95//AL022398
F-NT2RP2000328//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//1.9e-102:555:90//AL034430
F-NT2RP2000329//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//6.4e-105:639:87//M25757
F-NT2RP2000337//HS_2060_B1_E01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2060 Col=1 Row=J, genomic survey sequence.//0.78:218:60//AQ243333
F-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds.//3.6e-129:627:97//U83981
F-NT2RP2000369//HS_2182_B1_B11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=21 Row=D, genomic survey sequence.//2.5e-87:421:99//AQ024835
F-NT2RP2000412//Human DNA sequence from PAC 124O9 on chromosome 6q21. Contains DNAJ2 (HDJ1) like pseudogene, ESTs, STSs and GSSs.//0.72:170:65//AL021327
F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds.//5.0e-66:375:93//L28010
F-NT2RP2000420//Homo sapiens full-length insert cDNA YQ86E07.//9.2e-77:423:93//AF075093
F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//2.1e-126:609:96//AF102265
F-NT2RP2000438//CITBI-E1-2519O19.TR CITBI-E1 Homo sapiens genomic clone 2519O19, genomic survey sequence.//0.96:61:78//AQ276878
F-NT2RP2000448//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//7.1e-17:341:67//AC004691
F-NT2RP2000459//H.sapiens mRNA for imogen 38.//5.7e-21:158:87//Z68747
F-NT2RP2000498//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//3.2e-11:160:73//Z92844
F-NT2RP2000503//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//0.0031:187:66//AC005229
F-NT2RP2000510//Fugu rubripes GSS sequence, clone 066G04aC1, genomic survey sequence.//8.8e-07:179:64//AL026277
F-NT2RP2000516//Mus musculus t complex testis-specific protein (Tctex2) gene, wild type, promoter sequence.//0.19:72:81//U21671
F-NT2RP2000523//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 150C2, WORKING DRAFT SEQUENCE.//5.0e-115:570:96//AL022318
F-NT2RP2000603//Homo sapiens mRNA for MCM3 import factor, complete cds.//8.4e-37:196:98//AB005543
F-NT2RP2000617//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.81:354:60//AC005321
F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//1.3e-149:732:97//AB014514
F-NT2RP2000644//HS_3211_A1_F06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3211 Col=11 Row=K, genomic survey sequence.//3.6e-42:282:86//AQ175486
F-NT2RP2000656

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F-NT2RP2000658//CITBI-E1-2518N15.TF CITBI-E1 Homo sapiens genomic clone 2518N15, genomic survey sequence.//0.57:141:66//AQ278386
F-NT2RP2000668
F-NT2RP2000678//Homo sapiens clone DJ0891L14, WORKING DRAFT SEQUENCE, 12 unordered pieces.//4.3e-22:433:62//AC004916
F-NT2RP2000704//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//2.7e-22:270:75//AC005913
F-NT2RP2000710//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.4e-32:574:64//AC005122
F-NT2RP2000715//Homo sapiens PAC clone DJ1066K24 from 7p15, complete sequence.//4.8e-113:546:98//AC004540
F-NT2RP2000731//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42 unordered pieces.//0.97:115:70//AC004965
F-NT2RP2000758//Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds.//9.7e-16:162:77//U62293
F-NT2RP2000764//HS_2254_B2_D07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2254 Col=14 Row=H, genomic survey sequence.//0.071:45:95//AQ068887
F-NT2RP2000809
F-NT2RP2000812//Egernia stokesii clone EST3 microsatellite.//0.040:158:64//AF069698
F-NT2RP2000814
F-NT2RP2000816
F-NT2RP2000819
F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds.//1.1e-26:390:70//AB002292
F-NT2RP2000842//H.sapiens mRNA for G protein-coupled receptor Edg-2.//1.2e-44:255:93//Y09479
F-NT2RP2000845
F-NT2RP2000863//Human partial cDNA sequence, clone x874;.//5.9e-29:173:94//Z47045
F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds.//2.4e-140:732:94//AB018284
F-NT2RP2000892
F-NT2RP2000931//Homo sapiens mRNA for KIAA0723 protein, complete cds.//3.4e-129:610:98//AB018266
F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.8e-37:212:84//AC005014
F-NT2RP2000938//Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island.//1.6e-126:682:93//Z69890
F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//5.8e-112:533:98//AB018298
F-NT2RP2000965
F-NT2RP2000970//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence.//9.2e-101:505:96//AL021393
F-NT2RP2000985//Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence.//1.6e-72:498:82//AC005277
F-NT2RP2000987//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//7.4e-12:171:77//AC002394
F-NT2RP2001036//Homo sapiens chromosome 17, clone HRPC1096F1, complete sequence.//1.2e-37:390:76//AC004167
F-NT2RP2001044//HS_2253_B1_G01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=1 Row=N, genomic survey sequence.//0.21:276:61//AQ069224
F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488.//3.2e-144:696:97//AB007957
F-NT2RP2001065
F-NT2RP2001070//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA, complete cds.//4.3e-104:775:81//U91561
F-NT2RP2001081//Rattus norvegicus synaptotagmin XI mRNA, complete cds.//3.7e-69:488:82//AF000423
F-NT2RP2001094//Human DNA sequence from PAC 410B11 on chromosome X contains STS.//7.4e-11:490:61//Z86063
F-NT2RP2001119//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 745C22, WORKING DRAFT SEQUENCE.//5.1e-30:316:76//AL031596
F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds.//1.1e-31:519:63//D87072
F-NT2RP2001137//HS_2193_B2_D12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=24 Row=H, genomic survey sequence.//1.8e-11:136:78//AQ032187

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F-NT2RP2001149//Homo sapiens Chromosome 22q11.2 Cosmid Clone 2h In DGCR Region, complete sequence.//6.2e-29:247:78//AC000076
F-NT2RP2001168//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STss, GSSs, and a putative CpG island, complete sequence.//0.23:207:66//AL009178
F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds.//2.3e-112:567:96//AB007949
F-NT2RP2001174//RPCI11-58L2.TK RPCI11 Homo sapiens genomic clone R-58L2, genomic survey sequence.//7.6e-07:196:64//AQ237306
F-NT2RP2001196
F-NT2RP2001218
F-NT2RP2001226//Homo sapiens LERK-6 (EPLG6) gene, exon 1.//1.1e-09:320:65//U92893
F-NT2RP2001233//Human ZFP-36 mRNA for a zinc finger protein.//6.1e-71:681:72//X51760
F-NT2RP2001245//HS_3062_B1_F07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 Col=13 Row=L, genomic survey sequence.//1.5e-05:268:63//AQ143177
F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds.//2.5e-106:514:97//AB018353
F-NT2RP2001277//Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence.//0.32:183:64//AE001430
F-NT2RP2001290//M.musculus mRNA for I47 clone.//8.6e-102:641:86//X61455
F-NT2RP2001295//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y105E8, WORKING DRAFT SEQUENCE.//0.20:171:63//AL022594
F-NT2RP2001312//Bovine synaptophysin mRNA, complete cds.//0.98:253:58//M22967
F-NT2RP2001327//Human B12 protein mRNA, complete cds.//5.8e-29:359:71//M80783
F-NT2RP2001328//CIT-HSP-2335A5.TF CIT-HSP Homo sapiens genomic clone 2335A5, genomic survey sequence.//1.3e-65:366:94//AQ038539
F-NT2RP2001347//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//3.8e-31:325:77//AJ003147
F-NT2RP2001366//H.sapiens CpG island DNA genomic Mse1 fragment, clone 4e11, forward read cpg4e11.f1a.//1.7e-12:98:92//Z61305
F-NT2RP2001378//HS_3054_B2_A03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=6 Row=B, genomic survey sequence.//9.8e-17:131:89//AQ100721
F-NT2RP2001381//Arabidopsis thaliana BAC T2L5.//0.080:434:59//AF096371
F-NT2RP2001392//S.pristinaespiralis snbC gene & amp; snbDE gene.//0.019:267:59//Y11548
F-NT2RP2001394//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//1.9e-16:133:78//Z93242
F-NT2RP2001397//Bos taurus cyclin B2 (CYCB2) mRNA, complete cds.//1.3e-63:419:84//AF080219
F-NT2RP2001420//Mus musculus nuclear protein NIP45 mRNA, complete cds.//3.1e-98:747:79//U76759
F-NT2RP2001423//Xenopus laevis ER1 mRNA, complete cds.//3.7e-34:269:85//AF015454
F-NT2RP2001427//Homo sapiens Chromosome 2p13 BAC Clone h173, complete sequence.//3.2e-13:164:78//AC003065
F-NT2RP2001436//Mus musculus clone OST1784, genomic survey sequence.//3.0e-06:136:71//AF046702
F-NT2RP2001440//cDNA sequence coding for gamma protein.//7.9e-83:553:86//E02350
F-NT2RP2001445//P.falciparum complete gene map of plastid-like DNA (IR-A).//1.5e-09:829:57//X95275
F-NT2RP2001449//B.taurus mRNA for cleavage and polyadenylation specificity factor.//1.3e-136:766:90//X75931
F-NT2RP2001450
F-NT2RP2001467
F-NT2RP2001506//CIT-HSP-2374H21.TF CIT-HSP Homo sapiens genomic clone 2374H21, genomic survey sequence.//7.9e-14:151:80//AQ109561
F-NT2RP2001511//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.6e-22:462:64//AF005355
F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1.//2.0e-136:657:97//Y14494
F-NT2RP2001526//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence.//1.2e-37:357:64//AC004596
F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//1.6e-103:384:94//AF035586
F-NT2RP2001560
F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488.//4.4e-123:590:98//

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AB007957
F-NT2RP2001576//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds.//0.038:580:58//U32943
F-NT2RP2001581//Mus musculus semaphorin VIa mRNA, complete cds.//6.5e-09:222:66//AF030430
F-NT2RP2001597//Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds.//0.0057:361:60//U72648
F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds.//7.2e-137:647:98//AB018340
F-NT2RP2001613
F-NT2RP2001628//H.sapiens (xs128) mRNA, 380bp.//1.7e-15:279:68//Z36784
F-NT2RP2001634//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.//5.4e-123:606:96//AF030233
F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds.//4.2e-144:687:97//AF058718
F-NT2RP2001663//H.sapiens mRNA for 2-phosphopyruvate-hydratase-alpha-enolase.//1.0e-36:372:74//X84907
F-NT2RP2001675//S.pombe chromosome I cosmid c2G11.//0.070:507:59//Z54354
F-NT2RP2001677//Mouse BAC CitbCJ7 219m7, genomic sequence, complete sequence.//2.0e-60:232:96//AC005259
F-NT2RP2001678//HS_2007_A2_A04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2007 Col=8 Row=A, genomic survey sequence.//7.3e-62:370:91//AQ269699
F-NT2RP2001699//RPCI11-57B17.TK RPCI11 Homo sapiens genomic clone R-57B17, genomic survey sequence.//0.99:141:63//AQ115592
F-NT2RP2001720//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//9.4e-117:604:95//AC004079
F-NT2RP2001721//Homo sapiens DNA sequence from clone 46618 on chromosome Xq11.1-13.2. Contains an unknown gene similar to Coagulation Factor V (Activated Protein C Cofactor), Coagulation Factor VIII (Procoagulant Component) and Ceruloplasmin (EC 1.16.3.1, Ferroxidase). Contains ESTs and an STS, complete sequence.//1.0:273:61//AL030998
F-NT2RP2001740//Homo sapiens Chromosome 22q11.2 Cosmid Clone 8c In DGCR Region, complete sequence.//1.0:356:62//AC000090
F-NT2RP2001748//Human mRNA for KIAA0003 gene, complete cds.//3.7e-18:151:86//D14697
F-NT2RP2001762//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//6.0e-145:715:97//AC004783
F-NT2RP2001813//Plasmodium falciparum chromosome 2, section 15 of 73 of the complete sequence.//0.38:340:60//AE001378
F-NT2RP2001839//HS_3000_B1_C07_MR CIT Approved Human Genomic Sperm Library D_ Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey sequence.//0.026:253:60//AQ090347
F-NT2RP2001861//Homo sapiens mRNA for paraplegin.//0.89:146:71//Y16610
F-NT2RP2001869//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0.040:174:62//AF027219
F-NT2RP2001876//Cyprinus carpio mRNA for allograft inflammatory factor-1, complete cds.//2.8e-44:483:71//AB012309
F-NT2RP2001883//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.8e-87:496:92//AL031864
F-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end.//9.2e-112:633:90//M74161
F-NT2RP2001900//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone R08A5, WORKING DRAFT SEQUENCE.//0.0026:360:62//Z82281
F-NT2RP2001907//H.sapiens CpG island DNA genomic Mse1 fragment, clone 97f11, forward read cpg97f11.ft1a.//4.2e-26:206:84//Z64125
F-NT2RP2001926//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.5e-06:621:59//AC004688
F-NT2RP2001936//cSRL-47D9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-47D9, genomic survey sequence.//3.1e-50:282:93//B04856
F-NT2RP2001943//Drosophila melanogaster cosmid 25E8.//0.00036:248:60//AL009196
F-NT2RP2001946//Homo sapiens clone NH0140K04, complete sequence.//3.8e-78:232:99//AC005033
F-NT2RP2001947//Homo sapiens full-length insert cDNA clone ZD81B04.//2.0e-28:172:94//AF086442
F-NT2RP2001969//H.sapiens CpG island DNA genomic Mse1 fragment, clone 152a8, reverse read cpg152a8.rt1a.//1.0e-20:123:99//Z59378
F-NT2RP2001976

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F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds.//0.0023:235:62//AB011117
F-NT2RP2001991//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.//3.1e-35:180:80//L22022
F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds.//9.8e-61:314:97//AB018299
F-NT2RP2002032//Homo sapiens chromosome 5, Bac clone 5m9 (LBNL H220), complete sequence.//0.76:189:65//AC005895
F-NT2RP2002033//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.9e-12:160:79//AC004825
F-NT2RP2002041//Human BAC clone RG035E18 from 7q31, complete sequence.//0.0014:123:73//AC004029
F-NT2RP2002046//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete sequence.//2.2e-86:722:77//AC004552
F-NT2RP2002047//Human DNA sequence from clone 21F7 on chromosome 6q16.1-21. Contains part of an exon of a putative new gene and STSs and GSSs, complete sequence.//0.13:350:61//AL033375
F-NT2RP2002058//S.cerevisiae chromosome XII reading frame ORF YLR129w.//9.7e-11:480:60//Z73301
F-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//6.5e-97:610:86//U87306
F-NT2RP2002070//beta -ADD=adducin beta subunit 63 kda isoform/membrane skeleton protein, beta -ADD=adducin beta subunit 63 kda isoform/membrane skeleton protein {alternatively spliced, exon 10 to 13 region} [human, Genomic, 1851 nt, segment 3 of 3].//0.0059:107:73//S81083
F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.//1.0e-127:643:96//AF052183
F-NT2RP2002078//F12O16-T7.1 IGF Arabidopsis thaliana genomic clone F12016, genomic survey sequence.//0.14:191:64//AQ249805
F-NT2RP2002079//Homo sapiens clone DJ0892G19, complete sequence.//0.0094:325:60//AC004917
F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//9.8e-111:533:97//AJ007509
F-NT2RP2002105//H.sapiens CpG island DNA genomic Mse1 fragment, clone 10h8, forward read cpg10h8.ft1a.//2.4e-29:178:94//Z58857
F-NT2RP2002124//CIT-HSP-2023E9.TF CIT-HSP Homo sapiens genomic clone 2023E9, genomic survey sequence.//2.5e-32:202:92//B64468
F-NT2RP2002137//Human plasma membrane calcium ATPase (hPMCA4) mRNA, complete cds.//0.095:319:59//M25874
F-NT2RP2002154//Mus musculus mRNA for myosin, complete cds.//1.0:258:63//D85923
F-NT2RP2002172//HS_3020_B1_H02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3020 Col=3 Row=P, genomic survey sequence.//1.2e-11:124:82//AQ093169
F-NT2RP2002185//RPCI11-67B15.TJ RPCI11 Homo sapiens genomic clone R-67B15, genomic survey sequence.//2.8e-18:109:100//AQ201833
F-NT2RP2002192//Human PM-Scl-75 autoantigen (PM-sc1) mRNA, complete cds.//2.7e-36:363:78//U09215
F-NT2RP2002193//Rattus norvegicus potassium channel regulatory protein KChAP mRNA, complete cds.//9.5e-82:477:89//AF032872
F-NT2RP2002208
F-NT2RP2002219//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//1.0:378:58//AL034557
F-NT2RP2002231//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.60:560:56//AC005308
F-NT2RP2002235//P.falciparum glutamic acid-rich protein gnen, complete cds.//0.59:341:60//J03998
F-NT2RP2002252//Mus musculus mSin3A (sin3A) mRNA, complete cds.//3.5e-81:398:87//U22394
F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//6.6e-50:315:89//AF005418
F-NT2RP2002259//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 118J21, WORKING DRAFT SEQUENCE.//9.7e-67:340:89//AL033527
F-NT2RP2002270//RPCI11-77C23.TV RPCI11 Homo sapiens genomic clone R-77C23, genomic survey sequence.//2.9e-18:79:93//AQ268098
F-NT2RP2002292//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 321D2, WORKING DRAFT SEQUENCE.//1.0:290:60//AL031033
F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//1.5e-93:467:96//AF069532
F-NT2RP2002316//HS_2171_B2_D11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=22 Row=H, genomic survey sequence.//7.3e-94:463:97//AQ119673
F-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds.//3.9e-123:640:95//AB015594
F-NT2RP2002333
F-NT2RP2002373//F.rubripes GSS sequence, clone 026F10aB8, genomic survey sequence.//0.46:234:61//

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Z87330
F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//9.4e-138:673:97//AF038958
F-NT2RP2002394//P.falciparum complete gene map of plastid-like DNA (IR-A).//0.79:421:56//X95275
F-NT2RP2002408//F.rubripes GSS sequence, clone 080G11aA8, genomic survey sequence.//5.7e-15:220:71//AL015615
F-NT2RP2002426//Sus scrofa SCAMP1 gene, exon 9.//7.1e-71:582:80//AJ223742
F-NT2RP2002439//Caenorhabditis elegans cosmid T07D3.//0.0018:210:67//AF016682
F-NT2RP2002442//Caenorhabditis elegans cosmid T03F1.//2.8e-18:295:67//U88169
F-NT2RP2002457//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//1.9e-06:281:66//AC004381
F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds.//0.039:207:63//D42045
F-NT2RP2002475
F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//2.4e-123:607:96//AB005289
F-NT2RP2002498//Arabidopsis thaliana BAC F3D13.//0.73:395:57//AF069300
F-NT2RP2002503//Homo sapiens, clone hRPK.15_A_1, complete sequence.//7.2e-18:134:90//AC006213
F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds.//1.2e-157:761:97//AB018334
F-NT2RP2002520
F-NT2RP2002537
F-NT2RP2002546//Homo sapiens Chromosome 11q12 pac pDJ741n15, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.83:252:60//AC004127
F-NT2RP2002549//Human Chromosome 15q26.1 PAC clone pDJ457j11 containing DNA polymerase gamma (polg) gene, complete sequence.//5.9e-93:186:99//AC005317
F-NT2RP2002591//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE.//4.0e-38:175:78//Z98304
F-NT2RP2002595//Sequence 2 from patent US 5763220.//1.5e-84:430:95//AR012155
F-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds.//1.9e-43:282:87//U19181
F-NT2RP2002609//Mus musculus defender against death 1 (DAD1) gene, partial cds.//1.5e-11:99:90//AF051310
F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, splice variant, 1316 bp.//5.6e-27:460:63//Y10806
F-NT2RP2002621
F-NT2RP2002643//Rat calmodulin III gene for calmodulin, promoter region and exon 1.//0.023:322:60//D90397
F-NT2RP2002672//Homo sapiens chromosome 10 clone CIT-HSP-1326H7 map 10q24.3-10q25.1, complete sequence.//3.9e-149:794:94//AC005384
F-NT2RP2002701//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50O24, WORKING DRAFT SEQUENCE.//9.2e-10:129:75//AL034380
F-NT2RP2002706//S.griseus secA gene.//1.3e-05:311:63//Y10980
F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds.//2.5e-40:631:65//AB014572
F-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.//4.8e-65:600:73//AF041107
F-NT2RP2002736//S.pombe chromosome II cosmid c887.//0.17:352:58//AL033388
F-NT2RP2002740//Absidia glauca ORF, 3' end; (+) mating type surface protein (PSSP15) gene, complete cds; ORF, 5' end.//0.0073:274:66//M94861
F-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.//7.5e-29:628:62//D89016
F-NT2RP2002750//Homo sapiens Xp22 Bins 35-37 BAC GSHB-214D18 (Genome Systems Human BAC Library) complete sequence.//3.6e-31:568:67//AC005296
F-NT2RP2002752//Human BAC clone RG317M02 from 7p15-p21, complete sequence.//1.7e-08:206:63//AC002433
F-NT2RP2002753//Human DNA sequence from cosmid B11B7 on chromosome 22 contains ESTs.//2.8e-71:195:89//Z82171
F-NT2RP2002769//Streptomyces fradiae tylactone synthase, starter module and modules 1-7, (tylG) gene, complete cds.//0.0016:412:60//U78289
F-NT2RP2002778//CIT-HSP-2059C5.TF CIT-HSP Homo sapiens genomic clone 2059C5, genomic survey sequence.//6.8e-18:186:79//B69837
F-NT2RP2002800
F-NT2RP2002839//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.2e-41:134:94//AC006078
F-NT2RP2002857//Rat T-cell receptor active beta-chain V-region (V-beta6-J-beta2.5) mRNA, partial cds, clone

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TRB-4.//0.85:93:68//M18845
F-NT2RP2002862//HS_3084_A1_H03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=5 Row=O, genomic survey sequence.//5.0e-67:390:91//AQ186344
F-NT2RP2002880
F-NT2RP2002891//CIT-HSP-2310O14.TF CIT-HSP Homo sapiens genomic clone 2310O14, genomic survey sequence.//0.11:53:90//AQ019792
F-NT2RP2002925//Pig mRNA for carbonyl reductase, complete cds.//0.66:194:65//D16511
F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//2.3e-135:628:99//AF038392
F-NT2RP2002929//F.rubripes GSS sequence, clone 123I23aA1, genomic survey sequence.//3.9e-06:66:83//AL017246
F-NT2RP2002939
F-NT2RP2002954
F-NT2RP2002959//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//1.3e-47:411:79//U62483
F-NT2RP2002979//CIT-HSP-2340D12.TF CIT-HSP Homo sapiens genomic clone 2340D12, genomic survey sequence.//4.6e-96:476:97//AQ057233
F-NT2RP2002980//Sequence 20 from Patent EP0705842.//4.0e-13:100:94//A52230
F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.4e-09:272:61//AF059569
F-NT2RP2002987//Homo sapiens (subclone 6_d9 from P1 H21) DNA sequence, complete sequence.//1.0e-22:293:67//AC000958
F-NT2RP2002993//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds.//4.0e-74:502:84//AF025424
F-NT2RP2003000//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.3e-46:474:76//AC004765
F-NT2RP2003034//Homo sapiens chromosome 17, clone hRPK.849_N_15, complete sequence.//4.2e-23:202:82//AC005703
F-NT2RP2003073//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//3.4e-59:330:82//Z83822
F-NT2RP2003099//HS_3008_B2_C09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3008 Col=18 Row=F, genomic survey sequence.//1.4e-71:362:96//AQ089786
F-NT2RP2003108//Sequence 59 from patent US 5773577.//0.95:123:69//AR014362
F-NT2RP2003117//HS_2034_B2_D12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2034 Col=24 Row=H, genomic survey sequence.//1.5e-88:461:96//AQ230797
F-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//4.3e-46:470:72//AF079765
F-NT2RP2003125//Homo sapiens chromosome 19, cosmid R34382, complete sequence.//5.7e-10:436:61//AC005329
F-NT2RP2003129//P.thunbergii cab gene.//0.00044:541:60//X61915
F-NT2RP2003137//CIT-HSP-2300J6.TR CIT-HSP Homo sapiens genomic clone 2300J6, genomic survey sequence.//5.0e-78:393:97//AQ012976
F-NT2RP2003157//Human DNA sequence from cDNA 16pHQG;16 from chromosome 16p13.3.//5.4e-07:137:71//Z84716
F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds.//1.8e-111:581:93//D67025
F-NT2RP2003161//CITBI-E1-2506E20.TR CITBI-E1 Homo sapiens genomic clone 2506E20, genomic survey sequence.//0.0025:156:67//AQ262657
F-NT2RP2003164
F-NT2RP2003165//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//1.4e-43 :334:79//U91328
F-NT2RP2003177//Human signaling inositol polyphosphate 5 phosphatase SIP-110 mRNA, complete cds.//0.91:346:62//U50040
F-NT2RP2003194//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 996D20, WORKING DRAFT SEQUENCE.//1.7e-108:511:90//AL031597
F-NT2RP2003206
F-NT2RP2003228//H.sapiens P1-Cdc21 mRNA.//2.9e-136:726:93//X74794
F-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.6e-51:348:

BNSDOCID: <EP___1074617A2_I_>

86//AF023657
F-NT2RP2003237//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE.//2.6e-56:415:83//AL031447
F-NT2RP2003243//RPCI11-36J1.TP RPCI-11 Homo sapiens genomic clone RPCI-11-36J1, genomic survey sequence.//2.1e-16:112:93//AQ047107
F-NT2RP2003265//Muridae sp. (mouse-rat, neuroblastoma-glioma hybrid cell line NGD5) mRNA, complete cds.//6.0e-114:696:87//L38481
F-NT2RP2003272//RPCI11-67B15.TJ RPCI11 Homo sapiens genomic clone R-67B15, genomic survey sequence.//3.8e-16:110:94//AQ201833
F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.5e-145:714:96//AB014525
F-NT2RP2003280//RPCI11-14I2.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-14I2, genomic survey sequence.//6.4e-77:400:95//B85286
F-NT2RP2003286//CIT-HSP-2336D3.TF CIT-HSP Homo sapiens genomic clone 2336D3, genomic survey sequence.//5.3e-29:287:73//AQ041024
F-NT2RP2003293//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.5e-54:508:74//AC003973
F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds.//6.1e-85:416:97//AB006572
F-NT2RP2003297//S.pombe pho2 gene for specific p-nitrophenylphosphatase.//0.60:309:64//X62722
F-NT2RP2003307//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//1.0e-45:442:75//AF055666
F-NT2RP2003308//D.melanogaster crn mRNA.//1.1e-63:697:70//X58374
F-NT2RP2003329//Homo sapiens chromosome 17, clone hCIT.131_K_11, complete sequence.//0.040:145:64//AC005288
F-NT2RP2003339
F-NT2RP2003347//Plasmodium falciparum MAL3P7, complete sequence.//0.12:275:60//AL034559
F-NT2RP2003367//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//0.83:225:63//AC005510
F-NT2RP2003391
F-NT2RP2003393//HS_3218_A2_B09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=18 Row=C, genomic survey sequence.//0.021:93:79//AQ204356
F-NT2RP2003394
F-NT2RP2003401
F-NT2RP2003433//Rattus rattus sec61 homologue mRNA, complete cds.//4.2e-61:533:75//M96630
F-NT2RP2003445//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE.//2.1e-49:301:72//AP000023
F-NT2RP2003446
F-NT2RP2003456//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.0018:366:60//AJ235272
F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.//7.5e-16:189:68//AC004770
F-NT2RP2003480//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.9e-25:197:85//M21977
F-NT2RP2003499 2.1e-08:408:61//AB000826
F-NT2RP2003506//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.9e-33:192:96//AC005236
F-NT2RP2003511//Ceratopteris richardii mRNA for CRHB11, partial cds.//1.0:328:60//AB013801
F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds.//7.3e-76:403:93//D87460
F-NT2RP2003517//Human osteosarcoma cell line U-2 OS mRNA fragment for PDGF-B chain (PDGF= platelet-derived growth factor).//1.5e-24:151:95//X03702
F-NT2RP2003522//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.3e-101:564:91//M21977
F-NT2RP2003533//Human DNA sequence from cosmid F1121 on chromosome 6.//2.0e-40:315:75//Z80899
F-NT2RP2003543
F-NT2RP2003559//H.sapiens CpG island DNA genomic Mse1 fragment, clone 90a5, reverse read cpg90a5.rt1a.//1.1e-20:122:99//Z56144
F-NT2RP2003564//Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.//8.8e-27:664:63//M34551
F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds.//4.1e-113:541:98//AB007931
F-NT2RP2003581
F-NT2RP2003596//F.rubripes GSS sequence, clone 036L10aF12, genomic survey sequence.//J1.9e-11:210:65//AL012756

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F-NT2RP2003604//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.//1.9e-123:587:98//AF030233
F-NT2RP2003629
F-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.//7.8e-88:582:84//AJ006215
F-NT2RP2003668//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//5.6e-47:335:83//AC005081
F-NT2RP2003687//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//1.2e-06:133:74//AC003684
F-NT2RP2003691//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 525L6, WORKING DRAFT SEQUENCE.//1.7e-47:337:81//AL023807
F-NT2RP2003702//Rattus norvegicus ovarian-specific protein mRNA, complete cds.//1.3e-65:458:82//U44803
F-NT2RP2003704//H.sapiens CpG island DNA genomic Mse1 fragment, clone 2a9, reverse read cpg2a9.rt1e.//3.8e-17:170:84//Z60615
F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds.//2.6e-108:518:98//AB011097
F-NT2RP2003713//HS_2016_B1_B05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=9 Row=D, genomic survey sequence.//1.3e-11:102:90//AQ226895
F-NT2RP2003714//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.4e-27:249:78//AC003973
F-NT2RP2003727//RPCI11-77I19.TV RPCI11 Homo sapiens genomic clone R-77I19, genomic survey sequence.//3.4e-26:294:74//AQ268303
F-NT2RP2003737//Homo sapiens clone DJ1022I14, WORKING DRAFT SEQUENCE, 14 unordered pieces.//2.6e-74:194:91//AC004951
F-NT2RP2003751//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-911E12, complete sequence.//1.7e-92:165:96//AC003964
F-NT2RP2003760//B.primigenius mRNA for coat protein gamma-cop.//4.5e-76:696:73//X92987
F-NT2RP2003764//Homo sapiens gene for MTG16, exon 1b, partial sequence.//1.0:109:69//AB013275
F-NT2RP2003769
F-NT2RP2003770//Homo sapiens chromosome 17, clone hRPC.1050_D_4, complete sequence.//3.0e-96:467:98//AC004771
F-NT2RP2003777
F-NT2RP2003781//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].//7.2e-107:731:82//S70011
F-NT2RP2003793//CIT-HSP-2326L12.TF CIT-HSP Homo sapiens genomic clone 2326L12, genomic survey sequence.//7.0e-20:124:95//AQ038761
F-NT2RP2003825//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//8.9e-06:151:74//AC004491
F-NT2RP2003840//Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence, complete sequence.//0.018:145:69//AC005167
F-NT2RP2003857//HS_3227_A2_G04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3227 Col=8 Row=M, genomic survey sequence.//0.96:257:61//AQ303467
F-NT2RP2003859
F-NT2RP2003871//Homo sapiens 12q24 PAC RPCI1-74B13 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.0e-12:369:65//AC002375
F-NT2RP2003885//CITBI-E1-2514D6.TF CITBI-E1 Homo sapiens genomic clone 2514D6, genomic survey sequence.//0.13:167:64//AQ265722
F-NT2RP2003912//nek1=serine/threonine- and tyrosine-specific protein kinase [mice, erythroleukemia cells, mRNA, 4263 nt].//1.3e-136:838:86//S45828
F-NT2RP2003952
F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds.//2.1e-28:165:96//AB014458
F-NT2RP2003976//Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae) bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs, complete sequence.//2.6e-24:298:74//AL031282

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F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds.//9.9e-160:783:96//AB018347
F-NT2RP2003984
F-NT2RP2003986//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.7e-26:260:77//AC000382
F-NT2RP2003988//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE.//9.1e-61:701:70//AL031681
F-NT2RP2004013//Human DNA sequence from clone 372K1 on chromosome 6q24 Contains EST, STS, GSS and CpG Island, complete sequence.//3.0e-123:693:91//AL023580
F-NT2RP2004014
F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127, complete sequence.//5.8e-83:427:87//AC004780
F-NT2RP2004042
F-NT2RP2004066//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 134O19, WORKING DRAFT SEQUENCE.//5.6e-110:528:98//AL034555
F-NT2RP2004081
F-NT2RP2004098//HS_2216_A1_B12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2216 Col=23 Row=C, genomic survey sequence.//1.0e-07:86:84//AQ145694
F-NT2RP2004124//HS_3064_B2_A04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.0e-25:155:94//AQ136993
F-NT2RP2004142//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence.//1.0:220:62//AB007645
F-NT2RP2004152//Drosophila melanogaster DNA sequence (P1 DS02252 (D97)), complete sequence.//0.93:480:56//AC002493
F-NT2RP2004165//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.051:265:61//AC005140
F-NT2RP2004170//Homo sapiens distal-less homeobox protein (DLX7) gene, complete cds.//1.0:162:66//AF028235
F-NT2RP2004172//S.pombe chromosome II cosmid c24E9.//1.7e-06:466:59//AL021816
F-NT2RP2004187//Homo sapiens full-length insert cDNA YQ86E07.//3.5e-17:354:64//AF075093
F-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds.//9.4e-53:397:82//AF003998
F-NT2RP2004196
F-NT2RP2004207//Human von Willebrand factor pseudogene corresponding to exons 23 through 34.//0.0023:386:61//M60676
F-NT2RP2004226//HS_2186_A1_D03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2186 Col=5 Row=G, genomic survey sequence.//7.8e-58:370:87//AQ063813
F-NT2RP2004232//H.sapiens mRNA for protein kinase C mu.//1.2e-34:448:67//X75756
F-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds.//5.2e-108:510:99//AB015718
F-NT2RP2004240//Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (6/7).//1.1e-12:489:61//AP000006
F-NT2RP2004242
F-NT2RP2004245
F-NT2RP2004270//Streptomyces coelicolor cosmid 1A9.//7.5e-07:462:62//AL034446
F-NT2RP2004300//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//3.5e-11:299:64//AC005781
F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds.//4.5e-150:735:97//AF000416
F-NT2RP2004321//Drosophila melanogaster DNA sequence (P1 DS02110 (D147)), complete sequence.//0.98:267:59//AC004423
F-NT2RP2004339//Human Chromosome 16 BAC clone CIT987SK-A-355G7, complete sequence.//1.6e-40:419:75//AC002519
F-NT2RP2004347//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE.//1.2e-72:439:82//AL031650
F-NT2RP2004364
F-NT2RP2004365
F-NT2RP2004366//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//0.92:427:57//AL031864
F-NT2RP2004373//Homo sapiens cosmids Qc15C1 and 94B6 from Xq28, complete sequence.//2.6e-26:493:65//AF035397

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F-NT2RP2004389//HS_2183_B2_H04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=8 Row=P, genomic survey sequence.//2.9e-11:83:96//AQ063969
F-NT2RP2004392
F-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21, complete sequence.//1.1e-171:875:95//AC005164
F-NT2RP2004399//Homo sapiens SYBL1 gene.//1.4e-24:467:64//AJ004799
F-NT2RP2004400//Arabidopsis thaliana BAC T19B17 from chromsome IV, near 19.3 cM, complete sequence.//0.00074:455:59//AF069441
F-NT2RP2004412//H.sapiens CpG island DNA genomic Mse1 fragment, clone 34g4, reverse read cpg34g4.rt1a.//5.0e-27:154:98//Z65369
F-NT2RP2004425
F-NT2RP2004463//Streptomyces coelicolor cosmid 2E9.//0.0053:196:65//AL021530
F-NT2RP2004476//Drosophila melanogaster cosmid 67A9.//5.2e-15:377:63//AL034388
F-NT2RP2004490//Homo sapiens chromosome 16, P1 clone 94-10H (LANL), complete sequence.//4.3e-100:497:97//AC005591
F-NT2RP2004512//Plasmodium falciparum MAL3P5, complete sequence.//2.3e-07:815:57//AL034556
F-NT2RP2004523//Homo sapiens clone DJ0800G07, complete sequence.//8.5e-138:718:95//AC004890
F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cds.//1.4e-137:687:96//AB011163
F-NT2RP2004551//CIT-HSP-2387G7.TF.1 CIT-HSP Homo sapiens genomic clone 2387G7, genomic survey sequence.//2.1e-85 :484:91//AQ239555
F-NT2RP2004568//H.vulgare GAA-satellite DNA.//2.0e-07:292:62//Z50100
F-NT2RP2004580//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//4.5e-44:512:72//AL023755
F-NT2RP2004587//Candida albicans cytoskeleton assembly control protein (SLA2) gene, partial cds.//1.0:344:56//AF092908
F-NT2RP2004594//nbxb0019H13r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0019H13r, genomic survey sequence.//0.053:324:60//AQ258020
F-NT2RP2004600
F-NT2RP2004602//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//0.12:109:73//AC005176
F-NT2RP2004614
F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//2.6e-102:496:98//AJ006291
F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds.//1.6e-153:728:98//AB007929
F-NT2RP2004675//Homo sapiens chromosome 12q24.1, WORKING DRAFT SEQUENCE, 33 unordered pieces.//0.092:239:61//AC005805
F-NT2RP2004681//Human DNA sequence from clone 51J23 on chromosome Xq26.3-27.3. Contains an EST and GSSs, complete sequence.//1.0:236:61//AL031312
F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.3e-59:327:94//AB014525
F-NT2RP2004709//HS_2033_B2_E04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=8 Row=J, genomic survey sequence.//1.9e-15:187:74//AQ230714
F-NT2RP2004710//HS_3185_82_D07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=14 Row=H, genomic survey sequence.//9.9e-10:110:84//AQ172885
F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds.//6.4e-117:582:96//AB007947
F-NT2RP2004743//Human DNA sequence from PAC 37M17 chromosome X.//0.14:138:71//Z78022
F-NT2RP2004767//H.sapiens CpG island DNA genomic Mse1 fragment, clone 65c11, reverse read cpg65c11.rt1a.//1.3e-24:217:81//Z62210
F-NT2RP2004768//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//1.6e-45:541:71//AF024636
F-NT2RP2004775//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//5.8e-13:697:59//AE001398
F-NT2RP2004791//Human HeLa mRNA isolated as a false positive in a two-hybridscreen.//5.0e-53:353:84//U56252
F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//1.5e-116:594:95//AF058953 F-NT2RP2004802
F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds.//2.1e-101:495:97//AF054179
F-NT2RP2004841//Human DNA sequence from cosmid J138O17, between markers DXS6791 and DXS8038 on chromosome X contains EST CA repeat and an endogenous retroviral like element.//7.6e-82:531:84//Z72519
F-NT2RP2004861//Fugu rubripes GSS sequence, clone 040O17bA3, genomic survey sequence.//0.96:183:64//AL025645

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F-NT2RP2004897//Human Chromosome X clone bWXD187, complete sequence.//4.8e-142:710:96//AC004383
F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds.//2.0e-82:418:95//AB007144
F-NT2RP2004936
F-NT2RP2004959//HS_3197_A2_G11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=22 Row=M, genomic survey sequence.//3.5e-25:218:83//AQ150183
F-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1 (KS1) mRNA, complete cds.//2.5e-59:339:79//U56732
F-NT2RP2004962//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//3.6e-19:187:72//U91328
F-NT2RP2004967//Plasmodium falciparum MAL3P6, complete sequence.//0.0020:297:61//Z98551
F-NT2RP2004978//Chlamydomonas reinhardtii VSP-3 mRNA, complete cds.//0.22:162:69//L29029
F-NT2RP2004982//F26D4-Sp6 IGF Arabidopsis thaliana genomic clone F26D4, genomic survey sequence.//0.13:273:61//B12642
F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds.//1.5e-20:431:65//D63478
F-NT2RP2004999
F-NT2RP2005000//R.rattus gene for beta-1 subunit of Na,K-ATPase.//0.019:240:63//X63375
F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//6.0e-159:782:97//AB014515
F-NT2RP2005003//H.sapiens Staf50 mRNA.//3.1e-42:430:75//X82200
F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//1.4e-98:501:96//AF100141
F-NT2RP2005018//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence.//1.0:209:63//AC004849
F-NT2RP2005020
F-NT2RP2005022//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//3.0e-43:98:93//AC000380
F-NT2RP2005031//HS_2052_B2_G10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=20 Row=N, genomic survey sequence.//0.019:363:61//AQ231464
F-NT2RP2005037//Human 3' of immunoglobulin heavy chain locus (IGHA2) gene.//0.70:174:65//U64454
F-NT2RP2005038//Homo sapiens chromosome 17, clone hRPK.74_E_22, complete sequence.//0.20:519:57//AC005696
F-NT2RP2005108
F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds.//2.0e-103:495:98//AB014564
F-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//2.9e-27:157:98//X98743
F-NT2RP2005139//Amycolatopsis mediterranei genes encoding rifamycin polyketide synthases, ORFs 1 to 5.//0.00024:547:59//AJ223012
F-NT2RP2005140//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete sequence.//0.95:191:62//AC004527
F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//2.6e-89:447:96//AF045583
F-NT2RP2005147//HS_3184_A1_E01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=1 Row=I, genomic survey sequence.//0.10:294:60//AQ252226
F-NT2RP2005159//H.sapiens CpG island DNA genomic Mse1 fragment, clone 132g6, forward read cpg132g6.ft1a.//1.1e-13:93:97//Z59162
F-NT2RP2005162//Caenorhabditis elegans cosmid F01F1.//2.6e-20:394:64//U13070
F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//1.4e-125 :633:96//AJ007509
F-NT2RP2005204//Arabidopsis thaliana ubiquitin activating enzyme (UBA1) gene, complete cds.//0.00016:316:60//U80808
F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.51:52:92//AC005189
F-NT2RP2005239//S.pombe chromosome II cosmid c21D10.//1.3e-22:356:67//AL031536
F-NT2RP2005254
F-NT2RP2005270//H.sapiens genomic DNA (chromosome 3; clone NL197R).//0.58:132:65//X87513
F-NT2RP2005276//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//9.0e-103:656:85//D30666
F-NT2RP2005287//Cavia porcellus zinc finger protein (zfoC1) mRNA, complete cds.//3.4e-37:302:84//L26335
F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//7.1e-122:604:96//AF060219
F-NT2RP2005289//Homo sapiens mRNA for XRP2 protein.//4.0e-140:670:98//AJ007590
F-NT2RP2005293//HS_3245_B1_E10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

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nomic clone Plate=3245 Col=19 Row=J, genomic survey sequence.//8.2e-37:223:92//AQ217454
F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//1.1e-95:483:96//AB014576
F-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds.//8.2e-22:166:90//U11701
F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//0.39:353:62//AF032387
F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds.//8.8e-29:456:66//AB011138
F-NT2RP2005354//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//0.72:431:61//Z92844
F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//4.7e-99:489:96//AF072247
F-NT2RP2005360//Pan troglodytes huntingtin gene, partial exon.//0.93:105:67//L49358
F-NT2RP2005393//Rat parathyroid hormone receptor mRNA, complete cds.//2.4e-08:97:83//M77184
F-NT2RP2005407
F-NT2RP2005436//Homo sapiens chromosome 16, cosmid clone 2H2 (LANL), complete sequence.//0.014:235:62//AC005346
F-NT2RP2005441//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//4.0e-107:532:97//AQ055548
F-NT2RP2005453//F21C16TFC IGF Arabidopsis thaliana genomic clone F21C16, genomic survey sequence.//1.0:239:61//B97865
F-NT2RP2005457//B.taurus CI-B14.5b mRNA for NADH dehydrogenase (ubiquinone).//4.7e-25:245:79//X68647
F-NT2RP2005464//Human DNA sequence from clone 836E8 on chromosome 20p12 Contains EST, CA repeat, STS, GSS, retroviral sequence, complete sequence.//4.6e-111:724:86//AL031679
F-NT2RP2005465//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//6.5e-18:152:75//AC006116
F-NT2RP2005472//Human DNA sequence from clone 1118D24 on chromosome 1p36.11-36.33. Contains part of a novel gene similar to worm genes T08G11.1 and C25H3.9, part of a 60S Ribosomal Protein L10 LIKE (pseudo) gene and two 3' exons of the TNFR2 gene for Tumor Necrosis Factor Receptor 2 (75 kD) (TNF Binding Protein 2, TBPII, TNF-R2, CD120B, TNFBR). Contains ESTs, STSs, GSSs, genomic marker D1S434 and a ca repeat polymorphism, complete sequence.//4.4e-12:89:97//AL031276
F-NT2RP2005476//Homo sapiens BAC clone RG293F17 from 7p15-p21, complete sequence.//4.3e-40:463:73//AC004130
F-NT2RP2005490//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//3.2e-115:228:99//AC006030
F-NT2RP2005491//HS_2253_A2_G10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=20 Row=M, genomic survey sequence.//4.6e-23:234:80//AQ116847
F-NT2RP2005495
F-NT2RP2005496//HS_3064_A1_F08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=15 Row=K, genomic survey sequence.//5.3e-90:436:98//AQ143097
F-NT2RP2005498//Rabbit protein phosphatase 2A beta subunit mRNA, complete cds.//1.4e-63:503:78//M64931
F-NT2RP2005501//Homo sapiens chromosome 10 clone CIT987SK-1143A11 map 10q25, complete sequence.//0.86:183:63//AC005880
F-NT2RP2005509//Homo sapiens cosmid LM1937 from Xq28.//1.0:160:65//U82695
F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//3.9e-81:444:92//AF092563
F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds.//6.9e-18:112:99//AB018307
F-NT2RP2005531//Human structural protein 4.1 mRNA, complete cds.//1.1e-06:282:60//M14993
F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.9e-153:747:97//AJ012449
F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//5.9e-130:618:98//AB007963
F-NT2RP2005549//Mus musculus clone OST142, genomic survey sequence.//3.1e-43:277:89//AF046734
F-NT2RP2005555//HS_2188_A2_D04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=8 Row=G, genomic survey sequence.//8.0e-05:195:65//AQ086723
F-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds.//2.5e-44:473:71//AF062529
F-NT2RP2005581//Homo sapiens BAC clone GS180J15 from 7q31, complete sequence./0.99:213:65//AC005016
F-NT2RP2005600//H.sapiens CpG island DNA genomic Mse1 fragment, clone 172d12, reverse read cpg172d12.rt1a.//0.32:134:63//Z57359
F-NT2RP2005605

BNSDOCID: <EP___1074617A2_I_>

F-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//9.8e-91:447:97//AF062085
F-NT2RP2005622
F-NT2RP2005635//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//8.6e-17:411:61//U10556
F-NT2RP2005637//NATI (NATI*10)=acetyltransferase 1 {3' region, polyadenylation polymorphism} [human, unrelated Caucasians, mRNA Partial Mutant, 300 nt].//0.22:156:65//S78829
F-NT2RP2005640//Mouse U6 RNA gene.//5.5e-19:249:76//X06980
F-NT2RP2005645//HS_2201_B2_D07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2201 Col=14 Row=H, genomic survey sequence.//0.30:159:65//AQ066763
F-NT2RP2005651//H.sapiens DNA sequence.//0.00037:150:66//Z22493
F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds.//4.7e-07:351:62//AB006626
F-NT2RP2005669//Homo sapiens KE05 protein mRNA, complete cds.//8.2e-98:472:98//AF064605
F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//2.4e-94:462:98//AF089814
F-NT2RP2005683//HS-1024-B1-H05-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 803 Col=9 Row=P, genomic survey sequence.//0.99:156:64//B34405
F-NT2RP2005690//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//7.7e-10:328:61//M77836
F-NT2RP2005694
F-NT2RP2005701//Homo sapiens 12p13.3 BAC RPCI11-288K12 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.72:160:65//AC005183
F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//1.6e-124:599:97//AB018342
F-NT2RP2005719//R.norvegicus mRNA for metallothionein-III.//0.86:117:64//X89603
F-NT2RP2005722//Human zinc finger protein ZNF136.//2.6e-44:415:77//U09367
F-NT2RP2005723//Human BAC clone GS542D18 from 7q31-q32, complete sequence.//6.9e-15:153:81//AC002528
F-NT2RP2005726//Homo sapiens clone DJ0577P23, WORKING DRAFT SEQUENCE, 28 unordered pieces.//5.1e-41:138:95//AC005627
F-NT2RP2005732//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 291J10, WORKING DRAFT SEQUENCE.//0.61:303:60//Z93017
F-NT2RP2005741//Homo sapiens PALM gene, exon 1 and joined CDS.//0.52:116:67//Y16270
F-NT2RP2005748//Human Kox11 mRNA for zinc finger protein, partial.//0.11:136:66//X52342
F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//7.8e-22:134:96//AF068868
F-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//1.2e-100:486:98//AF082516
F-NT2RP2005763//Human mRNA for KIAA0111 gene, complete cds.//0.00073:425:56//D21853
F-NT2RP2005767//G.gallus PB1 gene.//2.1e-73:544:80//X90849
F-NT2RP2005773//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//6.2e-15:153:82//M77836
F-NT2RP2005775//Sus scrofa mRNA for soluble angiotesin-binding protein, complete cds.//1.2e-121:649:88//D11336
F-NT2RP2005781//Pseudomonas aeruginosa gene for MexX and MexY, complete cds//0.96:184:60//AB015853
F-NT2RP2005784//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE.//1.9e-63:222:96//AL034423
F-NT2RP2005804//Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds.//2.6e-07:232:64//AF010579
F-NT2RP2005812
F-NT2RP2005815//Streptomyces sp. gene for alkaline serine protease I.//0.031:358:59//X74103
F-NT2RP2005835//Rattus norvegicus mRNA for p47, complete cds.//2.5e-107:449:91//AB002086
F-NT2RP2005841//Human DNA sequence from cosmid U209G1 on chromosome X.//5.1e-05:144:73//Z68873
F-NT2RP2005853//RPCI11-24D4.TKBF RPCI-11 Homo sapiens genomic clone RPCI-11-24D4, genomic survey sequence.//6.4e-13:130:85//AQ013490
F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds.//1.7e-174:829:98//AF092564
F-NT2RP2005859//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 914P20, WORKING DRAFT SEQUENCE.//0.25:174:62//AL034553
F-NT2RP2005868//Fugu rubripes GSS sequence, clone 103I24aF4, genomic survey sequence.//7.8e-06:92:79//AL027276
F-NT2RP2005886//HS_3187_A2_D08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3187 Col=16 Row=G, genomic survey sequence.//7.1e-95:494:95//AQ155885

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F-NT2RP2005890//Mouse oncogene (ect2) mRNA, complete cds.//2.7e-32:660:66//L11316
F-NT2RP2005901//H.sapiens CpG island DNA genomic Mse1 fragment, clone 15b5, reverse read cpg15b5.rt1a.//0.0026:66:84//Z54729
F-NT2RP2005908//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.4e-49:481:75//AC004241
F-NT2RP2005933//Rattus norvegicus nucleoporin p54 mRNA, complete cds.//6.6e-61:657:73//U63840
F-NT2RP2005942//H.sapiens PAP mRNA.//1.6e-46:618:67//X76770
F-NT2RP2005980//Homo sapiens chromosome 17, clone hRPC.1081_P_3, complete sequence.//1.0e-48:533:71//AC005207
F-NT2RP2006023//HS_3048_A1_A11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3048 Col=21 Row=A, genomic survey sequence.//2.1e-25:167:91//AQ126553
F-NT2RP2006038//CIT-HSP-384K4.TR CIT-HSP Homo sapiens genomic clone 384K4, genomic survey sequence.//3.9e-06:102:74//B51912
F-NT2RP2006043//Human intercrine-alpha (hIRH) mRNA, complete cds.//1.9e-05:418:59//U19495
F-NT2RP2006052//Peromyscus polionotus ammobates dinucleotide microsatellite Ppa55.//0.0035:226:65//AF016861
F-NT2RP2006069//Human HepG2 partial cDNA, clone hmd3g02m5.//3.9e-11:121:85//D17047
F-NT2RP2006071
F-NT2RP2006098//Homo sapiens chromosome 21q22.2, cosmid D13C2, complete sequence.//0.46:264:59//AF027207
F-NT2RP2006100//Human Chromosome X, complete sequence.//3.2e-94:488:95//AC004073
F-NT2RP2006103//HS_2254_A2_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2254 Col=4 Row=G, genomic survey sequence.//5.7e-27:156:96//AQ129602
F-NT2RP2006106//Human Chromosome 11 pac pDJ1173a5, complete sequence.//11.2e-62:655:71//AC000378
F-NT2RP2006141//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SEQUENCE.//1.2e-69:316:98//AL034405
F-NT2RP2006166//Homo sapiens chromosome 4 clone B32I8, complete sequence.//3.1e-45:387:81//AC004063
F-NT2RP2006184//Cricetulus griseus beta-1,6-N-acetylglucosaminyltransferase Lec4A cell line point mutant mRNA, complete cds.//0.99:111:73//U62587
F-NT2RP2006186//Homo Sapiens mRNA for KIAA0654 protein, partial cds.//7.8e-113:567:96//AB014554
F-NT2RP2006196//Homo sapiens clone DJ1189D06, complete sequence.//2.8e-28:718:62//AC005232
F-NT2RP2006200//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//6.5e-83:239:94//AC006057
F-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.4e-116:618:93//X96484
F-NT2RP2006237//CIT-HSP-2300P9.TR CIT-HSP Homo sapiens genomic clone 2300P9, genomic survey sequence.//2.0e-18:118:97//AQ012480
F-NT2RP2006238//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//7.6e-102:635:86//U49055
F-NT2RP2006258//RPCI11-9N9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-9N9, genomic survey sequence.//8.6e-05:181:63//B71615
F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK.//0.44:111:71//X97630
F-NT2RP2006275//Pseudorabies virus UL[5,6,7,8,8.5,9,10,11,12,13] genes.//2.0e-05:501:59//X97257
F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.7e-138:679:97//AF035262
F-NT2RP2006320//P.falciparum pfmdr1 gene.//0.00013:425:60//X56851
F-NT2RP2006321//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.1e-19:545:62//AC003973
F-NT2RP2006323//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 745I14, WORKING DRAFT SEQUENCE.//8.9e-18:131:90//AL033532
F-NT2RP2006333//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//6.2e-125:602:98//AC004893
F-NT2RP2006334//Homo sapiens chromosome 19, cosmid R27139, complete sequence.//2.1e-06:241:65//AC005514
F-NT2RP2006365//Fugu rubripes GSS sequence, clone 171K15aC5, genomic survey sequence.//7.8e-06:148:70//AL029590
F-NT2RP2006393//Human DNA sequence from clone 80I19 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence.//6.8e-06:167:70//AL022727
F-NT2RP2006436//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//4.2e-92:363:84//AL023808

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F-NT2RP2006441
F-NT2RP2006454//Sequence 8 from Patent WO9517522.//2.9e-06:180:66//A45338
F-NT2RP2006456
F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//3.4e-148:545:98//AJ006266
F-NT2RP2006467//Sus scrofa IgM heavy chain gene, switch region and exons encoding ch1-ch4 and secretion domains, partial cds.//0.061:201:66//U50149
F-NT2RP2006472
F-NT2RP2006534//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence.//8.8e-10:273:66//Z93929
F-NT2RP2006554//Human DNA mismatch repair protein homolog (hMLH1) gene, exon 6.//0.71:174:59//U40965
F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds.//6.6e-114:669:90//AF038966
F-NT2RP2006571//Rabbit cytochrome P-450 isozyme 2 (type B2) mRNA, complete cds, clone B2-1.//6.0e-26:503:63//M20855
F-NT2RP2006573//Molluscum contagiosum virus subtype 1, complete genome.//0.44:134:71//U60315
F-NT2RP2006598//Human BRCA2 region, mRNA sequence CG033.//5.0e-16:140:85//U50537
F-NT2RP3000002//***ALU WARNING: Human Alu-Sc subfamily consensus sequence.//3.8e-32:214:89//U14571
F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//5.8e-136:637:98//AJ011972
F-NT2RP3000046//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//5.4e-05:571:60//L14320
F-NT2RP3000047
F-NT2RP3000050//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and-9.//1.0e-67:626:74//M27877
F-NT2RP3000055//Genomic sequence from Human 9q34, complete sequence.//3.5e-10:394:64//AC001227
F-NT2RP3000068
F-NT2RP3000072//Homo sapiens BAC clone RG290G13 from 7q21, complete sequence.//1.0:301:61//AC004746
F-NT2RP3000080//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 102D24, WORKING DRAFT SEQUENCE.//1.9e-44:297:79//AL021391
F-NT2RP3000085//Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase precursor mRNA, complete cds.//4.5e-33:528:65//U12536
F-NT2RP3000092//RPCI11-22M5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-22M5, genomic survey sequence.//3.3e-27:157:97//B84237
F-NT2RP3000109//Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds.//0.92:185:64//L29260
F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.2e-112:286:89//AC005189
F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//9.0e-181:849:98//AB011164
F-NT2RP3000149//Homo sapiens chromosome 17, clone hRPK.264_B_14, complete sequence.//4.2e-24:155:94//AC005884
F-NT2RP3000186//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 500L14, WORKING DRAFT SEQUENCE.//7.2e-43:269:81//AL023583
F-NT2RP3000197//Homo sapiens interleukin 9 receptor (IL9R) pseudogene, exons 1-9.//0.098:405:57//L39063
F-NT2RP3000207//Drosophila melanogaster DNA sequence (P1 DS00164 (D269)), complete sequence.//0.96:608:55//AC004716
F-NT2RP3000220
F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.0e-18:509:58//AF059569
F-NT2RP3000235//Mouse Cosmid ma53a016 from 14D1-D2, complete sequence.//3.5e-05:224:65//AC004101
F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds.//2.1e-109:691:86//D86972
F-NT2RP3000251//Caenorhabditis elegans cosmid ZK930, complete sequence.//0.20:119:68//Z70213
F-NT2RP3000252//Homo sapiens cosmid 1F1, complete sequence.//9.8e-78:174:88//AF065393
F-NT2RP3000255
F-NT2RP3000267
F-NT2RP3000299//Mus musculus Crk-associated substrate (Cas-b) mRNA, complete cds.//5.9e-48:374:82//U48853
F-NT2RP3000312//Fruit fly (D.melanogaster) Glued mRNA, complete cds.//4.9e-22:583:63//J02932

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F-NT2RP3000320//RPCI11-36J1.TP RPCI-11 Homo sapiens genomic clone RPCI-11-36J1, genomic survey sequence.//4.4e-06:87:88//AQ047107
F-NT2RP3000324//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//5.5e-26:283:79//U78090
F-NT2RP3000333//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 973M2, WORKING DRAFT SEQUENCE.//1.0:309:60//AL033533
F-NT2RP3000341//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//6.7e-42:465:74//Z97181
F-NT2RP3000348
F-NT2RP3000350//Homo sapiens cosmid 1F1, complete sequence.//3.4e-79:174:88//AF065393
F-NT2RP3000359//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//2.2e-127:816:85//M25757
F-NT2RP3000361//Schizosaccharomyces pombe DNA for pre-mRNA splicing factor, complete cds.//0.0075:288:58//D83743
F-NT2RP3000366//Mus musculus ras-related protein (rab18) mRNA, complete cds.//7.1e-134:693:94//L04966
F-NT2RP3000393//Rattus norvegicus mRNA for GABA-B R2 receptor.//0.049:308:60//AJ011318
F-NT2RP3000397//S.cerevisiae chromosome VII reading frame ORF YGL120c.//0.00012:441:58//Z72642
F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//5.0e-174:841:97//AF071185
F-NT2RP3000418//Homo sapiens chromosome 17, clone hRPK.1053_B_8, complete sequence.//7.9e-53:817:68//AC006083
F-NT2RP3000433//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE.//6.1e-31:590:63//AL031681
F-NT2RP3000439//Fugu rubripes GSS sequence, clone 075E22aB10, genomic survey sequence.//4.0e-19:169:81//AL026471
F-NT2RP3000441//Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG island.//2.4e-41:459:65//Z84488
F-NT2RP3000449//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE.//1.1e-100:365:87//AL031650
F-NT2RP3000451//HS_2024_A1_E10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2024 Col=19 Row=I, genomic survey sequence.//0.011:367:57//AQ229420
F-NT2RP3000456//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//1.5e-89:458:96//AQ055548
F-NT2RP3000484//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 90L6, WORKING DRAFT SEQUENCE.//0.043:147:70//Z97353
F-NT2RP3000487//H.sapiens CpG island DNA genomic Mse1 fragment, clone 11b11, forward read cpg11b11.ft1a.//1.7e-11:96:92//Z64440
F-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//9.7e-17:109:97//X16667
F-NT2RP3000526//Homo sapiens full-length insert cDNA clone YZ38E04.//4.1e-30:283:76//AF086071
F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds.//2.5e-34:706:63//D86966
F-NT2RP3000531//Mus musculus immunosuperfamily protein B12 mRNA, complete cds.//1.9e-14:220:70//AF061260
F-NT2RP3000542//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//0.00019:361:60//AC002554
F-NT2RP3000561//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//9.0e-171:827:98//AC006012
F-NT2RP3000562
F-NT2RP3000578//F.rubripes GSS sequence, clone 013G07cE7, genomic survey sequence.//1.7e-25:284:74//AL011271
F-NT2RP3000582//CIT978SK-A-56H4.TP CIT978SK Homo sapiens genomic clone A-56H4, genomic survey sequence.//5.8e-07:239:66//B73597
F-NT2RP3000584
F-NT2RP3000590//H.sapiens CpG island DNA genomic Mse1 fragment, clone 170d7, forward read cpg170d7.ft1a.//3.0e-22:128:100//Z59723
F-NT2RP3000592//CIT-HSP-2288J7.TR CIT-HSP Homo sapiens genomic clone 2288J7, genomic survey sequence.//2.2e-78:382:98//B98868
F-NT2RP3000596//CIT-HSP-2375J10.TR CIT-HSP Homo sapiens genomic clone 2375J10, genomic survey sequence.//0.00076:143:67//AQ109305
F-NT2RP3000599//Caenorhabditis elegans cosmid T19B10, complete sequence.//1.2e-13:295:66//Z74043

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F-NT2RP3000603//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.37:520:57//L14320
F-NT2RP3000605//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//8.8e-155:526:97//AC006128
F-NT2RP3000622//HS_3213_A2_D02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=4 Row=G, genomic survey sequence.//4.1e-29:238:85//AQ175104
F-NT2RP3000624//Homo sapiens clone DJ0800G07, complete sequence.//0.47:75:80//AC004890
F-NT2RP3000628//Human DNA sequence from clone 581F12 on chromosome Xq21. Contains Eukaryotic Translation Initiation Factor EIF3 P35 Subunit and 60S Ribosomal protein L22 pseudogenes. Contains ESTs, complete sequence.//0.078:393:58//AL031313
F-NT2RP3000632//Human zinc finger protein zfp6 (ZF6) mRNA, partial cds.//1.4e-96:541:79//U71363
F-NT2RP3000644//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//5.2e-46:421:77//AC005089
F-NT2RP3000661
F-NT2RP3000665//Human DNA sequence from clone 1191B2 on chromosome 22q13.2-13.3. Contains part of the BIK (NBK, BP4, BIP1) gene for BCL2-interacting killer (apoptosis-inducing), a 40S Ribososmal Protein S25 pseudogene and part of an alternatively spliced novel Acyl Transferase gene similar to C. elegans C50D2.7. Contains ESTs, STSs, GSSs, two putative CpG islands and genomic marker D22S1151, complete sequence.//1.7e-11:292:65//AL022237
F-NT2RP3000685//H.sapiens mRNA for novel protein.//2.4e-80:460:92//X99961
F-NT2RP3000690//H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA10F6.//1.0:141:65//Z77872
F-NT2RP3000736//Human mRNA for KIAA0140 gene, complete cds.//6.1e-20:127:96//D50930
F-NT2RP3000739//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//1.1e-46:622:67//AF015264
F-NT2RP3000742//Rattus norvegicus phospholipase C delta-4 mRNA, complete cds.//4.7e-37:429:70//U16655
F-NT2RP3000753
F-NT2RP3000759//Caenorhabditis elegans cosmid Y57G11C, complete sequence.//2.8e-38:519:69//Z99281
F-NT2RP3000815//HS_2237_A2_D12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=24 Row=G, genomic survey sequence.//0.79:151:61//AQ067252
F-NT2RP3000825//Campanula ramosa chloroplast NADH dehydrogenase (ndhF) gene, complete cds.//0.36:378:58//L39387
F-NT2RP3000826//Suid herpesvirus 1 Kaplan glycoprotein L (UL1) and uracil-DNA glycosylase (UL2) genes, complete cds, and (UL3) gene, partial cds.//0.0025:291:62//U02513 F-NT2RP3000836//Mouse complement factor H-related protein mRNA, complete cds, clone 9C4.//0.69:563:57//M29009
F-NT2RP3000841//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//2.1e-46:666:68//Z86062
F-NT2RP3000845//Homo sapiens chromosome 19, cosmid R31237, complete sequence.//3.4e-92:193:93//AC005581
F-NT2RP3000847//Human HepG2 3' region cDNA, clone hmd5d02.//3.4e-32:261:81//D16938
F-NT2RP3000850//Homo sapiens clone RG271G13, WORKING DRAFT SEQUENCE, 7 unordered pieces.//5.1e-44:358:81//AC005082
F-NT2RP3000852//Homo sapiens DNA sequence from PAC 117P20 on chromosome 1q24. Contains the LNHR (SELL) gene coding for Lymph Node Homing Receptor (L-Selectin precursor, LAM-1 Leukocyte Adhesion Molecule, Leukocyte surface antigen Leu-8, TQ1, GP90-MEL, LECAM1 Leukocyte-Endothelial Cell Adhesion Molecule 1, CD62L). Contains the SELE gene coding for E-Selectin precursor (CD62E, ELAM-1 Endothelial Leukocyte Adhesion Molecule 1, LECAM-2 Leukocyte-Endothelial Cell Adhesion Molecule 2). Contains an unknown gene with homology to predicted yeast, plant and worm proteins. Contains ESTs and STSs, complete sequence.//4.4e-123:150:98//AL021940
F-NT2RP3000859//T19M2TF TAMU Arabidopsis thaliana genomic clone T19M2, genomic survey sequence.//0.016:185:65//B60831
F-NT2RP3000865
F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//2.0e-29:766:60//U53445
F-NT2RP3000869//H.sapiens gene for plectin.//1.1e-12:700:60//Z54367
F-NT2RP3000875//HS_2236_B1_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2236 Col=19 Row=N, genomic survey sequence.//0.98:153:68//AQ154007
F-NT2RP3000901//Human herpesvirus 2 glycoprotein B precursor (UL27) gene, complete cds.//0.44:213:65//

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AF021340
F-NT2RP3000904//Rat Na+ channel mRNA, 3' end.//3.6e-106:505:99//M27223
F-NT2RP3000917//Mouse mRNA for Dhm1 protein, complete cds.//3.1e-132:691:93//D38517
F-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//3.2e-97:585:88//AF015264
F-NT2RP3000968//Human Chromosome 16 BAC clone CIT987SK-A-234F9, complete sequence.//5.8e-70:181:89//U91326
F-NT2RP3000980//R.norvegicus CYP3A1 gene, 5' flanking region.//6.1e-26:507:66//X98335
F-NT2RP3000994//HS-1049-B2-F03-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 771 Col=6 Row=L, genomic survey sequence.//1.5e-22:128:100//B39529
F-NT2RP3001004//H.sapiens CpG island DNA genomic Mse1 fragment, clone 39c1, reverse read cpg39c1.rt1a.//15.9e-27:150:99//Z60925
F-NT2RP3001007//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.11:610:57//AC006039
F-NT2RP3001055//Drosophila melanogaster; Chromosome 2R; Region 47F1-47F7; P1 clone DS02304, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23:352:67//AC005653
F-NT2RP3001057//H.sapiens HZF4 mRNA for zinc finger protein.//1.4e-49:437:77//X78927
F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//8.4e-50:534:74//AF060219
F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds.//1.2e-14:474:60//AB018325
F-NT2RP3001096//CIT-HSP-2305P8.TF CIT-HSP Homo sapiens genomic clone 2305P8, genomic survey sequence.//3.4e-37:222:93//AQ021278
F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds.//8.5e-33:712:64//D86969
F-NT2RP3001109//Human Chromosome 15q26.1 PAC clone pDJ457j11 containing DNA polymerase gamma (polg) gene, complete sequence.//2.7e-116:186:99//AC005317
F-NT2RP3001111
F-NT2RP3001113//Human DNA sequence from cosmid U157D4, between markers DXS366 and DXS87 on chromosome X.//2.4e-05:702:58//Z68871
F-NT2RP3001115//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.9e-170:821:98//AC005189
F-NT2RP3001116//HS_3075_A1_F01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=1 Row=K, genomic survey sequence.//7.3e-49:290:92//AQ120581
F-NT2RP3001119//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.4e-121:598:97//AL031864
F-NT2RP3001120//Human zinc finger protein ZNF136.//7.4e-76:687:75//U09367
F-NT2RP3001126//Bovine herpesvirus type 1 DNA for UL36, UL37, UL38, UL39, UL40 and UL41.//6.8e-05:344:64//Z49078
F-NT2RP3001133//Nephila clavipes minor ampullate silk protein MiSp1 mRNA, partial cds.//0.00021:529:60//AF027735
F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//3.6e-179:851:98//AB018305
F-NT2RP3001147//RPCI11-3M16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-3M16, genomic survey sequence.//2.1e-15:106:96//B48859
F-NT2RP3001150//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//2.0e-159:418:95//AL034379
F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//5.1e-190:891:98//AJ006266
F-NT2RP3001176//Human DNA sequence from clone 879K22 on chromosome 1q32.1-41 Contains GSS, complete sequence.//1.1e-69:207:97//AL034351
F-NT2RP3001214//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.16:475:58//AC005507
F-NT2RP3001216//Homo sapiens clone DJ0635O05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.3e-05:561:56//AC004845
F-NT2RP3001221
F-NT2RP3001232//Mouse mRNA for serine protease PC6, comlete cds.//1.0e-11:120:87//D12619
F-NT2RP3001236
F-NT2RP3001239//Mouse MAP1B mRNA for MAP1B microtubule-associated protein.//3.9e-19:501:61//X51396
F-NT2RP3001245//CITBI-E1-2505C1.TF.1 CITBI-E1 Homo sapiens genomic clone 2505C1, genomic survey sequence.//8.5e-70:337:100//AQ242007

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F-NT2RP3001253//CITBI-E1-2505N14.TR CITBI-E1 Homo sapiens genomic clone 2505N14, genomic survey sequence.//0.83:235:60//AQ260430
F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete cds.//3.8e-47:761:64//AB018269
F-NT2RP3001268//Homo sapiens zinc finger protein (HZF6) mRNA, 5' UTR and partial cds.//2.3e-64:618:72//AF027513
F-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein.//2.6e-99:669:83//Y18101
F-NT2RP3001274//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//0.99:400:58//U07561
F-NT2RP3001281//Homo sapiens chromosome 17, clone hRPK.318_A_15, complete sequence.//5.9e-39:304:70//AC005837
F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds.//7.6e-47:544:69//D87457
F-NT2RP3001307//Ambystoma tigrinum RPE65 protein mRNA, complete cds.//2.4e-27:547:63//AF047465
F-NT2RP3001318//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00022:624:60//AC004709
F-NT2RP3001325//Caenorhabditis elegans cosmid F36H12.//0.25:523:59//AF078790
F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds.//5.1e-29:345:73//D86966
F-NT2RP3001339//Rattus norvegicus mytonic dystrophy kinase-related Cdc42-binding kinase (MRCK) mRNA, complete cds.//1.2e-151:821:91//AF021935
F-NT2RP3001340//Homo sapiens HMG box factor SOX-13 mRNA, complete cds.//5.3e-27:247:81//AF083105
F-NT2RP3001355//Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 In CES Region, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-16:130:76//AC000052
F-NT2RP3001356
F-NT2RP3001374
F-NT2RP3001383//Homo sapiens DNA sequence from PAC 140C12 on chromosome 6q26-q27.//0.00082:365:61//AL008628
F-NT2RP3001384//Homo sapiens HRIHFB2018 mRNA, partial cds.//6.4e-157:743:98//AB015332
F-NT2RP3001392//Human DNA sequence from PAC 302D9 on chromosome 22q11.2-qter. Contains STS, complete sequence.//0.045:359:61//Z82198
F-NT2RP3001396//Drosophila melanogaster DNA sequence (P1 DS08860 (D181)), complete sequence.//1.3e-16:336:65//AC004296
F-NT2RP3001398//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//3.1e-100:711:82//U49046
F-NT2RP3001399//Homo sapiens PAC clone DJ1106E03 from 7q31.3-7q3, complete sequence.//5.4e-20:245:73//AC005521
F-NT2RP3001407//RPCI11-41A20.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41A20, genomic survey sequence.//0.051:306:59//AQ029031
F-NT2RP3001420//Human DNA sequence from PAC 12409 on chromosome 6q21. Contains DNAJ2 (HDJ1) like pseudogene, ESTs, STSs and GSSs.//0.90:170:65//AL021327
F-NT2RP3001426//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE.//2.9e-89:138:98//AL031447
F-NT2RP3001427//CIT-HSP-2302H24.TF CIT-HSP Homo sapiens genomic clone 2302H24, genomic survey sequence.//8.1e-36:212:94//AQ020997
F-NT2RP3001428//Human nuclear pore complex-associated protein TPR (tpr) mRNA, complete cds.//8.5e-73:431:91//U69668
F-NT2RP3001432//HS_3032_B1_A03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=5 Row=B, genomic survey sequence.//0.00024:111:76//AQ096619
F-NT2RP3001447
F-NT2RP3001449//Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae) bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs, complete sequence.//2.1e-105:223:99//AL031282
F-NT2RP3001453//Ralstonia sp. E2 positive phenol-degradative gene regulator (poxR), phenol hydroxylase components (poxA, poxB, poxC, poxD, poxE, poxF), and ferredoxin-like protein (poxG) genes, complete cds.//0.75:349:59//AF026065

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F-NT2RP3001457
F-NT2RP3001459
F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, complete cds.//1.3e-08:168:70//AF072836
F-NT2RP3001490
F-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//1.0e-26:191:90//U13395
F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//8.5e-171:804:98//AF064801
F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-A) mRNA, complete, cds.//8.9e-140:743:91//U36499
F-NT2RP3001529//Streptomyces griseus DNA for ribosoma protein L21, ribosomal protein L27, Obg, complete cds.//2.1e-14:517:59//D87916
F-NT2RP3001538//Capra hircus hircus clone 12 RAPD PCR sequence, genomic survey sequence.//4.7e-05:217:63//AF078176
F-NT2RP3001554//Rattus norvegicus microtubule-associated protein 1A MAP1A (Mtap-1) mRNA, complete cds.//4.3e-17:332:67//M83196
F-NT2RP3001580//RPCI11-91E19.TV RPCI11 Homo sapiens genomic clone R-91E19, genomic survey sequence.//4.2e-15:110:91//AQ281332
F-NT2RP3001587//S.pombe chromosome II cosmid c16H5.//6.6e-28:491:64//AL022104
F-NT2RP3001589//RPCI11-68M15.TK RPCI11 Homo sapiens genomic clone R-68M15, genomic survey sequence.//8.7e-108:517:98//AQ237629
F-NT2RP3001607//Homo sapiens Xp22 BAC GSHB-600G8 (Genome Systems Human BAC library) complete sequence.//1.0e-09:257:65//AC004674
F-NT2RP3001608//Methylococcus capsulatus methane monooxygenase component A alpha chain, methane monooxygenase A beta chain and methane monooxygenase component C genes, complete cds.//0.59:450:57//M90050
F-NT2RP3001621//Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.//1.8e-42:278:79//AL021808
F-NT2RP3001629
F-NT2RP3001634//Homo sapiens mRNA for Ariadne-2 protein.//1.5e-63:276:97//AJ130978
F-NT2RP3001642//Caenorhabditis elegans cosmid F45E6, complete sequence.//0.018:127:66//Z68117
F-NT2RP3001646
F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//3.4e-171:816:98//AJ012449
F-NT2RP3001672//Drosophila melanogaster transcriptional repressor protein (Scm) mRNA, complete cds.//1.6e-38:542:66//U49793
F-NT2RP3001676//HS_3090_B1_B04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3090 Col=7 Row=D, genomic survey sequence.//3.1e-07:333:64//AQ123250
F-NT2RP3001678//Drosophila melanogaster; Chromosome 3L; Region 63C5-63D3; P1 clone DS01859, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.0:539:57//AC004358
F-NT2RP3001679//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11.//2.8e-130:355:96//AB020860
F-NT2RP3001688//Rattus norvegicus glucocorticoid modulatory element binding protein 2 mRNA, complete cds.//2.1e-37:512:70//AF059273
F-NT2RP3001690//CIT-HSP-2300P9.TR CIT-HSP Homo sapiens genomic clone 2300P9, genomic survey sequence.//2.8e-19:123:95//AQ012480
F-NT2RP3001698//Rat mRNA for RhoGAP, complete cds.//9-4e-11:167:74//D31962
F-NT2RP3001708//H.sapiens CpG island DNA genomic Mse1 fragment, clone 4g7, reverse read cpg4g7.rt1d.//1.3e-17:113:97//Z61312
F-NT2RP3001712//M.musculus mRNA for HP1-BP74 protein.//2.2e-95:601:88//X99642
F-NT2RP3001716
F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//1.4e-159:565:97//AF054177
F-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2)-mRNA, partial cds.//1.7e-132:786:88//AF008554
F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds.//3.9e-104:811:78//D50918
F-NT2RP3001739//Homo sapiens Chromosome 22q11.2 PAC Clone p201m18 In DGCR Region, complete sequence.//6.5e-07:178:69//AC000097

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F-NT2RP3001752//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//5.2e-31:311:77//AL031311
F-NT2RP3001753//Sequence 29 from patent US 5658882.//0.11:513:58//I62381
F-NT2RP3001764//Sequence 6 from Patent WO9706245.//6.4e-47:673:66//A59888
F-NT2RP3001777//Caenorhabditis elegans cosmid T10E10.//0.078:290:63//U39644
F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds.//2.8e-151:710:98//AB007928
F-NT2RP3001792//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//1.2e-26:213:85//U13262
F-NT2RP3001799//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469D22, WORKING DRAFT SEQUENCE.//8.4e-51:168:95//AL031284
F-NT2RP3001819//S.glaucescens genes strU, strX, strV and strW for 5'-hydroxystreptomycin pruduction and transport polypeptides.//0.084:526:58//X89010
F-NT2RP3001844//HS_3110_B1_E10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3110 Col=19 Row=J, genomic survey sequence.//1.5e-40:232:82//AQ140433
F-NT2RP3001854//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.14:452:58//AC005505
F-NT2RP3001855//Mus musculus homeobox protein PKNOX1 (Pknox1) mRNA, complete cds.//2.7e-39:575:67//AF061270
F-NT2RP3001857//M.musculus tex292 mRNA (5'region).//8.7e-07:106:81//X80434
F-NT2RP3001896
F-NT2RP3001898//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 163G9, WORKING DRAFT SEQUENCE.//0.094:456:60//AL008733
F-NT2RP3001915//Caenorhabditis elegans cosmid C12D8, complete sequence.//0.58:482:56//Z73969
F-NT2RP3001926//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.42:401:58//AL034557
F-NT2RP3001929//Homo sapiens chromosome 16, cosmid clone RT102 (LANL), complete sequence.//3.1e-28:263:77//AC004651
F-NT2RP3001931
F-NT2RP3001938//CIT-HSP-2165E8.TR CIT-HSP Homo sapiens genomic clone 2165E8, genomic survey sequence.//3.6e-24:182:91//B95475
F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds.//1.8e-165:815:96//AB014575
F-NT2RP3001944
F-NT2RP3001969//Homo sapiens chromosome 12p13.3 clone RPCI11-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.//4.8e-62:304:89//AC005844
F-NT2RP3001989//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//8.2e-10:564:60//AF030694
F-NT2RP3002002//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//2.5e-57:361:80//Z83822
F-NT2RP3002004//Sequence 3 from patent US 5798245.//1.6e-26:104:100//AR025386
F-NT2RP3002007//Human Chromosome 15q11-q13 PAC clone pDJ223c9 from the Prader-Willi/Angelman Syndrome region, complete sequence.//0.0053:633:58//AC004137
F-NT2RP3002014//Drosophila melanogaster DNA sequence (P1s DS07528 (D169) and DS06665 (D220)), complete sequence.//1.3e-32:334:68//AC004640
F-NT2RP3002033//H.sapiens DNA sequence.//0.012:214:63//Z22493
F-NT2RP3002045//Rat mRNA for alpha-c large chain of the protein complex AP-2 associated with clathrin.//8.7e-116:713:86//X53773
F-NT2RP3002054//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.//1.6e-12:613:60//AL021841
F-NT2RP3002056//Human DNA sequence from PAC 358H7 on chromosome X.//0.17:566:59//Z77249
F-NT2RP3002057//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces.//3.3e-24:167:82//AC005682
F-NT2RP3002062
F-NT2RP3002063//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.24:508:58//AJ235272
F-NT2RP3002081//HS_2001_B1_E06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=11 Row=J, genomic survey sequence.//9.7e-22:155:90//AQ218494
F-NT2RP3002097//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) com-

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plete sequence.//9.6e-66:562:77//AC006210
F-NT2RP3002102//CIT-HSP-2307B10.TR CIT-HSP Homo sapiens genomic clone 2307B10, genomic survey sequence.//5.9e-16:214:74//AQ018040
F-NT2RP3002108
F-NT2RP3002142//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//7.6e-29:414:68//AC004020
F-NT2RP3002146//Pseudomonas fluorescens polyketide synthase type I (pltB) and polyketide synthase type I (pltC) genes, complete cds.//0.96:434:60//AF003370
F-NT2RP3002147//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 329F2, WORKING DRAFT SEQUENCE.//1.3e-63:380:91//AL031710
F-NT2RP3002151//Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence.//9.9e-60:315:80//U95742
F-NT2RP3002163
F-NT2RP3002165//M.musculus HCNGP mRNA.//1.4e-142:867:87//X68061
F-NT2RP3002166//Homo sapiens chromosome X, clone hCIT.200_L_4, complete sequence.//0.090:394:59//AC006121
F-NT2RP3002173//HS_3062_B1_G05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 Col=9 Row=N, genomic survey sequence.//3.3e-101:509:96//AQ193219
F-NT2RP3002181//Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.//4.5e-106:432:84//AL021808
F-NT2RP3002244//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.63:353:60//AC005321
F-NT2RP3002248//HS_3029_A1_D10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3029 Col=19 Row=G, genomic survey sequence.//3.5e-10:125:79//AQ094880
F-NT2RP3002255//Bovine herpesvirus type 1 immedidate-early transcriptional control protein (BICP4) gene, 5' end.//5.6e-09:629:59//L14321
F-NT2RP3002273//cSRL-165E12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-165E12, genomic survey sequence.//4.9e-35:366:74//B03004
F-NT2RP3002276//B.taurus mRNA for B15 subunit of NADH: ubiquinone oxidoreductase complex.//0.023:326:60//X64898
F-NT2RP3002303//Methanobacterium thermoautotrophicum from bases 172512 to 182957 (section 16 of 148) of the complete genome.//3.8e-12:643:57//AE000810
F-NT2RP3002304//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.6e-09:490:60//AC005504
F-NT2RP3002330//Human DNA sequence from cosmid L58b6, Huntington's Disease Region, chromosome 4p16.3, containing STS matches.//1.9e-93:572:88//Z49862
F-NT2RP3002343//HS_3010_A2_B08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3010 Col=16 Row=C, genomic survey sequence.//9.0e-75:373:97//AQ119068
F-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15).//4.9e-64:588:75//X16396
F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene, alternatively spliced form.//1.3e-164:770:98//Y16355
F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds.//1.4e-190:911:98//AB018331
F-NT2RP3002399
F-NT2RP3002402//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//7.2e-25:249:79//D89340
F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds.//1.2e-138:649:99//AB014578
F-NT2RP3002484//CIT-HSP-367N3.TP.1 CIT-HSP Homo sapiens genomic clone 367N3, genomic survey sequence.//5.0e-18:115:96//B78927
F-NT2RP3002501//Caenorhabditis elegans cosmid K01C8, complete sequence.//0.00020:170:65//Z49068
F-NT2RP3002512//Homo sapiens clone 664 unknown mRNA, partial sequence.//1.6e-59:308:97//AF091088
F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, complete cds.//1.4e-144:763:93//U35246
F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds.//1.8e-178:833:98//AB018272
F-NT2RP3002549//Homo sapiens clone DJ0098O22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-26:123:72//AC004821
F-NT2RP3002566//Streptomyces viridifaciens sigma factor (hrdD) gene, complete cds.//0.76:459:59//U60418
F-NT2RP3002587//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//4.6e-13:199:76//

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AC004617
F-NT2RP3002590//Porphyra purpurea chloroplast, complete genome.//0.88:284:60//U38804
F-NT2RP3002602//CIT978SK-A-441H11-2.TPB CIT978SK Homo sapiens genomic clone A-441H11, genomic survey sequence.//2.0e-22:140:95//B68331
F-NT2RP3002603
F-NT2RP3002628//C.acetobutylicum dnaJ and orfB genes.//2.0e-05:333:60//X69050
F-NT2RP3002631
F-NT2RP3002650//Mus musculus mRNA for cartilage-associated protein (CASP).//1.5e-20:641:62//AJ006469
F-NT2RP3002659//Bovine herpesvirus type 1 UL22-35 genes.//5.2e-05:621:59//Z78205
F-NT2RP3002660//Homo sapiens PAC clone DJ1006K12 from 7q31.2-q31, complete sequence.//0.98:453:57//AC004946
F-NT2RP3002663//Homo sapiens chromosome 19, cosmid F6697, complete sequence.//3.3e-22:407:67//AC006129
F-NT2RP3002671//S.pombe chromosome III cosmid c553.//1.0e-12:336:66//AL023704
F-NT2RP3002682//Caenorhabditis elegans cosmid F17C11, complete sequence.//1.3e-21:448:64//Z72507
F-NT2RP3002687//CIT978SK-A-789B1.TP CIT978SK Homo sapiens genomic clone A-789B1, genomic survey sequence.//2.5e-25:173:91//B51656
F-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kif1b), complete cds.//1.2e-73:728:74//D17577
F-NT2RP3002701//CITBI-E1-2507L14.TF CITBI-E1 Homo sapiens genomic clone 2507L14, genomic survey sequence.//0.0012:55:92//AQ263530
F-NT2RP3002713
F-NT2RP3002763//Caenorhabditis elegans cosmid T20F10, complete sequence.//0.98:209:63//Z81594
F-NT2RP3002770
F-NT2RP3002785//Homo sapiens laminin beta-4 chain precursor (LAMB4) mRNA, alternatively spliced short variant, partial cds.//0.78:515:57//AF029325
F-NT2RP3002799//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs, complete sequence.//1.9e-21:167:79//AL022718
F-NT2RP3002810//Homo sapiens chromosome 17, clone hRPK.215_E_13, complete sequence.//0.32:187:66//AC005549
F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete cds.//6.9e-54:615:70//AF004715
F-NT2RP3002861//Caenorhabditis elegans cosmid M03F4.//4.2e-05:226:65//U64601
F-NT2RP3002869//Mus musculus semaphorin VIa mRNA, complete cds.//2.0e-93:638:83//AF030430
F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds.//8.5e-89:557:88//AB001895
F-NT2RP3002877//Homo sapiens chromosome 12p13.3 clone RPCI11-433J6, WORKING DRAFT SEQUENCE, 100 unordered pieces.//7.9e-12:160:78//AC006087
F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//5.7e-180:853:98//AB018314
F-NT2RP3002911//RPCI11-24N15.TPC RPCI-11 Homo sapiens genomic clone RPCI-11-24N15, genomic survey sequence.//2.3e-13:442:61//B88815
F-NT2RP3002948//, complete sequence.//2.2e-110:637:91//AC005500
F-NT2RP3002953//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//1.7e-166:793:98//AC005754
F-NT2RP3002955//Human HepG2 partial cDNA, clone hmd3c02m5.//0.00011:61:95//D17024
F-NT2RP3002969//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//1.2e-128:808:85//D30666
F-NT2RP3002972//H.sapiens (xs168) mRNA, 381bp.//1.5e-43:312:85//Z36820
F-NT2RP3002978//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00044:527:57//AC005505
F-NT2RP3002985//Genomic sequence from Human 9q34, complete sequence.//0.92:341:60//AC001644
F-NT2RP3002988//HS_3015_A1_B07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3015 Col=13 Row=C, genomic survey sequence.//4.4e-05:379:58//AQ091708
F-NT2RP3003008//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//1.4e-72:197:79//AF109905
F-NT2RP3003032//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-80, complete sequence.//1.6e-08:809:58//AL010153
F-NT2RP3003059//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//4.1e-111:804:81//U78090

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F-NT2RP3003061//Human mRNA for ankyrin (variant 2.1).//1.4e-12:633:59//X16609
F-NT2RP3003068//Human BAC clone RG264L19 from 7p15-p21, complete sequence.//0.034:282:60//AC002410
F-NT2RP3003071//H.sapiens CpG island DNA genomic Mse1 fragment, clone 13d12, reverse read cpg13d12.rt1c.//6.8e-15:95:100//Z64565
F-NT2RP3003078
F-NT2RP3003101//Mouse mRNA for tetracycline transporter-like protein, complete cds.//8.1e-72:732:71//D88315
F-NT2RP3003121
F-NT2RP3003133//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//3.5e-12:168:76//AC004510
F-NT2RP3003138//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//4.0e-148:908:87//D12646
F-NT2RP3003139//Rattus norvegicus kappa opioid receptor gene, exon 4 and complete cds.//2.0e-31:658:63//U17995
F-NT2RP3003145//Mus musculus carboxypeptidase X2 mRNA, complete cds.//3.5e-22:430:63//AF017639
F-NT2RP3003150
F-NT2RP3003157//HS_3055_B1_G05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=9 Row=N, genomic survey sequence.//1.9e-92:493:94//AQ155489
F-NT2RP3003185//Rattus norvegicus brain-enriched guanylate kinase-associated protein 1 mRNA, complete cds.//8.6e-06:228:65//AF064868
F-NT2RP3003193//H.sapiens HZF10 mRNA for zinc finger protein.//7.4e-73:737:71//X78933
F-NT2RP3003197
F-NT2RP3003203//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//4.1e-48:640:67//AF015264
F-NT2RP3003204//Human Mermaid LINE-1 element mRNA sequence.//0.0033:69:81//U31059
F-NT2RP3003210//Homo sapiens SYBL1 gene.//1.1e-34:430:70//AJ004799
F-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//6.3e-75:776:74//U20286
F-NT2RP3003230//Rattus norvegicus mRNA for coronin-like protein.//1.8e-62:575:74//AJ006064
F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//3.7e-128:617:98//AF055460
F-NT2RP3003251//H.sapiens Staf50 mRNA.//3.5e-67:651:76//X82200
F-NT2RP3003264//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.015:473:58//AC004153
F-NT2RP3003278//H.sapiens CpG island DNA genomic Mse1 fragment, clone 28b4, forward read cpg28b4.ft1a.//4.0e-27:174:93//Z60555
F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//1.3e-131:694:93//L36983
F-NT2RP3003290//Homo sapiens nickel-specific induction protein (Cap43) mRNA, complete cds.//1.7e-64:662:71//AF004162
F-NT2RP3003301//Spinacia oleracea mRNA for ATP-dependent protease Lon, complete cds.//4.9e-37:682:64//D85610
F-NT2RP3003302//Homo sapiens, clone hRPK.15_A_1, complete sequence.//4.6e-95:680:82//AC006213
F-NT2RP3003311//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete sequence.//1.0:191:62//AC004527
F-NT2RP3003313//Streptomyces coelicolor cosmid 5A7.//0.0084:403:61//AL031107
F-NT2RP3003327//H.sapiens Staf50 mRNA.//2.5e-29:253:67//X82200
F-NT2RP3003330
F-NT2RP3003344
F-NT2RP3003346//Homo sapiens chromosome 17, clone hRPK.795_F_17, complete sequence.//9.0e-41:296:84//AC005284
F-NT2RP3003353//Human DNA sequence from PAC 970D1 on chromosome 1q24. Contains ESTs, STSs and a BAC end-sequence (GSS).//0.047:404:60//AL021069
F-NT2RP3003377//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//8.3e-122:632:96//AC005519
F-NT2RP3003384//Homo sapiens Chromosome 2 BAC Clone 376a1, WORKING DRAFT SEQUENCE, 17 unordered pieces.//0.0036:127:74//AC000360
F-NT2RP3003385//Mus musculus SKD3 mRNA, complete cds.//2.0e-110:843:79//U09874
F-NT2RP3003403//Human Chromosome X, complete sequence.//7.5e-21:647:61//AC002407
F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds.//1.0e-20:430:63//U90653

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F-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//4.2e-139:524:90//AF071317
F-NT2RP3003427//HS-1051-A1-D03-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 773 Col=5 Row=G, genomic survey sequence.//8.8e-18:111:97//B40173
F-NT2RP3003433//HS_2219_B2_A11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=22 Row=B, genomic survey sequence.//1.2e-57:410:83//AQ145866
F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.2e-181:853:98//AF004828
F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds.//1.6e-173:826:98//AB018268
F-NT2RP3003491//CIT-HSP-2344O1.TR CIT-HSP Homo sapiens genomic clone 2344O1, genomic survey sequence.//1.2e-39:213:97//AQ057124
F-NT2RP3003500//HS_3000_B1_C07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey sequence.//0.025:253:60//AQ090347
F-NT2RP3003543//Homo sapiens chromosome 16, cosmid clone 399H11 (LANL), complete sequence.//0.95:279:60//AC004234
F-NT2RP3003552//Homo sapiens clone UWGC:y54c222 from 6p21, complete sequence.//1.8e-88:166:84//AC006049
F-NT2RP3003555//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING DRAFT SEQUENCE.//8.9e-17:245:72//AL031985
F-NT2RP3003564//HS_3141_B1_G10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3141 Col=19 Row=N, genomic survey sequence.//2.7e-79:442:93//AQ187798
F-NT2RP3003572
F-NT2RP3003576//Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.//5.8e-55:275:84//AC005632
F-NT2RP3003589//Canine rab10 mRNA for ras-related GTP-binding protein.//1.1e-94:488:95//X56387
F-NT2RP3003621//Homo sapiens chromosome 16, cosmid clone 432A1 (LANL), complete sequence.//6.0e-88:463:84//AC004235
F-NT2RP3003625//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 390E6, WORKING DRAFT SEQUENCE.//0.98:307:60//AL031600
F-NT2RP3003656
F-NT2RP3003659//F.rubripes GSS sequence, clone 013G07cE7, genomic survey sequence.//1.7e-25:284:74//AL011271
F-NT2RP3003665//Homo sapiens chromosome 9q34, clone 63G10, complete sequence.//0.011:279:65//AC002096
F-NT2RP3003672
F-NT2RP3003680//Drosophila melanogaster; Chromosome 2R; Region 39B1-39B3; P1 clone DS05527, WORKING DRAFT SEQUENCE, 9 unordered pieces.//3.4e-16:425:64//AC005811
F-NT2RP3003686//HS_3064_B2_A04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-27:153:98//AQ136993
F-NT2RP3003701
F-NT2RP3003716//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//4.6e-107:788:82//U42975
F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds.//2.3e-148:700:98//AB018300
F-NT2RP3003746//CIT-HSP-2306A10.TF CIT-HSP Homo sapiens genomic clone 2306A10, genomic survey sequence.//0.39:212:61//AQ015785
F-NT2RP3003795//Human DNA sequence from clone 333H23 on chromosome 22q12.1-12.3. Contains the (possibly alternatively spliced) RPL3 gene for 60S Ribosomal Protein L3 and the threefold alternatively spliced gene for Synaptogyrin 1A, 1B and 1C (SYNGR1A, SYBGRIB, SYNGR1C), both genes downstream of a putative CpG island. Contains ESTs, an STS, GSSs, genomic marker D22S1155 and a ca repeat polymorphism, complete sequence.//4.2e-21:445:66//AL022326
F-NT2RP3003799//Homo sapiens DNA from chromosome 19-cosmids R31158, R31874, and R28125, genomic sequence, complete sequence.//1.0:257:63//AF038458
F-NT2RP3003800//Mouse neuronal proto-oncogene c-src mRNA encoding tyrosine-specific protein kinase, complete cds.//1.2e-63:484:81//M17031
F-NT2RP3003805//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.96:353:60//AC005321
F-NT2RP3003809//Bovine herpesvirus 1 complete genome.//7.2e-12:615:60//AJ004801
F-NT2RP3003819

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F-NT2RP3003825
F-NT2RP3003828//Human rRNA primary transcript internal transcribed spacer 2 (ITS2).//6.2e-16:543:62//X17626
F-NT2RP3003831//RPCI11-50N15.TJ RPCI11 Homo sapiens genomic clone R-50N15, genomic survey sequence.//1.1e-21:174:85//AQ082633
F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence.//8.0e-47:242:98//AF070611
F-NT2RP3003842//RPCI11-44E5.TJ RPCI11 Homo sapiens genomic clone R-44E5, genomic survey sequence.//9.7e-25:143:97//AQ195884
F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds.//4.2e-36:335:68//AB018268
F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds.//4.1e-174:805:99//AB018343
F-NT2RP3003876//Rattus norvegicus Rabin3 mRNA, complete cds.//2.7e-109:709:84//U19181
F-NT2RP3003914//Drosophila melanogaster UDP-glucose:glycoprotein glucosyltransferase mRNA, complete cds.//8.9e-11:193:70//U20554
F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//2.6e-47:404:77//AF057358
F-NT2RP3003932//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.68:597:55//AC005504
F-NT2RP3003989//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 404H4, WORKING DRAFT SEQUENCE.//0.37:548:56//AL031661
F-NT2RP3003992//Human cGMP-gated cation channel beta subunit (CNCG2) mRNA, complete cds.//0.021:433:58//U58837
F-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein.//1.4e-164:838:94//X84692
F-NT2RP3004016//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018K9, WORKING DRAFT SEQUENCE.//0.00042:356:62//AL031726
F-NT2RP3004041//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 809F4, WORKING DRAFT SEQUENCE.//6.8e-112:627:82//AL022400
F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds.//2.2e-61:774:67//AB002317
F-NT2RP3004070//Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family protein. Contains ESTs, STSs and GSSs, complete sequence.//7.9e-17:484:62//AL021939
F-NT2RP3004078//M.musculus (BALB/c) MRFX2 mRNA.//1.9e-102:684:83//X76089
F-NT2RP3004093//F24P17-Sp6 IGF Arabidopsis thaliana genomic clone F24P17, genomic survey sequence.//0.021:207:63//B09433
F-NT2RP3004095//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.5e-25:272:77//AC005038
F-NT2RP3004110//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//8.6e-28:223:73//AC003973
F-NT2RP3004125//Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds.//2.2e-28:637:63//AF000560
F-NT2RP3004145
F-NT2RP3004148
F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds.//6.5e-120:578:98//AF032900
F-NT2RP3004189//M.musculus tex292 mRNA (5'region).//1.1e-06:102:82//X80434
F-NT2RP3004206//D.melanogaster crn mRNA.//7.3e-69:715:71//X58374
F-NT2RP3004207//Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.//4.8e-42:650:66//D64009
F-NT2RP3004209//Human cosmid Q7A10 (D21S246) insert DNA, complete sequence.//8.4e-55:184:84//D42052
F-NT2RP3004215//Homo sapiens chromosome 5, Pac clone 9c13 (LBNL H127), complete sequence.//0.22:458:60//AC006084
F-NT2RP3004242//Caenorhabditis elegans cosmid ZK632, complete sequence.//1.6e-29:409:69//Z22181
F-NT2RP3004246//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence.//3.6e-117:242:100//AC005385
F-NT2RP3004253//H.sapiens 28S rRNA V8 region (LAN5-6).//2.6e-12:589:59//X69353
F-NT2RP3004258//Rattus norvegicus Zis mRNA, complete cds.//1.2e-88:489:91//AF013967
F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds.//3.1e-153:733:98//AF088982
F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds.//1.3e-24:597:61//AF007871
F-NT2RP3004332
F-NT2RP3004334//L.esculentum gene for fruit ripening polygalacturonase.//0.23:501:57//X80908
F-NT2RP3004341//Human DNA sequence from clone 503G16 on chromosome 6p23 Contains EST, CpG island, complete sequence.//0.0014:198:66//Z93020

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F-NT2RP3004348//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.4e-103:600:82//X67877
F-NT2RP3004349//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//5.1e-49:480:75//AC004025
F-NT2RP3004378//Drosophila melanogaster; Chromosome 2R; Region 47F1-47F7; P1 clone DS02304, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23 :352:67//AC005653
F-NT2RP3004399//H.sapiens mRNA for leucine-rich primary response protein 1.//7.2e-140:804:90//X97249
F-NT2RP3004424//Mus musculus mRNA for nuclear protein SA3.//6.8e-53:413:81//AJ005678
F-NT2RP3004428//Salmo salar DNA for a cryptic repeat.//3.2e-07:270:63//AJ012206
F-NT2RP3004451//RPCI11-51J15.TK RPCI11 Homo sapiens genomic clone R-51J15, genomic survey sequence.//8.8e-19:180:82//AQ052326
F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds.//6.2e-123:583:99//AB007917
F-NT2RP3004466//HS_3038_B2_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3038 Col=16 Row=L, genomic survey sequence.//0.41:172:59//AQ102458
F-NT2RP3004470//H.sapiens CpG island DNA genomic Mse1 fragment, clone 81a11, reverse read cpg81a11.rt1a.//7.0e-25:148:96//Z56029
F-NT2RP3004472//RPCI11-42M5.TJ RPCI11 Homo sapiens genomic clone R-42M5, genomic survey sequence.//1.6e-20:143:92//AQ052792
F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds.//3.0e-150:715:98//AB007925
F-NT2RP3004480//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//1.0e-119:679:90//U47024
F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds.//7.1e-155:752:97//AB012851
F-NT2RP3004498//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//4.0e-67:265:84//AC006023
F-NT2RP3004503//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//1.2e-55:415:78//AC004673
F-NT2RP3004504//M.musculus mRNA for CPEB protein.//2.0e-110:618:91//Y08260
F-NT2RP3004507//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.3e-46:433:76//AC005328
F-NT2RP3004527//Homo sapiens mRNA; transcriptional unit N144, 5' end.//1.1e-100:508:97//AJ002574
F-NT2RP3004534//Mouse oncogene (ect2) mRNA, complete cds.//2.0e-93:442:84//L11316
F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds.//8.5e-145:679:98//AB014532
F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds.//2.8e-169:793:98//AB011126
F-NT2RP3004566//Mus musculus krupple-related zinc finger protein (Emzf1) mRNA, complete cds.//6.9e-18:433:64//AF031955
F-NT2RP3004569//CITBI-E1-2522H6.TF CITBI-E1 Homo sapiens genomic clone 2522H6, genomic survey sequence.//5.3e-15:138:84//AQ280780
F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds.//1.0e-179:860:97//AF026445
F-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//4.2e-150:711:98//AB007946
F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//1.1e-158:796:95//AJ006266
F-NT2RP3004617//Homo sapiens clone DJ1152C17, WORKING DRAFT SEQUENCE, 1 unordered pieces.//9.3e-14:360:65//AC004977
F-NT2RP3004618//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.9e-52:539:73//AF005355
F-NT2RP3004669//Brn-3a=class V POU transcription factor [mice, CD/CD, embryo fibroblast cells, Genomic, 2160 nt].//0.046:437:57//S69350
F-NT2RP3004670//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 356B8, WORKING DRAFT SEQUENCE.//1.9e-05:625:59//Z98882
F-NT2RP4000008//Homo sapiens chromosome X, clone hCIT.200_L_4, complete sequence.//1.5e-155:844:92//AC006121
F-NT2RP4000023//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24G6, complete sequence.//0.012:417:59//AB012242
F-NT2RP4000035//Homo sapiens BAC clone NH0353P23 from 2, complete sequence.//8.0e-18:242:74//AC005035
F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds.//2.1e-81:556:85//AF029761
F-NT2RP4000051//Mus musculus mRNA for cartilage-associated protein (CASP).//1.6e-19:654:63//AJ006469
F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.5e-149:720:97//AJ012449
F-NT2RP4000102//Plasmodium falciparum MAL3P2, complete sequence.//0.28:336:57//AL034558

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F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//4.4e-166:774:99//AB011538
F-NT2RP4000111//B.taurus mRNA for cleavage and polyadenylation specificity factor.//2.6e-137:678:91//X75931
F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds.//3.3e-114:548:98//AB007952
F-NT2RP4000147//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//1.2e-104:677:85//U35776
F-NT2RP4000150//Rat proto-oncogene (Ets-1) mRNA, complete cds.//7.2e-54:327:74//L20681
F-NT2RP4000151//Homo sapiens clone 664 unknown mRNA, partial sequence.//2.2e-62:360:92//AF091088
F-NT2RP4000159//RPCI11-75N16.TJ RPCI11 Homo sapiens genomic clone R-75N16, genomic survey sequence.//2.6e-19:119:98//AQ267551
F-NT2RP4000167//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//3.3e-49:683:67//AC006210
F-NT2RP4000185//Homo sapiens clone DT1P1E11 mRNA, CAG repeat region.//1.1e-99:543:93//U92989
F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//4.9e-174:825:98//AB014600
F-NT2RP4000212//, complete sequence.//4.0e-131:233:94//AC005300
F-NT2RP4000214//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.8e-161:751:99//AC005261
F-NT2RP4000218//RPCI11-69B7.TJ RPCI11 Homo sapiens genomic clone R-69B7, genomic survey sequence.//1.7e-84:413:98//AQ268504
F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//2.6e-156:771:97//AJ006470
F-NT2RP4000246//Mus musculus neural variant mena+++ protein (Mena) mRNA, complete cds.//2.1e-120:707:87//U72523
F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence.//2.8e-128:604:99//AF091092
F-NT2RP4000263//CIT-HSP-2336N24.TF CIT-HSP Homo sapiens genomic clone 2336N24, genomic survey sequence.//0.27:124:69//AQ043515
F-NT2RP4000290//S.cerevisiae chromosome XIV reading frame ORF YNL132w.//8.6e-32:619:63//Z71408
F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds.//4.7e-41:685:63//D63481
F-NT2RP4000321//Mus musculus transcription factor HOXA13 (Hoxa13) gene, complete cds.//6.9e-05:756:59//U59322
F-NT2RP4000323
F-NT2RP4000355
F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//2.0e-140:654:99//AB018281
F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//2.6e-135:649:97//AF044195
F-NT2RP4000370//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//2.0e-23:524:62//AJ235272
F-NT2RP4000376//Sequence 1 from patent US 5580968.//1.6e-115:716:87//I30536
F-NT2RP4000381//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//4.3e-05:450:58//D63850
F-NT2RP4000398//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//9.2e-37:336:69//AC006116
F-NT2RP4000415//Caenorhabditis elegans cosmid C42D8.//0.30:222:60//U56966
F-NT2RP4000417//Drosophila melanogaster cosmid clone 86E4.//1.8e-48:580:69//AL021086
F-NT2RP4000424//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//1.6e-42:265:81//AC003101
F-NT2RP4000448//CIT-HSP-2370F8.TF CIT-HSP Homo sapiens genomic clone 2370F8, genomic survey sequence.//2.0e-56:287:98//AQ110194
F-NT2RP4000449//CIT-HSP-2366N18.TR CIT-HSP Homo sapiens genomic clone 2366N18, genomic survey sequence.//2.4e-42:236:95//AQ076183
F-NT2RP4000455//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//0.17:158:67//AC003982
F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP).//0.00034:532:57//Z72499
F-NT2RP4000480//Rhodothermus marinus R-21 DNA ligase gene, complete cds.//0.0094:616:58//U10483
F-NT2RP4000481
F-NT2RP4000498//S.cerevisiae chromosome IX cosmid 9150.//5.7e-24:633:60//Z38125
F-NT2RP4000500//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//2.4e-62:667:73//X74904
F-NT2RP4000515
F-NT2RP4000517//Homo sapiens chromosome 18, clone hRPK.474_N_24, complete sequence.//1.6e-179:851:98//AC006238

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F-NT2RP4000518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//6.7e-33:203:93//AJ010840
F-NT2RP4000519//Mus musculus tyrosine kinase growth factor receptor (Etk2/tyro3) gene, alternative 5' coding exon 2C.//0.26:162:61//U23720
F-NT2RP4000524//Rattus norvegicus rsec8 mRNA, partial cds.//1.2e-139:809:89//U32498
F-NT2RP4000528//Caenorhabditis elegans cosmid F59E12.//1.0e-06:404:59//AF003386
F-NT2RP4000541//Drosophila melanogaster DNA sequence (P1 DS02109 (D53)), complete sequence.//1.3e-05:498:58//AC002443
F-NT2RP4000556//Sequence 1 from Patent EP 0285405.//1.2e-18:586:61//I05465
F-NT2RP4000560//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//2.5e-53:183:82//AF059580
F-NT2RP4000588//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 414D7, WORKING DRAFT SEQUENCE.//0.00062:253:65//AL033543
F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//3.2e-138:666:98//AF067730
F-NT2RP4000638//HS_3042_B2_D05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3042 Col=10 Row=H, genomic survey sequence.//3.0e-06:78:89//AQ099333
F-NT2RP4000648//Homo sapiens KNSL4 and MAZ genes for kinesin-like DNA binding protein and Myc-associated zinc finger protein, complete cds.//1.9e-11:104:85//AB017335
F-NT2RP4000657//Mus musculus bone morphogenetic factor 11 (Bmp11) gene, exon 1.//0.34:350:62//AF100904
F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone IMAGE:300856.//3.3e-167:785:99//AB004852
F-NT2RP4000713//Gallus gallus atonal homolog 1 (Cath1) gene, complete cds.//3.7e-07:261:65//U61149
F-NT2RP4000724//Human endogenous retrovirus env mRNA.//9.2e-136:474:89//X82272
F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds.//3.1e-41:350:71//AB011178
F-NT2RP4000737//Myxococcus xanthus ATP-dependent protease (bsgA) gene, complete cds.//1.0:504:58//L19301
F-NT2RP4000739//CIT-HSP-2010O22.TR CIT-HSP Homo sapiens genomic clone 2010O22, genomic survey sequence.//1.1e-24:161:93//B57903
F-NT2RP4000781//Homo sapiens clone DJ0892G19, complete sequence.//0.052:493:58//AC004917
F-NT2RP4000787//Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mRNA, complete cds.//9.6e-18:259:68//U22818
F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds.//1.5e-174:816:98//AB007939
F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.97:52:92//AC005189
F-NT2RP4000837//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1112F19, WORKING DRAFT SEQUENCE.//2.1e-128:644:97//AL034420
F-NT2RP4000839//RPCI11-6D8.TP RPCI-11 Homo sapiens genomic clone RPCI-11-6D8, genomic survey sequence.//1.5e-44:281:91//B48216
F-NT2RP4000855//Rattus norvegicus mRNA for aminopeptidase-B, complete cds.//9.5e-43:722:64//D87515
F-NT2RP4000865//Human zinc finger protein ZNF136.//6.8e-95:415:78//U09367
F-NT2RP4000878//Mus musculus mRNA for myeloid associated differentiation protein.//7.0e-87:646:80//AJ001616
F-NT2RP4000879//N.tabaccum mRNA for ubiquitin activating enzyme E1.//9.0e-17:806:58//Y10804
F-NT2RP4000907//Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds.//6.8e-153:934:86//D45913
F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein.//9.4e-79:584:78//AJ224901
F-NT2RP4000918//Drosophila melanogaster DNA sequence (P1 DS04106 (D172)), complete sequence.//2.0e-08:609:58//AC004290
F-NT2RP4000925//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//3.5e-64:415:87//U42975
F-NT2RP4000927//H.sapiens genomic DNA (chromosome 3; clone NRL062R).//0.75:175:62//X87547
F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//3.5e-163:781:97//AF069532
F-NT2RP4000929//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.94:763:56//AC004688
F-NT2RP4000955//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//1.0e-128:673:96//AC005519
F-NT2RP4000973//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//1.6e-15:255:69//AL032657

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F-NT2RP4000975//CIT-HSP-2307I6.TF CIT-HSP Homo sapiens genomic clone 2307I6, genomic survey sequence.//6.5e-31:317:79//AQ015742
F-NT2RP4000979//Human bullous pemphigoid antigen mRNA, 3' end.//0.88:54:90//M22942
F-NT2RP4000984//Rhodobacter sphaeroides mRNA.//0.76:214:64//M83823
F-NT2RP4000989//F.rubripes GSS sequence, clone 011A11aE12, genomic survey sequence.//1.0:149:65//AL010911
F-NT2RP4000996//Penaeus setiferus microsatellite Pse017 repeat region.//3.3e-08:139:74//AF047358
F-NT2RP4000997//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds.//3.6e-126:824:84//AF025424
F-NT2RP4001004
F-NT2RP4001006//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.//1.4e-110:861:78//U83176
F-NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds.//2.0e-135:789:89//U67140
F-NT2RP4001029//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//3.7e-120:718:88//U20086
F-NT2RP4001041//Schizosaccharomyces pombe mRNA, partial cds, clone: SY 0717.//4.1e-22:452:64//D89170
F-NT2RP4001057
F-NT2RP4001064//Mus musculus mRNA for cartilage-associated protein (CASP).//1.2e-20:639:62//AJ006469
F-NT2RP4001078//Streptomyces coelicolor cosmid 1C2.//0.0025:474:59//AL031124
F-NT2RP4001079//Rat alternatively spliced mRNA.//1.4e-141:832:88//M93018
F-NT2RP4001080//H.sapiens PTB-4 gene for polypirimidine tract binding protein.//9.0e-64:628:70//X65372
F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds.//4.7e-84:604:86//AB011164
F-NT2RP4001095
F-NT2RP4001100//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//9.4e-17:185:79//AQ263402
F-NT2RP4001117//Canis familiaris sec61 homologue mRNA, complete cds.//1.0e-143:760:87//M96629
F-NT2RP4001122
F-NT2RP4001126//Homo sapiens shox gene, alternatively spliced products, complete cds.//4.2e-17:636:61//U82668
F-NT2RP4001138//Homo sapiens PAC clone DJ1121E10 from 7q21.1-q2, complete sequence.//2.5e-23:408:60//AC004969
F-NT2RP4001143//Sequence 5 from patent US 5753432.//1.8e-39:276:86//AR008079
F-NT2RP4001148//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.7e-116:684:89//AC005095
F-NT2RP4001149//Mouse mRNA for thymic epithelial cell surface antigen, complete cds.//3.0e-48:581:66//D67067
F-NT2RP4001150//Homo sapiens alone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.4e-25:193:67//AC004952
F-NT2RP4001159//Human FMR1 gene, 5' end.//0.28:130:66//L19476
F-NT2RP4001174//FMR1 {CGG repeats} [human, Fragile X syndrome patient, Genomic, 429 nt].//0.0014:187:67//S74494
F-NT2RP4001206//Dictyostelium discoideum random slug cDNA19 protein (rscl9) mRNA, partial cds.//0.032:453:58//U82511
F-NT2RP4001207//HS_2248_A1_C03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2248 Col=5 Row=E, genomic survey sequence.//0.00018:58:94//AQ192358
F-NT2RP4001210//Homo sapiens chromosome 10 clone CIT987SK-1019O18 map 10p11.2-10p12.1, complete sequence.//0.93:515:58//AC005877
F-NT2RP4001213//Human KRAB zinc finger protein (ZNF177) mRNA, splicing variant, complete cds.//3.6e-44:187:74//U37251
F-NT2RP4001219//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//1.3e-15:288:67//AL032657
F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.2e-26:855:60//AF059569
F-NT2RP4001235//RPCI11-18E11.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-18E11, genomic survey sequence.//2.7e-15:101:98//B88081
F-NT2RP4001256//Amycolatopsis mediterranei 3-amino-5-hydroxy benzoic acid synthase (rifD) gene, complete cds.//1.0:459:59//U33061
F-NT2RP4001260//Sequence 2 from Patent WO9601901.//0.0018:246:63//A48324

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F-NT2RP4001274//Homo sapiens, complete sequence.//2.5e-05:201:67//AC005854
F-NT2RP4001276//CIT-HSP-2324B15.TF CIT-HSP Homo sapiens genomic clone 2324B15, genomic survey sequence.//3.5e-18:138:92//AQ040728
F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//7.4e-30:535:65//AF043250
F-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//3.5e-145:795:91//AJ001119
F-NT2RP4001336//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence.//8.4e-16:109:94//B89870
F-NT2RP4001339//HS_3205_B1_E08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3205 Col=15 Row=J, genomic survey sequence.//7.1e-24:305:73//AQ183725
F-NT2RP4001343//Homo sapiens PAC clone DJ0894A10 from 7q32-q32, complete sequence.//1.9e-17:106:91//AC004918
F-NT2RP4001345//G.gallus mRNA for lecithin-cholesterol acyltransferase.//7.6e-40:631:66//X91011
F-NT2RP4001351//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 184J9, WORKING DRAFT SEQUENCE.//2.7e-30:608:64//AL031428
F-NT2RP4001353//Streptomyces coelicolor cosmid 5A7.//0.23:540:57//AL031107
F-NT2RP4001372//RPCI11-49L11.TJ RPCI11 Homo sapiens genomic clone R-49L11, genomic survey sequence.//8.5e-23:129:100//AQ051701
F-NT2RP4001373//G.gallus genomic DNA repeat region, clone 16E1.//0.15:213:61//X78609
F-NT2RP4001375
F-NT2RP4001379//Homo sapiens chromosome 17, clone hRPK.311_F_12, complete sequence.//7.3e-28:153:88//AC005722
F-NT2RP4001389//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//7.2e-47:518:73//AC004691
F-NT2RP4001407//P.falciparum glutamic acid-rich protein gnen, complete cds.//0.00079:686:57//J03998
F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds.//2.0e-76:818:71//D86957
F-NT2RP4001433//H.sapiens HZF10 mRNA for zinc finger protein.//3.5e-87:839:73//X78933
F-NT2RP4001442
F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds.//0.21:218:63//AB018326
F-NT2RP4001474//Human NotI linking clone 924A058R, genomic survey sequence.//7.6e-14:109:90//U49884
F-NT2RP4001483//Human mRNA for 2-oxoglutarate dehydrogenase, complete cds.//2.5e-59:480:75//D10523
F-NT2RP4001498//Homo sapiens huntingtin interacting protein HYPH mRNA, partial cds.//9.7e-39:392:72//AF049612
F-NT2RP4001502//H.sapiens (D8S135) DNA segment containing GT repeat.//2.7e-24:147:96//X61693
F-NT2RP4001507//Plasmid pSB24.2 (from S.cyanogenus) neomycin resistance protein gene, complete cds.//0.87:583:58//M32513
F-NT2RP4001524//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.93:394:58//AC005308
F-NT2RP4001529//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//3.1e-143:820:89//U20086
F-NT2RP4001547//S.cerevisiae chromosome XIV reading frame ORF YNR048w.//2.2e-05:319:61//Z71663
F-NT2RP4001551//S.pombe chromosome II p1 p8B7.//0.64:335:60//AL032684
F-NT2RP4001555//Homo sapiens 12q24.2 BAC RPCI11-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.0:309:58//AC004806
F-NT2RP4001567//HS_2166_B1_C07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2166 Col=13 Row=F, genomic survey sequence.//0.99:188:59//AQ086290
F-NT2RP4001568//Human mRNA for KIAA0167 gene, complete cds.//7.0e-53:566:72//D79989
F-NT2RP4001571//RPCI11-21F20.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21F20, genomic survey sequence.//2.8e-19:119:97//B85885
F-NT2RP4001574//B.primigenius mRNA for coat protein gamma-cop.//5.8e-129:813:85//X92987
F-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//3.4e-131:795:86//AJ223830
F-NT2RP4001592//S.aureus gene for isoleucyl-tRNA synthetase.//1.3e-14:663:59//X74219
F-NT2RP4001610//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//6.4e-10:135:73//AC002364
F-NT2RP4001614//HS_3042_B2_D05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3042 Col=10 Row=H, genomic survey sequence.//3.4e-06:78:89//AQ099333
F-NT2RP4001634
F-NT2RP4001638//cSRL-161F1-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic

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clone cSRL-161FI, genomic survey sequence.//4.9e-12:144:76//B02870
F-NT2RP4001644//M.musculus mRNA for map kinase interacting kinase, Mnk2.//3.8e-69:437:86//Y11092
F-NT2RP4001656//HS_2013_A1_D01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2013 Col=1 Row=G, genomic survey sequence.//2.0e-30:207:89//AQ224793
F-NT2RP4001677//Hylobates lar huntingtin gene, partial exon.//0.23:105:71//L49362
F-NT2RP4001679//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 462O23, WORKING DRAFT SEQUENCE.//2.7e-45:351:84//AL031431
F-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//1.8e-30:163:88//U96629
F-NT2RP4001725//Drosophila melanogaster DNA sequence (P1 DS08860 (D181)), complete sequence.//1.1e-13:402:63//AC004296
F-NT2RP4001730//RPCI11-37M21.TK RPCI-11 Homo sapiens genomic clone RPCI-11-37M21, genomic survey sequence.//0.88:177:67//AQ029840
F-NT2RP4001739
F-NT2RP4001753//H.sapiens telomeric DNA sequence, clone 12QTEL023, read 12QTELOO023.seq.//4.9e-36:192:98//Z96232
F-NT2RP4001760//Mouse oncogene (ect2) mRNA, complete cds.//2.3e-140:866:86//L11316
F-NT2RP4001790//Homo sapiens clone NH0569I24, complete sequence.//1.4e-29:327:74//AC005678
F-NT2RP4001803
F-NT2RP4001822//Homo sapiens tetraspan TM4SF (TSPAN-4) mRNA, complete cds.//1.0e-16:576:60//AF054841
F-NT2RP4001823//Human DNA sequence from clone 181C9 on chromosome 22q13.2-13.33. Contains a PHAPI2 Leucine Rich Acidic Nuclear Protein pseudogene, part of a putative novel gene, ESTs, STSs and GSSs, complete sequence.//2.1e-08:601:59//Z98743
F-NT2RP4001828
F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds.//2.2e-53:555:73//D31888
F-NT2RP4001841
F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds.//1.7e-55:813:65//AB014572
F-NT2RP4001861//Human simple repeat polymorphism.//0.0014:145:66//M87691
F-NT2RP4001889//HS_2052_B1_H06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=11 Row=P, genomic survey sequence.//1.0e-23:187:86//AQ270425
F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//7.3e-76:178:95//AC005014
F-NT2RP4001896//T3B4TFC TAMU Arabidopsis thaliana genomic clone T3B4, genomic survey sequence.//0.99:354:61//B26193
F-NT2RP4001901//Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.//0.031 :409:60//AB011413
F-NT2RP4001927//HS_2216_B1_D03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2216 Col=5 Row=H, genomic survey sequence.//4.9e-32:216:89//AQ184677
F-NT2RP4001938//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//1.2e-83:709:79//U49046
F-NT2RP4001946//HS_3021_B2_H10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3021 Col=20 Row=P, genomic survey sequence.//7.6e-09:120:76//AQ133185
F-NT2RP4001950//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-18:421:65//AL022577
F-NT2RP4001953//CIT-HSP-2294D14.TR CIT-HSP Homo sapiens genomic clone 2294D14, genomic survey sequence.//0.030:358:61//AQ005028
F-NT2RP4001966//Mus musculus DOC4 (Doc4) mRNA, complete cds.//2.5e-68:812:68//AF059485
F-NT2RP4001975//Homo sapiens chromosome 17, clone hCIT.91_J_4, complete sequence.//1.9e-57:555:75//AC003976
F-NT2RP4002018//cSRL-143G4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-143G4, genomic survey sequence.//8.9e-21:123:98//B01950 F-NT2RP4002047//Saccharomyces cerevisiae chromosome XII cosmid 8003.//1.6e-29:520:64//U17243
F-NT2RP4002052//CIT-HSP-2045A15.TF CIT-HSP Homo sapiens genomic clone 2045A15, genomic survey sequence.//2.8e-22:137:96//B80243
F-NT2RP4002058//T20L11-T7 TAMU Arabidopsis thaliana genomic clone T20L11, genomic survey sequence.//0.019:141:65//AQ248640

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F-NT2RP4002071//CIT-HSP-2314J9.TF CIT-HSP Homo sapiens genomic clone 2314J9, genomic survey sequence.//0.99:163:63//AQ027223
F-NT2RP4002075//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y57G11, WORKING DRAFT SEQUENCE.//0.15:506:59//Z92841
F-NT2RP4002078//RPCI11-73M20.TJ RPCI11 Homo sapiens genomic clone R-73M20, genomic survey sequence.//4.8e-21:130:96//AQ269030
F-NT2RP4002081//F.rubripes GSS sequence, clone 190O22bB9, genomic survey sequence.//0.0024:350:60//Z92062
F-NT2RP4002083//M.musculus tex27 mRNA.//8.2e-77:456:89//X80437
F-NT2RP4002408//Caenorhabditis elegans serine/threonine kinase LET-502 (let-502) mRNA, complete cds.//3.7e-18:541:62//U85515
F-NT2RP4002791
F-NT2RP4002888//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//4.7e-39:385:75//AC002383
F-NT2RP4002905//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//6.5e-91:672:83//AC004662
F-NT2RP5003459//Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds.//2.9e-37:193:99//M33197
F-NT2RP5003461//Human DNA sequence from PAC 506G2 contains ESTs.//7.9e-51:300:80//Z82901
F-NT2RP5003477//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.7e-77:150:100//AC000380
F-NT2RP5003492
F-NT2RP5003500//Human DNA sequence from cosmid 97K10, between markers DXS6791 and DXS8038 on chromosome X contains STSs and CpG island.//1.7e-111:623:93//Z81365
F-NT2RP5003506//H.sapiens CpG island DNA genomic Mse1 fragment, clone 71h2, reverse read cpg71h2.rt1a.//1.4e-49:283:93//Z62703
F-NT2RP5003512//HS_3084_A1_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=7 Row=G, genomic survey sequence.//7.7e-18:117:95//AQ186312
F-NT2RP5003522//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.8e-101:211:96//AC005236
F-NT2RP5003524//Homo sapiens beta-spectrin (HSpTB1) gene, exon 14 and partial cds.//0.00056:650:57//AF013178
F-NT2RP5003534//H.sapiens CpG island DNA genomic Mse1 fragment, clone 14c10, forward read cpg14c10.ft1b.//0.00013:70:91//Z54631
F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds.//1.2e-67:373:94//AB007934
F-OVARC1000004//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//5.8e-93:518:81//AC005510
F-OVARC1000006//Gallus gallus histone H2A (H2A-VIII) gene, complete cds.//9.1e-56:392:84//U38933
F-OVARC1000013
F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//5.6e-170:815:98//AF058922
F-OVARC1000017//Streptomyces glaucescens tcm operon.//0.37:347:60//M80674
F-OVARC1000035//Homo sapiens GA17 protein mRNA, complete cds.//6.8e-36:238:89//AF064603
F-OVARC1000058
F-OVARC1000060//Homo sapiens ribonuclease 6 precursor, mRNA, complete cds.//2.5e-36:192:98//U85625
F-OVARC1000068//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 404K8, WORKING DRAFT SEQUENCE.//0.14:554:57//AL023883
F-OVARC1000071//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 596C15, WORKING DRAFT SEQUENCE.//5.3e-104:197:100//AL031387
F-OVARC1000085//Human DNA sequence from clone 191N21 on chromosome 6q27 Contains genes for PDCD2 (PROGRAMMED CELL DEATH-2/RP8 HOMOLOG), TATA factor (TFIID), proteasome subunit HC5, EST, STS, GSS, complete sequence.//1.6e-116:588:96//AL031259
F-OVARC1000087//HS_2004_B2_E11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2004 Col=22 Row=J, genomic survey sequence.//7.1e-11:94:94//AQ221037
F-OVARC1000091//nbxb0020P17r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0020P17r, genomic survey sequence.//5.2e-05:238:64//AQ258489
F-OVARC1000092//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//1.1e-10:720:58//AC004617
F-OVARC1000106//HS_3212_B2_G12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

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nomic clone Plate=3212 Col=24 Row=N, genomic survey sequence.//9.9e-05:141:73//AQ175369
F-OVARC1000109
F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//1.6e-133:663:96//AF069250
F-OVARC1000114//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1111N9, WORKING DRAFT SEQUENCE.//2.3e-51:547:70//AL022574
F-OVARC1000133//Homo sapiens clone GS512I21, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.62:349:61//AC005027
F-OVARC1000139//Caenorhabditis elegans cosmid F09D1.//2.5e-18:314:64//AF040640
F-OVARC1000145//HS_2257_B2_D11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2257 Col=22 Row=H, genomic survey sequence.//5.8e-30:203:90//AQ304854
F-OVARC1000148//CIT-HSP-2345A22.TR CIT-HSP Homo sapiens genomic clone 2345A22, genomic survey sequence.//1.1e-26:146:100//AQ056703
F-OVARC1000151//Sequence 1 from patent US 5665588.//2.6e-61:677:70//I64695
F-OVARC1000168//Homo sapiens chromosome 19, cosmid R31343, complete sequence.//4.9e-19:381:63//AC005764
F-OVARC1000191//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//1.3e-06:745:57//AL034557
F-OVARC1000198//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//6.4e-161:781:97//AC004604
F-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//9.2e-33:511:65//AF068332
F-OVARC1000212//F.rubripes GSS sequence, clone 185L11aC1, genomic survey sequence.//1.1e-13:139:79//AL019910
F-OVARC1000240//Sequence 1 from patent US 5710024.//1.4e-129:623:98//I81226
F-OVARC1000241//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//1.1e-112:697:87//AF060194
F-OVARC1000288 2.2e-22:181:83//J00345
F-OVARC1000302//A-192A9.TP CIT978SK Homo sapiens genomic clone A-192A9, genomic survey sequence.//4.8e-18:110:99//B18003
F-OVARC1000304//Mouse mRNA from Mov10 locus.//5.5e-100:631:85//X52574
F-OVARC1000309
F-OVARC1000321//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.1e-122:325:95//AC005236
F-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//4.0e-46:339:84//U19614
F-OVARC1000335//Caenorhabditis elegans cosmid F15B10.//0.020:545:57//AF036696
F-OVARC1000347//Homo sapiens clone GS051M12, complete sequence.//0.71:252:59//AC005007
F-OVARC1000384//Homo sapiens expanded SCA7 CAG repeat.//2.2e-09:276:64//AF020275
F-OVARC1000408//Human Chromosome 11p15.5 PAC clone pDJ915f1 containing KvLQT1 gene, complete sequence.//0.61:343:59//AC003693
F-OVARC1000411//S.cerevisiae chromosome XI reading frame ORF YKL202w.//0.075:242:60//Z28201
F-OVARC1000414//Homo sapiens PAC clone DJ0905M06 from 7q31, complete sequence.//0.00088:285:62//AC005166
F-OVARC1000420//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 371H6, WORKING DRAFT SEQUENCE.//0.14:487:60//AL031718
F-OVARC1000427//Homo sapiens clone UWGC:rg041a03 from 7p14-15, complete sequence.//4.9e-30:195:84//AC005826
F-OVARC1000431//Plasmodium falciparum MAL3P2, complete sequence.//1.3e-05:651:59//AL034558
F-OVARC1000437//Chicken tensin mRNA, complete cds.//9.6e-54:296:78//M74165
F-OVARC1000440//Human PINCH protein mRNA, complete cds.//2.7e-19:116:99//U09284
F-OVARC1000442//Human DNA sequence from clone 816K17 on chromosome 20p12.2-13 Contains TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3 PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANSGLUTAMINASE 3), and another member of the Transglutaminase family, complete sequence.//1.0e-21:202:79//AL031678 F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds.//1.0e-138:566:99//AB014583
F-OVARC1000461
F-OVARC1000465//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//4.7e-

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124:650:93//AF023451
F-OVARC1000466//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//1.0e-15:510:59//AC004221
F-OVARC1000473//Ciona intestinalis genomic fragment, clone 3F4, genomic survey sequence.//2.5e-06:272:62//AJ227191
F-OVARC1000479//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.1e-117:652:90//E12829
F-OVARC1000486//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceeded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//1.7e-13:709:60//Z99297
F-OVARC1000496//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 455J7, WORKING DRAFT SEQUENCE.//6.0e-23:316:72//AL031733
F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.1e-113:539:99//AF051850
F-OVARC1000526//Homo sapiens clone GS438P06, WORKING DRAFT SEQUENCE, 17 unordered pieces.//8.0e-149:716:98//AC005024
F-OVARC1000533//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//5.8e-137:545:97//AC004510
F-OVARC1000543//HS_3055_A2_F10_MF CIT Approved Human Genomic_Sperm Library D Homo sapiens genomic clone Plate=3055 Col=20 Row=K, genomic survey sequence.//0.19:104:71//AQ102820
F-OVARC1000556//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//4.4e-136:670:97//AL022069
F-OVARC1000557//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence, complete sequence.//1.3e-15:262:69//AC002985
F-OVARC1000564//Mus musculus clone OST7314, genomic survey sequence.//1.9e-41:476:70//AF046733
F-OVARC1000573//HS_3241_B1_H03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=5 Row=P, genomic survey sequence.//2.2e-101:530:95//AQ211942
F-OVARC1000576//Human Chromosome X, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.7e-97:445:90//AC002414
F-OVARC1000578//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//9.1 e-27:354:72//AC003973
F-OVARC1000588//Human DNA sequence from clone 497J21 on chromosome 6q26-27. Contains a KOC (KH-domain containg transcript overexpressed in cancer) pseudogene, genomic marker D6S193, ESTs, STSs and GSSs, and a ca repeat polymorphism, complete sequence.//0.97:276:62//AL023775
F-OVARC1000605
F-OVARC1000622//Homo sapiens (subclone 2_d8 from P1 H42) DNA sequence, complete sequence.//7.2e-60:457:82//L81648
F-OVARC1000640//Human BAC clone RG326K09 from 7q21, complete sequence.//6.2e-58:499:80//AC002069
F-OVARC1000649//Human squamous cell carcinama of esophagus mRNA for GRB-7 SH2 domain protein, complete cds.//5.1e-77:424:93//D43772
F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds.//4.8e-99:536:94//AB011162
F-OVARC1000678//cSRL-29c7-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-29c7, genomic survey sequence.//2.5e-57:336:91//B04244
F-OVARC1000679//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//1.6e-81:291:84//AJ001713
F-OVARC1000681//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 257E24, WORKING DRAFT SEQUENCE.//8.2e-158:782:96//AL034424
F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.5e-151:549:99//AF027156
F-OVARC1000689//nbxb0003aG01f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0003M01f, genomic survey sequence.//0.17:499:60//AQ050003
F-OVARC1000700
F-OVARC1000703//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds.//3.5e-26:425:65//U34925
F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds.//3.7e-109:451:91//AF038661
F-OVARC1000730
F-OVARC1000746
F-OVARC1000769//HS_2056_B2_G06_T7 CIT Approved Human Genomic Sperm-Library D Homo sapiens genomic clone Plate=2056 Col=12 Row=N, genomic survey sequence.//8.8e-19:147:86//AQ245905

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F-OVARC1000771//M.musculus mRNA for GTP-binding protein.//2.2e-62:305:78//X95403
F-OVARC1000781//Sequence 5 from Patent WO9722695.//1.9e-89:705:78//A63552
F-OVARC1000787//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//3.0e-131:631:98//AC004542
F-OVARC1000800//Human Chromosome 11q23 PAC clone pDJ254e13, complete sequence.//1.7e-32:295:80//AC003691
F-OVARC1000802//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.//3.2e-55:356:88//AC004469
F-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//9.5e-27:163:94//Y17711
F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds.//6.0e-150:432:100//AB014543
F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//1.0e-135:632:99//AF045584
F-OVARC1000862//M.musculus mRNA for FT1.//2.6e-109:769:83//Z67963
F-OVARC1000876//S.cerevisiae chromosome IX cosmid 9150.//7.4e-21:541:61//Z38125
F-OVARC1000883//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//2.2e-08:98:88//U20086
F-OVARC1000885//B.subtilis 25 kb genomic DNA segment (from sspE to katA).//0.25:231:61//Z82044
F-OVARC1000886//CIT-HSP-2171H6.TR CIT-HSP Homo sapiens genomic clone 2171H6, genomic survey sequence.//0.00035:139:69//B89721
F-OVARC1000890
F-OVARC1000891
F-OVARC1000897//Human DNA sequence from clone 215F16 on chromosome 22q12.1-12.3. Contains part of a Homeobox domain containing gene and GSSs, complete sequence.//1.4e-18:473:64//AL024494
F-OVARC1000912//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//8.9e-08:378:63//L14320
F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds.//7.7e-85:440:95//AB011172
F-OVARC1000924//HS_2022_A1_C01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2022 Col=1 Row=E, genomic survey sequence.//5.7e-21:122:99//AQ269493
F-OVARC1000936//Human PAC clone DJ0093I03 from Xq23, complete sequence.//1.2e-113:476:91//AC003983
F-OVARC1000937//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20208, WORKING DRAFT SEQUENCE.//0.00066:436:61//AL031848
F-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//5.0e-89:556:86//AB005549
F-OVARC1000948//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.98:160:64//X95276
F-OVARC1000959//CIT-HSP-2348O16.TR CIT-HSP Homo sapiens genomic clone 2348O16, genomic survey sequence.//0.99:270:59//AQ062850
F-OVARC1000960//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat,.//3.9e-41:577:72//AL009181
F-OVARC1000964//P.falciparum malaria antigen (M26-32-2) gene, partial cds.//0.19:83:73//M63270
F-OVARC1000971//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y57G11, WORKING DRAFT SEQUENCE.//0.013:670:57//Z92841
F-OVARC1000984//Leishmania major chromosome 1, complete sequence.//0.80:345:58//AE001274
F-OVARC1000996//MO25 gene [mice, embryos, mRNA, 2322 nt].//2.6e-55:403:82//S51858
F-OVARC1000999//Synthetic construct galanin receptor type 3 (GALR3) gene, complete cds.//0.33:105:69//AF042785
F-OVARC1001000//HS_2247_A1_H05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2247 Col=9 Row=O, genomic survey sequence.//3.1e-60:315:96//AQ153910
F-OVARC1001004//Homo sapiens from UWGC:y18c282 from 6p21, complete sequence.//3:1e-124:595:98//AC004190
F-OVARC1001010//CIT-HSP-2034M3.TF CIT-HSP Homo sapiens genomic clone 2034M3, genomic survey sequence.//1.0:151:60//B74290
F-OVARC1001011//Human DNA sequence from cosmid U85A3, between markers DXS366 and DXS87 on chromosome X contains rad21 and T-cell cyclophorin pseudogenes, STS.//3.0e-08:149:79//Z78021
F-OVARC1001032//Yeast (S.cerevisiae) mitochondrial Tyr-tRNA gene.//3.2e-13:667:60//M12451
F-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//2.5e-119:737:86//AF001533
F-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds.//2.7e-150:733 :97//AF099149
F-OVARC1001040//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//9.8e-29:277:76//AC005081
F-OVARC1001044//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 364I1, WORKING DRAFT SEQUENCE.//0.0017:387:6.1//AL031319

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F-OVARC1001051//Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds.//0.012:112:74//AF053768
F-OVARC1001055//Sequence 1 from patent US 5580754.//3.3e-45:381:81//I30292
F-OVARC1001062//nbxb0026H08r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0026H08r, genomic survey sequence.//0.018:344:59//AQ271878
F-OVARC1001065//S.pombe chromosome I cosmid c29E6.//0.86:338:59//Z66525
F-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//2.0e-130:620:98//AF082657
F-OVARC1001072//Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions.//9.3e-24:285:65//AF003529
F-OVARC1001074//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//2.0e-07:652:59//AL022153
F-OVARC1001085//Homo sapiens c-syn protooncogene mRNA, complete cds.//5.0e-35:187:99//M14333
F-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//4.0e-74:289:95//AJ005897
F-OVARC1001107//Homo sapiens SKB1Hs mRNA, complete cds.//3.6e-72:351:86//AF015913
F-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//6.4e-150:710:98//AF051782
F-OVARC1001117//Homo sapiens chromosome 5, P1 clone 328E3 (LBNL H53), complete sequence.//0.99:148:67//AC005178
F-OVARC1001118//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.6e-35:302:74//AC000382
F-OVARC1001129//CIT-HSP-647P20.TP CIT-HSP Homo sapiens genomic clone 647P20, genomic survey sequence.//0.94:106:66//B79052
F-OVARC1001154//R.norvegicus mRNA for epithelin 1 and 2.//1.8e-95:462:79//X62322
F-OVARC1001161//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//2.9e-90:496:84//AC004069
F-OVARC1001162
F-OVARC1001167//Homo sapiens clone DJ1098J04, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00090:219:64//AC004961
F-OVARC1001169//Borrelia burgdorferi (section 27 of 70) of the complete genome.//1.0:265:59//AE001141
F-OVARC1001170//H.sapiens (xs170) mRNA, 350bp.//4.6e-58:355:90//Z36823
F-OVARC1001171//CIT-HSP-2285E22.TF CIT-HSP Homo sapiens genomic clone 2285E22, genomic survey sequence.//1.5e-25:152:83//AQ002315
F-OVARC1001173//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//0.0024:94:80//AL022323
F-OVARC1001176//Streptomyces plicatus B-N-acetylhexosaminidase (hex) gene, complete cds.//1.0:356:60//AF063001
F-OVARC1001180//G.gallus DNA for polyubiquitin gene Ub II.//0.0062:275:60//X58195
F-OVARC1001188//Homo sapiens full-length insert cDNA clone ZD93F03.//1.8e-32:180:97//AF086486
F-OVARC1001200
F-OVARC1001232//Caenorhabditis elegans cosmid F10B5, complete sequence.//0.013:128:67//Z48334
F-OVARC1001240//Human Chromosome 11 pac pDJ360p17, WORKING DRAFT SEQUENCE, 44 unordered pieces.//3.7e-131:811:87//AC001235
F-OVARC1001243//Human BAC clone GS117O10 from 7q21-q22, complete sequence.//0.044:457:59//AC003078
F-OVARC1001244//Human homolog of Drosophila female sterile homeotic mRNA, complete cds.//8.4e-18:118:95//M80613
F-OVARC1001261//Mus musculus putative membrane-associated guanylate kinase 1 (Magi-1) mRNA, alternatively spliced c form, partial cds.//1.4e-95 :649:84//AF027505
F-OVARC1001268//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//0.00051:72:83//U35776
F-OVARC1001270
F-OVARC1001271//Homo sapiens mRNA for KIAA0643 protein, partial cds.//2.1e-142:644:96//AB014543
F-OVARC1001282//RPCI11-60K8.TK RPCI11 Homo sapiens genomic clone R-60K8, genomic survey sequence.//0.0089:285:58//AQ195857
F-OVARC1001296//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//3.0e-20:263:73//U97018
F-OVARC1001306//nbxb0002M13r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0002M13r, genomic survey sequence.//0.98:170:66//AQ156061

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F-OVARC1001329//Homo sapiens BAC clone RG370M10 from 7p15, complete sequence.//1.3e-05:432:61//AC003986
F-OVARC1001330//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.027:444:59//AC005504
F-OVARC1001339//Homo sapiens chromosome 17, clone hCIT.124_H_2, complete sequence.//0.76:89:74//AC006071
F-OVARC1001341//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//0.99:45:86//AQ263402
F-OVARC1001342
F-OVARC1001344//HS-1059-A2-H02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 781 Col=4 Row=O, genomic survey sequence.//1.5e-07:254:67//B44456
F-OVARC1001357//Homo sapiens Xp22-149 BAC RPCI11-466O4 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.83:376:61//AC005297
F-OVARC1001360
F-OVARC1001369//Homo sapiens clone 162B15, complete sequence.//0.0066:99:76//AC004811
F-OVARC1001372//Homo sapiens liprin-alpha4 mRNA, partial cds.//2.7e-142:683:98//AF034801
F-OVARC1001376//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 850H21, WORKING DRAFT SEQUENCE.//1.9e-52:382:73//AL031680
F-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL.//1.2e-147:683:99//AJ224819
F-OVARC1001391//S.coelicolor whiB gene.//0.018:454:59//X62287
F-OVARC1001399//CIT-HSP-229118.TR CIT-HSP Homo sapiens genomic clone 229118, genomic survey sequence.//1.7e-11 :104:87//AQ007611
F-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds.//3.9e-149:707:98//AB006651
F-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds.//4.9e-48:586:69//U52426
F-OVARC1001425//Human DNA sequence from clone 1048E9 on chromosome 22q11.2-12.2 Contains pseudogene similar to ribosomal protein S3A and part of a gene similar to C.elegans protein CE02118, ESTs, STS, GSS, complete sequence.//0.0019:96:78//Z99714
F-OVARC1001436//Caenorhabditis elegans mitotic chromosome and X-chromosome associated MIX-1 protein (mix-1) mRNA, complete cds.//0.77:519:59//U96387
F-OVARC1001442//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 998H6, WORKING DRAFT SEQUENCE.//1.0:167:64//AL031687
F-OVARC1001453//Human DNA sequence from PAC 453D15 on chromosome 6 contains STS.//4.4e-64:376:79//Z84482
F-OVARC1001476//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y24F12, WORKING DRAFT SEQUENCE.//0.20:107:71//AL022277
F-OVARC1001480
F-OVARC1001489//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.20:281:63//AC005140
F-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//8.1e-85:479:92//AF016507
F-OVARC1001506//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13F4 ~complete genomic sequence, complete sequence.//1.2e-98:503:83//AC002039
F-OVARC1001525//Human beta-hexosaminidase alpha chain (HEXA) gene, exon 1.//1.7e-13:87:100//M16411
F-OVARC1001542//H.sapiens polymorphic repeat associated with glutamate dehydrogenase pseudogene 5.//0.43:190:68//X69219
F-OVARC1001547//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.017:533:56//AC005140
F-OVARC1001555//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//7.4e-159:416:99//AC005037
F-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//2.4e-115:540:99//AF031165
F-OVARC1001600//Homo sapiens chromosome 21q22.3 PAC 39C17, complete sequence.//5.5e-13:529:62//AF043945
F-OVARC1001610//, complete sequence.//1.4e-12:152:77//AC005409
F-OVARC1001611
F-OVARC1001615//Human DNA sequence from clone 873P14 on chromosome 20p12 Contains STS, GSS, complete sequence.//0.022:146:70//AL031682
F-OVARC1001668//Homo sapiens mRNA for MCM3 import factor, complete cds.//6.5e-109:358:96//AB005543

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F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds.//1.8e-47:393:81//AB006867
F-OVARC1001703//CIT-HSP-2164L6.TF CIT-HSP Homo sapiens genomic clone 2164L6, genomic survey sequence.//0.94:85:69//B92840
F-OVARC1001711//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 317C6, WORKING DRAFT SEQUENCE.//1.9e-06:489:61//Z97651
F-OVARC1001713//Rattus norvegicus neuroligin 2 mRNA, complete cds.//1.0:262:59//U41662
F-OVARC1001726//Human telomere associated repeat sequence, complete sequence.//7.5e-08:283:65//M57752
F-OVARC1001731//Mus musculus gene for beta-tropomyosin.//2.6e-83:606:81//X12650
F-OVARC1001745//HS_3007_B2_G09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=18 Row=N, genomic survey sequence.//0.00020:269:60//AQ164522
F-OVARC1001762//S.pombe chromosome III cosmid c338.//3.0e-17:624:61//AL023781
F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//4.2e-149:706:98//U97670
F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds.//3.0e-115:580:96//AB014575
F-OVARC1001768
F-OVARC1001791//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//5.7e-64:477:78//AC005066
F-OVARC1001795//Homo sapiens chromosome 4 clone B341C20 map 4q25, complete sequence.//6.5e-11:171:76//AC004704
F-OVARC1001802//CITBI-E1-2502A17.TR CITBI-E1 Homo sapiens genomic clone 2502A17, genomic survey sequence.//0.98:214:61//AQ264481
F-OVARC1001805//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//9.5e-151:712:99//AL023694
F-OVARC1001809//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//2.7e-56:522:75//AF068748
F-OVARC1001812//Homo sapiens chromosome 17, clone HCIT104N19, complete sequence.//1.7e-63:526:81//AC003662
F-OVARC1001813//Human DNA sequence from cosmid U144A10, between markers DXS366 and DXS87 on chromosome X contains STS.//0.17:214:65//Z70224
F-OVARC1001820//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 445N2, WORKING DRAFT SEQUENCE.//3.2e-55:379:82//AL031779
F-OVARC1001828//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence.//2.8e-17:509:62//AC005609
F-OVARC1001846//Human DNA sequence from cosmid U73E8, between markers DXS366 and DXS87 on chromosome X.//0.35:403:58//Z73361
F-OVARC1001861//CIT-HSP-2165M3.TR CIT-HSP Homo sapiens genomic clone 2165M3, genomic survey sequence.//2.4e-25:148:96//B94622
F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence.//1.2e-18:122:95//AF070611
F-OVARC1001879//HS_3026_B1_F09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=17 Row=L, genomic survey sequence.//4.9e-29:204:87//AQ207748
F-OVARC1001880//Human interferon regulatory factor 5 (Humirf5) mRNA, complete cds.//3.5e-05:489:60//U51127
F-OVARC1001883//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.9e-29:350:74//AC005020
F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//8.6e-56:300:96//AF061749
F-OVARC1001901//Human DNA sequence from clone 103M22 on chromosome 6p24. Contains STSs and GSSs, complete sequence.//2.3e-10:253:66//AL031904
F-OVARC1001911//HS_2196_B2_H11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196 Col=22 Row=P, genomic survey sequence.//3.4e-09:123:78//AQ294069
F-OVARC1001916//HS_3054_B1_C11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=21 Row=F, genomic survey sequence.//1.2e-31:126:97//AQ099979
F-OVARC1001928
F-OVARC1001942//H.sapiens CpG island DNA genomic Mse1 fragment, clone 21d7, forward read cpg21d7.ft1a.//7.2e-12:83:98//Z60390
F-OVARC1001943//Aplysia californica potassium channel modulatory factor mRNA, complete cds.//3.5e-50:535:69//AF059179

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F-OVARC1001949//Human KRAB zinc finger protein (ZNF177) mRNA, complete cds.//1.7e-16:294:67//U37263
F-OVARC1001950//Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRAFT SEQUENCE.//1.5e-20:261:68//AJ011929
F-OVARC1001987//D.melanogaster G6PD gene, exons 2-4.//0.99:447:57//Z19021
F-OVARC1001989//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.//2.9e-19:178:83//AC005995
F-OVARC1002044//Plasmodium falciparum MAL3P7, complete sequence.//0.17:232:62//AL034559
F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds.//2.1e-158:739:98//AB007934
F-OVARC1002066//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE.//3.0e-17:781:59//AP000011
F-OVARC1002082//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.4e-136:683:96//AC006015
F-OVARC1002107//Homo sapiens BAC clone RG276003 from 7q22-q31.1, complete sequence.//1.0:220:61//AC004668
F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//6.1e-115:557:98//AF041483
F-OVARC1002127//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence.//0.013:461:57//AC006241
F-OVARC1002138//Caenorhabditis elegans cosmid F32D1.//1.0e-29:545:64//AF016427
F-OVARC1002143//CIT-HSP-2343H20.TR CIT-HSP Homo sapiens genomic clone 2343H20, genomic survey sequence.//2.3e-11:258:67//AQ055576
F-OVARC1002156
F-OVARC1002158//F17O7-T7 IGF Arabidopsis thaliana genomic clone F17O7, genomic survey sequence.//1.8e-16:383:66//B11616
F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosinephosphatase.//0.0041:300:64//X79568
F-OVARC1002182//F.rubripes GSS sequence, clone 123I23aA7, genomic survey sequence.//1.4e-10:240:66//AL017241
F-PLACE1000004//CIT-HSP-2294H13.TF CIT-HSP Homo sapiens genomic clone 2294H13, genomic survey sequence.//8.2e-10:158:75//AQ003859
F-PLACE1000005//Mouse alpha-1 antitrypsin gene, segment 1.//4.8e-15:89:93//M12585
F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.//3.8e-51:550:72//AF022789
F-PLACE1000014
F-PLACE1000031//Homo sapiens alone DJ0098O22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.91:333:61//AC004821
F-PLACE1000040//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//2.6e-20:279:67//Z93023
F-PLACE1000048//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//3.6e-63:488:82//AC005177
F-PLACE1000050//Mus musculus chromosome 14 marker um-m24 GA dinucleotide DNA sequence.//2.3e-10:141:75//U31508
F-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//1.9e-30:190:94//L22154
F-PLACE1000066//Homo sapiens PAC clone DJ1106E03 from 7q31.3-7q3, complete sequence.//6.0e-63:597:74//AC005521
F-PLACE1000078//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.2e-09:143:73//AC005848
F-PLACE1000081//Human DNA from chromosome 19 specific cosmid R28461, genomic sequence, complete sequence.//0.52:390:60//AC002389
F-PLACE1000094
F-PLACE1000133//Human DNA sequence from clone 372K1 on chromosome 6q24 Contains EST, STS, GSS and CpG Island, complete sequence.//4.4e-129:731:92//AL023580
F-PLACE1000142//H.sapiens AUH mRNA.//6.4e-09:328:62//X79888
F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//7.7e-150:737:97//AF058291
F-PLACE1000185//Sequence 15 from patent US 5691147.//5.7e-106:558:94//I76211 F-PLACE1000213
F-PLACE1000214//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-06:644:57//AC005504
F-PLACE1000236//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 695O20, WORKING DRAFT SEQUENCE.//2.6e-39:191:83//AL032818

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F-PLACE1000246//HS_2008_A2_D04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=8 Row=G, genomic survey sequence.//0.96:153:61//AQ269813
F-PLACE1000292//Drosophila melanogaster Oregon-R mitochondrial A+T region.//5.1e-12:571:60//U11584
F-PLACE1000308//D.teissieri mitochondrial DNA for tRNA-fmet, tRNA-Ile, tRNA-Gln & amp; tRNA-Val.//0.00013:369:59//X54011
F-PLACE1000332//HS_2016_B2_D08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=16 Row=H, genomic survey sequence.//7.5e-83:424:96//AQ232106
F-PLACE1000347//CIT-HSP-2326A16.TV CIT-HSP Homo sapiens genomic clone 2326A16, genomic survey sequence.//0.13:46:100//AQ047350
F-PLACE1000374//Mus musculus putative CCAAT binding factor 1 (mCBF) mRNA, alternatively spliced transcript mCBF1, complete cds.//0.00048:84:83//U19891
F-PLACE1000380//F.rubripes GSS sequence, clone 047P21aA10, genomic survey sequence.//0.43:198:62//Z88163
F-PLACE1000383//Homo sapiens myotubularin related protein 1 (MTMR1) mRNA, partial cds.//8.7e-149:740:96//U58032
F-PLACE1000401//Pinctada fucata mRNA for insoluble protein, complete cds.//0.22:484:56//D86074
F-PLACE1000406//Human nuclear matrix protein 55 (nmt55) mRNA, complete cds.//3.3e-19:372:65//U89867
F-PLACE1000420//Homo sapiens chromosome 17, clone hRPK.227_G_15, complete sequence.//1.6e-85:421:87//AC005899
F-PLACE1000421//Human GT334 protein (GT334) gene, exons 16 and 17.//0.88:145:68//U61515
F-PLACE1000424//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.076:196:66//AC005189
F-PLACE1000435//HS_3217_A2_A12_MR CIT Approved Human Genomic-Sperm Library D Homo sapiens genomic clone Plate=3217 Col=24 Row=A, genomic survey sequence.//2.2e-47:438:76//AQ181698
F-PLACE1000444//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//6.9e-61:616:71//AC004382
F-PLACE1000453//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//5.8e-18:314:69//AF059580
F-PLACE1000481//Homo sapiens Chromosome 22q11.2 Cosmid Clone 94a In DGCR Region, complete sequence.//1.1e-33:349:76//AC002491
F-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//1.1e-34:256:83//U35245
F-PLACE1000540//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.099:336:58//X95276
F-PLACE1000547//Arabidopsis thaliana GDP-mannose pyrophosphorylase (GMP1) mRNA, complete cds.//5.4e-11:279:63//AF076484
F-PLACE1000562//, complete sequence.//1.7e-97:559:88//AC005409
F-PLACE1000564
F-PLACE1000583//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and-9.//3.3e-46:631:68//M27877
F-PLACE1000588//Human guanylate binding protein isoform I (GBP-2) mRNA, complete cds.//7.3e-84:503:88//M55542
F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//3.8e-164:798:97//AJ012449
F-PLACE1000599//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.018:295:61//X95276
F-PLACE1000610//HS_2056_A1_D10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=19 Row=G, genomic survey sequence.//5.3e-24:188:87//AQ235967
F-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2.4e-47:687:66//AF044201
F-PLACE1000636
F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//1.5e-152:747:96//AF102265
F-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin)).//2.3e-156:775:97//AJ005896
F-PLACE1000706//nuclear protein TIF1 [mice, mRNA, 3951 nt].//8.0e-60:675:70//S78219
F-PLACE1000712
F-PLACE1800716//HS-1057-A1-A03-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 779 Col=5 Row=A, genomic survey sequence.//2.7e-42:266:82//B43026
F-PLACE1000748//CIT-HSP-2372J8.TR CIT-HSP Homo sapiens genomic clone 2372J8, genomic survey sequence.//0.023:157:68//AQ113109

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F-PLACE1000749//Plasmodium falciparum MAL3P7, complete sequence.//0.099:664:57//AL034559
F-PLACE1000755//H.sapiens DNA 3' flanking simple sequence region clone wg2c3.//0.00068:206:62//X76589
F-PLACE1000769//RPCI11-3J18.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-3J18, genomic survey sequence.//6.5e-08:93:89//B63806
F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//3.5e-138:663:98//AB014548
F-PLACE1000786//Drosophila melanogaster cosmid 80H7.//1.4e-43:589:68//AL031027
F-PLACE1000793//H.sapiens CpG island DNA genomic Mse1 fragment, clone 13d12, reverse read cpg13d12.rt1c.//4.6e-09:71:100//Z64565
F-PLACE1000798//Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.//5.0e-14:235:72//AC002310
F-PLACE1000841//Homo sapiens clone NH0441G08, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.013:404:60//AC006158
F-PLACE1000849//H.sapiens CpG island DNA genomic Mse1 fragment, clone 72a10, reverse read cpg72a10.rt1a.//3.3e-09:82:92//Z62712
F-PLACE1000856//Hydra vulgaris HT4 mRNA for collagen-like protein, partial cds.//1.0:317:59//AB008935
F-PLACE1000863//H.sapiens CpG island DNA genomic Mse1 fragment, clone 53d2, forward read cpg53d2.ft1b.//7.3e-37:199:98//Z55621
F-PLACE1000909//H.sapiens CpG island DNA genomic Mse1 fragment, clone 173f8, reverse read cpg173f8.rt1a.//1.5e-17:128:92//Z57391
F-PLACE1000931//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.,//8.1e-55:647:72//AL009181
F-PLACE1000948
F-PLACE1000972//RPCI11-61B1.TJ RPCI11 Homo sapiens genomic clone R-61B1, genomic survey sequence.//1.0e-26:148:99//AQ194348
F-PLACE1000977//Homo sapiens mRNA for KIAA0672 protein, complete cds.//6.1e-08:413:61//AB014572
F-PLACE1000979//H.sapiens CpG island DNA genomic Mse1 fragment, clone 76e8, reverse read cpg76e8.rt1a.//2.7e-10:84:94//Z55963
F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds.//8.0e-140:694:96//AB018267
F-PLACE1001000//Herpetomonas muscarum muscarum kinetoplast 12S rRNA gene.//0.0056:443:58//U01011
F-PLACE1001007//CIT-HSP-2013L15.TF CIT-HSP Homo sapiens genomic clone 2013L15, genomic survey sequence.//0.99:277:58//B58681
F-PLACE1001010//Human cosmid g1572c101, complete sequence.//3.6e-55:294:88//AC000357
F-PLACE1001015//Homo sapiens PAC clone DJ0754J18 from 7p21, complete sequence.//7.2e-33:333:73//AC004741
F-PLACE1001024
F-PLACE1001036//CIT-HSP-2373I10.TF CIT-HSP Homo sapiens genomic clone 2373I10, genomic survey sequence.//1.1e-80:393:98//AQ108662
F-PLACE1001054//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence.//8.8e-40:483:66//AB013390
F-PLACE1001062//Mus musculus mRNA encoding lysine-ketoglutarate reductase/saccharopine dehydrogenase.//1.2e-23:224:80//AJ224761
F-PLACE1001076//HS_2195_B1_D05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=9 Row=H, genomic survey sequence.//0.0014:168:66//AQ066659
F-PLACE1001088
F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//3.1e-95:489:96//AF065485
F-PLACE1001104//Caprine arthritis-encephalitis virus envelope glycoprotein (env) gene, partial cds.//0.0073:253:62//U81400
F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds.//2.5e-64:676:71//AF022158
F-PLACE1001136//Human amphiregulin (AR) gene, exon 5, clones lambda-ARH(6,12).//3.8e-26:174:93//M30702
F-PLACE1001168
F-PLACE1001171//Homo sapiens subtelomeric cosmid 11b-1, complete sequence.//7.6e-23:245:68//AC005603
F-PLACE1001185//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte Marker-CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.010:102:70//AL031177
F-PLACE1001238//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//9.3e-82:684:

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77//D14336
F-PLACE1001241
F-PLACE1001257//Caenorhabditis elegans cosmid R12E2.//1.1e-16:480:60//AF067219
F-PLACE1001272//H.sapiens subunit of coatomer complex.//0.31:50:96//X70476
F-PLACE1001279//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.054:352:60//AC005507
F-PLACE1001280//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//1.0e-10:620:61//L14320
F-PLACE1001294//M.musculus GEG-154 mRNA.//5.0e-107:826:80//X71642
F-PLACE1001304//Mouse Zfp-35 mRNA for zinc finger protein ZFP-35.//1.2e-67:510:77//X17617
F-PLACE1001311//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-47:491:73//AC005282
F-PLACE1001323//HS-1007-A2-B10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 328 Col=20 Row=C, genomic survey sequence.//9.6e-26:142:100//B31181
F-PLACE1001351
F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cds.//8.6e-25:155:95//AB018342
F-PLACE1001377//H.sapiens MADM gene (exon 1).//1.6e-43:393:79//Z48614
F-PLACE1001383//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene. EST, CA repeats (D22S414, D22S925. D22S926), STS, GSS and CpG island, complete sequence.//1.5e-119:705:91//AL022324
F-PLACE1001384//Homo sapiens mRNA for multi PDZ domain protein.//5.7e-08:117:84//AJ001319
F-PLACE1001387//Sequence 3 from patent US 5610018.//1.7e-06:395:58//I57340
F-PLACE1001395//Plasmodium falciparum circular DNA rpoB and rpoC genes for beta and beta-prime subunits of RNA polymerase (EC 2.7.7.6).//7.2e-11:620:60//X52177
F-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.0e-145:700:98//AC005412
F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence.//2.0e-69:365:96//AF091087
F-PLACE1001414//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence.//8.2e-121:608:97//AC006241
F-PLACE1001440//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.3e-06:437:61//AC000384
F-PLACE1001456//Homo sapiens Xp22 GS-524I1 (Genome Systems Human BAC library), complete sequence.//0.98:348:60//AC003106
F-PLACE1001468//Homo sapiens DNA sequence from PAC 435A7 on chromosome Xq22.1-q22.3. Contains STS.//4.4e-05:358:62//AL022148
F-PLACE1001484//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 387E22, WORKING DRAFT SEQUENCE.//5.7e-31:195:93//AL031660
F-PLACE1001502//Human fibroblast growth factor receptor 3 (FGFR3) gene, exon L//0.00015:333:59//L78720
F-PLACE1001503//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//0.00016:161:66//AC004373
F-PLACE1001517//Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs.//3.7e-22:260:76//AL021786
F-PLACE1001534//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 620E11, WORKING DRAFT SEQUENCE.//1.1e-143:713:97//AL031667
F-PLACE1001545//Homo sapiens chromosome 3, clone hRPK.165_I_16, complete sequence.//2.7e-139:482:96//AC005669
F-PLACE1001551//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//6.9e-116:681:89//AC005261
F-PLACE1001570//HS_3105_A1_F06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3105 Col=11 Row=K, genomic survey sequence.//1.2e-10:137:79//AQ139817
F-PLACE1001602//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11.//1.8e-102:217:99//AB020860
F-PLACE1001603//Homo sapiens nitrilase homolog 1 (NIT1) gene, alternatively spliced product, complete cds.//3.7e-104:501:98//AF069984
F-PLACE1001608//HS_2189_A1_G07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2189 Col=13 Row=M, genomic survey sequence.//2.9e-60:429:84//AQ221959
F-PLACE1001610//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.4e-114:552:98//AC005037

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F-PLACE1001611//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//0.93:131:71//AL031587
F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds.//1.1e-74:702:75//AB018341
F-PLACE1001634//Human p190-B (p190-B) mRNA, complete cds.//1.2e-18:114:100//U17032
F-PLACE1001640//Homo sapiens chromosome 17, clone hRPK.651_L_9, complete sequence.//7.7e-159:788:97//AC005971
F-PLACE1001672//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055, complete sequence.//7.8e-36:365:73//AL022165
F-PLACE1001691//Homo sapiens chromosome 17, clone hRPK.294_J_22, complete sequence.//9.1e-149:760:96//AC005921
F-PLACE1001692//Rat medium-chain S-acyl fatty acid synthetase thio ester hydrolase (MCH), complete cds.//2.9e-57:643:71//M16200
F-PLACE1001705//Homo sapiens chromosome 17, clone hRPK.958_E_11, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.9e-18:284:71//AC005883
F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds.//6.6e-68:369:73//D83776
F-PLACE1001720//Homo sapiens Chromosome 22q11.2 Cosmid Clone 31f3 In IGLC Region, complete sequence.//1.0:274:59//AC000051
F-PLACE1001729//Streptomyces coelicolor cosmid 1C2.//0.22:433:57//AL031124
F-PLACE1001739//Caenorhabditis elegans cosmid C18H7.//0.049:341:61//AF067607
F-PLACE1001740//Homo sapiens chromosome 5, P1 clone 1108H7 (LBNL H81), complete sequence.//4.8e-26:372:68//AC005221
F-PLACE1001745
F-PLACE1001746//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//0.018:472:57//AL031744
F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//8.8e-159:773:97//AF061243
F-PLACE1001756//Homo sapiens chromosome 12p13.3 clone RPCI11-303E5, WORKING DRAFT SEQUENCE, 65 unordered pieces.//1.9e-54:274:81//AC005842
F-PLACE1001761//HS_3027_A1_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=3 Row=G, genomic survey sequence.//0.095:49:93//AQ130972
F-PLACE1001771//Homo sapiens transient receptor potential protein 6 mRNA, complete cds.//1.0e-146:709:97//AF080394
F-PLACE1001781 1.3e-08:238:65//AC005637
F-PLACE1001799//HS_3075_B1_H03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=5 Row=P, genomic survey sequence.//1.7e-09:166:69//AQ138474
F-PLACE1001810//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence.//0.00035:196:66//AB020749
F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//1.1e-108:546:96//AF058953
F-PLACE1001821//RPCI11-35D17.TK RPCI-11 Homo sapiens genomic clone RPCI-11-35D17, genomic survey sequence.//2.1e-55:300:97//AQ045286
F-PLACE1001844//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//2.8e-67:443:86//AC005177
F-PLACE1001845//Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence.//0.34:219:64//AC005850
F-PLACE1001869//Klebsiella pneumoniae ribitol kinase (rbtK) and ribitol transporter (rbtT) genes, complete cds.//7.1e-11:505:57//AF045244
F-PLACE1001897//RPCI11-46D15.TJ RPCI11 Homo sapiens genomic clone R-46D15, genomic survey sequence.//9.3e-08:383:63//AQ194408
F-PLACE1001912
F-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//7.3e-156:753:98//AF099935
F-PLACE1001928//HS_2220_B2_G04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2220 Col=8 Row=N, genomic survey sequence.//2.8e-43:233:97//AQ152361
F-PLACE1001983//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 745C22, WORKING DRAFT SEQUENCE.//1.6e-07:396:62//AL031596

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F-PLACE1001989//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//1.0e-109:602:93//AL023755
F-PLACE1002004//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 317E23, WORKING DRAFT SEQUENCE.//1.0e-69:475:87//AL020996
F-PLACE1002046//Mus musculus ligatin (Lgtn) mRNA, partial cds.//7.2e-97:623:85//U58337
F-PLACE1002052//HS_2178_B2_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=10 Row=H, genomic survey sequence.//4.8e-22:140:95//AQ307908
F-PLACE1002066//Apis mellifera NADH dehydrogenase subunit 2 (ND2) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.0063:371:60//U72284
F-PLACE1002072//Homo sapiens tight junction protein ZO (ZO-2) gene, alternative splice products, promoter and exon A.//0.97:248:60//AF043195
F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds.//1.3e-37:635:64//AB011178
F-PLACE1002090//Homo sapiens full-length insert cDNA clone ZA85C09.//7.0e-122:583:98//AF086131
F-PLACE1002115//nbxb0038A20r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0038A20r, genomic survey sequence.//0.039:210:69//AQ291086
F-PLACE1002119//Mus musculus IER5 (Ier5) mRNA, complete cds.//7.1e-61:540:77//AF079527
F-PLACE1002140//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-125:491:98//AL022162
F-PLACE1002150//Plasmodium falciparum MAL3P5, complete sequence.//0.12:408:61//AL034556
F-PLACE1002157//Homo sapiens BAC clone NH0335J18 from 2, complete sequence.//1.1e-44:515:71//AC005539
F-PLACE1002163//Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence.//0.98:210:65//AE000662
F-PLACE1002170//Homo sapiens Xp22 bins 16-17 BAC GSHB-531I17 (Genome Systems Human BAC Library) complete sequence.//1.2e-06:283:60//AC004805
F-PLACE1002171//Mus musculus interferon alpha/beta receptor (IFNAR) gene, exon 11 and partial cds.//1.0e-24:313:71//U06244
F-PLACE1002205//Drosophila melanogaster; Chromosome 3L; Region 79F1-80A2; BAC clone BACR48E05, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-05:428:60//AC005720
F-PLACE1002213//HS_3238_B1_G03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=5 Row=N, genomic survey sequence.//2.2e-74:371:98//AQ206965
F-PLACE1002227//HS-1056-B1-C01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 778 Col=1 Row=F, genomic survey sequence.//2.1e-07:174:71//B42800
F-PLACE1002256//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-72, complete sequence.//0.022:458:59//AL010142
F-PLACE1002259//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//3.5e-91:637:84//AL022324
F-PLACE1002319
F-PLACE1002342//Caenorhabditis elegans cosmid M03A1.//0.47:403:58//U49956
F-PLACE1002395//Homo sapiens chromosome 19, cosmid R28991, complete sequence.//1.9e-127:487:93//AC004623
F-PLACE1002399//Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence.//5.6e-05:474:59//AC005922
F-PLACE1002433//Drosophila melanogaster fidipidine gene, exons 1-7.//1.7e-11:613:58//AJ011928
F-PLACE1002437//M.musculus abc1 mRNA.//5.5e-62:452:85//X75926
F-PLACE1002438//Dictyostelium discoideum developmental protein DG1098 (DG1098) gene, partial cds.//0.013:372:59//AF081801
F-PLACE1002450//HS_3233_A1_G01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3233 Col=1 Row=M, genomic survey sequence.//3.1e-07:449:59//AQ204769
F-PLACE1002465
F-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//1.5e-110:720:85//U69262
F-PLACE1002477//Homo sapiens Xp22-171-173 BAC GSHB-312I4 (Genome Systems Human BAC Library) complete sequence.//3.9e-05:195:71//AC005926
F-PLACE1002493//Homo sapiens 3p22-8 PAC RPCI4-736H12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.020:301:60//AC006060
F-PLACE1002499

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F-PLACE1002500//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//2.1e-58:465:80//U50927
F-PLACE1002514//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 292E10, WORKING DRAFT SEQUENCE.//3.7e-08:139:76//Z93930
F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//9.0e-143:583:95//AB018256
F-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1, complete sequence.//0.00019:193:65//AC004774
F-PLACE1002537//Human DNA sequence from clone 127F18 on chromosome Xp11.4-21.3. Contains part of a novel gene with some similarity to parts of chicken Myosin Light Chain and various species' Interleukin-1 Receptor Type 1 (IL1-R-1). Contains GSSs, complete sequence.//4.7e-25:198:84//AL031575
F-PLACE1002571//Drosophila melanogaster actin-related protein mRNA, complete cds.//2.0e-13:400:60//L25314
F-PLACE1002578//Homo sapiens Xq28 BACs 360 F12, GSHB-555C13, complete sequence.//3.5e-11:167:72//AC002523
F-PLACE1002583//Mus musculus glutamate receptor subunit (GluR6) gene, partial cds.//4.2e-09:370:61//U31443
F-PLACE1002591//H.sapiens mRNA for coronin.//7.2e-26:279:74//X89109
F-PLACE1002598//Homo sapiens clone GS308H05, WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.0013:375:64//AC005537
F-PLACE1002604//Hansenula wingei mitochondrial DNA, complete sequence.//4.7e-05:556:59//D31785
F-PLACE1002625
F-PLACE1002655//Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.//1.6e-128:229:92//AC005281
F-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//3.6e-107:706:84//AF079765
F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//3.4e-186:804:97//AF068180
F-PLACE1002714//Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.//2.3e-16:474:64//AF051726
F-PLACE1002722//Sequence 1 from patent US 5686597.//1.7e-107:552:95//I73723
F-PLACE1002768//Human DNA sequence from clone 726F20 on chromosome 1p36.11-36.23. Contains ESTs and a GSS, complete sequence.//0.0076:161:70//AL031273
F-PLACE1002772//HS_3058_A1_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=3 Row=G, genomic survey sequence.//0.0046:192:64//AQ134567
F-PLACE1002775//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//7.6e-14:459:62//AF084259
F-PLACE1002782//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//3.6e-43:385:77//U50927
F-PLACE1002794//CIT-HSP-2368A17.TR CIT-HSP Homo sapiens genomic clone 2368A17, genomic survey sequence.//1.3e-71:368:96//AQ075879
F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds.//1.8e-44:567:70//D79994
F-PLACE1002815//Sequence 25 from patent US 5747660.//2.6e-07:150:73//AR005295
F-PLACE1002816//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//1.3e-68:687:73//AF039691
F-PLACE1002834//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and 9.//9.3e-41:240:93//M27877
F-PLACE1002839//Human BAC clone RG205G13 from 7q31, complete sequence.//0.00087:213:63//AC003045
F-PLACE1002851//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0032:269:66//AC005140
F-PLACE1002853//Leishmania tarentolae kinetoplast pre-edited mitochondrial maxicircle DNA complete transcribed region and flanks.//0.032:275:62//M10126
F-PLACE1002881//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 111B22, WORKING DRAFT SEQUENCE.//4.7e-38:355:76//Z98200
F-PLACE1002908//Gallus gallus beta-1,4-galactosyltransferase (CKII) mRNA, complete cds.//0.00012:200:64//U19889
F-PLACE1002941//Human BAC clone RG161K23 from 7q21, complete sequence.//1.1e-14:241:70//AC000120
F-PLACE1002962
F-PLACE1002968//Plasmodium falciparum MAL3P2, complete sequence.//0.21:410:59//AL034558
F-PLACE1002991//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//6.8e-121:605 :93//AL023755
F-PLACE1002993//CIT-HSP-2338I16.TF CIT-HSP Homo sapiens genomic clone 2338I16, genomic survey sequence.//1.9e-13:100:95//AQ054760
F-PLACE1002996//Mouse U6 RNA gene.//2.0e-13:113:90//X06980

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F-PLACE1003025//Plasmodium falciparum MAL3P6, complete sequence.//0.84:374:58//Z98551
F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds.//6.1e-130:632:97//AB011088
F-PLACE1003044//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.6e-123:687:91//E12829
F-PLACE1003045//H.sapiens CpG island DNA genomic Mse1 fragment, clone 47g6, forward read cpg47g6.ft1a.//0.0064:52:96//Z61200
F-PLACE1003092//CIT-HSP-387P22.TRB CIT-HSP Homo sapiens genomic clone 387P22, genomic survey sequence.//0.0031:249:63//B60158
F-PLACE1003100//Human Hep27 protein mRNA, complete cds.//8.9e-65:650:73//U31875
F-PLACE1003108
F-PLACE1003136//Homo sapiens chromosome 5, P1 clone 1130f1 (LBNL H40), complete sequence.//6.3e-46:606:68//AC004219
F-PLACE1003145
F-PLACE1003153//RPCI11-13P16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-13P16, genomic survey sequence.//2.7e-63:478:82//B76206
F-PLACE1003174//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003176//HS_2255_A2_B01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=2 Row=C, genomic survey sequence.//6.3e-09:137:76//AQ131934
F-PLACE1003190//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.4e-138:791:901/AC005095
F-PLACE1003200//P.falciparum complete gene map of plastid-like DNA (IR-B).//8.7e-06:728:57//X95276
F-PLACE1003205//Human BAC clone RG354L07 from 7q31, complete sequence.//7.5e-05:249:63//AC002466
F-PLACE1003238//HS_3239_A2_G02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3239 Col=4 Row=M, genomic survey sequence.//0.36:64:87//AQ209954
F-PLACE1003249
F-PLACE1003256
F-PLACE1003258//HS_3223_A1_G10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=19 Row=M, genomic survey sequence.//1.4e-07:227:65//AQ190317
F-PLACE1003296//CIT-HSP-2337F11.TF CIT-HSP Homo sapiens genomic clone 2337F11, genomic survey sequence.//1.1e-13:97:95//AQ057429
F-PLACE1003302//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and 9.//2.3e-92:485:95//M27877
F-PLACE1003334
F-PLACE1003342
F-PLACE1003343//Homo sapiens clone DJ1022I14, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.0e-20:179:84//AC004951
F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//8.0e-143:773:92//U92715
F-PLACE1003361//Human Cosmid g1248a143 from 7q31.3, complete sequence.//1.9e-30:402:70//AC004095
F-PLACE1003366
F-PLACE1003369//Plasmodium falciparum MAL3P2, complete sequence.//7.6e-07:378:60//AL034558
F-PLACE1003373//Homo sapiens PAC clone DJ0740L10 from 7p13-p14, complete sequence.//6.0e-18:471:61//AC005247
F-PLACE1003375
F-PLACE1003383//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epitherium cancer, segment 10/10.//2.3e-157:779:96//AB020878
F-PLACE1003394//Sprague-Dawley (clone LRB13) RAB14 mRNA, complete cds.//1.2e-104:596:91//M83680
F-PLACE1003401//RPCI11-71J5.TJ RPCI11 Homo sapiens genomic clone R-71J5, genomic survey sequence.//0.85:140:65//AQ268588
F-PLACE1003420//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y1E3, WORKING DRAFT SEQUENCE.//0.0015:286:60//AL021388
F-PLACE1003454//Plasmodium falciparum microsatellite pe63 sequence.//0.0084:219:61//AF015470
F-PLACE1003478//Homo sapiens calcium-dependent chloride channel-1 (hCLCA1) gene, complete cds.//1.3e-11:746:60//AF039401
F-PLACE1003493
F-PLACE1003516//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence.//8.2e-41:379:78//AC002994

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F-PLACE1003519//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.//6.2e-21:247:76//AF064859
F-PLACE1003521//Human DNA sequence from PAC 257A7 on chromosome 6p24. Contains two unknown genes and ESTs, STSs and a GSS.//4.4e-68:502:79//AL008729
F-PLACE1003528//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//1.0:323:58//AL022336
F-PLACE1003537//Homo sapiens multispanning membrane protein mRNA, complete cds.//0.0054:322:59//U94831
F-PLACE1003553//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//2.9e-78:267:88//AL031297
F-PLACE1003566//Plasmodium falciparum MAL3P3, complete sequence.//0.00026:514:58//Z98547
F-PLACE1003575//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.079:755:54//AC004688
F-PLACE1003583//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//1.1e-41:212:74//AL022324
F-PLACE1003584//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-56, complete sequence.//0.0038:465:57//AL010230
F-PLACE1003592//Homo sapiens chromosome 17, clone 296K1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//0.72:111:71//AC002557
F-PLACE1003593//Human PAC clone DJ318C15 from Xq23, complete sequence.//0.096:162:66//AC002476
F-PLACE1003596//Mus musculus integral membrane protein 1 (Itm1) mRNA, complete cds.//1.4e-54:685:68//L34260
F-PLACE1003602//Homo sapiens mRNA expressed in placenta.//1.1e-138:679:97//D83200
F-PLACE1003605//Homo sapiens chromosome 16, cosmid clone RT81 (LANL), complete sequence.//0.0074:265:63//AC005356
F-PLACE1003611//HS_2198_B1_D02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2198 Col=3 Row=H, genomic survey sequence.//2.1e-23:137:97//AQ184475
F-PLACE1003618//Homo sapiens chromosome 4 clone C0011C13 map 4p16, complete sequence.//3.0e-122:725:89//AC006226
F-PLACE1003625//HS_2238_B2_D11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=22 Row=H, genomic survey sequence.//4.8e-12:92:94//AQ065662
F-PLACE1003638//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD10, complete sequence.//0.043:264:63//AB011478
F-PLACE1003669
F-PLACE1003704//RPCI11-23H21.TKBF RPCI-11 Homo sapiens genomic clone RPCI-11-23H21, genomic survey sequence.//7.1e-31:199:91//AQ013830
F-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA, complete cds.//4.3e-132:669:95//AF053305
F-PLACE1003711//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//1.5e-31:166:99//AL021920
F-PLACE1003723//HS_2231_A2_C07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2231 Col=14 Row=E, genomic survey sequence.//1.2e-12:114:90//AQ235672
F-PLACE1003738//Human zinc finger protein 42 (MZF-1) mRNA, complete cds.//5.9e-33:592:67//M58297
F-PLACE1003760//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//3.6e-11:92:93//AF054840
F-PLACE1003762
F-PLACE1003768//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 7/15, WORKING DRAFT SEQUENCE.//4.8e-77:737:76//AP000014
F-PLACE1003771//Homo sapiens BAC clone GS164B05 from 7p21-p22, complete sequence.//2.1e-164:793:98//AC004160
F-PLACE1003783//HS_2190_A2_C02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2190 Col=4 Row=E, genomic survey sequence.//1.1e-26:147:100//AQ218757
F-PLACE1003784//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//4.5e-57:706:68//AC006210
F-PLACE1003795//Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyl-

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transferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq281u2 gene.//0.015:296:60//U52112
F-PLACE1003833//Homo sapiens DNA sequence from cosmid N75B3 on chromosome 22 Contains EST, exon trap, complete sequence.//0.52:212:64//AL022339
F-PLACE1003850//P.falciparum histidine-rich protein genes.//0.39:330:60//M17028
F-PLACE1003858//Human DNA sequence from PAC 332O11 on chromosome 1q24-1q25. Contains ESTs and STSs.//4.8e-07:461:59//Z98043
F-PLACE1003864//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.026:538:56//AC005139
F-PLACE1003870//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE.//6.5e-06:175:69//Z98304
F-PLACE1003885//Mus musculus poly(A) polymerase VI mRNA, complete cds.//9.4e-75:754:72//U58134
F-PLACE1003886//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.7e-20:432:64//AC006030
F-PLACE1003888//Human mRNA for phospholipase C, complete cds.//2.6e-53:702:67//D42108
F-PLACE1003892//RPCI11-24P17.TV RPCI-11 Homo sapiens genomic clone RPCI-11-24P17, genomic survey sequence.//3.3e-20:245:65//B86759
F-PLACE1003900//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 328E19, WORKING DRAFT SEQUENCE.//2.5e-17:260:71//AL022240
F-PLACE1003903//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds.//2.7e-86:533:87//U49385
F-PLACE1003915//Mus musculus clone OST1963, genomic survey sequence.//6.4e-29:251:80//AF046591
F-PLACE1003923//Homo sapiens full-length insert cDNA clone ZD40A05.//2.8e-25:316:70//AF086251
F-PLACE1003932//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.6e-05:652:58//AC005505
F-PLACE1003936//CIT-HSP-2387C11.TR.1 CIT-HSP Homo sapiens genomic clone 2387C11, genomic survey sequence-//1.0:223:62//AQ239494
F-PLACE1003968//Rattus norvegicus 5'-AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds.//5.2e-47:505:72//U42413
F-PLACE1004103//Homo sapiens chromosome 19, cosmid R28784, complete sequence.//6.7e-29:241:84//AC005954
F-PLACE1004104//Rattus norvegicus rsec5 mRNA, complete cds.//3.0e-115:719:86//AF032666
F-PLACE1004114//Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 In CES Region, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.5e-22:213:80//AC000052
F-PLACE1004118//Pseudorabies virus with upstream and downsteam sequences.//0.87:209:64//M34651
F-PLACE1004128//M.musculus G protein beta-subunit mRNA, complete cds.//2.5e-62:437:84//M63658
F-PLACE1004149//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//1.4e-16:342:65//AF005355
F-PLACE1004156//Homo sapiens DNA sequence from PAC 57E3 on chromosome 6p12.1-21.1. Contains GSSs and an STS with a TATC repeat polymorphism, complete sequence.//1.2e-26:299:74//AL022099
F-PLACE1004161
F-PLACE1004183//Homo sapiens for TOM1-like protein.//1.2e-146:731:96//AJ010071
F-PLACE1004197
F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.//4.0e-144:695:98//AF069493
F-PLACE1004242//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.3e-151:772:95//AL021326
F-PLACE1004256//HS_2010_B2_G04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2010 Col=8 Row=N, genomic survey sequence.//1.5e-44:372:79//AQ252434
F-PLACE1004257//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//0.00011:349:63//AC005034
F-PLACE1004258//Homo sapiens DNA sequence from PAC 779B17 on chromosome 22q13.1. Contains exon trap, complete sequence.//0.77:475:59//AL021806
F-PLACE1004270//Human IgA C alpha 1 switch region (Sa1).//1.7e-08:622:61//L19121
F-PLACE1004274//H.sapiens CpG island DNA genomic Mse1 fragment, clone 18g6, forward read cpg18g6.ft1b.//8.6e-37:196:98//Z57691
F-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds.//6.0e-156:756:

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97//AF084830
F-PLACE1004284//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI7, complete sequence.// 0.0060:635:57//AB011480
F-PLACE1004289//HS_3023_B1_E04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=7 Row=J, genomic survey sequence.//2.4e-12:86:98//AQ094451
F-PLACE1004302//Streptomyces coelicolor cosmid 7H1.//0.26:297:64//AL021411
F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//2.9e-150:797:94//Y11588
F-PLACE1004336//Drosophila melanogaster DNA sequence (P1 DS07968 (D117)), complete sequence.//0.87: 206:59//AC004267
F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//5.9e-139: 688:97//AF100153
F-PLACE1004376//Mus musculus clone OST20307, genomic survey sequence.//4.1e-81:498:89//AF046631
F-PLACE1004384//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1121J18, WORKING DRAFT SEQUENCE.//3.6e-41:482:73//AL031653
F-PLACE1004388//Caenorhabditis elegans cosmid K08F11.//8.6e-26:615:62//U70855
F-PLACE1004405//Homo sapiens clone GS512I21, WORKING DRAFT SEQUENCE, 9 unordered pieces.//9.2e-150:749:96//AC005027
F-PLACE1004425//Homo sapiens PAC clone DJ0733B09 from 7p14-p13, complete sequence.//2.4e-08:129:76// AC005532
F-PLACE1004428//R.norvegicus mRNA for Pristanoyl-CoA Oxidase.//7.0e-17:549:61//X95188
F-PLACE1004437//Human NAD+-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//3.1e-129:536:99//U49283
F-PLACE1004451//Human DNA sequence from PAC 214K23, BRCA2 gene region chromosome 13q12-13 contains BRCA2 exons 1-24, Interferon Induced 56Kd pseudogene and ESTs.//4.8e-23:231:71//Z74739
F-PLACE1004460//Homo sapiens PAC clone DJ1064B22 from 7q21, complete sequence.//0.96:454:56// AC004954
F-PLACE1004467//HS_2058_B1_C09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=17 Row=F, genomic survey sequence.//2.4e-87:433:98//AQ242700
F-PLACE1004471//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and-9.//1.4e-74:665:70// M27877
F-PLACE1004473//CIT-HSP-2045A15.TF CIT-HSP Homo sapiens genomic clone 2045A15; genomic survey sequence.//3.3e-20:140:92//B80243
F-PLACE1004491//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.9e-05:794:57//AC004709
F-PLACE1004506//Human Gx-alpha gene.//1.0e-05:231:63//D90150
F-PLACE1004510//Homo sapiens TATA binding protein associated factor (TAFII150) mRNA, complete cds.//3.2e-146:699:98//AF040701
F-PLACE1004516//Human DNA sequence from cosmid SRL9A13, chromosome region 11p13. Contains EST.// 1.4e-33:367:71//Z86001
F-PLACE1004518
F-PLACE1004548//Dictyostelium discoideum MigA (migA) gene, complete cds.//2.6e-05:318:62//U86962
F-PLACE1004550//Human FMR1 gene, 5' end.//0.0018:142:66//L19476
F-PLACE1004564//B.taurus mRNA for cleavage and polyadenylation specificity factor.//1.7e-114:513:85//X75931
F-PLACE1004629//Anolis carolinensis Brain-1 gene, complete cds.//0.00013:188:67//AB001868
F-PLACE1004645//Mycobacterium tuberculosis H37Rv complete genome: segment 138/162.//0.66:337:60// Z95120
F-PLACE1004646//Rattus norvegicus retinal pigment epithelium-specific protein (Rpe65) mRNA, complete cds.// 1.1e-19:326:63//AF035673
F-PLACE1004658//H.sapiens CpG island DNA genomic Mse1 fragment, clone 55h1, forward read cpg55h1.ft1a./ 12.4e-34:188:98//Z61632
F-PLACE1004664//Caenorhabditis elegans cosmid W10G6, complete sequence.//1.0:148:65//Z81140
F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//1.9e-101:182:95//U07561
F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds.//4.3e-109:625:91// AF035606
F-PLACE1004681//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//1.9e-152:759:96//AB020860
F-PLACE1004686//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the

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SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.// 1.2e-34:320:71//Z95152

F-PLACE1004691//HS_3044_A1_G01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3044 Col=1 Row=M, genomic survey sequence.//0.018:191:63//AQ098323

F-PLACE1004693//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.28:573:57//AL022577

F-PLACE1004716//Plasmodium falciparum MAL3P6, complete sequence.//0.00081:428:59//Z98551

F-PLACE1004722//HS_3052_B1_C10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=19 Row=F, genomic survey sequence.//2.3e-05:104:75//AQ134959

F-PLACE1004736//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 2365J21, genomic survey sequence.//1.3e-24:180:88//AQ080498

F-PLACE1004740//RPCI11-58A7.TJ RPCI11 Homo sapiens genomic clone R-58A7, genomic survey sequence.// 8.6e-26:522:65//AQ195766

F-PLACE1004743//Mus musculus ubiquitin-protein ligase E3-alpha (Ubr1) mRNA, complete cds.//1.1e-112:711: 86//AF061555

F-PLACE1004751

F-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds.//5.4e-171:828:97//AF084367

F-PLACE1004777//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//4.2e-134:763:90//AJ001713

F-PLACE1004793//Human DNA sequence from clone 323P24 on chromosome Xp11.21-11.23 Contains SPIN (spindlin homolog (PROTEIN DXF34), hypothetical protein EST, STS, GSS, complete sequence.//9.3e-132:759: 90//AL022157

F-PLACE1004804

F-PLACE1004813//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.5e-06:403:58//AC004710

F-PLACE1004814//Homo sapiens chromosome 17, clone hRPK.294_J_22, complete sequence.//9.8e-39:207: 99//AC005921

F-PLACE1004815//Homo sapiens PAC clone DJ0651K02 from 7p21-p22, complete sequence.//8.1e-15:203:73// AC004613

F-PLACE1004824//G.gallus PB1 gene.//1.1e-103:759:80//X90849

F-PLACE1004827//HS_2230_A2_A05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2230 Col=10 Row=A, genomic survey sequence.//4.1e-38:330:81//AQ299313

F-PLACE1004836//H.sapiens nidogen gene (exon 8).//0.97:116:68//X84825

F-PLACE1004838//HS_3241_A2_A04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=8 Row=A, genomic survey sequence.//1.8e-87:425:98//AQ206740

F-PLACE1004840//Sequence 2 from patent US 5728819.//6.7e-47:285:91//I92819

F-PLACE1004868

F-PLACE1004885//Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 9.//0.14:465:59//Z97344

F-PLACE1004900

F-PLACE1004902//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//3.6e-06:56:100//AQ261184

F-PLACE1004913//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//2.6e-151:770:91// AC005058

F-PLACE1004918//Mus musculus signaling molecule (ATTP) mRNA, complete cds.//2.6e-68:459:84//U97571

F-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds.//4.4e-106:545:95// AF070671

F-PLACE1004934//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//3.5e-45:226:84//AL020989

F-PLACE1004937

F-PLACE1004969

F-PLACE1004972//Homo sapiens PAC clone DJ0612F12 from 7p12-p14, complete sequence.//0.012:316:61// AC004843

F-PLACE1004979//Human DNA sequence from clone 142F18 on chromosome Xq26.3-27.2 Contains part of a gene similar to melanoma-associated antigen, EST, GSS and an inverted repeat, complete sequence.//4.7e-39: 394:77//AL031073

F-PLACE1004982//Caenorhabditis elegans cosmid B0507.//0.16:167:65//U64833

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F-PLACE1004985//Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence.//8.8e-14:590:61//AE001373
F-PLACE1005026
F-PLACE1005027
F-PLACE1005046
F-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SEQUENCE, 35 unordered pieces.//2.1e-135:675:97//AC005867
F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds.//1.9e-159:761:98//AB011148
F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//9.2e-10:757:56//AF059569
F-PLACE1005077
F-PLACE1005085//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//6.9e-29:253:77//AC004673
F-PLACE1005086//Homo sapiens chromosome 17, clone HCIT11023, complete sequence.//6.5e-52:446:78//AC002316
F-PLACE1005101//Homo sapiens clone DJ0414A15, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.0e-146:734:96//AC005225
F-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//9.8e-83:254:95//AC004476
F-PLACE1005108//Human BAC clone RG009H02 from 7q31, complete sequence.//0.46:179:64//AC003081
F-PLACE1005111
F-PLACE1005128//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.00051:287:63//L14320
F-PLACE1005146//HS_3071_A1_E03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=5 Row=I, genomic survey sequence.//7.4e-38:299:82//AQ103361
F-PLACE1005162//Human BAC clone GS306C12 from 7q21-q22, complete sequence.//2.6e-44:346:82//AC002451
F-PLACE1005176
F-PLACE1005181//CIT-HSP-2340O5.TR CIT-HSP Homo sapiens genomic clone 2340O5, genomic survey sequence.//0.99:211:63//AQ054651
F-PLACE1005187//CIT-HSP-2358N6.TR CIT-HSP Homo sapiens genomic clone 2358N6, genomic survey sequence.//2.7e-07:80:90//AQ074445
F-PLACE1005206//Human BAC clone 133K23 from 7q31.2, complete sequence.//0.98:216:61//AC000061
F-PLACE1005232//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42 unordered pieces.//0.70:245:63//AC004965
F-PLACE1005243
F-PLACE1005261//Caenorhabditis elegans cosmid T05H10, complete sequence.//0.00041:254:61//Z47812
F-PLACE1005266//H.sapiens mRNA (fetal brain cDNA a4_2g).//9.6e-33:177:98//Z70695
F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds.//1.6e-148:706:98//AB011182
F-PLACE1005287//Plasmodium falciparum (MESA) mRNA exons 1-2, complete cds.//2.8e-15:737:60//M69183
F-PLACE1005305//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//3.8e-111:728:84//M25757
F-PLACE1005308//Clethrionomys glareolus endogenous retroviral sequence ERV-L pol gene, clone ERV-L Vole Cg14.//1.0:128:67//AJ233621
F-PLACE1005313//Caenorhabditis elegans cosmid D2092.//8.8e-11:342:62//U88167
F-PLACE1005327//HS_3080_B2_A12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3080 Col=24 Row=B, genomic survey sequence.//4.1e-25:147:96//AQ139116
F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569, complete sequence.//1.4e-132:399:94//AC004794
F-PLACE1005335//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.5e-114:237:92//AC000380
F-PLACE1005373
F-PLACE1005374//Homo sapiens chromosome 7 common fragile site, complete sequence.//0.20:305:58//AF017104
F-PLACE1005409//Human BAC clone RG167B05 from 7q21, complete sequence.//2.5e-148:760:95//AC003991
F-PLACE1005453//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y48A6, WORKING DRAFT SEQUENCE.//0.00069:582:59//Z92854
F-PLACE1005467//Rat mRNA.//0.0014:131:70//M59859

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F-PLACE1005471//Human DNA sequence from clone 45I4 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//3.0e-23:530:67//AL023581
F-PLACE1005477//Human DNA sequence from clone J181N11, WORKING DRAFT SEQUENCE.//3.3e-131:814:88//Z82191
F-PLACE1005480//Homo sapiens DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D).TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.//7.0e-34:246:73//AL021878
F-PLACE1005481//RPCI11-74L17.TJ RPCI11 Homo sapiens genomic clone R-74L17, genomic survey sequence.//0.37:403:57//AQ266885
F-PLACE1005494//Homo sapiens transient receptor potential protein 6 mRNA, complete cds.//2.1e-67:325:99//AF080394
F-PLACE1005502//Homo sapiens BAC clone NH0161H12 from 7p14-p15, complete sequence.//0.015:403:61//AC005589
F-PLACE1005526//H.sapiens CpG island DNA genomic Mse1 fragment, clone 9f1, reverse read cpg9f1.rt1a.//3.6e-27:159:96//Z66485
F-PLACE1005528//Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.//2.6e-28:449:67//AP000038
F-PLACE1005530//Homo sapiens clone DJ0691L07, complete sequence.//6.5e-18:234:72//AC004860
F-PLACE1005550//Fugu rubripes GSS sequence, clone 048A08bH3, genomic survey sequence.//1.2e-14:123:75//AL025925
F-PLACE1005554//Leishmania tarentolae mitochondrial 12S ribosomal RNA gene.//0.43:209:66//X02354
F-PLACE1005557//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence.//9.3e-113:536:97//AC004707
F-PLACE1005574//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-10:514:59//AC005504
F-PLACE1005584//Homo sapiens mRNA for KIAA0617 protein, complete cds.//0.00056:289:63//AB014517
F-PLACE1005595//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence.//1.2e-111:262:89//AC004126
F-PLACE1005603
F-PLACE1005611//F16O5TFC IGF Arabidopsis thaliana genomic clone F16O5, genomic survey sequence.//2.0e-10:209:66//B98589
F-PLACE1005623
F-PLACE1005630//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.2e-93:230:98//AC005840
F-PLACE1005639//HS_3095_B1_A03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3095 Col=5 Row=B, genomic survey sequence.//1.2e-05:220:63//AQ123022
F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//6.4e-150:721:98//AF083255
F-PLACE1005656//H.sapiens RR2 mRNA for small subunit ribonucleotide reductase.//1.3e-51:480:74//X59618
F-PLACE1005666//RPCI11-78O15.TV RPCI11 Homo sapiens genomic clone R-78O15, genomic survey sequence.//8.7e-05:243:62//AQ284667
F-PLACE1005698//Human membrane-associated lectin type-C mRNA.//1.9e-63:374:85//M98457
F-PLACE1005727//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.69:633:57//AE001422
F-PLACE1005730//HS_2026_B1_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=21 Row=P, genomic survey sequence.//2.0e-24:286:74//AQ231147
F-PLACE1005739//Mus musculus IFN-gamma induced (Mg11) mRNA, complete cds.//2.8e-55:621:71//U15635
F-PLACE1005755//HS_2213_A2_H11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=22 Row=O, genomic survey sequence.//1.4e-25:290:75//AQ136844
F-PLACE1005763//Rat medium-chain S-acyl fatty acid synthetase thio ester hydrolase (MCH), complete cds.//4.5e-40:297:70//M16200
F-PLACE1005799//R.norvegicus mRNA for mitochondrial isoform of cytochrome b5.//0.91:287:63//Y12517
F-PLACE10058021/Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//5.0e-109:530:98//AC004827
F-PLACE1005803//HS_3092_B1_A10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=19 Row=B, genomic survey sequence.//2.4e-08:76:96//AQ103695
F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.4e-126:636:96//AF027156
F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//2.6e-154:739:98//AF065482

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F-PLACE1005828//Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.2e-37:355:77//AC004150
F-PLACE1005834//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-105, complete sequence.//0.00080:663:58//AL010283
F-PLACE1005845//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00015:340:58//AC004153
F-PLACE1005850//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence.//1.8e-46:278:85//AL031432
F-PLACE1005851
F-PLACE1005876//B.taurus mRNA for cleavage and polyadenylation specificity factor.//5.0e-120:701:89//X75931
F-PLACE1005884//CIT-HSP-2333O12.TR CIT-HSP Homo sapiens genomic clone 2333O12, genomic survey sequence.//4.6e-78:385:98//AQ039226
F-PLACE1005890//Schizosaccharomyces pombe bem1/bud5 suppressor (Bem46+) mRNA, partial cds.//9.3e-16:638:57//U29892
F-PLACE1005898//Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds.//1.0:178:65//U67136
F-PLACE1005921//M.musculus mRNA for immunity associated protein 38.//6.6e-17:614:59//Y08026
F-PLACE1005923//RPCI11-33G19.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-33G19, genomic survey sequence.//4.0e-10:535:57//AQ046151
F-PLACE1005925//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SEQUENCE.//0.17:159:65//AL034405
F-PLACE1005932
F-PLACE1005934//H.sapiens CpG island DNA genomic Mse1 fragment, clone 165g2, forward read cpg165g2.ft1a.//8.3e-43:247:93//Z57153
F-PLACE1005936//F.rubripes GSS sequence, clone 069K22aG2, genomic survey sequence.//0.91:116:68//AL014719
F-PLACE1005951//Rhodobacter sphaeroides DMSO/TMAO-sensor kinase (dorS), DMSO/TMAO-response regulator (dorR), DMSO/TMAO-cytochrome c-containing subunit (dorC), DMSO-membrane protein (dorB), and DMSO/TMAO-reductase (dorA) genes, complete cds.//0.0022:495:59//AF016236
F-PLACE1005953//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//2.9e-05:442:61//AC004081
F-PLACE1005955//Caenorhabditis elegans cosmid F01F1.//4.3e-20:409:64//U13070
F-PLACE1005966//P.falciparum aarp3 gene, exon.//0.0083:270:64//Y08925
F-PLACE1005968
F-PLACE1005990//Homo sapiens chromosome 12p13.3 clone RPCI11-407G6, WORKING DRAFT SEQUENCE, 51 ordered pieces.//1.0e-100:513:96//AC005866
F-PLACE1006002//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 229A8, WORKING DRAFT SEQUENCE.//2.5e-54:444:77//Z86090
F-PLACE1006003//HS-1059-A2-G01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 781 Col=2 Row=M, genomic survey sequence.//3.4e-05:214:64//B44442
F-PLACE1006011//Mus musculus poly-(ADPribosyl)-transferase homolog PARP mRNA, complete cds.//4.3e-71:580:79//AF072521
F-PLACE1006017//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 -complete genomic sequence, complete sequence.//8.6e-32:177:83//AC002299
F-PLACE1006037//Mus musculus B6D2F1 clone 2C11B mRNA.//1.8e-34:269:83//U01139
F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//3.4e-147:719:97//X99906
F-PLACE1006076//Homo sapiens DNA sequence from PAC 79C4 on chromosome 1q24. Contains the PMX1 gene, coding for two alternative forms of the Paired Mesoderm Homeobox protein 1 (PMX-1, PHOX-1). Contains ESTs, STSs and BAC end sequences (GSSs), complete sequence.//0.37:332:62//Z97200
F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.3e-145:679:99//AF039023
F-PLACE1006129
F-PLACE1006139//Saccharomyces cerevisiae chromosome VI cosmid 9965.//4.8e-27:693:60//D44597
F-PLACE1006143//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 169I5, WORKING DRAFT SEQUENCE.//4.7e-46:435:77//Z93015
F-PLACE1006157//Saguinus oedipus mRNA for membrane cofactor protein CD46, complete cds, clone:B2.//0.048:290:60//D85750
F-PLACE1006159//Homo sapiens chromosome 10 clone CIT987SK-1054O2 map 10q25, complete sequence.//3.2e-129:466:96//AC005661

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F-PLACE1006164//HS_3003_A1_F08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=15 Row=K, genomic survey sequence.//1.4e-70:388:93//AQ118200
F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//4.3e-78:385:86//AC005239
F-PLACE1006170//Mouse mRNA for alpha-adaptin (C).//3.5e-91:630:84//X14972
F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds.//3.9e-149:694:99//AF091433
F-PLACE1006195//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//2.5e-16:283:70//AC003658
F-PLACE1006196//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//2.2e-94:648:84//L25125
F-PLACE1006205//Human Xp22 cosmid U250A9, complete sequence.//0.15:533:58//U75931
F-PLACE1006223//F24L20-T7 IGF Arabidopsis thaliana genomic clone F24L20, genomic survey sequence.//0.0068:175:64//B19803
F-PLACE1006225//CIT-HSP-2335I23.TF CIT-HSP Homo sapiens genomic clone 2335I23, genomic survey sequence.//2.1e-19:149:90//AQ039880
F-PLACE1006236//Human chromosome 12p15 BAC clone CIT987SK-99D8 complete sequence.//0.51:290:58//U91327
F-PLACE1006239//Homo sapiens BAC clone RG118D07 from 7q31, complete sequence.//7.4e-158:452:96//AC004142
F-PLACE1006246//RPCI11-36I23.TK RPCI-11 Homo sapiens genomic clone RPCI-11-36I23, genomic survey sequence.//2.6e-31:176:97//AQ045400
F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//2.3e-166:791:98//AB014548
F-PLACE1006262//342E3.TVD CIT978SKA1 Homo sapiens genomic clone A-342E03, genomic survey sequence.//1.0:228:63//B16447
F-PLACE1006288//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20N2, WORKING DRAFT SEQUENCE.//6.6e-172:809:99//AL031320
F-PLACE1006318
F-PLACE1006325//Homo sapiens PAC clone DJ0988L12 from 7q11.23-q21.1, complete sequence.//0.079:396:59//AC004454
F-PLACE1006335//Mouse Ig third hypervariable region (HCDR3), nonproductively rearranged alpha-chain gene VHSB32-D-JH2 region.//1.0:90:67//M55721
F-PLACE1006357//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.16:445:56//AC005504
F-PLACE1006360//Plasmodium falciparum MAL3P7, complete sequence.//6.1e-05:625:57//AL034559
F-PLACE1006368//X.laevis mRNA for KLP2 protein.//3.0e-25:376:68//X94082
F-PLACE1006371//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence.//2.0e-146:711:97//AC004232
F-PLACE1006382
F-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//5.1e-110:539:97//AF062085
F-PLACE1006412//Homo sapiens BAC clone GS588G18 from 7p12-p14, complete sequence.//1.3e-23:463:68//AC005029
F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds.//1.3e-109:525:98//AF069735
F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds.//6.9e-23:531:65//AB011129
F-PLACE1006445//HS_3071_A1_C11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=21 Row=E, genomic survey sequence.//4.7e-74:392:95//AQ 103347
F-PLACE1006469//Rhodobacter capsulatus strain SB1003, partial genome.//1.1e-40:686:65//AF010496
F-PLACE1006470//T.brucei kinetoplast maxicircle variable region DNA.//0.99:250:59//Z15118
F-PLACE1006482//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 447C4, WORKING DRAFT SEQUENCE.//4.3e-120:328:98//AL021977
F-PLACE1006488//Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).//6.5e-86:478:91//X53744
F-PLACE1006492
F-PLACE1006506
F-PLACE1006521//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//0.0010:547:58//AC005083
F-PLACE1006531//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.6e-84:625:80//AF005355

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F-PLACE1006534//Caenorhabditis elegans cosmid Y40H7A, complete sequence.//0.00031:671:58//AL033510
F-PLACE1006540
F-PLACE1006552//P.falciparum glutamic acid-rich protein gnen, complete cds.//6.0e-10:636:59//J03998
F-PLACE1006598//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.//9.8e-25:170:77//AC006044
F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//6.7e-167:781:99//U97670
F-PLACE1006617//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence.//0.98:514:59//AC004470
F-PLACE1006626//H.sapiens DNA 3' flanking simple sequence region clone wg2c3.//0.00079:206:62//X76589
F-PLACE1006629//Human BAC clone RG333F24 from 7q11.2-q21, complete sequence.//0.0012:576:57//AC004015
F-PLACE1006640//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.0018:588:59//X95276
F-PLACE1006673//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0028:469:58//AC004688
F-PLACE1006678//Mus musculus UDP-Gal:betaGlcNAc beta 1,3-galactosyltranferase-I (b3GT1) gene, complete cds.//0.00011:184:64//AF029790
F-PLACE1006704//Mus musculus dentin sialophosphoprotein precursor (DSPP) mRNA, complete cds.//0.0013:380:62//U67916
F-PLACE1006731//Human DNA sequence from PAC 408N23 on chromosome 22q13. Contains HIP, HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN), ESTs and STS.//1.5e-78:520:86//Z98048
F-PLACE1006754//Homo sapiens chromosome 19, cosmid R29124, complete sequencer/1.9e-135:378:99//AC005626
F-PLACE1006760//CIT-HSP-2336O13.TR CIT-HSP Homo sapiens genomic clone 2336O13, genomic survey sequence.//0.018:147:66//AQ039246
F-PLACE1006779//Plasmodium falciparum chromosome 2, section 63 of 73 of the complete sequence.//2.6e-08:823:58//AE001426
F-PLACE1006782//Homo sapiens clone NH0005N18, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.043:252:65//AC005487
F-PLACE1006792//HS_3165_B1_H01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3165 Col=1 Row=P, genomic survey sequence.//1.4e-11:249:67//AQ149559
F-PLACE1006795//Mouse eph-related receptor tyrosine kinase (Mek4) mRNA, complete cds.//1.3e-12:155:80//M68513
F-PLACE1006800//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-92, complete sequence.//6.7e-05:391:62//AL010272
F-PLACE1006805//paramecium species 1,168 mt dna dimer: replication init. region.//9.1e-09:369:62//K00915
F-PLACE1006815//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 321D2, WORKING DRAFT SEQUENCE.//0.89:465:58//AL031033
F-PLACE1006819//Homo sapiens clone DJ1163L11, complete sequence.//1.5e-121:618:91//AC005230
F-PLACE1006829//Brn-3a=class V POU transcription factor [mice, CD/CD, embryo fibroblast cells, Genomic, 2160 nt].//0.011:145:68//S69350
F-PLACE1006860//Plasmodium falciparum MAL3P7, complete sequence.//2.2e-07:691:58//AL034559
F-PLACE1006867//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 323M4, WORKING DRAFT SEQUENCE.//1.5e-132:643:98//AL033378
F-PLACE1006878
F-PLACE1006883//Mycobacterium tuberculosis H37Rv complete genome; segment 138/162.//1.0:236:62//Z95120
F-PLACE1006901//Mus musculus t complex testis-specific protein (Tctex2) gene, t haplotype, promoter sequence.//2.7e-19:171:81//U21672
F-PLACE1006904
F-PLACE1006917//H.sapiens CpG island DNA genomic Mse1 fragment, clone 79g10, forward read cpg79g10.ft1a.//1.3e-21:131:98//Z63175
F-PLACE1006932//Mus musculus FKBP65 binding protein mRNA, complete cds.//0.99:248:61//L07063
F-PLACE1006935//Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families.//0.85:161:63//AF029308
F-PLACE1006956//Hylobates lar involucrin gene, complete cds.//0.077:355:61//M35447
F-PLACE1006958//Mus musculus osmotic stress protein 94 (Osp94) mRNA, complete cds.//2.9e-89:483:86//

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U23921
F-PLACE1006961//Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & amp; tRNA-Met genes.// 1.6e-06:651:58//AJ223323
F-PLACE1006962//H.sapiens ir1B mRNA.//7.1e-15:202:71//X63417
F-PLACE1006966//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y105E8, WORKING DRAFT SEQUENCE.//1.7e-26:451:61//AL022594
F-PLACE1006989//cSRL-172A4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-172A4, genomic survey sequence.//1.0:97:67//B03188
F-PLACE1007014//Rattus norvegicus equilbrative nitrobenzylthioinosine-insensitive nucleoside transporter mRNA, complete cds.//4.2e-07:592:58//AF015305
F-PLACE1007021//Homo sapiens chromosome 19, cosmid F16403; complete sequence.//5.1e-17:285:70// AC005777
F-PLACE1007045//Human DNA sequence from PAC 181N1 on chromosome X contains ESTs, STS polymorphic CA repeat*.//6.2e-131:775 :89//Z82899
F-PLACE1007053//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.7e-143:675:99//AC004895
F-PLACE1007068//Homo sapiens chromosome 17, clone hRPK.214_O_1, complete sequence.//1.3e-131:652: 97//AC005224
F-PLACE1007097//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucoronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.// 8.3e-158:768:97//AL021368
F-PLACE1007105//Mus musculus muskelin mRNA, complete cds.//4.1e-124:687:91//U72194
F-PLACE1007111//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-05:586:56//AC005139
F-PLACE1007112//HS_2234_B2_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2234 Col=20 Row=N, genomic survey sequence.//0.26:200:62//AQ087801
F-PLACE1007132//CIT978SK-A-211C6.TVB CIT978SK Homo sapiens genomic clone A-211C6, genomic survey sequence.//1.3e-40:255:92//B72112
F-PLACE1007140//QN1 orf [Coturnix coturnix, japonica, K2 neuroretinal cells, mRNA Partial, 3884 nt].//4.9e-15: 386:62//S68151
F-PLACE1007178//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.011:329:61//AC005140
F-PLACE1007226//Human lipocortin (LIP) 2 gene, upstream region.//0.0036:180:63//M62899
F-PLACE1007238//FMR1 {CGG repeats} [human, Fragile X syndrome patient, Genomic, 429 nt].//2.8e-08:269: 63//S74494
F-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//6.3e-57: 405:87//D50495
F-PLACE1007242//HS_3006_A1_B11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=21 Row=C, genomic survey sequence.//0.088:191:59//AQ089443
F-PLACE1007243//Human transporter protein (g17) mRNA, complete cds.//7.9e-12:245:66//U49082
F-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//5.2e-144:677:98//Y15908
F-PLACE1007274//HS_3003_A1_D08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=15 Row=G, genomic survey sequence.//7.4e-49:345:85//AQ294154
F-PLACE1007276//Fugu rubripes GSS sequence, clone 014O10aG11, genomic survey sequence.//0.0052:228: 62//AL024982
F-PLACE1007282//F.rubripes GSS sequence, clone 019O07aB3, genomic survey sequence.//0.024:289:58// AL011743
F-PLACE1007286//Human Chromosome 16 BAC clone CIT987SK-A-256A9, complete sequence.//0.0048:185: 69//AC002492
F-PLACE1007301//Dictyostelium discoideum gene for TRFA, complete cds.//0.069:761:57//AB009080
F-PLACE1007317
F-PLACE1007342
F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//5.4e-120: 567:98//AF096870
F-PLACE1007367//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.2e-59:613:75//AC005077

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F-PLACE1007375//Caenorhabditis elegans cosmid D2092.//1.8e-12:193:70//U88167
F-PLACE1007386
F-PLACE1007402//HS_2170_A2_D12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2170 Col=24 Row=G, genomic survey sequence.//5.6e-06:162:67//AQ125590
F-PLACE1007409//Homo sapiens mitoxantrone resistance protein 2 mRNA, complete sequence.//1.6e-25:165:93//AF093772
F-PLACE1007416
F-PLACE1007450//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.9e-34:764:62//AC003973
F-PLACE1007452//Mus musculus bet3 (Bet3) mRNA, complete cds.//4.1e-17:374:64//AF041433
F-PLACE1007454//Homo sapiens (clone s153) mRNA fragment.//8.1e-52:317:93//L40391
F-PLACE1007460//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//0.0019:280:64//AL031117
F-PLACE1007478//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 -complete genomic sequence, complete sequence.//2.5e-24:362:71//AC002302
F-PLACE1007484
F-PLACE1007488//Danio rerio faciogenital dysplasia protein (fgd) mRNA, complete cds.//3.8e-14:293:63//AF017370
F-PLACE1007507//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//4.6e-10:152:75//AL031311
F-PLACE1007511//Homo sapiens chromosome 17, clone hRPC.1110_E_20, complete sequence.//3.6e-139:477:98//AC004231
F-PLACE1007524//Plasmodium falciparum microsatellite 14C sequence.//0.0055:395:59//AF015461
F-PLACE1007525//Trypanoplasma borelli mitochondrion cytochrome oxidase subunit 1 (cox1), cytochrome oxidase subunit 2 (cox2), and apocytochrome b (cytb) genes, complete cds, and complete 9S rRNA gene and partial 12S rRNA gene.//0.0013:550:58//U11682 F-PLACE1007537//H.sapiens CpG island DNA genomic Mse1 fragment, clone 198g6, reverse read cpg198g6.rt1a.//0.98:121:67//Z60280
F-PLACE1007544//Mus musculus chromosome 14 marker um-m24 GA dinucleotide DNA sequence.//2.3e-10:141:75//U31508
F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete cds.//3.1e-69:733:71//AB014561
F-PLACE1007557//Drosophila yakuba mitochondrial DNA molecule.//0.022:393:61//X03240
F-PLACE1007583//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 545L17, WORKING DRAFT SEQUENCE.//3.6e-114:565:97//AL031665
F-PLACE1007598//CIT-HSP-2371G14.TF CIT-HSP Homo sapiens genomic clone 2371G14, genomic survey sequence.//2.0e-22:304:70//AQ111183
F-PLACE1007618//Homo sapiens chromosome 17, clone hRPK.642_C_21, complete sequence.//1.0:386:59//AC005245
F-PLACE1007621
F-PLACE1007632//Homo sapiens 12p13.3 PAC RPCI5-940J5 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0e-88:276:96//AC006064
F-PLACE1007645//Bovine elastin mRNA, partial cds.//2.1e-07:110:79//M26132
F-PLACE1007649
F-PLACE1007677//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//1.2e-21:567:64//AL023755
F-PLACE1007688//Pseudorabies virus immediate-early gene.//2.2e-05:287:66//X15120
F-PLACE1007690//Caenorhabditis elegans cosmid R07G3.//0.40:122:70//U23452
F-PLACE1007697//Mus musculus LIM/homeobox (Lhx3) gene fragment.//0.85:117:71//L40483
F-PLACE1007705//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE.//0.0035:75:88//AL031662
F-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//1.3e-147:709:97//AF061243
F-PLACE1007725//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBB18, complete sequence.//1.0:510:58//AB005231
F-PLACE1007729//Human endogenous retrovirus HML6 proviral clone HML6p, putative leader region, gag, pro and pol pseudogenes.//4.8e-136:516:89//U86698
F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//7.9e-155:728:98//AB014585
F-PLACE1007737//Homo sapiens clone DJ0847O08, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.8e-22:806:60//AC005484
F-PLACE1007743//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING

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DRAFT SEQUENCE, 3 unordered pieces.//1.1e-06:510:56//AC005504
F-PLACE1007746//HS_2268_B1_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=19 Row=N, genomic survey sequence.//0.10:171:63//AQ124780
F-PLACE1007791//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P6, WORKING DRAFT SEQUENCE.//0.63:241:58//AL031749
F-PLACE1007807//Homo sapiens chromosome 17, clone hRPK.879_D_6, complete sequence.//1.0e-120:743:87//AC005273
F-PLACE1007810//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//1.0e-113:739:86//AC003658
F-PLACE1007829//CIT-HSP-2383J22.TR CIT-HSP Homo sapiens genomic clone 2383J22, genomic survey sequence.//1.0e-47:254:97//AQ196438
F-PLACE1007843//F.rubripes GSS sequence, clone 162K02bC12, genomic survey sequence.//1.6e-10:148:72//AL006903
F-PLACE1007846//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//3.4e-177:844:98//AP000010
F-PLACE1007852//Mouse perlecan mRNA, complete cds.//8.5e-39:243:90//M77174
F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//3.9e-189:894:98//AB018309
F-PLACE1007866//CIT-HSP-2353D11.TF.1 CIT-HSP Homo sapiens genomic clone 2353D11, genomic survey sequence.//0.015:279:61//AQ263271
F-PLACE1007877
F-PLACE1007897
F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487.//2.3e-154:755:97//AB007956
F-PLACE1007946//Human chromosome Y cosmid 56B5 genomic sequence, WORKING DRAFT SEQUENCE.//1.1e-59:310:81//AC003097
F-PLACE1007954//Homo sapiens BAC clone NH0414C23 from Y, complete sequence.//2.1e-61:522:79//AC006157
F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//2.7e-171:813:98//AF084530
F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//2.5e-153:730:98//AF079529
F-PLACE1007969//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//3.4e-32:383:74//U13262
F-PLACE1007990//H.sapiens genomic DNA fragment (clone J31A212R).//6.6e-35:198:96//Z94758
F-PLACE1008000//Mus musculus veli 3 mRNA, complete cds.//1.5e-118:706:88//AF087695
F-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//6.4e-163:786:98//AC005628
F-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP107 mRNA, complete cds.//1.2e-95:625:84//L31840
F-PLACE1008045//Caenorhabditis elegans cosmid F17C8, complete sequence.//0.016:165:65//Z35719
F-PLACE1008080//Human DNA sequence from cosmid L118G10, Huntington's Disease Region, chromosome 4p16.3.//4.0e-07:251:64//Z68883
F-PLACE1008095//RPCI11-21F19.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21F19, genomic survey sequence.//1.5e-30:166:99//B85883
F-PLACE1008111//Aphidius picipes NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds.//7.5e-06:414:60//AF069163
F-PLACE1008122//S.cerevisiae chromosome XV reading frame ORF YOL125w.//0.046:477:59//Z74867
F-PLACE1008129//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase IIx genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0068:446:57//AC004586
F-PLACE1008132//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 316D5, WORKING DRAFT SEQUENCE.//3.6e-20:111:93//Z82199
F-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds.//2.5e-88:866:73//D14849
F-PLACE1008181//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE.//0.0033:727:56//AL034397
F-PLACE1008198//HS_3073_A1_C06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3073 Col=11 Row=E, genomic survey sequence.//2.3e-12:94:92//AQ171450
F-PLACE1008201//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.5e-

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162:791:97//AC005069
F-PLACE1008209
F-PLACE1008231//Mouse testis-specific protein mRNA, complete cds.//0.65:174:66//M26332
F-PLACE1008244//CIT-HSP-2337B4.TR CIT-HSP Homo sapiens genomic clone 2337B4, genomic survey sequence.//6.7e-28:165:95//AQ039317
F-PLACE1008273//B.primigenius mRNA for coat protein gamma-cop.//2.8e-71:709:71//X92987
F-PLACE1008275//D.discoideum actin A-13 gene, 5' flank.//0.12:131:64//M29123
F-PLACE1008280//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//0.011:96:73//AC005913
F-PLACE1008309//Rattus norvegicus putative four repeat ion channel mRNA, complete cds.//8.2e-86:672:77//AF078779
F-PLACE1008329//HS_2027_A1_C06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=11 Row=E, genomic survey sequence//8.7e-09:116:81//AQ244432
F-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//2.2e-141:670:98//AC005176
F-PLACE1008331//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-27:157:78//AC005000
F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds.//1.1e-137:659:98//AB014579
F-PLACE1008368//CIT-HSP-2311C9.TR CIT-HSP Homo sapiens genomic clone 2311C9, genomic survey sequence.//7.1e-08:398:60//AQ016352
F-PLACE1008369//HS_2251_B1_A02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2251 Col=3 Row=B, genomic survey sequence.//2.1e-35:217:93//AQ066512
F-PLACE1008392//Homo sapiens chromosome 17, clone hRPK.136_H_19, complete sequence.//1.4e-11:403:64//AC005856
F-PLACE1008398//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 215D11, WORKING DRAFT SEQUENCE.//3.7e-144:681:99//AL034417
F-PLACE1008401//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//2.8e-45:257:96//AC004604
F-PLACE1008402//Homo sapiens mRNA for p115, complete cds.//4.3e-148:711:98//D86326
F-PLACE1008405//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.089:672:56//AC004688
F-PLACE1008424
F-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 7/11.//1.0e-88:331:84//AB020864
F-PLACE1008429//Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence.//0.55:530:58//U62317
F-PLACE1008437//CIT-HSP-2376H4.TR CIT-HSP Homo sapiens genomic clone 2376H4, genomic survey sequence.//3.3e-78:349:94//AQ112479
F-PLACE1008455//HS_2064_B1_E09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2064 Col=17 Row=J, genomic survey sequence.//4.7e-59:471:81//AQ246589
F-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//8.9e-43:307:73//AC004526
F-PLACE1008465//CIT-HSP-2163F24.TR CIT-HSP Homo sapiens genomic clone 2163F24, genomic survey sequence.//8.9e-41:210:99//B90014
F-PLACE1008488//Mus musculus mRNA for testis-specific protein kinase 1, complete cds.//0.00013:516:58//AB003494
F-PLACE1008524//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 34B21, WORKING DRAFT SEQUENCE.//1.3e-161:778:98//AL031778
F-PLACE1008531//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//1.1e-78:191:100//AF045555
F-PLACE1008532//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 92N15, WORKING DRAFT SEQUENCE.//3.8e-24:257:70//Z93097
F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.//1.0e-13:215:71//AC004997
F-PLACE1008568//Human DNA sequence from PAC 388N15 on chromosome Xq21.1.//0.66:263:64//Z99571
F-PLACE1008584//Homo sapiens cosmid clone U39B3 from Xp22.1-22.2, complete sequence.//1.1e-19:315:68//U73023
F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete cds.//1.2e-173:812:98//AB018334

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F-PLACE1008621//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//3.9e-09:198:71//AC005077
F-PLACE1008625//Homo sapiens chromosome 5, PAC clone 45L14 (LBNL H91), complete sequence.//0.68:568:59//AC005373
F-PLACE1008626//HS_3221_A2_F03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=6 Row=K, genomic survey sequence.//1.7e-13:147:82//AQ180967
F-PLACE1008627//Cricetulus griseus mRNA for Zn finger factor.//9.7e-98:586:88//Y12836
F-PLACE1008629//CIT-HSP-2012I4.TR CIT-HSP Homo sapiens genomic clone 2012I4, genomic survey sequence.//0.00085:203:66//B53732
F-PLACE1008630//Sequence 26 from Patent WO9517522.//9.7e-05:97:80//A45356
F-PLACE1008643//Human mRNA for inter-alpha-trypsin inhibitor family heavy chain-related protein (IHRP), complete cds.//1.4e-23 :299:64//D38595
F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//1.1e-133:622:99//AF044333
F-PLACE1008693//CIT-HSP-2346F2.TF CIT-HSP Homo sapiens genomic clone 2346F2, genomic survey sequence.//0.24:89:76//AQ060732
F-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//1.4e-94:420:97//AF038406
F-PLACE1008715//CIT-HSP-2294K20.TR CIT-HSP Homo sapiens genomic clone 2294K20, genomic survey sequence.//2.1e-70:349:98//AQ007199
F-PLACE1008748//Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence.//0.14:347:59//AC004260
F-PLACE1008757//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//7.9e-25 :244:71//AC003037
F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds.//4.5e-120:503:97//AF060543
F-PLACE1008798//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//0.00026:370:61//AF001549
F-PLACE1008807//CIT-HSP-2334B19.TF CIT-HSP Homo sapiens genomic clone 2334B19, genomic survey sequence.//3.3e-08:220:65//AQ036643
F-PLACE1008808//Homo sapiens exonuclease homolog RAD1 (RAD1) mRNA, complete cds.//1.7e-120:470:97//AF030933
F-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//2.8e-87:504:89//AF032668
F-PLACE1008851//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//4.0e-21:212:74//AL021920
F-PLACE1008854
F-PLACE1008867//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//4.7e-77:477:84//Z82209
F-PLACE1008887//Homo sapiens BAC clone NH0335J18 from 2, complete sequence.//3.4e-53:699:70//AC005539
F-PLACE1008902//Mouse G-alpha-13 protein mRNA, complete cds.//2.1e-06:164:68//M63660
F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds.//6.4e-158:753:98//AB018308
F-PLACE1008925//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-180G2, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00013:400:63//AC002042
F-PLACE1008934//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1104E15, WORKING DRAFT SEQUENCE.//7.4e-05:145:71//AL022312
F-PLACE1008941//Human zinc finger protein (ZNF141) mRNA, complete cds.//4.3e-41:282:87//L15309
F-PLACE1008947//Pseudorabies virus with upstream and downsteam sequences.//5.9e-15:710:60//M34651
F-PLACE1009020//HS_3051_B1_H01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, genomic survey sequence.//1.9e-21:167:86//AQ253727
F-PLACE1009027//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//4.1e-152:763:97//AL031117
F-PLACE1009039//HS_2034_A2_F08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2034 Col=16 Row=K, genomic survey sequence.//0.17:252:59//AQ230137
F-PLACE1009045//HS_3185_B2_B03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=6 Row=D, genomic survey sequence.//1.9e-34:260:86//AQ172861
F-PLACE1009048//Pig pituitary glycoprotein hormone alpha subunit gene, 5'flank and exon 1.//4.7e-70:463:80//D00766

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F-PLACE1009050//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.63:280:61//AC004241
F-PLACE1009060//Mus musculus mRNA for Alix (ALG-2-interacting protein X), complete CDS.//5.9e-113:725:85//AJ005073
F-PLACE1009090//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1045J21, WORKING DRAFT SEQUENCE.//9.1e-27:222:84//AL021919
F-PLACE1009091//Homo sapiens clone DJ0968I16, complete sequence.//0.027:630:58//AC006016
F-PLACE1009094
F-PLACE1009099//Mouse zinc finger protein (mkr4) mRNA, partial cds.//2.1e-85:726:76//M36515
F-PLACE1009110
F-PLACE1009111//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 138B7, WORKING DRAFT SEQUENCE.//6.0e-12:362:64//Z98752
F-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//3.4e-138:671:97//AF035586
F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds.//3.6e-23:718:59//D25215
F-PLACE1009150//Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRAFT SEQUENCE.//6.1e-142:684:98//AJ011929
F-PLACE1009155//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE.//4.3e-36:227:77//AP000031
F-PLACE1009158//H.sapiens genomic sequence for ERCC2 gene 3'region involved in DNA excision repair.//1.0:173:60//X52222
F-PLACE1009166
F-PLACE1009172//Human BAC clone 7E17 from 12q, complete sequence.//4.0e-35:257:85//AC002070
F-PLACE1009174//Homo sapiens Xp22 bins 16-17 BAC GSHB-531I17 (Genome Systems Human BAC Library) complete sequence.//2.9e-19:288:72//AC004805
F-PLACE1009183//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence.//0.053:388:60//AB008266
F-PLACE1009186//Rattus norvegicus fracture callus 1 (FxC1) mRNA, complete cds.//1.8e-50:317:89//AF061242
F-PLACE1009190//RPCI11-81N5.TJ RPCI11 Homo sapiens genomic clone R-81N5, genomic survey sequence.//0.91:114:67//AQ281881
F-PLACE1009200//CITBI-E1-2509J16.TF CITBI-E1 Homo sapiens genomic clone 2509J16, genomic survey sequence.//2.8e-44:175:83//AQ262198
F-PLACE1009230//H.sapiens gene for pregnancy specific beta-1 glycoprotein.//1.1e-106:495:88//X63203
F-PLACE1009246//HS_3058_B1_A06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=11 Row=B, genomic survey sequence.//0.10:175:68//AQ185945
F-PLACE1009298//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//1.8e-94:575:89//U47024
F-PLACE1009308//Human clone mcag32 chromosome 7 CTG repeat region.//0.0017:350:62//U23862
F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mRNA, complete cds.//3.0e-06:411:59//U83192
F-PLACE1009328//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191P20, WORKING DRAFT SEQUENCE.//5.7e-138:830:86//AL034399
F-PLACE1009335//Human (lambda) DNA for immunoglobin light chain.//0.071:253:62//D87015
F-PLACE1009338//RPCI11-74N24 TV RPCI11 Homo sapiens genomic clone R-74N24, genomic survey sequence.//2.4e-34:180:100//AQ268811
F-PLACE1009368
F-PLACE1009375
F-PLACE1009388//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1014D13, WORKING DRAFT SEQUENCE.//2.0e-37:288:84//AL022311
F-PLACE1009398//Human DNA binding protein (HPF2) mRNA, complete cds.//4.3e-78:730:74//M27878
F-PLACE1009404//SmD homolog [mice, liver, mRNA Partial, 199 nt].//0.16:95:71//S71494
F-PLACE1009410//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence.//1.6e-150:701:99//AC005919
F-PLACE1009434//Mus musculus clone OST431, genomic survey sequence.//2.9e-73:442:88//AF046700
F-PLACE1009443//Mycobacterium tuberculosis H37Rv complete genome; segment 148/162.//0.012:582:56//AL022022
F-PLACE1009444//Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds.//4.6e-21:146:93//AF012872
F-PLACE1009459//Mus musculus clone OST9217, genomic survey sequence.//2.9e-31:264:81//AF046660

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F-PLACE1009468//Sequence 1 from patent US 5580968.//1.9e-83:567:84//I30536
F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence.//1.9e-142:704:97//AC004531
F-PLACE1009477//Human 11p14.3 PAC clone pDJ939m16, complete sequence.//2.2e-09:235:68//AC004601
F-PLACE1009493//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//2.9e-83:171:92//U91321
F-PLACE1009524//Homo sapiens DNA sequence from PAC 63G5 on chromosome 22q12.3-13.1. Contains part of a gene for a human SEC7 homolog B2-1 (cytohesin-2, Arno, ARF exchange factor) LIKE protein, an unknown gene and a gene coding for a Leucine rich protein. Contains ESTs, STSs and GSSs, complete sequence.//3.8e-69:175:92//Z94160
F-PLACE1009539//Mus musculus synaptojanin 2 isoform alpha mRNA, complete cds.//7.0e-26:237:78//AF041862
F-PLACE1009542//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//3.1e-10:126:79//AL031587
F-PLACE1009571//RPCI11-60K12.TK RPCI11 Homo sapiens genomic clone R-60K12, genomic survey sequence.//1.4e-05:68:91//AQ195869
F-PLACE1009581
F-PLACE1009595//Homo sapiens chromosome 5, P1 clone 1029A7 (LBNL H15), complete sequence.//6.6e-19:309:70//AC003959
F-PLACE1009596//Rattus norvegicus platelet-activating factor acetylhydrolase beta subunit (PAF-AH beta) gene, complete cds.//9.0e-09:485:59//AF016049
F-PLACE1009607//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 409J21, WORKING DRAFT SEQUENCE.//4.9e-43:714:66//Z83824
F-PLACE1009613//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.017:655:57//AC004157
F-PLACE1009621
F-PLACE1009622//HS-1016-B2-E08-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 791 Col=16 Row=J, genomic survey sequence.//2.7e-15:100:98//B33248
F-PLACE1009637//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.63:130:67//AC005308
F-PLACE1009639//S.pombe chromosome II cosmid c24E9.//0.86:509:58//AL021816
F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds.//1.4e-171:816:98//AB011159
F-PLACE1009665//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//3.4e-67:437:87//AC005177
F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//2.5e-147:701:98//AF062534
F-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence.//1.5e-98:228:100//AC006011
F-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete sequence.//2.2e-130:736:91//AC000109
F-PLACE1009731//M.musculus mRNA for immunity associated protein 38.//1.1e-13:311:64//Y08026
F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds.//4.2e-125:602:98//AF046024
F-PLACE1009794
F-PLACE1009798//Hnman DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//1.3e-73:271:84//AL030996
F-PLACE1009845
F-PLACE1009861//B.tauris cathepsin B mRNA, 3' end.//0.00023:147:65//M64620
F-PLACE1009879//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE.//4.9e-27:725:63//AL034397
F-PLACE1009886//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SEQUENCE.//8.2e-12:135:82//AL031427
F-PLACE1009888//F14G3-T7 IGF Arabidopsis thaliana genomic clone F14G3, genomic survey sequence.//0.0044:232:60//AQ251431
F-PLACE1009908//S.pombe chromosome I cosmid c3F10.//1.5e-19:559:59//Z69369
F-PLACE1009921//Homo sapiens cosmid clone HDAB (1S149) insert DNA, complete cosmid.//5.9e-48:304:87//M63005
F-PLACE1009924//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-2011O4, WORKING DRAFT SE-

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QUENCE, 4 unordered pieces.//2.4e-51:481:78//AC004529
F-PLACE1009925//nbxb0027C22r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0027C22r, genomic survey sequence.//0.98:220:67//AQ272066
F-PLACE1009935//Sequence 16 from patent US 5552281.//0.030:152:67//I25655
F-PLACE1009947//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.6e-12:322:67//AC006026
F-PLACE1009971
F-PLACE1009992//HS_3178_B1_F04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3178 Col=7 Row=L, genomic survey sequence.//4.9e-23:142:95//AQ150311
F-PLACE1009995//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.00019:231:64//Z81029
F-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds.//7.9e-87:552:80//U48288
F-PLACE1010023
F-PLACE1010031//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//6.9e-101:181:98//AL031775
F-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//2.3e-136:689:95//X84692
F-PLACE1010069//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 212A2, WORKING DRAFT SEQUENCE.//0.0090:383:60//Z95114
F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//1.8e-166:792:98//AF065482
F-PLACE1010076//Mouse mRNA for TGF-beta type I receptor, complete cds.//7.5e-13:203:77//D25540
F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds.//3.0e-152:727:98//AB007925
F-PLACE1010089//HS_3111_A1_E08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3111 Col=15 Row=I, genomic survey sequence.//4.8e-07:124:78//AQ101268
F-PLACE1010096//R.norvegicus mRNA for 100 kDa protein.//1.2e-108:700:85//X64411
F-PLACE1010102//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-07:476:60//AC005506
F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//3.8e-25:728:60//AF059569
F-PLACE1010106//Human DNA sequence from PAC 127B14 on chromosome Xq22.//6.5e-25:488:63//Z93928
F-PLACE1010134//S.pombe chromosome I cosmid c29B12.//1.9e-13:238:67//Z99164
F-PLACE1010148//Homo sapiens partial human cDNA (660 bp).//4.8e-83 :409:98//AJ222636
F-PLACE1010152//CIT-HSP-2381F24.TF CIT-HSP Homo sapiens genomic clone 2381F24, genomic survey sequence.//1.5e-28:163:98//AQ196757
F-PLACE1010181//Homo sapiens PAC clone DJ1139I01 from Xq23, complete sequence.//2.4e-15:197:72//AC004973
F-PLACE1010194//Ictalurus punctatus tumor supressor p53 mRNA, complete cds.//3.0e-14:181:74//AF074967
F-PLACE1010202//Homo sapiens mRNA for MBNL protein.//1.2e-27:509:66//Y13829
F-PLACE1010231//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 287G14, WORKING DRAFT SEQUENCE.//2.3e-101:194:95//AL033377
F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds.//5.8e-145:693:97//AB007917
F-PLACE1010270//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence; WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.1e-05:347:60//AC004710
F-PLACE1010274//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.00040:231:64//Z81029
F-PLACE1010293//Homo sapiens chromosome 2 PAC RPCI3-417E16 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.5e-25:344:70//AC004464
F-PLACE1010310//Homo sapiens DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence.//3.5e-I 0:185:67//AL031005
F-PLACE1010321//Human DNA sequence from clone 299D3 on chromosome 22q13.3, complete sequence.//0.010:524:58//Z84468
F-PLACE1010324//CIT-HSP-2335J21.TR CIT-HSP Homo sapiens genomic clone 2335J21, genomic survey sequence.//9.1e-90:448:97//AQ041837
F-PLACE1010329//Apis mellifera ligustica complete mitochondrial genome.//2.8e-08:384:64//L06178
F-PLACE1010341//HS-1047-A2-C04-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=8 Row=E, genomic survey sequence.//4.1e-21:141:92//B38252
F-PLACE1010362//Mycobacterium tuberculosis H37Rv complete genome: segment 155/162.//0.94:398:57//AL022121

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F-PLACE1010364//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y102G3, WORKING DRAFT SEQUENCE.//0.11:404:56//AL020985
F-PLACE1010383//Homo sapiens chromosome 17, clone hCIT.186_H_2, complete sequence.//0.066:88:76//AC004675
F-PLACE1010401//CIT-HSP-2367K17.TR CIT-HSP Homo sapiens genomic clone 2367K17, genomic survey sequence.//2.4e-71:454:88//AQ076825
F-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds.//7.5e-134:722:93//AF003927
F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds.//2.2e-150:702:99//AF039081
F-PLACE1010492
F-PLACE1010522//Homo sapiens cosmid LM1937 from Xq28.//0.022:405:60//U82695
F-PLACE1010529//Sequence 1 from patent US 5776717.//2.9e-145 :684:98//AR016417
F-PLACE1010547//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//1.0:283:61//AL031677
F-PLACE1010562//RPCI11-65I16.TK RPCI11 Homo sapiens genomic clone R-65I16, genomic survey sequence.//0.017:216:67//AQ200831
F-PLACE1010579//Homo sapiens full-length insert cDNA YI23D12.//3.9e-19:147:89//AF075014
F-PLACE1010580//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//6.4e-96:559:89//L25125
F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14p (PEX14) mRNA, complete cds.//3.1e-146:707:97//AF045186
F-PLACE1010616//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.045:454:59//AC005308
F-PLACE1010622//Plasmodium falciparum MAL3P2, complete sequence.//9.1e-07:378:60//AL034558
F-PLACE1010624//Streptomyces coelicolor cosmid 5A7.//1.4e-05:518:61//AL031107
F-PLACE1010628//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//5.0e-137:675:97//AC004846
F-PLACE1010629//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-259H10, complete sequence.//2.5e-17:187:80//AC004682
F-PLACE1010630//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence.//0.21:159:64//AB016872
F-PLACE1010631//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.2e-144:720:97//AC005069
F-PLACE1010661
F-PLACE1010662//Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project).//0.90:257:61//AL021960
F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds.//3.3e-73:697:74//U35376
F-PLACE1010714//Human Chromosome 15q11-q13 PAC clone pDJ778a2, complete sequence.//0.010:447:59//AC004583
F-PLACE1010720//Mouse TPA-induced TIS11 mRNA.//2.0e-86:535:88//X14678
F-PLACE1010739//HS_2013_B2_B10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2013 Col=20 Row=D, genomic survey sequence.//5.7e-87:435:97//AQ235864
F-PLACE1010743//R.norvegicus mRNA for myr5.//1.7e-87:582:85//X77609
F-PLACE1010761//Homo sapiens chromosome 17, clone hRPK.294_J_22, complete sequence.//4.7e-45:235:99//AC005921
F-PLACE1010771//M.musculus HCNGP mRNA.//1.6e-135:801:88//X68061
F-PLACE1010786//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-15, complete sequence.//0.35:334:60//AL010221
F-PLACE1010800//RPCI11-79H17.TV RPCI11 Homo sapiens genomic clone R-79H17, genomic survey sequence.//5.8e-18:168:82//AQ284252
F-PLACE1010802//Human Chromosome X clone bWXD531, complete sequence.//1.6e-30:693:63//AC004384
F-PLACE1010811//RPCI11-51N5.TK RPCI11 Homo sapiens genomic clone R-51N5, genomic survey sequence.//8.3e-11:142:78//AQ052380
F-PLACE1010833//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 467K16, WORKING DRAFT SEQUENCE.//7.3e-40:147:88//AL031283
F-PLACE1010856//M.musculus mRNA for utrophin.//7.3e-17:150:86//Y12229
F-PLACE1010857//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11.//1.4e-94:422:95//AB020868

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F-PLACE1010870//M.musculus mRNA for ZT3 zinc finger factor.//1.3e-93:530:90//Z67747
F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//1.1e-147:694:98//AB011182
F-PLACE1010891
F-PLACE1010896//Mouse BAC mbac20 from 14D1-D2 (T-Cell Receptor Alpha Locus), complete sequence.//3.9e-26:394:68//AC003997
F-PLACE1010900
F-PLACE1010916//HS_2242_A1_C04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=7 Row=E, genomic survey sequence.//1.0e-78:391:97//AQ146687
F-PLACE1010917
F-PLACE1010925//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.11:629:56//AC004688
F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds.//9.5e-138:653:98//AB011126
F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds.//5.6e-90:437:98//AF064243
F-PLACE1010944//Homo sapiens full-length insert cDNA clone ZD38E12.//1.4e-09:208:68//AF086247
F-PLACE1010947
F-PLACE1010954//CIT-HSP-2283D9.TR CIT-HSP Homo sapiens genomic clone 2283D9, genomic survey sequence.//2.1e-29:190:91//B98965
F-PLACE1010960//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-52, complete sequence.//0.00074:421:60//AL010226
F-PLACE1010965//CIT-HSP-2386K24:TF.1 CIT-HSP Homo sapiens genomic clone 2386K24, genomic survey sequence.//1.8e-84:412:99//AQ240696
F-PLACE1011026//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-20, complete sequence.//0.00037:257:64//AL008972
F-PLACE1011032//Homo sapiens chromosome 5, BAC clone 118L13 (LBNL H176), complete sequence.//3.8e-06:315:65//AC005348
F-PLACE1011041//Human Fas-ligand associated factor 3 mRNA, partial cds.//1.5e-56:286:98//U70669
F-PLACE1011046//Rat phospholipase C-1 mRNA, complete cds.//1.3e-24:278:76//M20636
F-PLACE1011054//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 981L23, WORKING DRAFT SEQUENCE.//3.8e-27:196:84//AL031686
F-PLACE1011056//Ovis aries bactinecin 11 (Bac11) gene, exon 4, and complete cds.//5.4e-06:182:67//U77049
F-PLACE1011057//protein kinase PRK2 [human, DX3 B-cell myeloma cell line, mRNA, 3255 nt].//3.2e-31:169:100//S75548
F-PLACE1011090//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 998H6, WORKING DRAFT SEQUENCE.//5.1e-80:479:89//AL031687
F-PLACE1011109//Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.//2.3e-24:192:84//L14684
F-PLACE1011114//S.cerevisiae chromosome XI reading frame ORF YKR024c.//1.4e-14:346:60//Z28249
F-PLACE1011133//T7E9-T7.1 TAMU Arabidopsis thaliana genomic clone T7E9, genomic survey sequence.//0.010:345:60/B19698
F-PLACE1011143//CIT-HSP-2375J10.TR CIT-HSP Homo sapiens genomic clone 2375J10, genomic survey sequence.//0.00013:95:76//AQ109305
F-PLACE1011160//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//3.7e-111:692:87//AC004893
F-PLACE1011165//H.sapiens galactokinase (GK2) mRNA, complete cds.//8.4e-31:194:92//M84443
F-PLACE1011185//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-249B10, complete sequence.//3.1e-43:447:72//AC002288
F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyltransferase mRNA, complete cds.//3.3e-124:584:99//AF038664
F-PLACE1011214//HS_2046_A2_B01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2046 Col=2 Row=C, genomic survey sequence.//2.0e-39:346:81//AQ305965
F-PLACE1011219
F-PLACE1011221//CITBI-E1-2513F18.TR CITBI-E1 Homo sapiens genomic clone 2513F18, genomic survey sequence.//2.4e-20:119:100//AQ279801
F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds.//4.4e-146:675:99//AB011101
F-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.7e-42:212:84//AC005014
F-PLACE1011273//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y37D8, WORKING DRAFT SEQUENCE.//1.0:214:60//Z92819

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F-PLACE1011291//RPCI11-16P9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-16P9, genomic survey sequence.//8.0e-08:66:98//B81770
F-PLACE1011296//Homo sapiens chromosome 16, cosmid clone 443G8 (LANL), complete sequence.//0.027:135:67//AC004647
F-PLACE1011310//H.sapiens CpG island DNA genomic Mse1 fragment, clone 53c10, reverse read cpg53c10.rt1b.//1.4e-05:57:100//Z61496
F-PLACE1011325//Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds.//0.077:193:60//L02290
F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//3.1e-150:699:99//AF102265
F-PLACE1011340//Homo sapiens chromosome 17, clone hRPK.388_F_14, complete sequence.//2.4e-38:186:83//AC005375
F-PLACE1011371//Mus musculus PK-120 precursor (itih-4) mRNA, complete cds.//6.0e-35:689:63//AF023919
F-PLACE1011375//Mus musculus Kv3.4 gene, exon 4.//6.0e-88:584:86//AJ010310
F-PLACE1011399//paramecium species 7,325 mt dna dimer: replication init. region.//0.00011:255:63//K00919
F-PLACE1011419//Homo sapiens chromosome 21 PAC LLNLP704G1150Q13.//0.067:337:62//AJ006996
F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds.//4.6e-157:743:98//AB011102
F-PLACE1011452//Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRAFT SEQUENCE.//1.1e-53:557:73//AJ011929
F-PLACE1011465//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//3.5e-71:498:80//AC004605
F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds.//4.8e-151:703:99//AB018255
F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//5.2e-145:675:99//AF065482
F-PLACE1011492//Ray (T.californica) acetylcholine receptor beta-subunit mRNA.//1.0:448:59//J00964
F-PLACE1011503
F-PLACE1011520//Homo sapiens clone DJ1119N05, complete sequence.//3.8e-147:692:99//AC004968
F-PLACE1011563//R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).//0.00036:296:61//X83546
F-PLACE1011567//Homo sapiens PAC clone DJ1164K10 from 7p21-p22, complete sequence.//1.1e-38:315:82//AC004984
F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds.//1.3e-65:268:86//AF054180
F-PLACE1011586//Homo sapiens chromosome 17, clone HRPC890E16, complete sequence.//2.0e-82:188:96//AC004477
F-PLACE1011635//Homo sapiens chromosome 17, clone hRPK.214_O_1, complete sequence.//1.8e-153:752:97//AC005224
F-PLACE1011641//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//4.8e-05:190:67//AE000660
F-PLACE1011643//Alcaligenes eutrophus phaP gene.//0.16:466:59//X85729
F-PLACE1011646//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1013A10, WORKING DRAFT SEQUENCE.//9.1e-19:156:76//AL033383
F-PLACE1011649
F-PLACE1011650//Homo sapiens retinol dehydrogenase gene, complete cds.//6.4e-09:172:74//AF037062
F-PLACE1011664//D.melanogaster crn mRNA.//1.1e-52:650:68//X58374
F-PLACE1011675//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.11:443:58//AC005507
F-PLACE1011682//Human DNA sequence from clone 342B11 on chromosome 22q12.1-12.3. Contains ESTs and a GSS, complete sequence.//0.31:127:71//AL008719
F-PLACE1011719//Human BAC clone RG369K23 from 7q31, complete sequence.//4.6e-52:461:77//AC002487
F-PLACE1011725
F-PLACE1011729//Human Chromosome 15q11-q13 clone pDJ276c12 from the Prader-Willi/Angelman syndrome region, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.011:320:62//AC004737
F-PLACE1011749//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.00031:544:59//AC004157
F-PLACE1011762//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//2.4e-115:682:90//AC004003
F-PLACE1011778//RPCI11-22D17.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-22D17, genomic survey sequence.//2.7e-114:611:93//AQ008944

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F-PLACE1011783//CIT-HSP-2317N1.TF CIT-HSP Homo sapiens genomic clone 2317N1, genomic survey sequence.//2.3e-17:120:94//AQ042330
F-PLACE1011858//Gallus domesticus filamin mRNA, complete cds.//4.1e-24:565:64//U00147
F-PLACE1011874//Homo Sapiens Chromosome X clone bWXD312, complete sequence.//2.5e-141:678:98//AC004478
F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cds.//1.6e-108:526:98//AB011152
F-PLACE1011891//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 439F8, WORKING DRAFT SEQUENCE.//0.0014:330:62//AL021392
F-PLACE1011896//Mus musculus Wnt10a mRNA, complete cds.//1.4e-89:678:82//U61969
F-PLACE1011922//Caprine arthritis-encephalitis virus envelope glycoprotein (env) gene, partial cds.//0.069:246:61//U81400
F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//1.2e-138:664:98//AF059617
F-PLACE1011962//HS_3212_B2_G12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3212 Col=24 Row=N, genomic survey sequence.//2.4e-07:154:74//AQ175369
F-PLACE1011964//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 322P7, WORKING DRAFT SEQUENCE.//3.7e-22:369:69//AL023799
F-PLACE1011982//HS-1041-A1-B01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 823 Col=1 Row=C, genomic survey sequence.//0.44:309:58//B36529
F-PLACE1011995//Homo sapiens Xq28 BAC RPCI11-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//8.8e-53:687:71//AC006054
F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//1.2e-146:690:98//AB018256
F-PLACE2000003//Homo sapiens chromosome 17, clone hRPK.318_A_15, complete sequence.//1.7e-62:293:88//AC005837
F-PLACE2000006//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//1.4e-116:261:91//AC006057
F-PLACE2000007
F-PLACE2000011//Homo sapiens chromosome 19, cosmid F20887, complete sequence.//5.2e-102:489:99//AC005578
F-PLACE2000014//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1111N9, WORKING DRAFT SEQUENCE.//0.0095:307:62//AL022574
F-PLACE2000015//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.0e-36:316:81//AC005069
F-PLACE2000017//HS_3042_A1_F08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3042 Col=15 Row=K, genomic survey sequence.//1.0:184:61//AQ098074
F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, complete cds.//4.6e-84:844:72//AF082556
F-PLACE2000030//Human Chromosome 11 Cosmid cSRL16b6, complete sequence.//2.3e-22:233:77//U73638
F-PLACE2000033//C.capitata mRNA for chorion protein s18.//0.0019:342:62//Y08913
F-PLACE2000034//Rattus norvegicus transmembrane receptor Robo1 mRNA, complete cds.//2.8e-13:335:63//AF041082
F-PLACE2000039//Rattus norvegicus cytoplasmic dynein heavy chain (MAP 1C), mRNA, complete cds.//7.7e-84:489:90//L08505
F-PLACE2000047//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//5.0e-28:327:76//U95626
F-PLACE2000050//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//1.1e-32:527:68//AC003101
F-PLACE2000061//CIT-HSP-2346L20.TF CIT-HSP Homo sapiens genomic clone 2346L20, genomic survey sequence.//1.1e-05:89:83//AQ059010
F-PLACE2000062//Human membrane-associated lectin type-C mRNA.//9.0e-113:662:86//M98457
F-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//2.2e-133:631:98//AF027219
F-PLACE2000097//Homo sapiens chromosome 12p13.3 clone RPCI11-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//1.6e-16:119:93//AC005910
F-PLACE2000100//HS_3184_A1_D06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=11 Row=G, genomic survey sequence.//1.5e-80:409:97//AQ150004
F-PLACE2000103//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20208, WORKING DRAFT SEQUENCE.//1.0e-172:830:98//AL031848
F-PLACE2000111//Homo sapiens DNA, trinucleotide repeats region.//1.0:200:64//AB018491
F-PLACE2000115

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F-PLACE2000124//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence.//6.2e-43:362:80//AC004531
F-PLACE2000132//RPCI11-79F15.TV RPCI11 Homo sapiens genomic clone R-79F15, genomic survey sequence.//5.4e-35:206:94//AQ284166
F-PLACE2000136//Human BAC clone 7E17 from 12q, complete sequence.//2.7e-12:814:59//AC002070
F-PLACE2000140//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 11703, WORKING DRAFT SEQUENCE.//3.6e-165:799:97//AL020995
F-PLACE2000164//Canine histamine H2 receptor gene, complete cds.//0.10:392:56//M32701
F-PLACE2000170
F-PLACE2000172//Homo sapiens PAC clone DJ0811017 from 7q21-22, complete sequence.//3.9e-91:552:88//AC006005
F-PLACE2000176//Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 In BCRL2-GGT Region, complete sequence.//0.98:201:64//AC004032
F-PLACE2000187
F-PLACE2000216
F-PLACE2000223//RPCI11-12L17.TP RPCI-11 Homo sapiens genomic clone RPCI-11-12L17, genomic survey sequence.//0.00039:325:58/B75888
F-PLACE2000235//Human Chromosome 16 BAC clone CIT987SK-254P9, complete sequence.//7.5e-55:237:78//AC003003
F-PLACE2000246//Homo sapiens chromosome 3p clone RPCI4-544D10, WORKING DRAFT SEQUENCE, 58 unordered pieces.//2.4e-92:236:94//AC005902
F-PLACE2000264//Human DNA sequence from clone 391022 on chromosome 6p21.2-21.31 Contains pseudogenes similar to ribosomal protein, ESTs, GSSs, complete sequence.//1.4e-32:331:78//AL031577
F-PLACE2000274//Anthocidaris crassispina mRNA for B2HC, partial cds.//8.5e-48:765:66//AB012308
F-PLACE2000302//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//8.3e-08:662:58//US2064
F-PLACE2000305//Homo sapiens clone DJ1129L24, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.4e-08:95:81//AC006021
F-PLACE2000317//HS_3183_B2_F05_MR CIT Approved Human Genomic Sperm-Library D Homo sapiens genomic clone Plate=3183 Col=10 Row=L, genomic survey sequence.//2.5e-71:346:99//AQ172747
F-PLACE2000335//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.7e-14:402:65//AC004952
F-PLACE2000341//Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete cds.//4.5e-77:555:82//AF026554
F-PLACE2000342//Suid herpesvirus 1 UL5 gene, partial cds, UL6 and UL7 genes, complete cds, UL8 gene, partial cds.//1.8e-14:259:71//U66829
F-PLACE2000347//Human DNA from overlapping chromosome 19-specific cosmids R32543,, and F15613 containing ZNF gene family member, genomic sequence, complete sequence.//6.0e-34:376:74//AC003006
F-PLACE2000359//RPCI11-23J20.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-23J20, genomic survey sequence.//8.4e-21:288:69//AQ013849
F-PLACE2000366//Human Tigger1 transposable element, complete consensus sequence.//5.0e-114:692:80//U49973
F-PLACE2000371//Homo sapiens 12p13.3 PAC RPCI1-29K11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.38:356:58//AC005182
F-PLACE2000373//RPCI11-49C18.TJ RPCI11 Homo sapiens genomic clone R-49C18, genomic survey sequence.//0.064:132:68//AQ051776
F-PLACE2000379//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//1.6e-130:776:88//AC003658
F-PLACE2000394//Homo sapiens chromosome 18 BAC RPCI11-128D14 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//5.4e-113:808:83//AC005909
F-PLACE2000398//Mouse hexamer repeat sequence (117) homologous to Drosophila 'period' gene.//0.87:286:63//X06967
F-PLACE2000399
F-PLACE2000404//Caenorhabditis elegans cosmid R74, complete sequence.//2.9e-59:532:68//Z36238
F-PLACE2000411//Acanthamoeba castellanii transformation-sensitive protein homolog mRNA, complete cds.//0.44:553:56//U89984
F-PLACE2000419//Human adenosine deaminase (ADA) gene, complete cds.//1.4e-56:303:86//M13792
F-PLACE2000425//HS_3047_A1_H05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

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nomic clone Plate=3047 Col=9 Row=O, genomic survey sequence.//2.8e-42:224:97//AQ126949
F-PLACE2000427
F-PLACE2000433//Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence.//1.1e-19:363:67//AC005821
F-PLACE2000435//HS_3036_B1_F11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=21 Row=L, genomic survey sequence.//3.1e-06:184:66//AQ096999
F-PLACE2000438//Caenorhabditis elegans cosmid Y45F10D, complete sequence.//4.6e-23:550:62//AL021492
F-PLACE2000450//Homo sapiens PAC clone DJ1188N21 from 7q11.23-q21.1, complete sequence.//1.0e-78:604:80//AC006025
F-PLACE2000455//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//8.2e-05:330:63//AC002300
F-PLACE2000458//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//5.7e-168:816:97//AC005740
F-PLACE2000465//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.//4.3e-33:296:79//AC002037
F-PLACE2000477//Homo sapiens clone RG052H06, WORKING DRAFT SEQUENCE, 11 unordered pieces.//3.4e-59:598:74//AC005057
F-PLACE3000004//Human EYA3 homolog (EYA3) mRNA, complete cds.//7.6e-49:361:84//U81602
F-PLACE3000009//Human placenta (Diff48) mRNA, complete cds.//3.0e-58:713:69//U49187
F-PLACE3000020//R.norvegicus type III adenylyl cyclase mRNA, complete cds.//6.1e-103:600:89//M55075
F-PLACE3000029
F-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//4.4e-115:718:86//Y17267
F-PLACE3000070//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//1.8e-17:250:74//AC005368
F-PLACE3000103//Caenorhabditis elegans cosmid C13F10.//4.6e-07:408:61//U97006
F-PLACE3000119//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.5e-58:291:86//AC004670
F-PLACE3000121//Rattus norvegicus rsec15 mRNA, complete cds.//8.1e-81:837:71//AF032668
F-PLACE3000124//Homo sapiens chromosome 17, clone hRPK.85_B_7, complete sequence.//1.8e-48:330:79//AC005695
F-PLACE3000136
F-PLACE3000142//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 349A12, WORKING DRAFT SEQUENCE.//0.011:294:62//AL033520
F-PLACE3000145//Gallus gallus tensin mRNA, 3' end.//6.9e-52:659:68//L06662
F-PLACE3000147//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//5.1e-37:305:81//AL031053
F-PLACE3000148//Homo sapiens chromosome Y, clone 47511, complete sequence.//4.7e-32:766:63//AC004474
F-PLACE3000155//Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence.//7.4e-173:822:98//AC005277
F-PLACE3000156//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//2.2e-81:783:74//AC003682
F-PLACE3000157
F-PLACE3000158//, complete sequence.//1.0e-180:845:97//AC005500
F-PLACE3000160//CIT978SK-152K7.TV CIT978SK Homo sapiens genomic clone 152K7, genomic survey sequence.//0.080:259:59//B50878
F-PLACE3000169//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//9.8e-158:749:98//AC006130
F-PLACE3000194
F-PLACE3000197//F.rubripes GSS sequence, clone 075N04bB7, genomic survey sequence.//1.4e-08:164:68//AL003352
F-PLACE3000199//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//0.0019:277:58//Z82207
F-PLACE3000207//Homo sapiens BAC clone GS165L15 from 7p15, complete sequence.//6.6e-21:312:67//AC005013
F-PLACE3000208//Homo sapiens (clones: CW52-2, CW27-6, CW15-2, CW26-5, 11-67) collagen type VII intergenic region and (COL7A1) gene, complete cds.//1.0:279:61//L23982
F-PLACE3000218//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//9.3e-43:383:79//AC004086

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F-PLACE3000220//RPCI11-54B4.TV RPCI11 Homo sapiens genomic clone R-54B4, genomic survey sequence.// 2.4e-36:381:76//AQ082056
F-PLACE3000221//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces//7.2e-135:721:91//AC005231
F-PLACE3000226
F-PLACE3000230//Homo sapiens c1cr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//3.3e-80:498:78//U95626
F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//2.6e-54:254:92//Z98046
F-PLACE3000244//M.musculus mRNA for 200 kD protein.//1.4e-139:850:86//X80169
F-PLACE3000254//Ateline herpesvirus 3 complete genome.//1.3e-10:399:61//AF083424
F-PLACE3000271//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//1.8e-21:350:68//AF001548
F-PLACE3000276//HS_2026_B1_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=21 Row=P, genomic survey sequence.//5.7e-45:376:81//AQ231147
F-PLACE3000304//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//1.6e-138:650:99//AC005328
F-PLACE3000310
F-PLACE3000320//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//1.9e-41:379:77//AL034379
F-PLACE3000322//Homo sapiens chromosome 17, clone hRPK.209_J_20, complete sequence.//3.3e-35:419:68//AC005822
F-PLACE3000331//CIT-HSP-2347D24.TR CIT-HSP Homo sapiens genomic clone 2347D24, genomic survey sequence.//2.7e-20:119:99//AQ061543
F-PLACE3000339//Rhodobacter sphaeroides magnesium chelatase subunits BchI (bchI) and BchD (bchD) genes, complete cds; and BchO (bchO) gene, partial cds.//0.99:310:58//AF017642
F-PLACE3000341//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//7.5e-159:752:98//AC006055
F-PLACE3000350//Rattus norvegicus serine/threonine protein kinase TAO1 mRNA, complete cds.//2.3e-107:592:92//AF084205
F-PLACE3000352//Human DNA sequence from PAC 293L6 on chromosome 22, complete sequence.//2.1e-37:480:70//Z83732
F-PLACE3000353
F-PLACE3000362//Homo sapiens chromosome 17, clone hRPK.215_P_18, complete sequence.//0.00011:373:60//AC005969
F-PLACE3000363
F-PLACE3000365//Human DNA sequence from PAC 227P17, between markers DXS6791 and DXS8038 on chromosome X contains CpG island, EST.//0.074:279:61//Z81007
F-PLACE3000373//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.8e-118:653:92//Z92545
F-PLACE3000388//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//2.2e-25:288:71//AC005154
F-PLACE3000399//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 466N1, WORKING DRAFT SEQUENCE.//2.3e-69:303:86//Z97630
F-PLACE3000400//Caenorhabditis elegans cosmid H03A11, complete sequence.//0.0063:435:58//Z93239
F-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.// 5.8e-25 :292:73//AC006023
F-PLACE3000402//RPCI11-20D6.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-20D6, genomic survey sequence.//1.1e-10:154:74//AQ008761
F-PLACE3000405//Homo sapiens chromosome 17, clone hRPK.628_E_12, complete sequence.//2.9e-41:515:72//AC005701
F-PLACE3000406//cSRL-179E11-u cSRL flow sorted Chromosome 11 specific cosmid Homosapiens genomic clone cSRL-179E11, genomic survey sequence.//2.8e-91:540:89//B03443
F-PLACE3000413
F-PLACE3000416//F19L8-Sp6 IGF Arabidopsis thaliana genomic clone F19L8, genomic survey sequence.//

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0.0018:664:55//B11305
F-PLACE3000425//Human DNA sequence from clone 231L4 on chromosome Xq27.1-27.3 Contains GSS, STS, complete sequence.//1.1e-16:284:70//AL022719
F-PLACE3000455//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469D22, WORKING DRAFT SEQUENCE.//3.6e-146:732:96//AL031284
F-PLACE3000475//HS_2164_A2_H10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2164 Col=20 Row=O, genomic survey sequence.//1.5e-07:159:71//AQ132983
F-PLACE3000477//Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs, CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) like gene and STSs.//2.9e-11:213:70//Z83843
F-PLACE4000009//Sequence 93 from patent US 5616500.//9.9e-08 :692:60//I39845
F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds.//1.1e-116:331:100//AB018352
F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.//5.0e-05:244:63//AC004131
F-PLACE4000049//Homo sapiens Xp22-171-173 BAC GSHB-312I4 (Genome Systems Human BAC Library) complete sequence.//1.2e-37:385:74//AC005926
F-PLACE4000052//M.musculus abcl mRNA.//1.5e-110:671:88//X75926
F-PLACE4000063
F-PLACE4000089//M.musculus BOX DNA for regulatory element and promoter region related to EC cell differentiation.//3.7e-12:114:85//X74311
F-PLACE4000093//CIT-HSP-2380K5.TF CIT-HSP Homo sapiens genomic clone 2380K5, genomic survey sequence.//0.11:245:60//AQ108342
F-PLACE4000100//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20208, WORKING DRAFT SEQUENCE.//2.9e-19:384:65//AL031848
F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds.//1.2e-145:684:99//AB007931
F-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds.//3.7e-62:541:78//AF091234
F-PLACE4000129
F-PLACE4000131//HS_3139_B2_F12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3139 Col=24 Row=L, genomic survey sequence.//2.3e-14:221:70//AQ183207
F-PLACE4000147//Human DNA sequence from clone 740A11 on chromosome Xq22.2-23. Contains part of the COL4A5 gene for Collagen Alpha 5(IV) Chain Precursor. Contains GSSs, complete sequence.//0.28:412:58//AL031622
F-PLACE4000156//Human zinc finger protein ZNF136.//7.2e-88:764:76//U09367
F-PLACE4000192
F-PLACE4000211
F-PLACE4000222//344J1.TVB CIT978SKA1 Homo sapiens genomic clone A-344J01, genomic survey sequence.//1.2e-14:177:76//B17158
F-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds.//9.8e-116:662:89//AF030430
F-PLACE4000233//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//5.2e-54:363:70//AC003973
F-PLACE4000247
F-PLACE4000250//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//0.0053:229:65//AC004673
F-PLACE4000252
F-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD protein.//2.0e-25:191:87//Z70200
F-PLACE4000261//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//2.6e-23:314:71//AF084259
F-PLACE4000269//Rattus norvegicus rexo70 mRNA, complete cds.//5.5e-122:734:88//AF032667
F-PLACE4000270
F-PLACE4000300
F-PLACE4000320//Human FKBP-rapamycin associated protein (FRAP) mRNA, complete cds.//1.4e-21:135:96//L34075
F-PLACE4000323//HS_2165_B1_B02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2165 Col=3 Row=D, genomic survey sequence.//4.3e-08:170:71//AQ125036
F-PLACE4000326//Mouse DNA with homology to EBV IR3 repeat, segment 1, clone Mu2.//2.8e-06:311:63//M10296
F-PLACE4000344//Plasmodium falciparum chromosome 2, section 38 of 73 of the complete sequence.//0.014:252:60//AE001401
F-PLACE4000367

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F-PLACE4000369
F-PLACE4000379//CIT-HSP-2350B9.TF CIT-HSP Homo sapiens genomic clone 2350B9, genomic survey sequence.//9.2e-46:282:86//AQ062661
F-PLACE4000387//CIT-HSP-2382F11.TR CIT-HSP Homo sapiens genomic clone 2382F11, genomic survey sequence.//0.96:102:70//AQ080649
F-PLACE4000392//Rattus norvegicus polymorphic marker D20UIA1 sequence.//1.2e-05:222:68//AF054088
F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds.//9.6e-46:605:71//AB014540
F-PLACE4000411//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 173D1, WORKING DRAFT SEQUENCE.//3.2e-29:179:79//AL031984
F-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//4.0e-44:263:92//Z70200
F-PLACE4000445//HS-1053-B1-D02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775 Col=3 Row=H, genomic survey sequence.//0.070:47:100//B41346
F-PLACE4000450
F-PLACE4000465//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//2.3e-07:273:65//AC005065
F-PLACE4000487//Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence.//4.1e-34:351:70//AC005821
F-PLACE4000489//HS_3012_B1_G05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3012 Col=9 Row=N, genomic survey sequence.//2.0e-36:220:92//AQ095537
F-PLACE4000494//Homo sapiens 12p13.3 PAC RPCI5-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.3e-57:395:79//AC005865
F-PLACE4000521//Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRAFT SEQUENCE.//1.6e-163:770:98//AJ011929
F-PLACE4000522//Feline leukemia virus Notch2 gene, clone FeLV/Notch2-C, partial cds.//4.0e-124:686:90//U47645
F-PLACE4000548
F-PLACE4000558//Bothrops atrox batroxobin gene (EC 3.4.21.29).//0.049:435:59//X12747
F-PLACE4000581
F-PLACE4000590//Homo sapiens chromosome Y, clone 475I1, complete sequence.//3.6e-20:747:59//AC004474
F-PLACE4000593//Caenorhabditis elegans cosmid F25D7, complete sequence.//5.6e-16:326:65//Z78418
F-PLACE4000612//Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.//1.7e-163:785:97//AC005281
F-PLACE4000638//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.7e-74:707:74//AC006039
F-PLACE4000650
F-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//1.1e-145:840:89//Y17267
F-PLACE4000670//Sequence 13 from patent US 5712381.//1.0:311:59//I82816
F-SKNMC1000011//Gallus gallus bone sialoprotein II mRNA, complete cds.//0.014:92:73//U10577
F-SKNMC1000013//Orang-utan involucrin gene, complete cds.//0.021:417:59//M25312
F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds.//7.6e-147:706:98//AB014554
F-SKNMC1000050//Sequence 5 from patent US 5789181.//1.6e-52:330:90//AR020616
F-SKNMC1000091//Human NK homeobox protein (Nkx6.1) gene, exon 1.//0.0018:375:60//U66797
F-THYRO1000017//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA, complete cds.//6.6e-97:542:84//U91561
F-THYRO1000026//Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains genes for NCF4 (P40PHOX) protein,cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS, complete sequence.//3.5e-46:353:82//AL008637
F-THYRO1000034//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 90L6, WORKING DRAFT SEQUENCE.//0.83:227:61//Z97353
F-THYRO1000035//Human Chromosome X clone bWXD187, complete sequence.//1.2e-39:303:83//AC004383
F-THYRO1000040
F-THYRO1000070//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//1.3e-05:613:58//AC005383
F-THYRO1000072//Homo sapiens mRNA for KIAA0657 protein, partial cds.//2.7e-84:722:77//AB014557
F-THYRO1000085
F-THYRO1000092//CIT-HSP-2013L16.TFB CIT-HSP Homo sapiens genomic clone 2013L16, genomic survey sequence.//0.31:186:61//B60606
F-THYRO1000107

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F-THYRO1000111//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//6.4e-110:690:87//Z93403
F-THYRO1000121//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//1.4e-127:816:85//U49055
F-THYRO1000124//H.sapiens CpG island DNA genomic Mse1 fragment, clone 72a7, forward read cpg72a7.ft1a.//9.5e-26:169:94//Z62724
F-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds.//8.5e-154:732:98//AF087142
F-THYRO1000132//Homo sapiens chromosome 9q34, clone 63G10, complete sequence.//3.7e-39:315:82//AC002096
F-THYRO1000156//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//1.2e-21:335:71//AL023574
F-THYRO1000163//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-A-218C7, complete sequence.//8.4e-52:301:88//AC002331
F-THYRO1000173//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//4.0e-89:821:74//M62419
F-THYRO1000186//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//7.2e-39:293:85//Z82207
F-THYRO1000187//Clostridium tetani gene for tetanus toxin.//0.041:473:57//X06214
F-THYRO1000190//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence.//0.38:184:64//AC005746
F-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//7.5e-174:805:99//AJ005698
F-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//1.2e-86:616:84//AB014552
F-THYRO1000206//HS_3047_A1_A05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=A, genomic survey sequence.//0.51:331:63//AQ099134
F-THYRO1000221//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.092:738:56//AC004157
F-THYRO1000241//Gallus gallus genome fragment with pentamer tandem repeats.//0.43:191:62//X00186
F-THYRO1000242//Human zinc finger gene HZF7.//2.8e-43:534:64//X60156
F-THYRO1000253//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.95:139:68//AC006055
F-THYRO1000270
F-THYRO1000279//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 531H16, WORKING DRAFT SEQUENCE.//1.4e-174:826:98//AL031664
F-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//3.9e-179:848:98//AB016068
F-THYRO1000320//Mus musculus sphingosine-1-phosphate lyase mRNA, complete cds.//1.0e-44:331:83//AF036894
F-THYRO1000327//Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds.//5.7e-112:641:91//L35233
F-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//2.2e-162:763:98//AB018333
F-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds.//2.2e-32:177:84//U29091
F-THYRO1000368//Caenorhabditis elegans cosmid W09G3, complete sequence.//0.97:206:60//Z82080
F-THYRO1000381//Arthrobacter sp. glcI gene for beta-1,3-glucanase, complete cds.//0.27:427:62//D23668
F-THYRO1000387//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//9.7e-147:698:98//AC006019
F-THYRO1000394//HS_2061_A2_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2061 Col=8 Row=E, genomic survey sequence.//1.6e-29:202:91//AQ247672
F-THYRO1000395//Drosophila melanogaster ring canel protein and ORF2 mRNA, complete cds.//4.3e-15:512:59//L08483
F-THYRO1000401 3.2e-116:504:80//AF051908
F-THYRO1000438//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.4e-09:539:59//AC005308
F-THYRO1000452//RPCI11-1C19.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-1C19, genomic survey sequence.//0.27:132:64//B49573
F-THYRO1000471//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.3e-38:332:81//AC005229
F-THYRO1000484//Homo sapiens BAC378, complete sequence.//2.2e-37:254:76//U85196
F-THYRO1000488//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//6.3e-130:327:97//AC005740
F-THYRO1000501//H.sapiens Staf50 mRNA.//9.8e-74:615:77//X82200

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F-THYRO1000502//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.//0.076:380:59//Z94056
F-THYRO 1000505
F-THYRO1000558//Human PAC clone 127H14 from 12q, complete sequence.//2.4e-27:412:69//AC002563
F-THYRO1000569//HS_2178_B2_E03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=6 Row=J, genomic survey sequence.//1.9e-27:326:74//AQ307499
F-THYRO1000570
F-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds.//7.4e-167:808:97//AF075587
F-THYRO1000596//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//0.99:280:61//U91323
F-THYRO1000602//HS_3037_B2_E04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=8 Row=J, genomic survey sequence.//1.2e-05:109:75//AQ097057
F-THYRO1000605//Homo sapiens map 2p11.2; 83cM from GATA85A06 repeat region, complete sequence.//1.0:84:70//AF067777
F-THYRO1000625//Homo sapiens chromosome 19, cosmid R29425, complete sequence.//3.4e-174:820:98//AC005546
F-THYRO1000637//Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin Gene, part of cytochrome C oxidase gene, EST, CpG island, complete sequence.//3.6e-38:289:84//AL024474
F-THYRO1000641//Plasmodium falciparum MAL3P7, complete sequence.//6.8e-07:540:56//AL034559
F-THYRO1000658//Homo sapiens chromosome 17, clone hRPK.74_E_22, complete sequence.//1.1e-68:468:84//AC005696
F-THYRO1000662//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence.//0.0072:141:70//AB016874
F-THYRO1000666//Mus musculus mRNA for motor domain of KIF9, partial cds.//4.7e-58:367:87//AB001437
F-THYRO1000676//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//1.2e-36:396:71//AC005778
F-THYRO1000684//Fugu rubripes cosmid 165K09 DNA for GRM7, TRIP, Sand, PRGFR3 genes.//6.6e-13:236:69//AJ010317
F-THYRO1000699//RPCI11-50D4.TK RPCI11 Homo sapiens genomic clone R-50D4, genomic survey sequence.//2.7e-09:135:78//AQ052641
F-THYRO1000712//Homo sapiens BAC clone RG041D11 from 7q21, complete sequence.//5.2e-17:290:67//AC005053
F-THYRO1000715//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//8.6e-08:517:60//L14320
F-THYRO1000734//HS_3233_B1_B04_T7 CIT Approved Human Genomic Sperm Library D-Homo sapiens genomic clone Plate=3233 Col=7 Row=D, genomic survey sequence.//6.0e-72:463:89//AQ182143
F-THYRO1000748//Homo sapiens KIAA0411 mRNA, complete cds.//9.7e-34:339:74//AB007871
F-THYRO1000756//M.musculus mRNA for Gal beta1, 3GalNAc alpha2,3-sialyltransferase.//0.00034:349:60//X73523
F-THYRO1000777//S.griseus strO gene and sts gene cluster.//8.2e-05:625:59//Y08763
F-THYRO1000783//Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds.//4.0e-70:860:69//U37373
F-THYRO1000787//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 366D1, WORKING DRAFT SEQUENCE.//5.3e-09:221:66//Z97986
F-THYRO1000793
F-THYRO1000796//Cristatella mucedo clone 5.9 microsatellite sequence.//0.34:173:63//AF085422
F-THYRO1000805//Homo sapiens Xp21 PAC RPCI1-37A12 containing exons 10 to 16 of the Duchenne Muscular Dystrophy gene, complete sequence.//7.8e-43:677:66//AC004468
F-THYRO1000815//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135), complete sequence.//5.5e-43:405:77//AC005914
F-THYRO1000829//CIT-HSP-2387C10.TF.1 CIT-HSP Homo sapiens genomic clone 2387C10, genomic survey sequence.//2.0e-20:159:88//AQ240053
F-THYRO1000843
F-THYRO1000852//Homo sapiens chromosome 19, cosmid R31855, complete sequence.//1.8e-33:445:72//AC005782
F-THYRO1000855//Mus musculus potassium channel alpha subunit (Kv9.1) mRNA, complete cds.//0.038:208:

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64//AF008573
F-THYRO1000865//Homo sapiens PAC clone DJ0283M22 from 14, complete sequence.//1.9e-30:286:74//AC005477
F-THYRO1000895//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 385E7, WORKING DRAFT SEQUENCE.//2.8e-18:186:80//AL031720
F-THYRO1000916//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.6e-78:432:93//AC006015
F-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//9.2e-178:839:98//AF079529
F-THYRO1000934//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//3.5e-32:759:63//M77836
F-THYRO1000951//Homo sapiens Chromosome 11q12 pac pDJ57114, WORKING DRAFT SEQUENCE, 29 unordered pieces.//4.9e-76:224:93//AC004229
F-THYRO1000952
F-THYRO1000974//HS_3238_B2_F01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=2 Row=L, genomic survey sequence.//12.4e-26:154:96//AQ219846
F-THYRO1000975//Plasmodium falciparum TopoII gene.//0.32:491:58//X79345
F-THYRO1000983//Mvwf9A3 exon amplification products from BACs in Mvwf region Mus musculus genomic, genomic survey sequence.//7.0e-16:112:94//AQ010457
F-THYRO1000984//CIT-HSP-2167O17.TR CIT-HSP Homo sapiens genomic clone 2167O17, genomic survey sequence.//0.00015:186:66//B91313
F-THYRO1000988//Human Chromosome 11q12.2 PAC clone pDJ756b9 containing human ferritin heavy chain mRNA (FTH), WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.024:267:63//AC004588
F-THYRO1001003
F-THYRO1001031//Homo sapiens chromosome 17, clone hRPC.859_O_20, complete sequence.//1.1e-55:543:72//AC003695
F-THYRO1001033//Methanobacterium thermoautotrophicum from bases 48264 to 58328 (section 5 of 148) of the complete genome.//0.94:445:58//AE000799
F-THYRO1001062//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 199H16, WORKING DRAFT SEQUENCE.//4.4e-45:441:75//AL022320
F-THYRO1001093//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence.//4.9e-34:353:76//AC006241
F-THYRO1001100//Human DNA-binding protein mRNA, 3'end.//1.1e-72:742:74//L14787
F-THYRO1001120//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-76:521:86//AC005522
F-THYRO1001121//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 671O14, WORKING DRAFT SEQUENCE.//0.00078:594:58//AL031595
F-THYRO1001133//Homo sapiens PAC clone DJ1200I23 from 7p15, complete sequence.//4.0e-35:349:76//AC004996
F-THYRO1001134//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.0:154:66//AC005486
F-THYRO1001142//Human DNA sequence from clone B79B4 on chromosome 22 Contains CA repeat and GSS, complete sequence.//1.4e-44:374:80//Z82178
F-THYRO1001173
F-THYRO1001177//Human pigment epithelium-derived factor gene, complete cds.//1.9e-42:250:86//U29953
F-THYRO1001189//HS_3171_B2_F10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3171 Col=20 Row=L, genomic survey sequence.//1.8e-28:246:83//AQ302330
F-THYRO1001204//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds.//4.9e-39:657:64//U34925
F-THYRO1001213//, complete sequence.//1.7e-45:257:84//AC005300
F-THYRO1001262//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//1.5e-40:274:87//AP000036
F-THYRO1001271//Streptomyces coelicolor cosmid 1A6.//0.033:364:61//AL023496
F-THYRO1001287//Drosophila melanogaster cosmid clone 86E4.119.6e-49:586:69//AL021086
F-THYRO1001290//HS_2045_B1_H09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2045 Col=17 Row=P, genomic survey sequence.//4.4e-13:156:78//AQ248237
F-THYRO1001313//S. lavendulae bla gene for beta-lactamase, complete cds.//1.0:229:64//D12693
F-THYRO1001320//Homo sapiens Chromosome 22q11.2 PAC Clone p_n5 In BCRL2-GGT Region, complete sequence.//1.1e-88:672:82//AC002472

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F-THYRO1001321//Human PAC clone DJ527C21 from Xq23, complete sequence.//1.2e-115:740:87//AC000114
F-THYRO1001322//HS_3205_B2_C12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3205 Col=24 Row=F, genomic survey sequence.//0.00031:285:61//AQ304025
F-THYRO1001347//Homo sapiens mRNA for KIAA0745 protein, partial cds.//2.2e-43:638:64//AB018288
F-THYRO1001363//Homo sapiens PAC clone DJ0845I21 from 7q11.21-q11.23, complete sequence.//1.0e-09:189:74//AC004905
F-THYRO1001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map-10q25, complete sequence.//7.6e-168:821:97//AC005660
F-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds.//2.3e-155:740:97//AB014607
F-THYRO1001401//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//3.2e-07:138:73//AC005239
F-THYRO1001403//Homo sapiens chromosome 12p13.3 clone RPCI3-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces.//3.6e-70:360:86//AC005845
F-THYRO1001405//Bos taurus mRNA for NDP52, complete cds.//2.6e-14:559:63//AB008852
F-THYRO1001406//Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.//1.0e-91:631:82//AF064635
F-THYRO1001411//Homo sapiens chromosome 19, cosmid F18718, complete sequence.//5.5e-42:509:71//AC006126
F-THYRO1001426//*** SEQUENCING IN PROGRESS *** Homo sapiens genomic DNA (PAC 1118i22) from chromosome 11; HTGS phase 1, WORKING DRAFT SEQUENCE.//2.7e-31:172:81//AJ002553
F-THYRO1001434//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.0:98:70//AC000384
F-THYRO1001458//Bos taurus non-muscle myosin heavy chain mRNA, partial cds.//1.9e-58:653:71//U87265
F-THYRO1001480//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//7.5e-42:357:80//AC006001
F-THYRO1001487//H.sapiens DNA sequence.//0.92:160:64//Z22449
F-THYRO1001534//Homo sapiens chromosome 17, clone hCIT.468_F_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.8e-47:266:80//AC004666
F-THYRO1001537//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 998H6, WORKING DRAFT SEQUENCE.//1.3e-79:479:89//AL031687
F-THYRO1001541//Human DNA sequence from clone 399M14 on chromosome Xq26.1-26.3. Contains ESTs, an STS and GSSs, complete sequence.//0.0034:106:77//Z96074
F-THYRO1001559//Rattus norvegicus simple sequence repeat D18Mco6.//1.6e-09:351:63//AF006056
F-THYRO1001570//RPCI11-49B23.TJ RPCI11 Homo sapiens genomic clone R-49B23, genomic survey sequence.//1.4e-65:384:91//AQ052105
F-THYRO1001573//Homo sapiens clone 24778 unknown mRNA.//8.2e-104:546:95//AF070572
F-THYRO1001584//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 2365J21, genomic survey sequence.//1.3e-24:180:88//AQ080498
F-THYRO1001595//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//8.7e-145:779:93//AL023808
F-THYRO1001602//Homo sapiens chromosome 17, clone hRPK.786_O_4, complete sequence.//2.9e-26:393:68//AC005863
F-THYRO1001605//Dictyostelium discoideum filopodin (talA) gene, complete cds.//0.0012:436:58//U14576
F-THYRO1001617//Homo sapiens full-length insert cDNA clone ZD69D05.//8.6e-43:342:82//AF086381
F-THYRO1001637//Homo sapiens clone DJ1019E05, WORKING DRAFT SEQUENCE, 10 unordered pieces.//6.2e-15:318:66//AC004950
F-THYRO1001656//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.5e-05:147:68//AC004827
F-THYRO1001661
F-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//2.5e-164:780:98//AJ225089
F-THYRO1001673//Homo sapiens clone RG161A02, complete sequence.//4.4e-40:770:64//AC005071
F-THYRO1001703//S.coelicolor plasmid SCP2 transfer region DNA.//0.14:414:59//X72857
F-THYRO1001706//Homo sapiens BAC clone RG281B09 from 7q21.1-q31.1, complete sequence.//2.6e-43:308:75//AC004745
F-THYRO1001721//, complete sequence.//9.9e-134:770:91//AC005500
F-THYRO1001738//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 355C18, WORKING DRAFT SEQUENCE.//0.99:163:61//AL022327

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F-THYRO1001745
F-THYRO1001746
F-THYRO1001772//HS_3069_B1_C05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3069 Col=9 Row=F, genomic survey sequence.//1.5e-61:360:91//AQ171021
F-THYRO1001793//B.taurus mRNA for beta-subunit of rod photoreceptor CNG-channel.//0.028:446:58//X89626
F-THYRO 1001809
F-THYRO1001828//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 110F11, WORKING DRAFT SEQUENCE.//1.3e-175:841:98//AL033526
F-THYRO1001854//Homo sapiens chromosome 17, clone hCIT54K19, complete sequence.//7.9e-07:445:59//AC003664
F-THYRO1001895
4.4e-13:248:68//AB012576
F-THYRO1001907//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//2.9e-15:144:77//AC005058
F-VESEN1000122//HS_3075_B1_C09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=17 Row=F, genomic survey sequence.//1.1e-16:130:90//AQ143749
F-Y79AA1000013
F-Y79AA1000033//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//2.9e-95:300:94//AC006027
F-Y79AA1000037//Human prot-oncogene (BMI-1) mRNA, complete cds.//2.4e-19:230:66//L13689
F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, complete cds.//2.2e-38:629:64//U78521
F-Y79AA1000065//Human DNA sequence from cosmid J256K24, between markers DXS6791 and DXS8038 on chromosome X contains EST.//5.3e-10:117:83//Z72005
F-Y79AA1000131//Homo sapiens LERK-6 (EPLG6) gene, exon 1.//7.6e-10:381:64//U92893
F-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.4e-165:732:99//AL031864
F-Y79AA1000202//Drosophila melanogaster DNA sequence (P1 DS06882 (D310)), complete sequence.//9.1e-20:339:65//AC005115
F-Y79AA1000214//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//3.7e-72:397:93//AC004854
F-Y79AA1000230
F-Y79AA1000231//Mus musculus SIK similar protein mRNA, complete cds.//8.5e-151:833:90//AF053232
F-Y79AA1000258//Leishmania donovani histidine secretory acid phosphatase (SAcP-1) gene, complete cds.//0.0099:547:58//U78522
F-Y79AA1000268//Mus musculus Nip21 mRNA, complete cds.//4.0e-11:424:62//AF035207
F-Y79AA1000313
F-Y79AA1000328//CIT-HSP-386A20.TF CIT-HSP Homo sapiens genomic clone 386A20, genomic survey sequence.//5.9e-07:173:69//B55085
F-Y79AA1000342//RPCI11-57J6.TK.1 RPCI11 Homo sapiens genomic clone R-57J6, genomic survey sequence.//5.2e-27:151:99//AQ115511
F-Y79AA1000346//B.primigenius mRNA for coat protein gamma-cop.//5.7e-69:694:71//X92987
F-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//1.8e-98:535:92//X84692
F-Y79AA1000355//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.6e-21:129:85//AC005484
F-Y79AA1000368//H.sapiens CpG island DNA genomic Mse1 fragment, clone 12f1, reverse read cpg12f1.rt1c.//0.00016:53:98//Z56610
F-Y79AA1000405//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P4, WORKING DRAFT SEQUENCE.//0.069:366:59//AL031747
F-Y79AA1000410//Human DNA sequence from PAC 117P19 on chromosome X.//1.0e-25:235:80//Z86061
F-Y79AA1000420//H.sapiens CpG island DNA genomic Mse1 fragment, clone 82c3, forward read cpg82c3.ft1a.//2.0e-36:194:98//Z63378
F-Y79AA1000469//Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete cds.//8.5e-121:696:89//U41736
F-Y79AA1000480//HS_2175_A2_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2175 Col=22 Row=O, genomic survey sequence.//2.5e-26:178:89//AQ307693
F-Y79AA1000538//Homo sapiens clone DJ1158B01, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.67:111:72//AC004980

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F-Y79AA1000539//HS_2237_B2_F10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=20 Row=L, genomic survey sequence//1.2e-14:168:77//AQ153503
F-Y79AA1000540//Homo sapiens clone DJ0655N24, WORKING DRAFT SEQUENCE, 8 unordered pieces//0.94:127:67//AC005193
F-Y79AA1000560//Mouse mRNA for alpha-adaptin (C)//1.7e-114:776:84//X14972
F-Y79AA1000574//M.musculus tex23 mRNA (5'region)//1.8e-23:291:75//X80424
F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence//8.6e-153:755:97//AF091080
F-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//5.2e-135:644:98//AF060503
F-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1//6.9e-148:902:86//X69942
F-Y79AA1000734//Homo sapiens PEX11 beta mRNA for peroxisome assembly factor, complete cds//4.8e-180:850:98//AB018080
F-Y79AA1000748//Caenorhabditis elegans cosmid F25B5//0.00019:308:60//U23172
F-Y79AA1000752//Oryctolagus cuniculus mRNA for hnRNP-E1 protein//1.7e-40:513:68//AJ003023
F-Y79AA1000774
F-Y79AA1000782
F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds//3.5e-177:847:97//AF098799
F-Y79AA1000794//H.sapiens CpG island DNA genomic Mse1 fragment, clone 45a4, forward read cpg45a4.ft1a//2.5e-13:104:92//Z61120
F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds//0.98:244:60//AF056085
F-Y79AA1000802
F-Y79AA1000805//Human Chromosome 11 Cosmid cSRL30h11, complete sequence//9.3e-76:528:85//U73642
F-Y79AA1000824//RPCI11-26B4.TP RPCI-11 Homo sapiens genomic clone RPCI-11-26B4, genomic survey sequence//4.4e-14:99:95//B84538
F-Y79AA1000827//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1177I5, WORKING DRAFT SEQUENCE//1.5e-08:249:69//AL022315
F-Y79AA1000833//Macaca fascicularis mRNA for alpha-tubulin.//1.8e-103:603:89//X04757
F-Y79AA1000850
F-Y79AA1000962//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat.//0.038:468:59//Z82203
F-Y79AA1000966//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//9.7e-150:865:89//AF071314
F-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//6.4e-122:717:88//U38253
F-Y79AA1000969//Mouse chromosome 6 BAC-284H12 (Research Genetics mouse BAC library) complete sequence.//1.0:155:63//AC002397
F-Y79AA1000976//Caenorhabditis elegans cosmid F54C1//4.3e-06:130:73//U88165
F-Y79AA1000985//Mus musculus pericentrin mRNA, complete cds.//2.4e-44:428:77//U05823
F-Y79AA1001023
F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds//2.3e-13:90:100//U63329
F-Y79AA1001048//Human mRNA for very-long-chain acyl-CoA dehydrogenase (VLCAD), complete cds.//2.6e-28:772:60//D43682
F-Y79AA1001061//Homo sapiens chromosome 4 clone B331M8 map 4q25, complete sequence//9.4e-36:292:82//AC004701
F-Y79AA1001068//tipAL-AS complex: tipA=TipAL-AS [Streptomyces lividans, Genomic, 1146 nt].//0.17:537:59//S64314
F-Y79AA1001077//Zea mays mRNA for aldehyde oxidase-2, complete cds.//0.17:231:64//D88452
F-Y79AA1001078
F-Y79AA1001105//Zebrafish otx2 mRNA for otx homeoprotein, complete cds.//3.1e-63:529:77//D26173
F-Y79AA1001145//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.3e-23:228:76//AC005015
F-Y79AA1001167
F-Y79AA1001177//M.musculus mRNA for NfiX1-protein.//4.0e-10:398:64//Y07688
F-Y79AA1001185//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 169I5, WORKING DRAFT SEQUENCE.//1.1e-113:666:90//Z93015
F-Y79AA1001211//HS_3124_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence.//5.5e-12:87:96//AQ187492
F-Y79AA1001216
F-Y79AA1001228//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.//0.028:188:67//

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AL021841
F-Y79AA1001233//Human placental 17-beta-hydroxysteroid dehydrogenase mRNA, complete cds.//3.5e-24:731:60//M36263
F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin)).//1.2e-133:441:97//AJ005892
F-Y79AA1001281//HS_2241_B2_F09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2241 Col=18 Row=L, genomic survey sequence.//5.0e-27:169:94//AQ217497
F-Y79AA1001299//Human Ini1 mRNA, complete cds.//6.7e-115:323:93//U04847
F-Y79AA1001312
F-Y79AA1001323
F-Y79AA1001384
F-Y79AA1001391//Mus musculus transcription factor HOXA13 (Hoxa13) gene, complete cds.//5.8e-42:245:74//U59322
F-Y79AA1001394//Caenorhabditis elegans cosmid F54B3, complete sequence.//7.8e-18:636:58//Z48583
F-Y79AA1001402//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.2e-110:738:85//AC005924
F-Y79AA1001493//H.sapiens DNA sequence.//2.0e-27:254:82//Z22497
F-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//1.1e-158:804:95//AL034430
F-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//1.7e-100:820:78//D14336
F-Y79AA1001541//HS_3197_A2_G11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=22 Row=M, genomic survey sequence.//5.1e-28:218:86//AQ150183
F-Y79AA1001548//Homo sapiens chromosome 19, cosmid R28738, complete sequence.//5.4e-21:167:86//AC004151
F-Y79AA1001555//R.norvegicus mRNA for drebrin A.//0.88:463:59//X59267
F-Y79AA1001581//FMR1 {CGG repeats} [human, Fragile X syndrome patient, Genomic, 429 nt].//0.00051:252:65//S74494
F-Y79AA1001585//Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds.//7.2e-33:375:76//M26434
F-Y79AA1001594
F-Y79AA1001603//Homo sapiens PAC 128M19 derived from chromosome 21q22.3, containing the HMG-14 and CHD5 genes, complete cds, complete sequence.//4.2e-06:338:66//AF064861
F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds.//0.024:520:57//AB014583
F-Y79AA1001647//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y53F4, WORKING DRAFT SEQUENCE.//0.014:331:61//Z92860
F-Y79AA1001665//Human DNA sequence from clone 299D3 on chromosome 22q13.3, complete sequence.//0.99:273:63//Z84468
F-Y79AA1001679//O.cuniculus lambda-crystallin mRNA, complete cds.//1.2e-97:682:81//M22743
F-Y79AA1001692//insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1292 nt, segment 1 of 4].//5.6e-05:426:59//S37712
F-Y79AA1001696//Rice endogenous double-stranded RNA encoding polyprotein (containing putative helicase and putative RNA-dependent RNA polymerase domains), complete cds.//1.0:437:60//D32136
F-Y79AA1001705//M.musculus fkh-5 gene.//0.18:153:64//X71943
F-Y79AA1001711//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 328E19, WORKING DRAFT SEQUENCE.//5.4e-76:191:98//AL022240
F-Y79AA1001781//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 10/15, WORKING DRAFT SEQUENCE.//0.99:227:63//AP000017
F-Y79AA1001805//H.sapiens CpG island DNA genomic Mse1 fragment, clone 13d12, reverse read cpg13d12.rt1c.//2.6e-13:88:100//Z64565
F-Y79AA1001827//Oryctolagus cuniculus PiUS mRNA, complete cds.//3.7e-130:775:88//U74297
F-Y79AA1001846//CIT-HSP-2300M6.TR CIT-HSP Homo sapiens genomic clone 2300M6, genomic survey sequence.//8.3e-17:218:76//AQ012369
F-Y79AA1001848//Human mRNA for KIAA0390 gene, complete cds.//4.2e-10:378:62//AB002388
F-Y79AA1001866//Rattus norvegicus Cys2/His2 zinc finger protein (rKr1) mRNA, complete cds.//6.9e-41:441:71//U41164
F-Y79AA1001874//Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spliced isoform of Jagged2, complete cds.//0.00017:412:62//AF029779

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F-Y79AA1001875//CTT-HSP-2317G18.TR CIT-HSP Homo sapiens genomic clone 2317G18, genomic survey sequence.//1.9e-09:271:67//AQ042654
F-Y79AA1001923//H.sapiens CpG island DNA genomic Mse1 fragment, clone 193c12, forward read cpg193c12.ft1a.//0.0031:108:75//Z60186
F-Y79AA1001963//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//1.8e-05:56:100//AQ261184
F-Y79AA1002027//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds.//3.3e-13:451:62//AF028340
F-Y79AA1002083//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 526I14, WORKING DRAFT SEQUENCE.//0.91:134:65//Z82214
F-Y79AA1002089
F-Y79AA1002093//Mus musculus transcription factor like protein 4 TCFL4 mRNA, partial cds.//1.2e-112:678:88//U43548
F-Y79AA1002103//HS_3052_B1_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=15 Row=P, genomic survey sequence.//6.5e-18:238:72//AQ135014
F-Y79AA1002115
F-Y79AA1002125//H.sapiens (D8S135) DNA segment containing GT repeat.//1.5e-14:99:96//X61693
F-Y79AA1002139//Saccharomyces cerevisiae dnaJ homolog Hlj1p (HLJ1) gene, complete cds.//2.5e-07:208:64//U19358
F-Y79AA1002204//HS_2235_B2_D12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2235 Col=24 Row=H, genomic survey sequence.//2.9e-13:89:98//AQ154260
F-Y79AA1002208//CIT-HSP-2006M21.TV CIT-HSP Homo sapiens genomic clone 2006M21, genomic survey sequence.//3.7e-27:154:98//B56397
F-Y79AA1002209//E.coli tyrS gene coding for tyrosyl-tRNA synthetase.//2.8e-05:143:70//J01719
F-Y79AA1002210//Homo sapines chromosome 19, cosmid R28058, complete sequence.//8.3e-22:229:78//AC005615
F-Y79AA1002211//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.0e-06:241:67//AC003043
F-Y79AA1002220//CIT-HSP-2374P23.TR CIT-HSP Homo sapiens genomic clone 2374P23, genomic survey sequence.//1.3e-68:375:95//AQ109738
F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds.//0.12:203:63//D42045
F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//1.3e-174:821:98//AB014592
F-Y79AA1002246//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.50:470:60//AC005015
F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds.//6.8e-159:748:98//AB014555
F-Y79AA1002298//Human density enhanced phosphatase-1 mRNA, complete cds.//0.036:278:62//U10886
F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//6.4e-129:622:97//AB014534
F-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.0e-116:693:82//X67877
F-Y79AA1002351//S.clavuligerus pah and cas genes.//1.0:369:58//X84101
F-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//5.4e-105:762:80//Y18208
F-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence.//1.0e-159:411:100//AC005920
F-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//1.1e-118:609:84//AC004662
F-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds.//4.4e-90:529:88//U49385
F-Y79AA1002431//Chlamydomonas reinhardtii novel protein kinase mRNA, complete cds.//1.0:166:66//U36196
F-Y79AA1002433//CIT-HSP-384K8.TF CIT-HSP Homo sapiens genomic clone 384K8, genomic survey sequence.//0.24:85:72//B51917
F-Y79AA1002472//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.9e-13:242:69//AC006116
F-Y79AA1002482//Homo sapiens full-length insert cDNA clone ZC18H06.//1.2e-35:462:71//AF088022
F-Y79AA1002487//Bovine herpesvirus type 1 genes for UL[27,28,29,30,31].//0.93:215:60//X94677

Homology Search Result Data 3.

[0303] The result of the homology search of the GenBank using the clone sequence of 3'-end except EST and STS.

[0304] Data include

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the name of clone,
definition of the top hit data,
the P-value: the length of the compared sequence: identity (%), and
the Accession No. of the top hit data, as in the order separated by //.

[0305] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

[0306] Data are not shown for the clones in which the P-value was higher than 1.

R-HEMBA1000005//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds.//3.6e-60:504:78//L16953
R-HEMBA1000030//F.rubripes GSS sequence, clone 063K10bD3, genomic survey sequence.//0.28:117:68//Z88864
R-HEMBA1000042//RPCI11-77G23.TV RPCI11 Homo sapiens genomic clone R-77G23, genomic survey sequence.//1.3e-56:292:97//AQ268240
R-HEMBA1000046//Homo sapiens chromosome X map Xq28, complete sequence.//9.8e-56:401:82//U82696
R-HEMBA1000050//Human cosmid insert containing polymorphic marker DXS455.//0.0010:175:68//L31948
R-HEMBA1000076//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//4.9e-41:364:79//AC005520
R-HEMBA1000111//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//4.7e-30:229:84//AC003684
R-HEMBA1000129//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//2.4e-93:503:93//AC003104
R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds.//6.5e-99:514:94//AB018340
R-HEMBA1000150//Homo sapiens clone RG086D03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.7e-37:289:83//AC005060
R-nnnnnnnnnnnn//Homo sapiens scaffold attachment factor B (SAF-B) mRNA, partial cds.//3.1e-21:417:64//L43631
R-HEMBA1000158
R-nnnnnnnnnnnn
R-HEMBA1000180//Plasmodium falciparum encoding Pfg27/25.//0.073:292:56//X84904
R-HEMBA1000185//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//5.3e-40:286:85//AC006146
R-HEMBA1000193
R-HEMBA1000201//Homo sapiens SNF5/INI1 gene, exon 9.//2.0e-24:137:99//Y17126
R-HEMBA1000213//Caenorhabditis elegans cosmid C44C8.//0.025:192:68//AF100655
R-HEMBA1000216//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//2.5e-31:269:79//AF001548
R-nnnnnnnnnnnn
R-HEMBA1000231//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat,.//4.3e-24:400:68//AL009181
R-HEMBA1000243//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//1.3e-19:319:69//AC004526
R-HEMBA1000244
R-HEMBA1000251//Meloidogyne hapla mitochondrial COII gene, 3' end of cds; transfer RNA-His gene; 16S ribosomal RNA gene; ND3 gene, complete cds; cytochrome b (cytb) gene, 5' end of cds.//0.16:338:60//L76262
R-HEMBA1000264//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 5/15, WORKING DRAFT SEQUENCE.//0.00093:300:66//AP000012
R-nnnnnnnnnnnn//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//3.5e-10:238:70//AC003037
R-HEMBA1000282//Arabidopsis thaliana BAC IG002P16.//0.71:344:60//AF007270
R-HEMBA1000288//Homo sapiens Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.//4.8e-33:267:82//AC003046
R-HEMBA1000290//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//2.2e-15:249:69//AC004223
R-HEMBA1000302//CIT-HSP-2173N10.TF CIT-HSP Homo sapiens genomic clone 2173N10, genomic survey sequence.//1.0:215:61//B95105
R-nnnnnnnnnnnn//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//1.0e-77:551:82//AF030131
R-nnnnnnnnnnnn//Rattus norvegicus Ca2+-dependent activator protein (CAPS) mRNA, complete cds.//2.0e-96:546:90//U16802

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R-HEMBA1000307//Mus musculus mRNA for CDV-1 protein.//3.8e-36:315:68//Y10496
R-nnnnnnnnnnn//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.078:379:59//AC005505
R-HEMBA1000338//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 620E11, WORKING DRAFT SEQUENCE.//2.0e-33:399:72//AL031667
R-HEMBA1000351//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//1.7e-39:272:87//AJ003147
R-HEMBA1000355//Human primary Alu transcript.//0.0045:67:85//U67829
R-HEMBA1000357//Homo sapiens (subclone 9_h8 from PI H16) DNA sequence.//8.7e-93:426:88//L42086
R-HEMBA1000366//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//1.7e-12:130:83//AC006012
R-HEMBA1000369//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//1.9e-69:355:97//AL031587
R-HEMBA1000376//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//3.7e-66:410:89//AC006116
R-HEMBA1000387//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.0e-43:363:81//AC002993
R-HEMBA1000390//Homo sapiens BAC clone RG041D11 from 7q21, complete sequence.//4.6e-23:417:69//AC005053
R-HEMBA1000392//Human Chromosome 11p14.3 PAC clone pDJ59m18, complete sequence.//6.2e-05:174:68//AC004582
R-HEMBA1000396//Homo sapiens DNA sequence from PAC 159A15 on chromosome Xp11.21-p11.23. Contains inter-alpha-trypsin inhibitor heavy chain H3 precursor-like protein.//1.4e-62:564:77//AL022575
R-HEMBA1000411
R-HEMBA1000418//Liverwort Marchantia polymorpha chloroplast genome DNA.//0.94:210:60//X04465
R-HEMBA1000422//CIT-HSP-2382A6.TR CIT-HSP Homo sapiens genomic clone 2382A6, genomic survey sequence.//4.4e-12:98:92//AQ078233
R-HEMBA1000428//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs, complete sequence.//2.0e-93 :526:90//Z95400
R-HEMBA1000434//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//2.7e-07:452:60//AC004826
R-HEMBA1000442//E.caballus microsatellite DNA, clone HMB4.//0.39:135:62//Y07733
R-HEMBA1000456//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-52, complete sequence.//2.6e-05:174:70//AL010226
R-HEMBA1000459//Arabidopsis thaliana putative transmembrane protein G1p (AtG1), putative nuclear DNA-binding protein G2p (AtG2), Em1 protein (ATEM1), putative chlorophyll synthetase (AtG4), putative transmembrane protein G5p (AtG5), putative acyl-coA dehydrogenase (AtG6), and calcium dependent protein kinase genes, complete cds; and unknown genes.//0.013:212:63//AF049236
R-HEMBA1000460//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//8.6e-114:556:98//AC004839
R-HEMBA1000464//Caenorhabditis elegans cosmid C34B7, complete sequence.//0.086:334:61//Z83220
R-HEMBA1000469//Homo sapiens BAC clone RG442F18 from 2, complete sequence.//1.8e-52:472:79//AC005104
R-HEMBA1000488//, complete sequence.//3.3e-68:200:99//AC005500
R-HEMBA1000490//Caenorhabditis elegans cosmid Y53C12B, complete sequence.//0.97:233:6l//Z99278
R-HEMBA1000491
R-HEMBA1000504//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-64, complete sequence.//1.7e-08:440:60//AL009014
R-HEMBA1000505//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 1/11.//0.37:189:62//AB020858
R-HEMBA1000508//Human DNA sequence from cosmid V210E9, between markers DXS366 and DXS87 on chromosome X.//1.1e-25:248:80//Z70280
R-HEMBA1000518//RPCI11-6022.TV RPCI-11 Homo sapiens genomic clone RPCI-11-6022, genomic survey sequence.//0.0035:293:61//B49544
R-HEMBA1000519
R-HEMBA1000520//Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence.//0.30:255:63//AC006232

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R-HEMBA1000523//Human cleavage stimulation factor 77kDa subunit mRNA, complete cds.//1.2e-53:203:92//U15782
R-HEMBA1000531//CIT-HSP-388J17.TR CIT-HSP Homo sapiens genomic clone 388J17, genomic survey sequence.//2.7e-24:137:99//B55638
R-HEMBA1000540//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 510D11, WORKING DRAFT SEQUENCE.//0.00014:329:60//Z98044
R-HEMBA1000545//Homo sapiens Xp22 BAC GS-619J3 (Genome Systems Human BAC library) complete sequence.//6.9e-87:552:87//AC004103
R-nnnnnnnnnnnn//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 134019, WORKING DRAFT SEQUENCE.//8.9e-121:584:98//AL034555
R-HEMBA1000557//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//5.7e-45:307:87//AC004381
R-HEMBA1000561//Mus musculus clone OST20235, genomic survey sequence.//1.3e-43:279:90//AF046762
R-HEMBA1000563//Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence.//3.8e-05:506:56//AE001368
R-HEMBA1000568//RPCI11-49P8.TK.1 RPCI11 Homo sapiens genomic clone R-49P8, genomic survey sequence.//1.7e-101:498:97//AQ116293
R-nnnnnnnnnnnn
R-HEMBA1000575//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 754E20, WORKING DRAFT SEQUENCE.//1.3e-47:458:75//AL022335
R-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//2.9e-62:447:81//AF045573
R-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein.//1.2e-111:591:9411AJ007509
R-HEMBA1000592//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-10, complete sequence.//3.5e-09:421:60//AL010216
R-HEMBA1000594//Homo sapiens clone RG004N09, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.1e-15:421:66//AC005044
R-HEMBA1000604//HS_2220_A1_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2220 Col=19 Row=M, genomic survey sequence.//1.0e-51:306:92//AQ151991
R-HEMBA1000608
R-HEMBA1000622//H.sapiens CpG island DNA genomic Mse1 fragment, clone 155e4, reverse read cpg155e4.rt1a.//4.5e-16:105:98//Z56962
R-HEMBA1000636//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 1/15, WORKING DRAFT SEQUENCE.//4.8e-62:421:86//AP000008
R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds.//1.2e-97:443:97//AB014590
R-HEMBA1000655//Homo sapiens chromosome 19, cosmid R26349, complete sequence.//9.8e-61:311:90//AC005953
R-HEMBA1000657
R-HEMBA1000662
R-HEMBA1000673//Human DNA sequence from PAC 448E20 on chromosome Xq26.1 contains ESTs and STS.//1.0e-13:351:63//Z97196
R-HEMBA1000682//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-50:298:79//AC005377
R-HEMBA1000686//HS_3018_B1_H10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00048:210:62//AQ093513
R-HEMBA1000702//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//9.7e-54:317:88//AC005000
R-HEMBA1000705//Glossonotus uhivittatus 12S mitochondrial ribosomal RNA, small subunit, mitochondrial gene, partial sequence.//0.080:138:65//U77850
R-HEMBA1000719//Rattus norvegicus mRNA for TESK1, complete cds.//0.96:291:58//D50864
R-HEMBA1000722
R-HEMBA1000726//Homo sapiens PAC clone DJ0701016 from 7q33-q36, complete sequence.//4.4e-26:284:77//AC005531
R-HEMBA1000727//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-89, complete sequence.//9.1e-05:351:60//AL010266
R-HEMBA1000747//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.5e-16:123:93//AL021326

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R-HEMBA1000749//Human Chromosome 16 BAC clone CIT987SK-327O24, complete sequence.//2.8e-32:298:79//AC003108

R-HEMBA1000752//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.8e-90:542:90//Z92545

R-HEMBA1000769//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.7e-36:405:75//AC005031

R-HEMBA1000773//HS_3050_A2_B08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=16 Row=C, genomic survey sequence.//0.00053:268:60//AQ105619

R-HEMBA1000774//Homo sapiens PAC clone DJ0630C24 from 7q31-q32, complete sequence.//4.7e-46:338:85//AC004690

R-HEMBA1000791//'***ALU WARNING: Human Alu-Sc subfamily consensus sequence.//5.3e-47:279:91//U14571

R-HEMBA1000817/Sequence 1 from Patent WO 8904839.//0.86:148:67//I09339

R-HEMBA1000822//T.brucei kinetoplast maxicircle variable region DNA.//0.00061:246:61//Z15118

R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRM160) mRNA, complete cds.//6.9e-43:228:98//AF048977

R-HEMBA1000843//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//1.7e-41:319:84//AL022394

R-HEMBA1000851//Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence.//0.40:168:67//AC004260

R-HEMBA1000852//Homo sapiens Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//1.5e-112:572:96//AC005295

R-HEMBA1000867//Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.//0.11:121:71//AC004938

R-HEMBA1000869//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-180G2, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-22:186:76//AC002042

R-HEMBA1000870//Human BAC clone GS542D18 from 7q31-q32, complete sequence.//0.0060:283:63//AC002528

R-HEMBA1000872//Rattus norvegicus polymorphic satellite repetitive elements.//3.8e-05:269:61//M98801

R-HEMBA1000876//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//6.5e-38:327:77//AC006057

R-HEMBA1000908//CIT-HSP-2373I4.TR CIT-HSP Homo sapiens genomic clone 2373I4, genomic survey sequence.//5.0e-34:221:90//AQ108658

R-HEMBA1000910//T.pigmentosa UM1060 macronuclear rDNA telomeric region 3' term.//0.19:280:61//X04205

R-HEMBA1000918//RPCI11-68E14.TK RPCI11 Homo sapiens genomic clone R-68E14, genomic survey sequence.//1.3e-32:172:100//AQ267293

R-HEMBA1000919

R-HEMBA1000934//Homo sapiens DNA sequence from PAC 874C20 on chromosome 6p22.1-22.3. Contains a Zinc Finger Protein ZFP47 LIKE gene, a Zinc Finger Protein pseudogene and a Zinc Finger Protein SRE-ZBP pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.6e-18:284:71//AL021997

R-HEMBA1000942//Homo sapiens clone RG350L10, WORKING DRAFT SEQUENCE, 15 unordered pieces.//1.4e-17:217:76//AC005098

R-HEMBA1000943//Homo sapiens chromosome 17, clone hRPK.640_I_15, complete sequence.//9.0e-113:586:95//AC005324

R-HEMBA1000946//T5N8TFB TAMU Arabidopsis thaliana genomic clone T5N8, genomic survey sequence.//0.030:369:59//B26224

R-HEMBA1000960//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.5e-52:494:77//AC005096

R-HEMBA1000968//Homo sapiens P1 clone 797a11 containing MHC class II DQ-beta (HLA-DQB) and MHC class II DC-alpha (HLA-DCA) genes, complete cds.//3.5e-77:568:83//U92032

R-HEMBA1000971//RPCI11-54D1.TJ RPCI11 Homo sapiens genomic clone R-54D1, genomic survey sequence.//2.3e-27:153:98//AQ081552

R-HEMBA1000972//Human DNA sequence from clone 111F4 on chromosome Xq23 Contains GSSs, complete sequence.//7.3e-43:375:79//AL023876

R-HEMBA1000974//Homo sapiens clone DA0091H08, complete sequence.//2.8e-104:521:97//AC004817

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R-HEMBA1000975//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//8.0e-22:352:68//AL031311
R-HEMBA1000985//Homo sapiens PAC clone DJ0797C05 from 7q31, complete sequence.//8.5e-05:306:63//AC004888
R-HEMBA1000986//Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.//5.7e-37:296:83//AC005632
R-HEMBA1000991//RPCI11-22017.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-22017, genomic survey sequence.//6.5e-44:162:90//AQ008952
R-HEMBA1001007
R-HEMBA1001008//Homo sapiens chromosome 16, P1 clone 79-2A (LANL), complete sequence.//0.082:313:60//AC005365
R-HEMBA1001009//O.sativa osr40g2 gene.//0.99:203:62//Y08987
R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds.//1.0e-113:587:95//AB007937
R-HEMBA1001019//Bos taurus cyclin-dependent kinase 1 (cdk1/cdc2) mRNA, complete cds.//7.4e-24:215:82//L26547
R-HEMBA1001020//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 732E4, WORKING DRAFT SEQUENCE.//2.8e-18:449:64//AL008722
R-HEMBA1001022
R-HEMBA1001024//Homo sapiens BAC clone 393I22 from 8q21, complete sequence.//6.6e-48:536:74//AF070717
R-HEMBA1001026//T33H14TF TAMU Arabidopsis thaliana genomic clone T33H14, genomic survey sequence.//0.013:180:66//B97363
R-nnnnnnnnnnnn//Caenorhabditis elegans cosmid R10H10, complete sequence.//1.2e-25:438:65//Z70686
R-HEMBA1001051//Homo sapiens 12q24.1 PAC RPCI3-521E19 (Roswell Park Cancer Institute Human PAC library) complete sequence.//7.3e-38:188:89//AC004217
R-HEMBA1001052//Rabbit alpha-1-globin gene to theta-1-globin pseudogene region.//2.4e-24:279:74//X04751
R-HEMBA1001060//HS_2056_B1_C01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=1 Row=F, genomic survey sequence.//4.1e-14:137:83//AQ245004
R-HEMBA1001071//M.musculus COL3A1 gene for collagen alpha-I.//6.9e-38:513:70//X52046
R-HEMBA1001077//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 150C2, WORKING DRAFT SEQUENCE.//1.9e-22:507:61//AL022318
R-HEMBA1001080
R-HEMBA1001085//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase IIx genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.2e-43:317:83//AC004586
R-HEMBA1001088//Caenorhabditis elegans cosmid C18H7.//0.46:301:60//AF067607
R-HEMBA1001094//Homo sapiens clone RG491N20, complete sequence.//5.3e-98:501:96//AC005105
R-HEMBA1001099
R-HEMBA1001109//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 118J21, WORKING DRAFT SEQUENCE.//3.1e-39:335:80//AL033527
R-HEMBA1001121//Human cosmid LL12NC01-132B11A, ETV6 gene, intron 2.//9.8e-11:122:81//U81833
R-HEMBA1001122//Plasmodium falciparum MAL3P6, complete sequence.//0.0024:284:63//Z98551
R-HEMBA1001123//Human NFE genomic fragment.//3.6e-26:318:72//M98511
R-HEMBA1001133
R-HEMBA1001137//Homo sapiens full-length insert cDNA clone ZD29F04.//4.2e-88:426:98//AF086241
R-HEMBA1001140//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.0e-41:304:84//AC005077
R-HEMBA1001172//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE.//3.7e-36:261:85//Z98304
R-HEMBA1001174//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//1.0:219:58//AE001398
R-HEMBA1001197
R-HEMBA1001208//HS_2233_A1_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2233 Col=19 Row=M, genomic survey sequence.//0.083:174:68//AQ170789
R-HEMBA1001226//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-59:553:75//AC005377
R-HEMBA1001235//RPCI11-50E6.TJ RPCI11 Homo sapiens genomic clone R-50E6, genomic survey sequence.//2.6e-08:97:76//AQ052666
R-HEMBA1001247//Caenorhabditis elegans cosmid C01F1.//2.4e-05:319:63//U58761

BNSDOCID: <EP___1074617A2_I_>

R-HEMBA1001257//Rattus norvegicus alpha-methylacyl-CoA racemase mRNA, complete cds.//1.5e-24:439:66//U89905
R-HEMBA1001265//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//9.9e-21:537:63//AC004491
R-nnnnnnnnnnn//Homo sapiens chromosome 17, clone HCIT75G16, complete sequence.//0.022:169:65//AC003042
R-HEMBA1001286
R-HEMBA1001289
R-HEMBA1001294//HS_3219_A2_G01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=2 Row=M, genomic survey sequence.//0.24:251:63//AQ189882
R-HEMBA1001299//Homo sapiens, clone hRPK.12_A_1, complete sequence.//1.3e-38:381:76//AC006222
R-HEMBA1001302//cDNA encoding a human homologue of a mouse novel polypeptide derived from stromal cell.//4.1e-28:114:92//E12258
R-HEMBA1001303//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//0.00011:382:58//AL031744
R-HEMBA1001310
R-HEMBA1001319//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.2e-09:491:58//AC005504
R-HEMBA1001323//Drosophila yakuba mitochondrial DNA molecule.//8.3e-06:485:60//X03240
R-HEMBA1001326//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucoronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//2.2e-14:277:69//AL021368
R-HEMBA1001327//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.15:360:61//AL024509
R-HEMBA1001330//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-27:481:67//AC004216
R-HEMBA1001351//Homo sapiens chromosome 18, clone hRPK.474_N_24, complete sequence.//7.1e-45:252:94//AC006238
R-HEMBA1001361//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence.//1.4e-113:569:97//AC006241
R-HEMBA1001375//Homo sapiens full-length insert cDNA clone ZE09H03.//2.8e-89:428:99//AF086542
R-HEMBA1001377//Homo sapiens PAC clone DJ0728D04, complete sequence.//2.3e-32:324:77//AC004865
R-HEMBA1001383
R-HEMBA1001387
R-HEMBA1001388//Homo sapiens clone RG189J21, WORKING DRAFT SEQUENCE, 15 unordered pieces.//8.9e-06:108:83//AC005073
R-HEMBA1001391//Yeast mitochondrial aapl gene for ATPase subunit 8.//7.3e-08:500:59//X00960
R-HEMBA1001398//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//2.3e-48:315:88//AP000050
R-HEMBA1001405//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.//5.5e-35 :464:68//AL034380
R-HEMBA1001407
R-HEMBA1001411//Yeast (S.cerevisiae) mitochondria Ser-tRNA-UCN gene and flanks.//0.00029:301:62//K01981
R-HEMBA1001413
R-HEMBA1001415//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 41018, WORKING DRAFT SEQUENCE.//5.6e-101:512:96//AL031732
R-HEMBA1001432//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//6.3e-37:302:81//AC006146
R-HEMBA1001433//Human DNA sequence from PAC 339A18 on chromosome Xp11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of S.cerevisiae, DNA binding protein similar to URE-B1, ESTs and STS.//1.9e-32:242:79//Z97054
R-HEMBA1001435//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete sequence.//5.7e-59:457:82//AC004527
R-HEMBA1001442//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//0.051:276:63//Z98950

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R-HEMBA1001446//HS_3207_A1_A08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3207 Col=15 Row=A, genomic survey sequence.//8.9e-06:119:73//AQ175385
R-HEMBA1001450//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//0.0043:266:63//AC005065
R-HEMBA1001454//Homo sapiens PAC clone DJ0673011 from 7q31, complete sequence.//7.1e-25:210:82//AC004855
R-HEMBA1001455//Homo sapiens chromosome 17, clone hRPK.640_I_15, complete sequence.//2.7e-08:316:62//AC005324
R-HEMBA1001463//Homo sapiens chromosome 17, clone hRPK.1064_E_11, complete sequence.//0.57:219:60//AC005208
R-HEMBA1001476//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//9.3e-50:252:80//AC004840
R-HEMBA1001478
R-HEMBA1001497
R-HEMBA1001510/Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//3.5e-41:282:86//U89337
R-HEMBA1001515//Human DNA sequence from PAC 238J17 on chromosome 6q22. Contains EST and STS.//1.9e-79:529:86//Z98753
R-HEMBA1001517//Homo sapiens BAC clone RG459N13 from 7p15, complete sequence.//4.3e-18:335:71//AC004549
R-HEMBA1001522
R-HEMBA1001526//Human DNA sequence from cosmid 444G9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs and CpG islands.//5.6e-08:265:67//Z98258
R-HEMBA1001533//Human DNA sequence from PAC 179M20 on chromosome 20q12-13.1. Contains adenosine deaminase (ADA), placental protein Diff33, CA repeat, ESTs, STS.//7.8e-16:235:72//Z97053
R-HEMBA1001557
R-HEMBA1001566//Human Chromosome X clone bWXD187, complete sequence.//2.2e-44:416:78//AC004383
R-HEMBA1001569//Sequence 15 from patent US 5693476.//1.8e-59:389:88//I77040
R-HEMBA1001570//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//1.1e-44:316:87//AC004453
R-HEMBA1001579//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0047:437:60//AC005506
R-HEMBA1001581//P.falciparum complete gene map of plastid-like DNA (IR-B).//2.3e-07:491:58//X95276
R-HEMBA1001585//Caenorhabditis elegans cosmid C06A6.//0.68:224:62//U41012
R-HEMBA1001589
R-HEMBA1001595//CIT-HSP-2349G19.TF CIT-HSP Homo sapiens genomic clone 2349G19, genomic survey sequence.//8.0e-69:337:99//AQ060483
R-HEMBA1001608//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//9.5e-59:514:78//AC005177
R-HEMBA1001620//S.polyrrhiza mRNA for D-myo-inositol-3-phosphate synthase.//4.5e-12:289:65//Z11693
R-nnnnnnnnnnnn//HS_2195_A1_E09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=17 Row=I, genomic survey sequence.//5.8e-09:358:58//AQ292688
R-HEMBA1001636//Human putative potassium channel subunit (h-erg) mRNA, complete cds.//0.77:225:59//U04270
R-HEMBA1001640//Human DNA sequence from PAC 50J22 on chromosome 6p21. Contains ETS related protein TEL like and GS2 like genes, ESTs and an STS.//6.0e-49:404:79//Z84484
R-nnnnnnnnnnnn
R-HEMBA1001655//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//1.1e-103:532:95//AC005368
R-HEMBA1001658//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//1.0:197:64//AL023808
R-HEMBA1001661//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//1.5e-100:457:93//AC005740
R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//1.2e-90:496:91//AF072247
R-HEMBA1001675
R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA, complete cds.//1.3e-101:534:94//AF038962

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R-HEMBA1001681//CIT-HSP-2345M7.TF CIT-HSP Homo sapiens genomic clone 2345M7, genomic survey sequence.//0.21:124:68//AQ056593
R-HEMBA1001702//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//8.3e-06:279:63//AC004801
R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete cds.//1.9e-96:483:96//AB014598
R-HEMBA1001711//Human HepG2 3' region cDNA, clone hmd2b02.//2.3e-31:169:100//D16886
R-HEMBA1001712//HS-1015-B1-E01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 790 Col=1 Row=J, genomic survey sequence.//0.0025:200:65/B32577
R-HEMBA1001714//Rattus norvegicus mitochondrial ATPase inhibitor gene, complete cds.//6.6e-27:316:75//U12250
R-HEMBA1001718//CIT-HSP-2171J2.TR CIT-HSP Homo sapiens genomic clone 2171J2, genomic survey sequence.//3.1e-41:167:87//B89781
R-HEMBA1001723//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//0.53:275:61//AF018261
R-HEMBA1001731//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 322P7, WORKING DRAFT SEQUENCE.//2.9e-48:292:84//AL023799
R-HEMBA1001734//Homo sapiens Chromosome 15q22.3-23 PAC 88m3, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.2e-33:290:81//AC005959
R-HEMBA1001744//Human DNA sequence from clone 134E15 on chromosome 6q21 Contains Blimp-1, apoptosis specific protein similar to yeast APG5 ESTs, GSSs and retroviral sequence, complete sequence.//0.98:203:62//AL022067
R-HEMBA1001745//Homo sapiens BAC clone RG298G08 from 7p15-p21, complete sequence.//0.00019:312:59//AC005084
R-HEMBA1001746//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.045:457:61//AC004153
R-HEMBA1001761//Homo sapiens chromosome X, clone hCIT.200_L_4, complete sequence.//3.8e-39:331:80//AC006121
R-HEMBA1001781//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//0.0062:245:60//AC004554
R-HEMBA1001784//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.1e-22:370:63//AC005740
R-HEMBA1001791//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//3.0e-50:408:80//AL023575
R-HEMBA1001800//CIT-HFP-2049N5.TF CIT-HSP Homo sapiens genomic clone 2049N5, genomic survey sequence.//9.0e-37:335:77//AQ009222
R-HEMBA1001803//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.86:536:56//AC005506
R-nnnnnnnnnnnn//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//2.9e-93:553:89//M21977
R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//2.8e-112:548:98//AB007969
R-HEMBA1001809
R-HEMBA1001815//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//2.6e-48:363:84//AC004025
R-HEMBA1001819//Homo sapiens *** SEQUENCING IN PROGRESS *** from PAC 1577, WORKING DRAFT SEQUENCE.//1.1e-15:275:68//AJ009612
R-HEMBA1001820//HS_3022_B1_A09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022 Col=17 Row=B, genomic survey sequence.//0.00054:335:59//AQ165107
R-nnnnnnnnnnnn//Xenopus laevis intersectin mRNA, complete cds.//1.4e-19:533:63//AF032118
R-HEMBA1001824//S.clavuligerus linear plasmid pSCL (complete sequence).//0.62:189:65//X54107
R-HEMBA1001835//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191J18, WORKING DRAFT SEQUENCE.//1.0:450:60//AL024507
R-HEMBA1001844//Human familial Alzheimer's disease (STM2) gene, complete cds.//1.6e-07:170:68//U50871
R-HEMBA1001847
R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds.//3.3e-108:553:96//AB014517
R-HEMBA1001864//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463
R-HEMBA1001866//HS_2258_B2_D01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2258 Col=2 Row=H, genomic survey sequence.//2.8e-39:397:75//AQ221138

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R-nnnnnnnnnnnn//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//5.9e-56:303:94//AC005065

R-HEMBA1001888//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.7e-43:281:88//AC006210

R-HEMBA1001896

R-HEMBA1001910

R-HEMBA1001912//Homo sapiens chromosome 5, P1 clone 1308e5 (LBNL H13), complete sequence.//0.10:307:61//AC004775

R-HEMBA1001913

R-HEMBA1001915//HS_2037_A1_E12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037 Col=23 Row=I, genomic survey sequence.//0.071:206:64//AQ233106

R-HEMBA1001918//Homo sapiens chromosome 5, P1 clone 1308e5 (LBNL H13), complete sequence.//0.97:449:59//AC004775

R-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//2.0e-105:534:96//AF000145

R-HEMBA1001939//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 508I15, WORKING DRAFT SEQUENCE.//4.6e-13:120:82//AL021707

R-HEMBA1001940//Homo sapiens clone DJ1093I16, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.2e-36:301:81//AC005629

R-HEMBA1001942//Human PAC clone DJ0205E24 from Xq23, complete sequence.//1.9e-10:208:68//AC003013

R-HEMBA1001945//Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence.//1.2e-06:393:60//AE001433

R-HEMBA1001950//R.prowazekii genomic DNA fragment (clone A437R).//0.33:122:66//Z82646

R-HEMBA1001960//Borrelia afzelii VS461 outer surface protein D (ospD) gene, complete cds.//0.0086:427:59//U05329

R-HEMBA1001962//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//4.5e-07:176:70//AC004069

R-HEMBA1001964//HS_2215_B1_H01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2215 Col=1 Row=P, genomic survey sequence.//7.3e-25:215:74//AQ151931

R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs, complete sequence.//1.7e-51:209:95//AL031178

R-HEMBA1001979//CIT-HSP-2387I12.TF.1 CIT-HSP Homo sapiens genomic clone 2387I12, genomic survey sequence.//4.9e-06:153:71//AQ240461

R-HEMBA1001987//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence.//3.1e-46:437:77//AL033521

R-HEMBA1001991//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.1e-48:446:78//AL020997

R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase 2C (beta).//5.1e-90:448:97//AJ005801

R-HEMBA1002008//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//3.2e-42:317:84//Z97181

R-HEMBA1002018//HS_3006_B1_D10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=19 Row=H, genomic survey sequence.//1.0:63:74//AQ089717

R-HEMBA1002022//Homo sapiens chromosome 18, clone hRPK.453_M_1, complete sequence.//0.93:339:59//AC006203

R-HEMBA1002035//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//1.4e-11:285:67//AC003694

R-HEMBA1002039

R-HEMBA1002049//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 117I5, WORKING DRAFT SEQUENCE.//5.3e-52:266:84//AL022315

R-HEMBA1002084//CIT-HSP-2357LI1.TR CIT-HSP Homo sapiens genomic clone 2357L11, genomic survey sequence.//0.0013:185:66//AQ063078

R-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//2.7e-70:479:86//U92703

R-HEMBA1002100//Homo sapiens thyroid receptor interactor (TRIP7) mRNA, 3' end of cds.//8.5e-32:206:91//L40357

R-HEMBA1002102//Homo sapiens Chromosome 15q26.1 PAC clone pDJ427d15, complete sequence.//4.3e-42:302:85//AC005800

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R-HEMBA1002113//Human chromosome 12p13 sequence, complete sequence.//1.6e-64:550:80//U47924
R-HEMBA1002119//Human Chromosome 11 pac pDJ1173a5, complete sequence.//1.2e-92:435:92//AC000378
R-HEMBA1002125
R-HEMBA1002139//Human nebulin mRNA, partial cds.//0.056:68:88//U35637
R-HEMBA1002144//Homo sapiens Chromosome 11p14.3 PAC clone 6-130a9 containing tryptophan hydroxylase gene, complete sequence.//2.0e-26:323:70//AC005728
R-HEMBA1002150//Human DNA sequence from clone 742C19 on chromosome 22q12.3-13.1. Contains a pseudogene similar to Cytochrome C Oxidase Polypeptide VB and (parts of) up to four novel genes, two with homology to Phorbolin genes and one a novel Chromobox protein gene. Contains ESTs, an STS, GSSs and putative CpG islands, complete sequence.//1.0:371:61//AL031846
R-HEMBA1002151
R-HEMBA1002153//Human BAC 367D17 from chromosome 18, complete sequence.//2.4e-21:322:70//AC003971
R-HEMBA1002160//Human DNA sequence from PAC 339A18 on chromosome Xp11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of S.cerevisiae, DNA binding protein similar to URE-B1, ESTs and STS.//2.5e-38:216:84//Z97054
R-HEMBA1002161//CIT-HSP-2163F10.TF CIT-HSP Homo sapiens genomic clone 2163F10, genomic survey sequence.//3.1e-58:284:80//B89969
R-HEMBA1002162//Caenorhabditis elegans cosmid F48C11, complete sequence.//0.0079:286:57//Z80789
R-HEMBA1002166//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//5.9e-53:326:80//AC002980
R-HEMBA1002177
R-HEMBA1002185//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 745I14, WORKING DRAFT SEQUENCE.//9.5e-37:356:76//AL033532
R-HEMBA1002189//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//3.4e-43:244:77//AC003684
R-HEMBA1002191//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.3e-37:323:78//AC005077
R-HEMBA1002199//Human Cosmid g5129g124 from 7q31.3, complete sequence.//1.4e-89:564:87//AC002498
R-HEMBA1002204//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC Region, complete sequence.//1.5e-31:313:71//AC000053
R-HEMBA1002212//K.lactis mitochondrial COX1 and A8 genes for cytochrome oxidase subunit I and ATPase subunit 8.//0.0023:346:60//X57546
R-HEMBA1002215//M.musculus mRNA for testin.//4.7e-61:414:84//X78989
R-HEMBA1002226//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 2705, WORKING DRAFT SEQUENCE.//4.6e-46:375:77//AL033529
R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.6e-46:238:98//AF089814
R-HEMBA1002237//Homo sapiens 12q13 PAC RPCI1-316M24 (Roswell Park Cancer Institute Human PAC library) complete sequence.//4.3e-26:469:67//AC004242
R-HEMBA1002253//Homo sapiens BAC clone GS180J15 from 7q31, complete sequence.//5.1e-23:162:82//AC005016
R-HEMBA1002257
R-HEMBA1002267//Equus caballus dermatan sulfate proteoglycan II mRNA, complete cds.//4.6e-44:300:88//AF03 8127
R-HEMBA1002270//Human BAC clone RG067M09 from 7q21-7q22, complete sequence.//1.9e-19:176:85//AC000057
R-HEMBA1002321
R-HEMBA1002328//HS_3061_A1_D06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3061 Col=11 Row=G, genomic survey sequence.//1.0:151:65//AQ127617
R-HEMBA1002337//Saccharomyces cerevisiae RNA polymerase II holoenzyme component (SRB7) gene, complete cds.//3.7e-07:328:63//U23811
R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds.//2.4e-128:642:96//AB018314
R-HEMBA1002348//Human DNA sequence from clone 409O10 on chromosome 20q12 Contains CA repeat, GSS, STS, complete sequence.//3.7e-07:587:58//AL031256
R-HEMBA1002349//Leishmania tarentolae maxicircle DNA fragment.//0.018:341:58//X02438
R-nnnnnnnnnnnn//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//1.2e-121:661:93//AF092563
R-HEMBA1002381//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and

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non-small cell lung cancer , segment 11/11.//1.1e-70:559:79//AB020868
R-HEMBA1002389//HS_3218_B2_E08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=16 Row=J, genomic survey sequence.//0.0011:122:72//AQ213602
R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784, complete sequence.//4.2e-81:232:97//AC005954
R-HEMBA1002419//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence.//0.50:231:64//AC004848
R-HEMBA1002430//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.0023:604:56//X95276
R-HEMBA1002439//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.4e-23:183:80//AC006026
R-HEMBA1002458//Human DNA sequence from clone 146H21 on chromosome Xq22 Contains cleavage stimulation factor, 64 KD subunit, gene similar to CYTOCHROME B-245 HEAVY CHAIN. pseudogene similar to hnRNP A1 protein and ESTs, complete sequence.//7.7e-32:161:83//Z83819
R-HEMBA1002460//Homo sapiens clone DJ1137M13, complete sequence.//2.6e-100:305:100//AC005378
R-HEMBA1002462//Sequence 43 from patent US 5708157.//2.0e-10:131:77//I80068
R-nnnnnnnnnnnn
R-HEMBA1002477//Homo sapiens PAC clone DJ0607J23 from 7q21.2-q31.1, complete sequence.//6.6e-33:279:80//AC004841
R-HEMBA1002486//***ALU WARNING: Human Alu-Sq subfamily consensus sequence.//2.1e-50:290:92//U14573
R-HEMBA1002495//CITBI-E1-2515J10.TR CITBI-E1 Homo sapiens genomic clone 2515J10, genomic survey sequence.//1.0:122:68//AQ261762
R-HEMBA1002498//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces.//2.8e-22:210:78//AC004963
R-HEMBA1002503//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//2.7e-17:435:58//AC003043
R-HEMBA1002508//Homo sapiens, clone hRPK.15_A_1, complete sequence.//3.7e-09:408:61//AC006213
R-nnnnnnnnnnnn//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//7.1e-112:456:92//AJ011972
R-HEMBA1002515
R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds.//1.6e-104:564:93//AB007923
R-HEMBA1002542//HS_3197_B2_B10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=20 Row=D, genomic survey sequence.//2.8e-25:186:86//AQ188792
R-HEMBA1002547//Mus musculus agrin gene, exon 36.//0.0095:93:75//M92658
R-HEMBA1002552//Homo sapiens clone DJ1137M13, complete sequence.//4.0e-49:308:90//AC005378
R-HEMBA1002555//Homo sapiens full-length insert cDNA clone YR87G10.//8.3e-65:318:99//AF085957
R-HEMBA1002558//, complete sequence.//2.3e-38:264:89//AC005409
R-HEMBA1002561//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//7.1e-44:192:80//AL008634
R-nnnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds.//4.5e-119:587:97//AF075587
R-HEMBA1002583
R-HEMBA1002590//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//9.4e-42:248:88//Z95152
R-HEMBA1002592//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//2.6e-56:302:84//AC004510
R-HEMBA1002621
R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//6.7e-76:380:97//AB018351
R-HEMBA1002628//P.falciparum complete gene map of plastid-like DNA (IR-A).//8.8e-05:327:60//X95275
R-HEMBA1002629//Mus musculus clone OST16705, genomic survey sequence.//4.3e-06:205:66//AF046247
R-HEMBA1002645//***ALU WARNING: Human Alu-J subfamily consensus sequence.//7.1e-39:281:84//U14567
R-HEMBA1002651//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//1.1e-104:500:95//AC004839
R-HEMBA1002659//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//1.2e-61:280:92//AL022323
R-HEMBA1002661//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 225E12, WORKING DRAFT SEQUENCE.//3.2e-41:325:81//AL031772
R-HEMBA1002666//Homo sapiens full-length insert cDNA clone YY74A07.//0.00037:79:84//AF088008
R-HEMBA1002678//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1137F22, WORK-

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ING DRAFT SEQUENCE.//2.3e-107:561:94//AL034421
R-nnnnnnnnnnn//CIT-HSP-2287E8.TF CIT-HSP Homo sapiens genomic clone 2287E8, genomic survey sequence.//5.4e-17:137:88//B99281
R-HEMBA1002688//Homo sapiens chromosome 5, P1 clone 1354A7 (LBNL H47), complete sequence.//0.033:146:70//AC004503
R-HEMBA1002696
R-HEMBA1002712//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//6.2e-44:302:87//AC003982
R-HEMBA1002716//Mus musculus mRNA for ELM1, complete cds.//1.1e-31:332:76//AB004873
R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds.//1.2e-35:287:81//AB014521
R-HEMBA1002730//D.discoideum actin M6 gene, 5' flank.//0.018:233:66//M29109
R-HEMBA1002742//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1108H3, WORKING DRAFT SEQUENCE.//2.6e-13:419:62//AL033525
R-HEMBA1002746//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//0.019:202:65//AC003694
R-HEMBA1002748//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 404K8, WORKING DRAFT SEQUENCE.//0.046:263:60//AL023883
R-HEMBA1002750//Human DNA sequence from PAC 452H17 on chromosome X contains sodium-and chloride-dependent glycine transporter 1 (GLYT-1) like, ESTs.//0.052:421:58//Z96810
R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds.//1.2e-104:545:95//AB011126
R-HEMBA1002770//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//3.0e-07:523:59//AC005140
R-HEMBA1002777
R-HEMBA1002779//Human HepG2 3' region MboI cDNA, clone hmd1e03m3.//9.4e-25:158:93//D17139
R-HEMBA1002780//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y214H10, WORKING DRAFT SEQUENCE.//1.6e-42:463:75//AL022344
R-HEMBA1002794//Plasmodium falciparum MAL3P8, complete sequence.//2.2e-05:417:59//AL034560
R-HEMBA1002801//Meloidogyne javanica mitochondrial transfer RNA His, 16S ribosomal RNA (16S rRNA) genes, ND3 gene, complete cds, and cytochrome b gene, 5' end of CDS.//0.00055:444:59//L76261
R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//4.4e-115:559:97//AF071185
R-HEMBA1002816//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.3e-88:329:94//AC005043
R-HEMBA1002826//Homo sapiens genomic DNA, chromosome 21q11.1, segment 12/28, WORKING DRAFT SEQUENCE.//1.9e-22:262:67//AP000041
R-HEMBA1002833//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence.//1.3e-79:396:97//AC004707
R-HEMBA1002850//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.013:393:61//AC005506
R-HEMBA1002863//Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.//4.1e-73:489:85//AC005562
R-HEMBA1002876//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.21:549:55//AL034557
R-HEMBA1002886//CIT-HSP-2013C4.TR CIT-HSP Homo sapiens genomic clone 2013C4, genomic survey sequence.//0.30:431:56//B53836
R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds.//3.9e-106:541:95//AF037261
R-HEMBA1002921
R-HEMBA1002924//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epitherium cancer, segment 7/10.//4.6e-19:139:78//AB020875
R-HEMBA1002934//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE.//7.5e-45:282:89//AL031681
R-HEMBA1002935//CIT-HSP-2282P14.TFB CIT-HSP Homo sapiens genomic clone 2282P14, genomic survey sequence.//1.5e-102:514:97//AQ008584
R-HEMBA1002937//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 745114, WORKING DRAFT SEQUENCE.//3.3e-87:444:97//AL033532
R-HEMBA1002939
R-HEMBA1002944//HS_3107_A1_C05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3107 Col=9 Row=E, genomic survey sequence.//6.3e-21:250:73//AQ103952
R-HEMBA1002951//Xerolycosa miniata mitochondrial 12S rRNA gene.//0.013:228:63//AJ008020

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R-HEMBA1002954//HS_3246_A2_G09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3246 Col=18 Row=M, genomic survey sequence.//5.8e-42:258:91//AQ218005
R-HEMBA1002968//Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence.//4.2e-38:300:83//AC005553
R-HEMBA1002970//Slime mold (D.discoideum) prestalk D11 gene, complete cds.//5.0e-05:541:57//M11012
R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds.//7.2e-29:162:99//AB014579
R-HEMBA1002973//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//9.1e-36:520:69//AC006128
R-nnnnnnnnnnnn//Homo Sapiens Chromosome X clone bWXD691, complete sequence.//0.00040:504:59//AC004386
R-HEMBA1002999//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//3.7e-66:556:79//U19614
R-HEMBA1003021//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//1.6e-44:530:70//AC000406
R-HEMBA1003033//Homo sapiens full-length insert cDNA clone ZC34B10.//4.6e-78:414:94//AF086194
R-HEMBA1003034//Homo sapiens chromosome 19, cosmid R29351, complete sequence.//9.0e-52:322:75//AC004026
R-HEMBA1003035//HS_2008_A2_G08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=16 Row=M, genomic survey sequence.//4.0e-68:343:97//AQ269839
R-HEMBA1003037//347G15.TVB CIT978SKA1 Homo sapiens genomic clone A-347G15, genomic survey sequence.//0.57:188:58//B17694
R-HEMBA1003041//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//6.3e-30:350:72//AC004983
R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds.//4.1e-118:578:97//AF054182
R-HEMBA1003064//Human cosmid LL12NC01-N-136B11, located centromeric to the ETV6 gene, chromosome 12p12-13.//0.0018:271:60//U59962
R-HEMBA1003067//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 633019, WORKING DRAFT SEQUENCE.//5.3e-48:464:76//AL022302
R-HEMBA1003071//CIT-HSP-2370D6.TR CIT-HSP Homo sapiens genomic clone 2370D6, genomic survey sequence.//0.19:48:87//AQ110136
R-HEMBA1003077//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//4.9e-69:494:84//U42975
R-HEMBA1003078//Human DNA sequence from PAC 339A18 on chromosome Xp11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of S.cerevisiae, DNA binding protein similar to URE-B1, ESTs and STS.//1.1e-11:331:64//Z97054
R-HEMBA1003079//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//4.6e-116:576:98//AC004673
R-HEMBA1003083//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0442P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.1e-43:280:83//AC005798
R-HEMBA1003086//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3-unordered pieces.//1.2e-43:281:88//AC006039
R-HEMBA1003096//Human DNA sequence from clone J506G21, WORKING DRAFT SEQUENCE.//0.00037:421:59//Z82213
R-HEMBA1003098//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0024K08; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.4e-30:303:78//AC005598
R-HEMBA1003117
R-HEMBA1003129//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 407F11, WORKING DRAFT SEQUENCE.//7.9e-11:109:85//AL022329
R-HEMBA1003133//Homo sapiens chromosome 9, P1 clone 11659, complete sequence.//3.9e-99:484:98//AC004472
R-HEMBA1003136//CIT-HSP-2281L22.TF CIT-HSP Homo sapiens genomic clone 2281L22, genomic survey sequence.//2.0e-10:93:92//B99861
R-HEMBA1003142//Homo sapiens 12q24.2 PAC RPCI1-128M12 (Roswell Park Cancer Institute Human PAC library) complete sequence.//9.8e-40:270:87//AC004024
R-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//1.1e-116:586:96//AJ005670
R-HEMBA1003166//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//6.4e-35:364:70//Z83822

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R-HEMBA1003175//Human IFNAR gene for interferon alpha/beta receptor.//1.9e-30:282:77//X60459
R-HEMBA1003197
R-HEMBA1003199//HS_2166_A1_E12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2166 Col=23 Row=I, genomic survey sequence.//0.00026:271:61//AQ164162
R-HEMBA1003202//Homo sapiens clone DJ0592G07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.4e-44:291:83//AC005480
R-HEMBA1003204//Human BAC clone RG072E11 from 7q21-7q22, complete sequence.//3.1e-10:293:62//AC000118
R-HEMBA1003212//Homo sapiens clone DJ0902E20, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.0:118:69//AC006148
R-HEMBA1003220//HS_3092_B1_F09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=17 Row=L, genomic survey sequence.//0:00014:59:91//AQ128202
R-HEMBA1003222//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y43F8, WORKING DRAFT SEQUENCE.//0.84:214:62//Z95393
R-HEMBA1003229//RPCI11-16F15.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16F15, genomic survey sequence.//0.42:167:64//B83610
R-HEMBA1003235//CIT-HSP-2320G19.TF CIT-HSP Homo sapiens genomic clone 2320G19, genomic survey sequence.//3.6e-36:195:81//AQ037231
R-HEMBA1003250//HS_2168_A2_C09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=18 Row=E, genomic survey sequence.//1.4e-22:158:89//AQ125356
R-HEMBA1003257//Human PCP4 gene, exon 3 and complete cds.//0.96:268:61//U53709
R-HEMBA1003273//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence.//1.0e-32:255:84//AC002549
R-HEMBA1003276//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0044:212:60//AC005308
R-HEMBA1003278//Homo sapiens 12q24.1 PAC RPCI1-315L5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.1e-34:286:74//AC002395
R-HEMBA1003281//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.8e-53:428:83//AC005840
R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//3.0e-115:551:99//AB011109
R-HEMBA1003296//CIT-HSP-2196L16.TR CIT-HSP Homo sapiens genomic clone 2196L16, genomic survey sequence.//2.9e-20:337:65//AQ003073
R-HEMBA1003304//Sequence 23 from patent US 5552281.//1.8e-31:179:97//I25662
R-HEMBA1003309//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete sequence.//0.00019:334:60//AB017061
R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds.//2.8e-111:545:97//AB001872
R-HEMBA1003322//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//0.60:274:61//AL022153
R-HEMBA1003327//Homo sapiens BAC clone RG351J01 from 7q22-q31, complete sequence.//0.00028:172:65//AC005099
R-HEMBA1003328//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//2.2e-44:268:90//AC005081
R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds.//2.7e-61:312:97//AF026029
R-HEMBA1003348//***ALU WARNING: Human Alu-J subfamily consensus sequence.//7.2e-38:186:83//U14567
R-HEMBA1003369//Caenorhabditis elegans cosmid F59C6, complete sequence.//0.00012:465:59//Z79600
R-HEMBA1003370//Homo sapiens chromosome 17, clone hRPC867C24, complete sequence.//3.2e-42:301:87//AC002558
R-HEMBA1003373//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUCI, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete sequence.//7.4e-34:375:74//AL022721
R-HEMBA1003376//Homo sapiens chromosome 16, cosmid clone RT102 (LANL), complete sequence.//1.6e-46:309:88//AC004651
R-HEMBA1003380//HS_3184_B2_E06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=12 Row=J, genomic survey sequence.//1.0e-35:237:88//AQ189144

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R-HEMBA1003384//HS_2193_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=16 Row=P, genomic survey sequence.//0.00029:96:76//AQ032212
R-HEMBA1003395//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.6e-21:139:86//AC002993
R-HEMBA1003402//CIT-HSP-2166E19.TR CIT-HSP Homo sapiens genomic clone 2166E19, genomic survey sequence.//0.99:144:61//B91549
R-nnnnnnnnnnnn
R-HEMBA1003417//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//2.5e-112:547:98//AL031321
R-HEMBA1003418//Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence.//0.082:352:59//AC004879
R-HEMBA1003433//Homo sapiens cell cycle regulatory protein p95 (NBS1) mRNA, complete cds.//9.9e-114:544:98//AF058696
R-HEMBA1003461
R-HEMBA1003463
R-HEMBA1003480//Homo sapiens clone NH0523H20, complete sequence.//9.1e-106:533:96//AC005041
R-HEMBA1003528
R-HEMBA1003531//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//3.4e-08:333:64//AC002454
R-HEMBA1003538//Human mRNA for complement component C1r.//1.4e-23:333:68//X04701
R-HEMBA1003545//Zebrafish mRNA for zflsl-2 (insulin gene enhancer binding protein homolog), complete cds.//0.030:144:68//D38453
R-HEMBA1003548//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0017:487:57//AC004153
R-HEMBA1003555//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 371H6, WORKING DRAFT SEQUENCE.//2.8e-99:503:96//AL031718
R-HEMBA1003556//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//1.6e-114:574:97//AC005913
R-HEMBA1003560//Diplolepis rosae microsatellite clone DR04096.//0.24:116:67//AF034416
R-HEMBA1003568//Homo sapiens clone NH0215P16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.9e-05:422:63//AC006036
R-HEMBA1003569//Homo sapiens full-length insert cDNA clone ZD82D06.//8.7e-108:545:95//AF086450
R-HEMBA1003571//Homo sapiens PAC clone DJ0886O08 from 7q32-q35, complete sequence.//4.6e-51:570:71//AC004914
R-HEMBA1003579//HS_3237_B2_E05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3237 Col=10 Row=J, genomic survey sequence.//8.5e-97:495:95//AQ209302
R-HEMBA1003581//Mouse mRNA for talin.//8.3e-12:128:82//X56123
R-HEMBA1003591//Homo sapiens chromosome 16, BAC clone 2603 (LANL), complete sequence.//2.9e-87:251:95//AC005774
R-HEMBA1003595//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a ggtt repeat polymorphism, complete sequence.//4.5e-52:384:83//AL008715
R-HEMBA1003597//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//4.6e-41:442:74//Z84480
R-HEMBA1003598//Homo sapiens PAC clone DJ0537P09 from 7p11.2-p12, complete sequence.//1.8e-23:177:88//AC005153
R-HEMBA1003615
R-HEMBA1003617//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.039:494:57//AC005139
R-HEMBA100362111*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0052I22; HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.3e-26:309:75//AC004599
R-HEMBA1003622//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//7.1e-56:545:75//AC002980
R-HEMBA1003630//Homo sapiens CC chemokine gene cluster, complete sequence.//2.8e-32:546:68//AF088219
R-HEMBA1003637//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//8.0e-25:457:68//AC002454
R-HEMBA1003640//Homo sapiens chromosome X, PAC 671D9, complete sequence.//2.8e-40:280:86//AF031078

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R-HEMBA1003645//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32B1, WORKING DRAFT SEQUENCE.//1.7e-33:297:82//AL023693
R-HEMBA1003646//Plasmodium falciparum MAL3P7, complete sequence.//0.44:319:59//AL034559
R-HEMBA1003656//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//6.9e-36:242:80//AC004382
R-HEMBA1003662//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence.//8.6e-117:588:96//AC005746
R-HEMBA1003667//Sequence 8 from patent US 5420245.//1.8e-21:170:88//I12222
R-HEMBA1003679//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//1.6e-22:180:87//AC005065
R-HEMBA1003680//C. elegans cosmid ZK353.//1.1e-06:270:61//L15313
R-HEMBA1003684//Colias alexandra alexandra cytochrome oxidase subunit I (cox1) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.77:171:66//AF044872
R-HEMBA1003690//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-104:523:97//AC004466
R-HEMBA1003692//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 508I15, WORKING DRAFT SEQUENCE.//1.7e-41:414:77//AL021707
R-HEMBA1003711//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//1.6e-29:304:77//AC000406
R-HEMBA1003714
R-HEMBA1003715//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-685D8, WORKING DRAFT SEQUENCE, 16 unordered pieces.//1.4e-63:578:77//AC005136
R-HEMBA1003720//Homo sapiens, WORKING DRAFT SEQUENCE, 135 unordered pieces.//2.4e-36:350:78//AC002353
R-HEMBA1003725//Homo sapiens chromosome 19, cosmid R31973, complete sequence.//6.3e-42:250:75//AC004699
R-HEMBA1003729//RPCI11-22D14.TV RPCI-11 Homo sapiens genomic clone RPCI-11-22D14, genomic survey sequence.//1.0:234:62//B86158
R-HEMBA1003733//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//7.7e-80:558:83//AL008634
R-HEMBA1003742//HS_3080_B2_H06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3080 Col=12 Row=P, genomic survey sequence.//3.4e-55:331:91//AQ139179
R-HEMBA1003758//Human DNA sequence from PAC 295C6 on chromosome 1q24. Contains ESTs, CA repeat, STS and CpG istand.//4.5e-59:521:75//Z97876
R-HEMBA1003760
R-HEMBA1003773//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//2.6e-72:467:86//U17343
R-HEMBA1003783//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//1.0e-77:557:81//AF084259
R-HEMBA1003784
R-HEMBA1003799//Homo sapiens PAC clone DJ1032B10 from 7p15.3-p21, complete sequence.//2.1 e-49:390:72//AC004455
R-HEMBA1003803
R-HEMBAI003804//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence.//9.4e-99:359:99//AC004596
R-HEMBA1003805//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//8.0e-113:567:96//AL031781
R-HEMBA1003807//Bovine dinucleotide microsatellite HUJII77.//5.4e-18:194:78//M96348
R-HEMBA1003836//Human DNA from overlapping chromosome 19 cosmids R31396, F2545L and R31076 containing COX6B and UPKA, genomic sequence, complete sequence.//3.4e-40:256:85//AC002115
R-HEMBA1003838//CIT-HSP-2380F18.TF CIT-HSP Homo sapiens genomic clone 2380F18, genomic survey sequence.//9.7e-25:150:96//AQ196624
R-HEMBA1003856//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence.//4.8e-33:486:68//Z93929
R-HEMBA1003864//, complete sequence.//4.4e-100:531:94//AC005300

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R-HEMBA1003866//HS_3203_B2_C01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3203 Col=2 Row=F, genomic survey sequence.//2.6e-05:206:64//AQ180298
R-HEMBA1003879//Homo sapiens chromosome 10 clone CIT987SK-1119P3 map 10q25.1, WORKING DRAFT SEQUENCE, 1 ordered pieces.//4.7e-17:170:79//U82207
R-HEMBA1003880//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//7.8e-103:526:96//AP000036
R-HEMBA1003885//Human apolipoprotein apoC-IV (APOC4) gene, complete cds.//3.5e-45:299:87//U32576
R-HEMBA1003893//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1137F22, WORKING DRAFT SEQUENCE.//1.1e-41:386:77//AL034421
R-HEMBA1003902//HS_3031_B2_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3031 Col=14 Row=J, genomic survey sequence.//5.3e-50:293:93//AQ165549
R-HEMBA1003908//CIT-HSP-2367K7.TR CIT-HSP Homo sapiens genomic clone 2367K7, genomic survey sequence.//1.2e-32:220:92//AQ076795
R-HEMBA1003926//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//3.1e-58:294:85//AC005368
R-HEMBA1003937//Homo sapiens chromosome 3 subtelomeric region.//8.0e-111:590:93//AF109718
R-HEMBA1003939
R-HEMBA1003942//Homo sapiens clone DJ0828F13, complete sequence.//2.2e-08:474:58//AC004904
R-HEMBA1003950//Plasmodium vivax from Brazil cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.034:258:62//AF069619
R-HEMBA1003953//Plasmodium falciparum MAL3P8, complete sequence.//0.096:492:57//AL034560
R-HEMBA1003958//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 64K7, WORKING DRAFT SEQUENCE.//7.3e-40:382:78//AL031668
R-HEMBA1003959//Amaranthus hypochondriacus betaine aldehyde dehydrogenase (ahybadh4) gene, complete cds.//0.11:428:60//AF000132
R-HEMBA1003976//Homo sapiens PAC clone DJ0724E13 from 7p11.2-p12, complete sequence.//1.0:222:62//AC004414
R-HEMBA1003978//Sequence 31 from patent US 5708157.//1.9e-14:159:77//I80060
R-HEMBA1003985//Homo sapiens 12p13.3 PAC RPCI5-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.6e-14:136:83//AC004804
R-HEMBA1003987//Human chromosome 12p13 sequence, complete sequence.//3.2e-26:268:79//U47924
R-HEMBA1003989//RPCI11-52K22.TJ RPCI11 Homo sapiens genomic clone R-52K22, genomic survey sequence.//2.2e-86:443:95//AQ052484
R-HEMBA1004000
R-HEMBA1004011
R-HEMBA1004012//Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.//4.7e-38:284:85//AC005670
R-HEMBA1004015//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//0.48:460:58//AL023575
R-HEMBA1004024//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//2.5e-21:159:80//AC005081
R-HEMBA1004038//Homo sapiens Xq28 BAC RPCI11-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//7.9e-10:231:66//AC006054
R-HEMBA1004042//Homo sapiens clone DJ0968I16, complete sequence.//0.00071:263:68//AC006016
R-HEMBA1004045//Homo sapiens PAC clone DJ0074M20 from X, complete sequence.//8.8e-23:196:69//AC006143
R-HEMBA1004048//CIT-HSP-2288N20.TF CIT-HSP Homo sapiens genomic clone 2288N20, genomic survey sequence.//0.013:162:67//AQ007283
R-HEMBA1004049//Human hsp 70 gene 3' region for 70 kDa heat shock protein.//7.7e-30:176:96//X04677
R-HEMBA1004055//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.4e-05:395:63//AC005504
R-HEMBA1004056//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-61:551:77//AC005484
R-HEMBA1004074//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.98:275:63//AC004952
R-HEMBA1004086//Sequence 65 from patent US 5691147.//2.8e-54:313:92//I76237
R-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//1.8e-11:323:63//AF091234
R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds.//9.3e-42:534:69//D50918

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R-HEMBA1004132//Homo sapiens chromosome 17, clone hCIT.211_P_7, complete sequence.//6.0e-49:491:76//AC003665
R-HEMBA1004133//HS_3229_B2_E09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 Col=18 Row=J, genomic survey sequence.//1.1e-72:374:97//AQ192003
R-HEMBA1004138//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 417M14, WORKING DRAFT SEQUENCE.//3.1e-09:277:66//AL024498
R-HEMBA1004143//Plasmodium falciparum MAL3P4, complete sequence.//0.53:239:61//AL008970
R-HEMBA1004146//Homo sapiens clone DJ0038I10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.0e-35:165:88//AC004820
R-HEMBA1004150//CITBI-E1-2517I2.TR CITBI-E1 Homo sapiens genomic clone 2517I2, genomic survey sequence.//0.56:379:59//AQ277616
R-HEMBA1004164//Human BAC clone GS200K05 from 7q21-q22, complete sequence.//4.6e-49:448:77//AC002429
R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//2.4e-110:563:96//AF067855
R-HEMBA1004199//S.pombe chromosome I cosmid c8A4.//0.73:187:64//Z66569
R-HEMBA1004200//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete sequence.//6.3e-30:293:77//AC004552
R-HEMBA1004202//rah=ras-related homolog [mice, HT4 neural cell line, mRNA, 993 nt].//3.0e-64:517:80//S72304
R-HEMBA1004203//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//1.0e-97:303:98//AC005488
R-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//3.6e-116:573:97//U50748
R-HEMBA1004225//Drosophila melanogaster mitochondrial DNA with 12 tRNAs and 7 genes.//5.4e-11:493:60//M37275
R-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//6.1e-76:443:86//AF095927
R-HEMBA1004238//Homo sapiens chromosome 19, cosmid R28341, complete sequence.//1.1e-42:330:83//AC005763
R-HEMBA1004241
R-HEMBA1004246//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE.//1.1e-45:288:85//AP000011
R-HEMBA1004248//Homo sapiens PAC clone DJ0828B12 from 7q11.23-q21.1, complete sequence.//5.2e-09:516:61//AC004903
R-HEMBA1004264
R-HEMBA1004267//HS_2255_A2_H12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=24 Row=O, genomic survey sequence.//8.6e-59:318:95//AQ068854
R-HEMBA1004272//Homo sapiens 12p13.3 PAC RPCIS-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.1e-113:576:96//AC005831
R-nnnnnnnnnnnn//Homo sapiens clone 617 unknown mRNA, complete sequence.//4.4e-110:553:96//AF091081
R-HEMBA1004276
R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.//1.9e-106:538:97//AF022795
R-HEMBA1004289//RPCI11-74010.TJ RPCI11 Homo sapiens genomic clone R-74O10, genomic survey sequence.//2.3e-37:248:76//AQ266668
R-HEMBA1004295//Baboon apolipoprotein A-VI mRNA, 3' end.//0.0016:273:64//L13174
R-HEMBA1004306//HS_3175_B2_F01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3175 Col=2 Row=L, genomic survey sequence.//1.6e-28:190:77//AQ169206
R-HEMBA1004312//Human BAC clone RG119P24 from 7q31, complete sequence.//6.3e-36:267:82//AC003088
R-HEMBA1004321//Homo sapiens *** SEQUENCING IN PROGRESS *** from PAC 10155, WORKING DRAFT SEQUENCE.//4.1e-111:576:95//AJ009611
R-HEMBA1004323//CIT-HSP-2374C8.TR CIT-HSP Homo sapiens genomic clone 2374C8, genomic survey sequence.//2.7e-42:136:91//AQ114933
R-HEMBA1004327//CIT-HSP-2303L24.TF CIT-HSP Homo sapiens genomic clone 2303L24, genomic survey sequence.//1.0:78:67//AQ017600
R-HEMBA1004330//Homo sapiens clone DJ1173120, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.3e-119:580:98//AC004987
R-HEMBA1004334//Pimpinella brachycarpa Phybl mRNA, complete cds.//3.3e-14:238:69//AF082024
R-HEMBA1004335//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.//1.8e-

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21:291:71//AC004638
R-HEMBA1004341
R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds.//4.1e-74:444:90//D89667
R-HEMBA1004354//Human DNA from overlapping chromosome 19-specific cosmids R29515 and R28253, genomic sequence, complete sequence.//7.0e-38:287:82//AC003002
R-HEMBA1004356//Sequence 2 from patent US 5652144.//3.7e-108:588:92//I58611
R-HEMBA1004366//WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-14:446:63//AC005949
R-HEMBA1004372//CIT-HSP-2005C13.TF CIT-HSP Homo sapiens genomic clone 2005C13, genomic survey sequence.//0.010:334:61//B55811
R-HEMBA1004389//Homo sapiens full-length insert cDNA clone ZE09A11.//1.5e-19:170:83//AF086540
R-HEMBA1004394//Human (D21S198) DNA segment containing (TG)23 repeat.//1.0:50:84//X58124
R-HEMBA1004396//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//8.2e-34:459:69//AC004057
R-HEMBA1004405//Homo sapiens BAC clone GS589P19 from 7p13-p14, complete sequence.//2.8e-42:314:84//AC005030
R-HEMBA1004408
R-HEMBA1004429//M.musculus of DNA encoding DNA-binding protein.//1.6e-66:449:82//Z54200
R-HEMBA1004433//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.//7.2e-32:460:68//AJ011930
R-HEMBA1004460//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//3.9e-113:581:96//AC004846
R-HEMBA1004461//HS_3244_A2_F12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=24 Row=K, genomic survey sequence.//8.0e-83:397:99//AQ220876
R-HEMBA1004479//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//1.7e-40:485:70//AC006012
R-HEMBA1004482//Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence.//2.2e-11:513:59//AE001370
R-HEMBA1004502//Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.//2.0e-08:245:66//AC005951
R-HEMBA1004506//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 34606, WORKING DRAFT SEQUENCE.//4.2e-81:582:83//Z84487
R-HEMBA1004507//Caenorhabditis elegans cosmid C40C9, complete sequence.//0.56:235:64//Z70266
R-HEMBA1004509
R-HEMBA1004534//Sequence 58 from patent US 5691147.//1.9e-61:430:83//I76230
R-HEMBA1004538//HS_3189_B2_C03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3189 Col=6 Row=F, genomic survey sequence.//6.1e-21:140:92//AQ170330
R-HEMBA1004554//CIT-HSP-712K9.TP CIT-HSP Homo sapiens genomic clone 712K9, genomic survey sequence.//1.7e-16:116:93//B73329
R-HEMBA1004560//Human mRNA for KIAA0281 gene, complete cds.//2.2e-14:213:71//D87457
R-HEMBA1004573
R-HEMBA1004577//Human DNA sequence from cosmid L247F6, Huntington's Disease Region, chromosome 4p16.3 contains protein similar to Mouse SH3 binding protein 3BP2, multiple ESTs and a CpG island.//1.0:352:60//Z68279
R-HEMBA1004586
R-nnnnnnnnnnnn//Plasmodium falciparum MAL3P6, complete sequence.//0.0012:359:60//Z98551
R-HEMBA1004610//S.pombe chromosome II cosmid c354.//0.0011:362:62//AL022071
R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501./1.4e-50:327:85//AB007970
R-HEMBA1004629//Homo sapiens Xp22 bins 16-17 BAC GSHB-531I17 (Genome Systems Human BAC Library) complete sequence.//4.4e-13:527:63//AC004805
R-HEMBA1004631//Rattus norvegicus Nclone10 mRNA.//2.9e-24:364:71//U31866
R-HEMBA1004632
R-HEMBA1004637//Homo sapiens clone DJ0982E09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.7e-117:573:98//AC005534
R-HEMBA1004638//H.sapiens mRNA for DGCR2.//3.8e-19:118:99//X84076
R-HEMBA1004666//Arabidopsis thaliana chromosome II BAC T4E14 genomic sequence, complete sequence.//0.00013:501:58//AC005171
R-HEMBA1004669//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel

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genes, ESTs, GSSs and CpG islands, complete sequence.//1.5e-120:571:98//AL031432
R-HEMBA1004670//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 222E13, WORKING DRAFT SEQUENCE.//4.4e-12:110:88//Z93241
R-HEMBA1004672//Human DNA sequence from PAC 308I13 on chromosome 1p35-1p36.3.//3.4e-38:324:81//Z99291
R-HEMBA1004693//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence.//0.86:309:57//AB006702
R-HEMBA1004697//T33B22TF TAMU Arabidopsis thaliana genomic clone T33B22, genomic survey sequence.//0.29:331:61//B97342
R-HEMBA1004705//Plasmodium falciparum MAL3P7, complete sequence.//0.051:424:58//AL034559
R-HEMBA1004709//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.//1.7e-49:497:76//AC004638
R-HEMBA1004711//Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.//1.6e-38:362:79//AC005562
R-HEMBA1004725
R-HEMBA1004730//Homo sapiens Chromosome 17p13 Cosmid Clone cos26, complete sequence.//1.1e-58:489:79//AC002085
R-HEMBA1004733
R-HEMBA1004734//Human DNA sequence from clone 273N12 on chromosome 6q16.1-16.3. Contains the gene for the N-Oct5a (N-Oct3, N-Oct5b) POU domain proteins and an unknown gene. Contains a putative CpG island, ESTs, STS; and GSSs, complete sequence.//0.0030:362:61//AL022395
R-HEMBA1004736//Homo sapiens clone DJ0981O07, complete sequence.//1.9e-58:282:87//AC006017
R-HEMBA1004748//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//3.6e-34:287:81//AC004953
R-HEMBA1004751//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//5.3e-40:266:89//Z98950
R-HEMBA1004752//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 495010, WORKING DRAFT SEQUENCE.//3.3e-39:281:85//AL031121
R-HEMBA1004753//Homo sapiens ribosomal protein S20 (RPS20) mRNA, complete cds.//2.6e-65:475:84//L06498
R-HEMBA1004756//Homo sapiens DNA sequence from PAC 86C11 on chromosome 6p21.31-22.1. Contains histone genes H2A/1,H2B.1A,H4,H2A.1b,H3 pseudogene, pheromone receptor pseudogene, ESTs, STS and CpG island.//1.8e-08:516:59//AL021807
R-HEMBA1004758//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//5.1e-45:577:72//AC004057
R-HEMBA1004763
R-HEMBA1004768//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Aminotransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//4.1e-60:435:78//AL022310
R-HEMBA1004770//Plasmodium falciparum chromosome 2, section 8 of 73 of the complete sequence.//8.7e-05:476:61//AE001371
R-HEMBA1004771//Homo sapiens Xp22 Cosmid U152D7 (Lawrence Livermore human cosmid library) complete sequence.//5.0e-08:113:80//AC003047
R-HEMBA1004776
R-HEMBA1004778//***ALU WARNING: Human Alu-J subfamily consensus sequence.//1.1e-35:288:84//U14567
R-nnnnnnnnnnnn/HS_3192_B1_F09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3192 Col=17 Row=L, genomic survey sequence.//1.9e-44:233:98//AQ155855
R-HEMBA1004803//Homo sapiens minisatellite ms31 repeat region.//3.0e-67:318:87//AF048728
R-HEMBA1004806
R-HEMBA1004807//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.6e-20:333:69//AC005015
R-HEMBA1004816//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//6.3e-13:148:77//Z92545
R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds.//1.5e-12:141:85//M74002
R-HEMBA1004847//Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).//7.6e-80:297:85//X53744

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R-HEMBA1004850
R-HEMBA1004863//Human DNA sequence from PAC 345P10 on chromosome 22q12-qter contains ESTs and STS and polymorphic CA repeat D22S927.//2.0e-14:159:79//Z82201
R-HEMBA1004864
R-HEMBA1004865//Homo sapiens Xp22-149 BAC RPCI11-466O4 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.90:76:76//AC005297
R-HEMBA1004880//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.// 1.9e-49:551:73//AC004826
R-HEMBA1004889//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 223B1, WORKING DRAFT SEQUENCE.//0.0021:189:65//AL031943
R-HEMBA1004900//Homo sapiens chromosome 17, clone hRPK.180_P_8, complete sequence.//6.6e-11:144: 7711AC005972
R-HEMBA1004909//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//7.6e-46:341:83//Z98052
R-HEMBA1004918//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 994L9, WORKING DRAFT SEQUENCE.//1.6e-54:301:89//AL034554
R-HEMBA1004923//Homo sapiens 47kB DNA fragment from Xq28, proximal to MTM1 gene.//2.0e-07:182:69// Y15994
R-HEMBA1004929
R-HEMBA1004930//Homo sapient chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.7e-66:547:79//AC005848
R-HEMBA1004933//H.sapiens Humig mRNA.//0.13:233:62//X72755
R-HEMBA1004934//CIT-HSP-2021I16.TF CIT-HSP Homo sapiens genomic-clone 2021I16, genomic survey sequence.//0.66:268:62//B65345
R-HEMBA1004944//CIT-HSP-2281L12.TR CIT-HSP Homo sapiens genomic clone 2281L12, genomic survey sequence.//3.8e-20:104:82//B99849
R-HEMBA1004954//Homo sapiens chromosome 17, clone hRPK.146_P_2, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.00082:385:60//AC005341
R-HEMBA1004956//CIT-HSP-2305H22.TF CIT-HSP Homo sapiens genomic clone 2305H22, genomic survey sequence.//1.6e-84:411:99//AQ020408
R-HEMBA1004960//Human DNA sequence from PAC 358H7 on chromosome X.//3.3e-22:249:74//Z77249
R-HEMBA1004972//nbxb0003aF01f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0003K01f, genomic survey sequence.//0.52:171:64//AQ049982
R-HEMBA1004973//*** SEQUENCING IN PROGRESS *** EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//0.69:179:64//AC003656
R-HEMBA1004977//Caenorhabditis elegans cosmid F08G2, complete sequence.//7.6e-07:492:58//Z81495
R-HEMBA1004978//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.20:427:60//AL024509
R-HEMBA1004980//CIT-HSP-2379K5.TF CIT-HSP Homo sapiens genomic clone 2379K5, genomic survey sequence.//1.6e-53:331:88//AQ108614
R-HEMBA1004983//Genomic sequence from Human 17, complete sequence.//0.00061:473:58//AC000389
R-HEMBA1004995//Homo sapiens chromosome 16, cosmid clone 306E5 (LANL), complete sequence.//1.6e-90: 527:89//AC004224
R-HEMBA10050087/Human DNA sequence from clone 461P17 on chromosome 20q12-13.2. Contains four novel (pseudo)genes for proteins with Kunitz/Bovine pancreatic trypsin inhibitor and/or WAP-type (Whey Acidic Protein) 'four-disulfide core' domains, COX6C (Cytochrome C Oxidase Polypeptide VIC, EC 1.9.3.1) and RPL5 (60S Ribosomal Protein L5) pseudogenes, a pseudogene similar to part of the HSPD1 (HSP60, Mitochondrial Matrix Protein P1 precursor, Heat Shock Protein 60, GROEL protein, HUCHA60) gene, and the Major Epididymis-specific protein E4 precursor (HE4, Epididymis Secretory protein E4, WAP-type (Whey Acidic Protein) 'four-disulfide core' domain) gene. Contains ESTs, an STS, GSSs and a putative CpG island, complete sequence.//5.4e-65:357:83// AL031663
R-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//5.6e-107:550:96//AF041474
R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds.//6.3e-104:542:94//AB014548
R-HEMBA1005029//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c),

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H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence.//3.1e-67:493:83//AL009179
R-HEMBA1005035//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence.//7.4e-101:537:94//AC004596
R-HEMBA1005039//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE.//9.5e-30:446:68//AL031650
R-HEMBA1005047//Mus musculus mRNA for Rab24 protein.//1.4e-34:229:88//Z22819
R-HEMBA1005050//Human Chromosome X PAC RPCI1-290C9 from the Pieter de Jong Human PAC library; complete sequence.//4.0e-43:371:80//AC002404
R-HEMBA1005062//Homo sapiens chromosome 17, clone hCIT.186_H_2, complete sequence.//2.3e-15:269:66//AC004675
R-HEMBA1005066//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE. 1 unordered pieces.//4.0e-30:305:74//AC006030
R-HEMBA1005075
R-HEMBA1005079//Homo sapiens clone HS 19.11 Alu-Ya5 sequence.//6.5e-48:245:91//AF015156
R-HEMBA1005083//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE.//1.3e-15:142:83//AL034423
R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//5.3e-110:545:96//AF080561
R-HEMBA1005113//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y53C10, WORKING DRAFT SEQUENCE.//0.026:252:64//Z93340
R-HEMBA1005123//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//7.1e-55:306:82//AL022336
R-HEMBA1005133//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//6.4e-45:309:87//AL022345
R-HEMBA1005149//Human cosmid LL12NC01-95H4, ETV6 gene, exon 2 and partial cds.//3.2e-31:310:76//U81834
R-HEMBA1005152//Homo sapiens DNA sequence from PAC 13D10 on chromosome 6p22.3-23. Contains CpG island.//1.4e-33:361:79//AL021407
R-HEMBA1005159//Human DNA sequence from clone 163016 on chromosome 1p35.1-36.13 Contains CA repeat, STS, complete sequence.//2.7e-22:440:66//AL031279
R-HEMBA1005185//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y105E8, WORKING DRAFT SEQUENCE.//0.0017:381:58//AL022594
R-HEMBA1005201//P.falciparum complete gene map of plastid-like DNA (IR-B).//8.5e-05:457:57//X95276
R-HEMBA1005202//Human 18S ribosomal RNA.//4.7e-38:236:91//X03205
R-HEMBA1005219
R-HEMBA1005223//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//1.0:209:65//AC004854
R-HEMBA1005232//Homo-sapiens chromosome Y, clone 264,M,20, complete sequence.//0.0040:439:58//AC004617
R-HEMBA1005241//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//4.2e-111:568:96//AC005154
R-HEMBA1005244//HS_3092_B2_C11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=22 Row=F, genomic survey sequence.//4.9e-12:116:84//AQ127947
R-HEMBA1005251//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//3.2e-27:210:84//AC004548
R-HEMBA1005252//Homo sapiens chromosome 17, clone hRPK.318_A_15, complete sequence.//4.6e-105:437:97//AC005837
R-HEMBA1005274//Slime mold mitochondrial DNA, binding region to the membrane system.//0.011:339:59//D86630
R-HEMBA1005275//Homo sapiens PAC clone DJ0886O08 from 7q32-q35, complete sequence.//3.4e-17:269:71//AC004914
R-HEMBA1005293//Human DNA sequence from PAC 130N4, BRCA2 gene region chromosome 13q12-13 contains xs7 mRNA, ESTs.//6.9e-20:193:73//Z75887
R-HEMBA1005296//HS_3037_B1_D01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=1 Row=H, genomic survey sequence.//0.26:184:64//AQ117120
R-HEMBA1005304//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//

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1.5e-58:445:78//AC006146
R-HEMBA1005311//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796E4, WORKING DRAFT SEQUENCE.//9.3e-42:383:78//AL022337
R-HEMBA1005314//Caenorhabditis elegans cosmid F23H11.//0.80:179:65//AF003389
R-HEMBA1005315//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.// 2.4e-40:409:71//AC006030
R-HEMBA1005318//S.pombe chromosome I cosmid c2E11.//0.97:370:61//AL031181
R-HEMBA1005331//Homo sapiens chromosome 17, clone hRPK.214_C_8, complete sequence.//1.9e-112:577: 95//AC005803
R-HEMBA1005353//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 429E7, WORKING DRAFT SEQUENCE.//8.9e-80:406:97//AL031722
R-HEMBA1005359//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.2e-50:320:84//AC005412
R-HEMBA1005367//RPCI11-85E23.TV RPCI11 Homo sapiens genomic clone R-85E23, genomic survey sequence.//0.39:148:67//AQ281915
R-HEMBA1005372//Homo sapiens full-length insert cDNA YH93B03.//2.6e-108:557:95//AF074997
R-HEMBA1005374//Homo sapiens full-length insert cDNA clone ZA95D11.//1.9e-110:531:98//AF086142
R-HEMBA1005389//Human DNA sequence from clone 245G19 on chromosome Xp22.11-22.2 Contains serine-threonine kinase (Txp3) gene, a pseudogene similar to ALPHA-1 PROTEIN ((CONNEXIN 43, CX43, GAP JUNCTION 43 KD HEART PROTEIN)), and the 3' end of the RS (X-linked juvenile retinoschisis precursor protein) gene. Contains ESTs, STSs and GSSs, complete sequence.//6.0e-41:432:75//Z92542
R-HEMBA1005394//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 681N20, WORKING DRAFT SEQUENCE.//4.9e-107:585:93//AL031670
R-HEMBA1005403//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//5.1e-118:586:97//AL034379
R-HEMBA1005408//Bos taurus retina membrane guanylate cyclase ROS-GC2 mRNA, complete cds.//1.6e-06: 204:68//U95958
R-HEMBA1005410//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 732E4, WORKING DRAFT SEQUENCE.//1.2e-23:452:66//AL008722
R-HEMBA1005411//RPCI11-66N19.TK RPCI11 Homo sapiens genomic clone R-66N19, genomic survey sequence.//2.2e-38:222:79//AQ237442
R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.//5.6e-117: 453:99//AF041248
R-HEMBA1005426//Human DNA sequence from PAC 448E20 on chromosome Xq26.1 contains ESTs and STS.// 0.86:278:60//Z97196
R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment.//5.4e-46:305:87//L40391
R-HEMBA1005447//Human DNA sequence from clone 48G12 on chromosome Xq27.1-27.3. Contains STSs and GSSs, complete sequence.//3.3e-79:531:86//AL031054
R-HEMBA1005468//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence.//4.0e-27:469: 66//AC004894
R-HEMBA1005469//Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence.//7.2e-40:410: 76//AC005212
R-HEMBA1005472//Human DNA Sequence *** SEQUENCING IN PROGRESS *** from clone 1090E8, WORKING DRAFT SEQUENCE.//3.1e-40:296:85//AL033524
R-HEMBA1005475//HS_2266_B2_C04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2266 Col=8 Row=F, genomic survey sequence.//0.49:209:61//AQ069377
R-HEMBA1005497
R-HEMBA1005500//Homo sapiens PAC clone DJ1093O17 from 7q11.23-q21, complete sequence.//4.5e-116:580: 97//AC004957
R-HEMBA1005506//Arabidopsis thaliana BAC T26D22.//0.0050:442:59//AF058826
R-HEMBA1005508//Sigalphus sp. 16S ribosomal RNA gene, partial sequence.//0.020:391:59//AF003509
R-HEMBA1005511//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.// 0.44:195:63//Z96811
R-HEMBA1005517//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.44:470:57//L14320
R-HEMBA1005518//M.musculus mRNA for paladin gene.//6.2e-29:183:81//X99384
R-HEMBA1005520//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.// 7.2e-40:281:86//AC004913

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R-HEMBA1005526//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 341D10, WORKING DRAFT SEQUENCE.//3.9e-40:482:73//Z97985
R-HEMBA1005528//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11.//3.8e-84:309:99//AB020860
R-HEMBA1005530//Homo sapiens PAC clone 946B23 SCA2 region, SP6 end, genomic sequence, genomic survey sequence.//8.1e-25:154:94//U84091
R-HEMBA1005548//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 970A17, WORKING DRAFT SEQUENCE.//5.3e-105:534:96//AL034431
R-HEMBA1005552//Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence.//2.8e-69:432:88//AC004743
R-HEMBA1005558
R-HEMBA1005568//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//5.9e-33:367:74//AC004087
R-HEMBA1005570//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//2.2e-67:399:91//AL020989
R-HEMBA1005576//Homo sapiens chromosome 16, BAC clone 97H22 (LANL), complete sequence.//1.0:156:631/AC005737
R-HEMBA1005577
R-HEMBA1005581//Homo sapiens mRNA for MEGFS, partial cds.//9.7e-27:561:64//AB011538
R-HEMBA1005582//Torulopsis glabrata mitochondrial intergenic region ATPase 9 -cytochrome oxidase 2 genes.//2.3e-10:404:62//X02171
R-HEMBA1005583//HS_3014_B1_D05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3014 Col=9 Row=H, genomic survey sequence.//3.0e-81:442:94//AQ154499
R-HEMBA1005588//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//1.8e-54:490:77//Z98046
R-HEMBA1005593//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence.//2.2e-28:262:79//AC005746
R-HEMBA1005595//HS_2224_A2_G03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2224 Col=6 Row=M, genomic survey sequence.//3.6e-48:263:95//AQ033446
R-HEMBA1005606//Human PAC clone DJ0093I03 from Xq23, complete sequence.//2.5e-08:355:63//AC003983
R-HEMBA1005609//HS_2182_B1_H06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=11 Row=P, genomic survey sequence.//2.2e-82:400:99//AQ023130
R-HEMBA1005616//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 124K22, WORKING DRAFT SEQUENCE.//0.80:308:60//AL031176
R-HEMBA1005621//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 330012, WORKING DRAFT SEQUENCE.//7.4e-76:338:98//AL031731
R-HEMBA1005627//Homo sapiens full-length insert cDNA clone ZD53D02.//4.5e-72:398:93//AF086321
R-HEMBA1005631//Homo sapiens PAC clone DJ1086D14, complete sequence.//3.8e-17:548:60//AC004460
R-HEMBA1005632//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//1.4e-13:172:75//AL022069
R-HEMBA1005634//RPCI11-13O15.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-13015, genomic survey sequence.//1.0e-28:153:82//B73293
R-HEMBA1005666//Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs.//4.5e-51:343:87//AL021786
R-HEMBA1005670//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 11703, WORKING DRAFT SEQUENCE.//2.5e-33:288:78//AL020995
R-HEMBA1005679//Human esterase D mRNA, 3'end.//4.2e-49:322:88//M13450
R-HEMBA1005680//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.0e-36:285:83//AC005924
R-HEMBA1005685//H.sapiens (MAR8) chromosome 19 DNA, 343bp.//0.022:65:86//Z35281
R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds.//5.4e-46:376:84//U66406
R-HEMBA1005705//RPCI11-13014.TP RPCI-11 Homo sapiens genomic clone RPCI-11-13O14, genomic survey sequence.//0.071:182:59//B76186
R-HEMBA1005717//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATPSG3) like pseudogene, ESTs and STSs.

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Contains polymorphic CA repeat.//1.0:189:66//Z92545
R-HEMBA1005732//Human Chromosome 11q12 pac pDJ363p2, WORKING DRAFT SEQUENCE, 22 unordered pieces.//2.1e-47:449:75//AC003023
R-HEMBA1005737
R-nnnnnnnnnnnn//H.sapiens DNA for repeat unit locus D18S51 (285 bp).//0.11:174:63//X91255
R-HEMBA1005755//Human DNA-sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//0.15:160:65//AL008634
R-HEMBA1005765//Human Xq28 cosmids U225B5 and U236A12, complete sequence.//5.2e-39:422:74//U71148
R-HEMBA1005780//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//0.037:261:61//AP000010
R-HEMBA1005813//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//1.7e-26:242:80//AL023808
R-HEMBA1005815//Bufo boreas MVZ 145227 c-mos gene, partial cds.//0.17:199:62//U52805
R-HEMBA1005822//Plasmodium falciparum MAL3P7, complete sequence.//0.26:437:56//AL034559
R-HEMBA1005829//Human Cosmid g1572c035, complete sequence.//3.8e-05:366:61//AC000124
R-HEMBA1005834//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//8.2e-107:551:96//AL031781
R-HEMBA1005852//F.rubripes GSS sequence, clone 163A22aA4, genomic survey sequence.//2.6e-17:225:72//AL018730
R-HEMBA1005853//Human Chromosome 15 pac pDJ24m8, complete sequence.//1.1e-27:314:75//AC000379
R-HEMBA1005884//Homo sapiens 12p13.3 BAC RPCI3-488H23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//2.6e-20:328:67//AC006207
R-HEMBA1005891//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//2.0e-102:543:95//AC004945
R-HEMBA1005894
R-HEMBA1005909
R-HEMBA1005911//CIT-HSP-2342E5.TR CIT-HSP Homo sapiens genomic clone 2342E5, genomic survey sequence.//0.0012:315:60//AQ058081
R-HEMBA1005921//P.chrysogenum mitochondrion genes for tRNA-Arg, tRNA-Asn, tRNA-Tyr, small subunit rRNA, and ATPase subunit 6.//0.0090:445:58//Z23072
R-HEMBA1005931//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE.//1.7e-46:351:83//Z98304
R-HEMBA1005934//Homo sapiens chromosome 17, clone hRPK.261_A_13, complete sequence.//0.0052:179:71//AC005138
R-HEMBA1005962//Homo sapiens clone RG012D21, complete sequence.//1.1e-11:149:74//AC005045
R-HEMBA1005963//HS_3055_A1_E08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=15 Row=I, genomic survey sequence.//5.4e-79:403:97//AQ147357
R-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//6.9e-112:580:95//AF082516
R-HEMBA1005991//Human DNA sequence from clone 58A9 on chromosome 1q24.1-24.3. Contains STSs, GSSs, genomic marker D1S210 and a ca repeat polymorphism, complete sequence.//2.6e-39:299:82//AL031285
R-HEMBA1005999//Homo sapiens clone DJ0691F11, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.1e-29:260:70//AC004859
R-HEMBA1006002//Rattus norvegicus s-nexilin mRNA, complete cds.//6.3e-15:174:78//AF056035
R-HEMBA1006005//Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds.//2.6e-112:574:95//AF036405
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0725 protein, partial cds.//7.6e-27:444:67//AB018268
R-HEMBA1006035//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.025:373:60//AC005139
R-HEMBA1006036//Homo sapiens Chromosome 16 BAC clone CIT987SK-625P11, complete sequence.//0.0056:535:59//AC004125
R-HEMBA1006042//HS_2169_A1_B11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2169 Col=21 Row=C, genomic survey sequence.//1.7e-73:390:95//AQ132995
R-nnnnnnnnnnnn
R-HEMBA1006081
R-HEMBA1006090//HS_2262_A2_A01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2262 Col=2 Row=A, genomic survey sequence.//2.1e-70:360:97//AQ216324

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R-HEMBA1006091
R-HEMBA1006100//Homo sapiens DNA sequence from PAC 212G6 on chromosome Xp11.3-p11.4. Contains synapsin 1, brain protein 4.1, properdin, tyrosine kinase (ELK1) oncogene, ESTs, STS, GSS, complete sequence.// 1.6e-36:354:77//AL009172
R-HEMBA1006108
R-HEMBA1006121
R-HEMBA1006124//Human DNA sequence from BAC 175E3 on chromosome 22q11.2-qter. Contains ESTs, STSs and polymorphic CA repeat.//1.3e-12:327:64//Z95113
R-HEMBA1006130//WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.60:326:62//AC005948
R-nnnnnnnnnnnn//Homo sapiens chromosome 19, cosmid F16403, complete sequence.//4.3e-52:321:80// AC005777
R-HEMBA100614211, complete sequence.//1.0e-13:160:78//AC005500
R-HEMBA1006155//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0013:389:60//AC004688
R-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//1.4e-119: 574:98//AF048693
R-HEMBA1006173//Mus musculus protein tyrosine phosphatase STEP61 mRNA, complete cds.//4.1e-43:307:86// U28217
R-HEMBA1006182//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//1.7e-30:300:71// AC004491
R-HEMBA1006198//***ALU WARNING: Human Alu-J subfamily consensus sequence.//1.3e-36:284:85//U14567
R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//2.1e-110:545:97//AF070557
R-HEMBA1006248//Homo sapiens mRNA for KIAA0667 protein, partial cds.//0.46:365:58//AB014567
R-HEMBA1006252//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//2.8e-41:438: 71//U91323
R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds.//1.8e-28:179:91//AF083384
R-HEMBA1006259//RPCI11-44N14.TJ RPCI11 Homo sapiens genomic clone R-44N14, genomic survey sequence.//1.5e-48:348:85//AQ203161
R-HEMBA1006268
R-HEMBA1006272//Human DNA sequence from clone 1198H6 on chromosome 1p36.11-36.31. Contains two Melanoma Preferentially Expressed Antigen PRAME LIKE genes. Contains GSSs and ESTs, complete sequence.// 2.8e-73:273:87//AL023753
R-nnnnnnnnnnn//H.sapiens PAP mRNA.//1.6e-54:585:71//X76770
R-HEMBA1006283//Sequence 7 from patent US 5776683.//9.7e-18:113:98//AR016240
R-HEMBA1006284//Homo sapiens chromosome 17, clone hRPC.1028_K_7, complete sequence.//0.97:447:59// AC004585
R-HEMBA1006291//Homo sapiens full-length insert cDNA clone ZB76B10.//2.9e-94:454:98//AF086161
R-HEMBA1006293//Sequence 8 from patent US 5721351.//8.1e-10:111:72//I89415
R-HEMBA1006309//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//8.6e-37:288:84//AC005412
R-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//6.5e-29:132:81//AF076183
R-HEMBA1006328//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 894K16, WORKING DRAFT SEQUENCE.//3.3e-50:340:75//AL034429
R-HEMBA1006334
R-HEMBA1006344//Rattus norvegicus nitzin mRNA, partial cds.//8.7e-22:259:72//AF087945
R-HEMBA1006347//Human prostasin gene, complete cds.//1.8e-78:170:100//U33446
R-HEMBA1006349//Rat brain calcium channel alpha-1 subunit mRNA, complete cds.//0.00051:120:73//M57682
R-HEMBA1006359//CITBI-E1-2516C16.TR CITBI-E1 Homo sapiens genomic clone 2516C16, genomic survey sequence.//4.7e-74:576:82//AQ277951
R-HEMBA1006364//G.gallus gene for transforming growth factor-beta2, exons 5-7.//2.5e-21:118:85//X59080
R-HEMBA1006377//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//5.7e-68:367:85// AC005239
R-HEMBA1006380//Human BAC clone RG007J15 from 7q31, complete sequence.//6.1e-47:300:83//AC003989
R-HEMBA1006381//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135), complete sequence.//1.5e-47: 336:86//AC005914
R-HEMBA1006398//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence.//1.5e-67:501:83//AC005609

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R-HEMBA1006416//Homo sapiens chromosome 17, clone 347_H_5, complete sequence.//4.4e-37:319:76//AC002119
R-HEMBA1006419//Homo sapiens chromosome 17, clone HCIT542B22, complete sequence.//2.9e-50:502:75//AC004253
R-HEMBA1006421//Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown genes.//4.1e-116:572:97//AF107885
R-HEMBA1006424//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//9.4e-117:578:97//AL031781
R-HEMBA1006426//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 291J10, WORKING DRAFT SEQUENCE.//2.2e-08:353:63//Z93017
R-HEMBA1006438//HS_2008_A1_D04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=7 Row=G, genomic survey sequence.//1.2e-29:194:91//AQ245162
R-HEMBA1006445//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.011:330:60//AC005075
R-HEMBA1006446//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//0.032:256:61//AE001398
R-HEMBA1006461//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//5.6e-35:229:77//AC002364
R-HEMBA1006467//Homo sapiens Chromosome 9p22 Cosmid clone 34a5, complete sequence.//1.1e-14:354:63//AC002052
R-HEMBA1006471
R-HEMBA1006474//p40, p24 [Borna disease virus BDV, WT-1, Hallc B1/91, horse brain, field isolate, Genomic RNA, 1138 nt, segment 1 of 3].//1.1e-14:442:60//S67502
R-HEMBA1006483//Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence.//3.7e-37:290:82//U95742
R-HEMBA1006485//H.sapiens mRNA for aminopeptidase.//7.6e-91:517:91//Y07701
R-HEMBA1006486//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.1e-33:289:81//AC005089
R-HEMBA1006489//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//6.0e-07:485:60//AL020989
R-HEMBA1006492//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.//4.3e-112:572:95//AC005828
R-HEMBA1006494//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence.//2.3e-10:186:67//AC002994
R-HEMBA1006497//RPCI11-16L10.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16L10, genomic survey sequence.//1.5e-10:75:100//B88015
R-HEMBA1006502//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence.//3.3e-36:516:70//Z93929
R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds.//1.2e-115:570:96//AB014566
R-HEMBA1006521//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE.//2.2e-20:266:71//Z98304
R-HEMBA1006530//RPCI11-52M1.TJ RPCI11 Homo sapiens genomic clone R-52M1, genomic survey sequence.//0.00015:227:64//AQ052526
R-HEMBA1006535//HS_2234_B1_B07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2234 Col=13 Row=D, genomic survey sequence.//7.5e-33:191:95//AQ129525
R-HEMBA1006540//Homo sapiens clone GS051M12, complete sequence.//0.026:497:58//AC005007
R-HEMBA1006546//Homo sapiens chromosome 19, cosmid R33496, complete sequence.//5.2e-41:289:86//AC004603
R-HEMBA1006559//Mus musculus PRAJA1 (Praja1) mRNA, complete cds.//3.4e-64:551:78//U06944
R-HEMBA1006562//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//5.7e-09:266:66//AC002554
R-HEMBA1006566//HS_2171_B1_B04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=7 Row=D, genomic survey sequence.//0.012:306:61//AQ125421
R-HEMBA1006569//Ovis aries beta actin mRNA, complete cds.//3.8e-70:529:82//U39357
R-HEMBA1006579//Homo sapiens BAC clone NH0115E20 from Y, complete sequence.//1.0:141:65//AC006032

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R-HEMBA1006583//CIT-HSP-2377M16.TR CIT-HSP Homo sapiens genomic clone 2377M16, genomic survey sequence.//1.7e-31:271:76//AQ111875
R-HEMBA1006595//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.093:270:61//AC004709
R-HEMBA1006597//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.7e-45:371:80//AC005031
R-HEMBA1006612
R-nnnnnnnnnnnn//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 8B22, WORKING DRAFT SEQUENCE.//2.1e-20:229:77//AL031737
R-HEMBA1006624//Human DNA sequence from clone 406A7 on chromosome 6q23-24. Contains three pseudogenes similar to Elongation Factor 1-Alpha (EF-1-ALPHA, Statin S1), 60S Acidic Ribosomal Protein P1 and NADH-Ubiquinone Oxidoreductase 15 kDa subunit, and part of the Microtuble Associated Protein E-MAP-115 gene. Contains ESTs, STSs and GSSs, complete sequence.//4.8e-40:321:83//AL023284
R-HEMBA1006631//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 202O8, WORKING DRAFT SEQUENCE.//1.5e-45:477:77//AL031848
R-HEMBA1006635//***ALU WARNING: Human Alu-Sp subfamily consensus sequence.//8.0e-40:245:91//U14572
R-HEMBA1006639
R-HEMBA1006643
R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds.//2.5e-106:567:94//U40282
R-HEMBA1006652//Human BAC clone RG308B22 from 7q22-q31, complete sequence.//8.7e-54:334:76//AC002089
R-HEMBA1006653//Homo sapiens 7q telomere, complete sequence.//5.0e-36:207:89//AF027390
R-HEMBA1006665//HS_3213_B2_D04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=8 Row=H, genomic survey sequence.//1.2e-21:235:67//AQ175625
R-HEMBA1006674//H.sapiens telomeric DNA sequence, clone 9QTEL023, read 9QTELOO023.seq.//2.6e-32:212:83//Z96776
R-HEMBA1006676//Plasmodium falciparum MAL3P6, complete sequence.//1.9e-10:436:60//Z98551
R-HEMBA1006682//Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds.//6.1e-06:477:59//L40608
R-HEMBA1006695//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//1.8e-30:266:80//AC005096
R-HEMBA1006696
R-HEMBA1006708
R-HEMBA1006709//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 715N11, WORKING DRAFT SEQUENCE.//6.8e-14:139:82//AL031674
R-HEMBA1006717
R-HEMBA1006737//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.//9.9e-18:365:66//AC005828
R-HEMBA1006744//Human Chromosome 16 BAC clone CIT987SK-327O24, complete sequence.//1.3e-37:380:75//AC003108
R-HEMBA1006754//Homo sapiens chromosome 5, P1 clone 962c5 (LBNL H87), complete sequence.//2.1e-75:338:85//AC003951
R-HEMBA1006758//Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.//1.2e-112:579:95//AC005752
R-HEMBA1006767//Plasmodium falciparum MAL3P6, complete sequence.//0.00022:528:58//Z98551
R-HEMBA1006779//Homo sapiens chromosome 17, clone hRPK.628_E_12, complete sequence.//2.3e-46:305:87//AC005701
R-HEMBA10067801/Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//7.2e-39:305:82//AL022323
R-HEMBA1006789//Streptomyces coelicolor cosmid 6G4.//0.0085:449:61//AL031317
R-HEMBA1006795//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//4.1e-43:355:801/AC006120
R-HEMBA1006796//HS_3038_B2_H11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3038 Col=22 Row=P, genomic survey sequence.//0.99:158:63//AQ102483
R-HEMBA1006807//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//8.4e-47:481:75//AC004854
R-HEMBA1006821//Homo sapiens chromosome 17, clone hRPC.62_O_9, complete sequence.//3.0e-08:84:90//AC004797

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R-HEMBA1006824//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//3.7e-54:496:76//Z93023
R-HEMBA1006832//Homo sapiens chromosome 17, clone hRPK.243_K_12, complete sequence.//0.70:206:65//AC005668
R-HEMBA1006849//Homo sapiens 12q24.1 PAC RPCI3-521E19 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.2e-46:281:91//AC004217
R-HEMBA1006865//Mus musculus clone 101 B1 repeat region sequence.//0.61:115:70//AF056074
R-nnnnnnnnnnnn//Mus musculus mRNA for oxysterol-binding protein, complete cds.//3.3e-102:618:87//AB017026
R-HEMBA1006885 4.2e-14:379:63//AG006839
R-HEMBA1006900//CIT-HSP-2006M20.TR CIT-HSP Homo sapiens genomic clone 2006M20, genomic survey sequence.//2.6e-07:230:66//B56395
R-HEMBA1006921//Homo sapiens PAC clone DJ0777O23 from 7p14-p15, complete sequence.//2.1e-68:267:86//AC005154
R-HEMBA1006926
R-HEMBA1006929//HS_3244_A2_C01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=2 Row=E, genomic survey sequence.//6.9e-21:191:83//AQ207500
R-HEMBA1006936
R-HEMBA1006938//Colias philodice eriphyle large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//0.11:309:59//AF044853
R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.//2.0e-75:371:98//AJ010841
R-HEMBA1006949//Homo sapiens PAC clone DJ0777G09 from 7q34-q36, complete sequence.//0.47:240:63//AC005518
R-HEMBA1006973//HS_2009_A2_A12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2009 Col=24 Row=A, genomic survey sequence.//9.6e-05:407:60//AQ232302
R-HEMBA1006976//RPCI11-49L11.TJ RPCI11 Homo sapiens genomic clone R-49L11, genomic survey sequence.//0.0018:184:63//AQ051701
R-HEMBA1006993//Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial cds for thymopoietin beta.//1.9e-47:394:79//U18271
R-HEMBA1006996//CIT-HSP-2172D17.TF CIT-HSP Homo sapiens genomic clone 2172D17, genomic survey sequence.//1.8e-07:365:62//B93406
R-HEMBA1007002//Plasmodium falciparum MAL3P2, complete sequence.//0.0012:505:56//AL034558
R-HEMBA1007017//Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence.//5.6e-41:437:71//AC005277
R-HEMBA1007018//G.gallus mRNA for dynein light chain-A.//8.2e-73:556:80//X79088
R-HEMBA1007045
R-HEMBA1007051//Human DNA sequence from cosmid N69F4 on chromosome 22q11.2-qter contains EST.//9.9e-27:342:71//Z72006
R-HEMBA1007052//Homo sapiens FSHD-associated repeat DNA, proximal region.//5.4e-85:558:87//U85056
R-HEMBA1007062
R-HEMBA1007066
R-HEMBA1007073//Homo sapiens chromosome 17, clone hRPK.421_E_14, complete sequence.//2.0e-66:476:85//AC006141
R-HEMBA1007078//Homo sapiens chromosome 17, clone hRPK.60_A_24, complete sequence.//1.0e-38:179:82//AC005325
R-HEMBA1007085//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.2e-49:551:73//AC006015
R-HEMBA1007087//Human Chromosome 11 pac pDJ392a17, complete sequence.//1.0:261:61//AC000385
R-HEMBA1007112//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 37 unordered pieces.//0.043:295:62//AC004803
R-HEMBA1007113//Homo sapiens (subclone 6_a8 from P1 H16) DNA sequence.//1.4e-52:307:87//L43392
R-HEMBA1007129//Human DNA sequence from PAC 863K19 on chromosome X. Contains STS.//1.2e-08:131:75//Z92547
R-HEMBA1007147//H.sapiens CpG island DNA genomic Mse1 fragment, clone 65f1, reverse read cpg65f1.rt1a.//0.16:187:64//Z62246
R-HEMBA1007149//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//7.6e-108:543:96//AC005239
R-HEMBA1007151//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//0.14:323:58//

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AC004875
R-nnnnnnnnnnnn//Homo sapiens epsin 2a mRNA, complete cds.//5.1e-103:529:94//AF062085
R-HEMBA1007178//Homo sapiens chromosome 12p13.3 clone RPCI11-372B4, WORKING DRAFT SEQUENCE, 129 ordered pieces.//5.4e-106:537:96//AC005911
R-HEMBA1007194//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//4.1e-39:262:80//AC003035
R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds.//5.3e-61:332:95//D86987
R-HEMBA1007206//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//1.9e-50:436:81//Z93023
R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds.//2.3e-96:471:97//AB018340
R-HEMBA1007251//Homo sapiens chromosome 5, PAC clone 247f3 (LBNL H85), complete sequence.//0.011:349:62//AC004777
R-HEMBA1007256//Homo sapiens PAC clone DJ0676L20 from 7q35-q36, complete sequence.//2.8e-10:224:70//AC004856
R-HEMBA1007267//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.4e-53:362:86//AC005924
R-HEMBA1007273
R-HEMBA1007279//Rickettsia prowazekii strain Madrid E, complete genome; segment 4/4.//0.042:454:57//AJ235273
R-HEMBA1007281//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.99:288:60//AJ235272
R-HEMBA1007288//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence.//7.4e-107:554:95//AL031003
R-HEMBA1007300//Caenorhabditis elegans cosmid C48C5.//0.22:474:59//U39994
R-HEMBA1007301
R-HEMBA1007319//Campylobacter jejuni repetitive DNA, clone pINT.//4.9e-08:524:58//Y14425
R-HEMBA1007320//Homo sapiens genomic DNA, chromosome 21q11.1, segment 14/28, WORKING DRAFT SEQUENCE.//3.4e-16:244:71//AP000043
R-HEMBA1007322//Homo sapiens BAC clone RG324D18 from 7p15-p21, complete sequence.//3.9e-83:383:85//AC005251
R-HEMBA1007327//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 7706, WORKING DRAFT SEQUENCE.//1.6e-38:533:71//Z96804
R-HEMBA1007341//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 268D13, WORKING DRAFT SEQUENCE.//3.6e-21:394:66//AL023513
R-HEMBA1007342//Human BAC clone GS368F15 from 7q31, complete sequence.//1.7e-15:190:73//AC003080
R-HEMBA1007347//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone N38G6, WORKING DRAFT SEQUENCE.//2.2e-47:455:77//Z96802
R-HEMBB1000005//Homo sapiens 3p21.1-9 PAC RPCI4-793P23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.1e-62:539:79//AC006208
R-HEMBB1000008//Homo sapiens chromosome 17, clone hCIT.211_P_7, complete sequence.//1.2e-36:285:83//AC003665
R-HEMBB1000018//Homo sapiens clone DJ0038I10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.2e-51:416:79//AC004820
R-HEMBB1000024//Human DNA sequence from BAC 175E3 on chromosome 22q11.2-qter. Contains ESTs, STSs and polymorphic CA repeat.//3.9e-18:211:79//Z95113
R-HEMBB1000025//HS_3064_B2_B07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=14 Row=D, genomic survey sequence.//5.9e-40:254:90//AQ132765
R-HEMBB1000030//Human DNA sequence from clone 108K11 on chromosome 6p21 Contains SRP20 (SR protein family member), Ndr protein kinase gene similar to yeast suppressor protein SRP40, EST and GSS, complete sequence.//1.5e-32:452:70//Z85986
R-HEMBB1000036//CIT-HSP-2024L15.TF CIT-HSP Homo sapiens genomic clone 2024L15, genomic survey sequence.//9.3e-63:541:77//B66264
R-HEMBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//7.6e-91:467:97//AF084928
R-HEMBB1000039//Homo sapiens chromosome 17, clone hRPK.401_O_9, complete sequence.//2.4e-44:456:68//AC005291
R-HEMBB1000044//Human BAC clone RG016J04 from 7q21, complete sequence.//1.4e-54:307:80//AC002064
R-HEMBB1000048//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//3.8e-

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09:330:63//AC002300
R-HEMBB1000050//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.//6.7e-12:225:65//Z94056
R-HEMBB1000054//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence.//8.9e-76:557:82//AL033521
R-HEMBB1000055//Human housekeeping (Q1Z 7F5) gene, exons 2 through 7, complete cds.//1.6e-88:350:86//M81806
R-HEMBB1000059//Homo sapiens clone DJ0850I01, WORKING DRAFT SEQUENCE, 1 unordered pieces.//4.9e-12:356:65//AC006009
R-HEMBB1000083//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.7e-41:311:82//AC004840
R-HEMBB1000089//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.6e-34:314:78//AC005520
R-HEMBB1000099//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a ggtt repeat polymorphism, complete sequence.//8.8e-32:434:71//AL008715
R-HEMBB1000103//Human DNA sequence from BAC 445C9 on chromosome 22q12.1. Contains CRYBB1, beta B1 crystallin, CRYBA4, beta A4 crystallin, high mobility group-1 protein (HMG-1), ESTs.//2.5e-16:207:74//Z95115
R-HEMBB1000113//HS_3013_A1_B08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3013 Col=15 Row=C, genomic survey sequence.//0.94:211:63//AQ118730
R-HEMBB1000119//Homo sapiens ASMTL gene.//1.9e-106:531:96//Y15521
R-HEMBB1000136//Human Chromosome X, complete sequence.//0.00073:359:59//AC002407
R-HEMBB1000141//Homo sapiens chromosome 21q22.3 PAC 39C17, complete sequence.//6.8e-41:280:74//AF043945
R-HEMBB1000144//Homo sapiens chromosome 17, clone hCIT.507_E_2, complete sequence.//0.00083:206:66//AC004134
R-HEMBB1000173//Homo sapiens, WORKING DRAFT SEQUENCE, 97 unordered pieces.//2.5e-82:401:90//AC004085
R-HEMBB1000175
R-HEMBB1000198//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucoronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//0.91:428:56//AL021368
R-HEMBB1000215//Homo sapiens DNA sequence from PAC 69E11 on chromosome 1q23-24. Contains a NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ) LIKE pseudogene, a 60S Ribosomal protein L34 LIKE pseudogene, an unknown gene similar to yeast YPR037W and worm C02C2.6 predicted genes, a predicted CpG island, ESTs and an STS, complete sequence.//4.4e-54:298:91//AL021397
R-HEMBB1000217
R-HEMBB1000218//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.8e-32:517:70//AC004216
R-HEMBB1000226//Human DNA sequence from cosmid COS12 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs, Flanking sequences of 3' alpha globin HVR and CpG island.//2.5e-77:450:92//Z69706
R-HEMBB1000240//Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families.//4.1e-05:310:62//AF029308
R-HEMBB1000244//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1112F19, WORKING DRAFT SEQUENCE.//1.3e-43:278:85//AL034420
R-HEMBB1000250//Human DNA sequence from clone 34B20 on chromosome 6p21.31-22.2. Contains seventeen Histone (pseudo)genes and a 40S Ribosomal protein S10 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.8e-16:484:64//AL031777 R-HEMBB1000258//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//4.3e-11:286:67//U91328
R-HEMBB1000264//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//1.2e-42:406:79//AF079765
R-HEMBB1000266//RPCI11-76C20.TV RPCI11 Homo sapiens genomic clone R-76C20, genomic survey sequence.//1.0:232:59//AQ265533

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R-HEMBB1000272//HS_3032_B1_H06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=11 Row=P, genomic survey sequence.//0.0082:209:62//AQ096702
R-HEMBB1000274//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC Region, complete sequence.//1.6e-45:277:72//AC000053
R-HEMBB1000284//Homo sapiens full-length insert cDNA clone YY88A05.//6.9e-112:572:96//AF088018
R-HEMBB1000307//Homo sapiens chromosome 17, clone hRPK.471_L_13, complete sequence.//5.7e-96:523:93//AC005244
R-HEMBB1000312//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32B1, WORKING DRAFT SEQUENCE.//7.5e-21:218:67//AL023693
R-HEMBB1000317//Toxoplasma gondii chloroplast, complete genome.//0.062:354:58//U87145
R-HEMBB1000318//Human DNA sequence from PAC 292H14 on chromosome Xp21. Contains STS and CA repeat polymorphism.//4.5e-52:302:81//AL008710
R-HEMBB1000335//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence.//1.9e-16:139:84//AC005179
R-HEMBB1000336//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//0.0062:231:64//AJ003147
R-HEMBB1000337//CIT-HSP-2329010.TF CIT-HSP Homo sapiens genomic clone 2329O10, genomic survey sequence.//1.2e-31:192:92//AQ035976
R-HEMBB1000338//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//1.9e-39:477:71//AC004605
R-HEMBB1000339//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE.//4.1e-54:357:76//AL031681
R-HEMBB1000341//Homo sapiens 12q24 PAC RPCI3-424M6 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.8e-19:501:63//AC002350
R-HEMBB1000343//Homo sapiens chromosome 16, cosmid clone 367E12 (LANL), complete sequence.//3.6e-41:457:72//AC004644
R-HEMBB1000354//Human DNA sequence from PAC 560B9 on chromosome 1q24-1q25. Contains profilin-like pseudogene, 60S ribosomal protein L4 pseudogene RNA binding protein, ESTs, GSS.//7.2e-36:325:74//Z98751
R-HEMBB1000369//Homo sapiens chromosome 4 clone B366O24 map 4q25, complete sequence.//9.0e-25:179:79//AC004067
R-HEMBB10003741/Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 75N14, WORKING DRAFT SEQUENCE.//8.4e-58:332:79//Z97199
R-HEMBB1000376//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.1e-47:309:88//D87675
R-HEMBB1000391//Homo sapiens clone RG269P13, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.7e-46:302:85//AC005080
R-HEMBB1000399//Homo sapiens Rad17-like protein (RAD17) mRNA, complete cds.//1.0e-107:531:97//AF076838
R-HEMBB1000402//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//1.1e-25:441:67//Z98052
R-HEMBB1000404//HS_2246_A2_D01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2246 Col=2 Row=G, genomic survey sequence.//0.0025:196:63//AQ084251
R-HEMBB1000420//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC Region, complete sequence.//1.2e-29:358:72//AC000053
R-HEMBB1000434//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//2.8e-51:299:89//AC004069
R-HEMBB1000438//HS_2239_B2_E08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2239 Col=16 Row=J, genomic survey sequence.//1.3e-10:76:100//AQ067700
R-HEMBB1000441//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//4.4e-60:281:90//Z82207
R-HEMBB1000449//Homo sapiens clone DJ0898O18, WORKING DRAFT SEQUENCE, 8 unordered pieces.//4.8e-11:228:68//AC004920
R-HEMBB1000455//Homo sapiens clone GS051M12, complete sequence.//3.1e-14:388:65//AC005007
R-HEMBB1000472//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//4.9e-34:320:79//AC003104
R-HEMBB1000480//Human DNA sequence from Fosmid 65B7 on chromosome 22q11.2-qter. Contains exons 6-12 of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter), complete sequence.//3.4e-36:285:82//Z83849
R-HEMBB1000487

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R-HEMBB1000490//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE.//1.5e-34:281:81//AL034423
R-HEMBB1000491//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//8.5e-37:483:72//Z93023
R-HEMBB1000493//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUCI, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete sequence.//7.6e-14:217:71//AL022721
R-HEMBB1000510//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27K12, WORKING DRAFT SEQUENCE.//7.1e-44:221:80//AL033397
R-HEMBB1000518//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//3.5e-51:280:90//AC002477
R-HEMBB1000523//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//1.7e-53:304:82//AC004079
R-HEMBB1000530//Homo sapiens chromosome 17, clone hCIT.162_E_12, complete sequence.//4.2e-74:428:92//AC006236
R-HEMBB1000550//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//5.6e-13:112:80//U91321
R-HEMBB1000554//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 409J21, WORKING DRAFT SEQUENCE.//5.1e-14:239:63//Z83824
R-HEMBB1000556//Homo sapiens envoplakin (EVPL) mRNA, complete cds.//0.031:275:60//U53786
R-HEMBB1000564//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135), complete sequence.//3.1e-17:227:76//AC005914
R-HEMBB1000573//Borrelia afzelii (strain NT28) DNA, internal transcribed spacer.//0.078:161:63//D84405
R-HEMBB1000575//Homo sapiens chromosome 17, clone hRPC.859_O_20, complete sequence.//7.2e-52:260:80//AC003695
R-HEMBB1000586//Human DNA sequence from cosmid V210E9, between markers DXS366 and DXS87 on chromosome X.//2.0e-33:305:79//Z70280
R-HEMBB1000589//Homo sapiens chromosome 17, clone hRPK.1064_E_11, complete sequence.//1.3e-14:409:65//AC005208
R-HEMBB1000591//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//6.2e-39:493:71//AC005184
R-HEMBB1000592//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.6e-08:254:64//AC005831
R-HEMBB1000598//Homo sapiens chromosome 11 pac pDJ159ol, complete sequence.//3.3e-38:407:76//AC000381
R-HEMBB1000623//CIT-HSP-2374P17.TR CIT-HSP Homo sapiens genomic clone 2374P17, genomic survey sequence.//1.3e-41:212:100//AQ109717
R-HEMBB1000630//Human DNA sequence from clone 413H6 on chromosome 6p22.3-24.3. Contains a hamster Androgen-dependent Expressed Protein like protein gene, ESTs and GSSs, complete sequence.//5.2e-31:319:78//AL022724
R-HEMBB1000631//Sequence 28 from patent US 5708157.//6.8e-20:208:80//I80058
R-HEMBB1000632//Homo sapiens Cosmid C4, WORKING DRAFT SEQUENCE, 1 ordered pieces.//7.4e-47:457:75//AC004176
R-HEMBB1000637//Human BAC clone RG094H21 from 7q21-q22, complete sequence.//2.9e-45:263:87//AC003085
R-HEMBB1000638//Genomic sequence from Human 6, complete sequence.//9.1e-34:375:73//AC002112
R-HEMBB1000643//HS_2242_A2_B07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=14 Row=C, genomic survey sequence.//0.010:239:60//AQ065993
R-HEMBB1000649//Homo sapiens RBP56/hTAFII68 gene, exon 7.//8.3e-63:306:100//AB010061
R-HEMBB1000652//Human DNA sequence from PAC 467D16 on chromosome 6p22.3-24.1. Contains the 3' part of the SCA1 (ataxin-1) gene with a poly-glutamine (CAG repeat) polymorphism, the 3' part of the GMPR (GMP reductase, Guanosine 5'-monophosphate oxidoreductase) gene, ESTs and an STS with a polymorphic CA repeat.//3.3e-14:450:64//AL009031
R-HEMBB1000665//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXA21, complete sequence.//0.98:251:63//AB005247
R-HEMBB1000671//Human DNA sequence from PAC 106C24, between markers DXS294 and DXS730 on chro-

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mosome X.//6.8e-58:296:85//Z83313
R-HEMBB1000673//CITBI-E1-2506F20.TR CITBI-E1 Homo sapiens genomic clone 2506F20, genomic survey sequence.//0.98:71:76//AQ264731
R-HEMBB1000684//Human DNA sequence from clone 1158E12 on chromosome Xp11.23-11.4 Contains EST, STS, GSS, CpG island, complete sequence.//2.6e-11:153:77//AL031584
R-nnnnnnnnnnnn//Homo sapiens neuroan1 mRNA, complete cds.//2.0e-50:287:93//AF040723
R-HEMBB1000705//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//3.4e-18:340:65//AC005943
R-HEMBB1000706//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 462C17, WORKING DRAFT SEQUENCE.//4.7e-10:358:64//AL033380
R-HEMBB1000709//RPCI11-79A8.TV RPCI11 Homo sapiens genomic clone R-79A8, genomic survey sequence.//1.4e-40:262:89//AQ282374
R-HEMBB1000725//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGN6, complete sequence.//0.00018:386:60//AB017066
R-HEMBB1000726//Homo sapiens PAC clone DJ1185I07 from 7q11.23-q21, complete sequence.//1.5e-48:316:88//AC004990
R-HEMBB1000738//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//7.1e-53:382:85//AC004875
R-HEMBB1000749//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.5e-51:438:80//AC005069
R-HEMBB1000763//Plasmid Col Ib-P9 (from E.coli K12) colicin Ib promoter region and 5' coding region.//1.0:115:63//K02071
R-HEMBB1000770//Human Rhesus blood group antigen (RHCE) gene, intron 6, partial sequence.//5.6e-24:183:86//U83205
R-HEMBB1000781//Homo sapiens Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.//0.00054:154:67//AC003046
R-HEMBB1000789//RPCI11-2I14.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-2I14, genomic survey sequence.//3.0e-09:299:64//B63628
R-HEMBB1000790//Human Chromosome 16 BAC clone CIT987SK-A-362G6, complete sequence.//4.5e-46:185:85//U95740
R-HEMBB1000794//HS_3253_A1_G06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3253 Col=11 Row=M, genomic survey sequence.//5.7e-13:172:65//AQ216291
R-HEMBB1000807
R-HEMBB1000810//Human BAC clone RG114A06 from 7q31, complete sequence.//1.3e-24:385:71//AC002542
R-HEMBB1000821
R-HEMBB1000822//CITBI-E1-2517E13.TF CITBI-E1 Homo sapiens genomic clone 2517E13, genomic survey sequence.//4.5e-08:278:64//AQ279944
R-HEMBB1000826//Homo sapiens genomic DNA, chromosome 21q11.1, segment 14/28, WORKING DRAFT SEQUENCE.//1.2e-44:521:72//AP000043
R-HEMBB1000827//Homo sapiens clone DJ0981O07, complete sequence.//6.8e-43:319:84//AC006017
R-HEMBB1000831//HS_3247_B2_A09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3247 Col=18 Row=B, genomic survey sequence.//5.5e-74:381:96//AQ223850
R-HEMBB1000835//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucoronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//4.2e-17:167:80//AL021368
R-HEMBB1000840//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.9e-26:220:73//AC005283
R-HEMBB1000848//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//7.8e-39:356:79//AC004086
R-HEMBB1000852//HS_3075_A2_B07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=14 Row=C, genomic survey sequence.//3.4e-11:151:75//AQ138816
R-HEMBB1000870//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 72E17, WORKING DRAFT SEQUENCE.//1.8e-44:454:75//AL033523
R-HEMBB1000876//Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin Gene, part of cytochrome C oxidase gene, EST, CpG island, complete sequence.//0.0016:227:65//AL024474
R-HEMBB1000883//Homo sapiens chromosome 19, cosmid F19678, complete sequence.//0.62:238:62//

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AC005621
R-HEMBB1000887//Synthetic human/adenovirus type 5 recombination junction.//9.9e-24:275:76//M34061
R-HEMBB1000888//CIT-HSP-2282A13.TR CIT-HSP Homo sapiens genomic clone 2282A13, genomic survey sequence.//2.4e-05:310:60//AQ000826
R-HEMBB1000890//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.//6.5e-44:305:84//AC005995
R-HEMBB1000893//Homo sapiens BAC clone RG363E19 from 7q31.1, complete sequence.//3.7e-30:265:80//AC004492
R-HEMBB1000908//RPCI11-13P12.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13P12, genomic survey sequence.//0.98:183:61//B76199
R-HEMBB1000910//Homo sapiens Chromosome 22q11.2 Cosmid Clone 50d10 In IGLC Region, complete sequence.//1.7e-28:302:76//AC000024
R-HEMBB1000913//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//4.1e-34:314:76//AC003037
R-HEMBB1000915//Human chromosome 16p11.2-p12 BAC clone CIT987SK-224D6 complete sequence.//6.3e-09:536:59//U95739
R-HEMBB1000917//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1691S, WORKING DRAFT SEQUENCE.//1.6e-47:234:86//Z93015
R-HEMBB1000927
R-HEMBB1000947//CIT-HSP-2287M13.TF CIT-HSP Homo sapiens genomic clone 2287M13, genomic survey sequence.//0.090:115:69//B99228
R-HEMBB1000959//Homo sapiens chromosome 17, clone HRPC905N1, complete sequence.//5.7e-89:544:90//AC003098
R-HEMBB1000973//Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence.//0.038:377:58//AC005560
R-HEMBB1000975//Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence.//1.0e-05:342:62//AC006234
R-HEMBB1000981//CIT-HSP-2386J13.TF.1 CIT-HSP Homo sapiens genomic clone 2386J13, genomic survey sequence.//1.1e-18:231:74//AQ239443
R-HEMBB1000985//HS_3184_A1_D12_T7 CIT Approved Human Genomic Sperm Library D. Homo sapiens genomic clone Plate=3184 Col=23 Row=G, genomic survey sequence.//6.3e-52:286:95//AQ150008
R-HEMBB1000991
R-HEMBB1000996//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//1.4e-42:343:81//AC002368
R-HEMBB1001004
R-HEMBB1001008//CITBI-E1-2504L23.TF CITBI-E1 Homo sapiens genomic clone 2504L23, genomic survey sequence.//3.1e-57:317:94//AQ262056
R-HEMBB1001011//HS_3017_B1_G03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3017 Col=5 Row=N, genomic survey sequence.//7.3e-34:237:86//AQ101944
R-HEMBB1001014//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE.//2.4e-49:417:80//AL031662
R-HEMBB1001020//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence.//7.6e-41:303:76//AC002549
R-HEMBB1001024//Homo sapiens (subclone 2_g5 from P1 H16) DNA sequence.//7.4e-48:341:85//L48475
R-HEMBB1001037//Homo sapiens 22q11 BAC Clone 489d1 In MDR Region, complete sequence.//2.0e-50:416:82//AC005527
R-HEMBB1001047//Homo sapiens chromosome 19, cosmid R31973, complete sequence.//8.4e-22:288:71//AC004699
R-HEMBB1001051//H.sapiens mRNA for FAN protein.//7.1e-18:114:98//X96586
R-HEMBB1001056//Homo sapiens clone DJ0953A04, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.1e-94:520:93//AC006014
R-HEMBB1001058//Homo sapiens clone UWGC:y17c131 from 6p21, complete sequence.//1.1e-56:242:82//AC004187
R-HEMBB1001060//Human Tigger1 transposable element, complete consensus sequence.//4.2e-66:323:81//U49973
R-HEMBB1001063//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 523G1, WORKING DRAFT SEQUENCE.//4.0e-114:556:98//AL034375
R-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.8e-105:512:97//AF034803

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R-HEMBB1001096//Human DNA sequence from PAC 246O8, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//2.4e-13:225:69//Z76735
R-HEMBB1001102//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.4e-35:295:80//AL022577
R-HEMBB1001105//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 462O23, WORKING DRAFT SEQUENCE.//7.9e-46:380:80//AL031431
R-HEMBB1001114//Homo sapiens DNA sequence from PAC 119E23 on chromosome Xq25-q27.1. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2),5'UTR. ESTs, STS.//1.1e-38:306:84//Z99570
R-HEMBB1001117//RPCI11-35I8.TK RPCI-11 Homo sapiens genomic clone RPCI-11-35I8, genomic survey sequence.//1.5e-08:67:100//AQ047113
R-HEMBB1001119//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//9.0e-26:481:67//AC003071
R-HEMBB1001126//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.045:127:69//Z99495
R-HEMBB1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subunit mRNA, complete cds.//5.0e-23:285:73//M25077
R-HEMBB1001137//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-09, complete sequence.//2.5e-07:334:62//AL010222
R-HEMBB1001142//Human BAC clone RG164L14 from 7q21-q22, complete sequence.//2.5e-46:412:79//AC002564
R-HEMBB1001151//Mus musculus IFN alpha-treated embryonic fibroblast mRNA.//1.8e-11:148:77//U51904
R-HEMBB1001153//RPCI11-10L7.TP RPCI-11 Homo sapiens genomic clone RPCI-11-10L7, genomic survey sequence.//2.3e-34:213:82//B71766
R-HEMBB1001169//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence.//0.040:465:56//AC003070
R-nnnnnnnnnnnn//Sequence 1 from patent US 5618695.//2.8e-15:176:80//I40055
R-HEMBB1001177
R-HEMBB1001182//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-52, complete sequence.//1.9e-05:174:70//AL010226
R-HEMBB1001199
R-HEMBB1001208
R-HEMBB1001209//RPCI11-41E13.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41E13, genomic survey sequence.//1.1e-95:473:97//AQ029098
R-HEMBB1001210//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence.//6.2e-08:412:61//AC005199
R-HEMBB1001218//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13L8, genomic survey sequence.//1.0e-46:498:74//B75158
R-HEMBB1001221//RPCI11-62024.TJ RPCI11 Homo sapiens genomic clone R-62024, genomic survey sequence.//3.2e-09:215:68//AQ200950
R-HEMBB1001234
R-HEMBB1001242
R-HEMBB1001249//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.4e-33:361:72//AC005377
R-HEMBB1001253//Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence.//3.8e-105:517:98//AF042089
R-HEMBB1001254//Methanococcus jannaschii section 3 of 150 of the complete genome.//0.96:203:61//U67461
R-HEMBB1001267//Human DNA sequence from clone 14O9 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//2.8e-39:320:80//Z98046
R-HEMBB1001271//Homo sapiens chromosome 17, clone hRPK.349_A_8, complete sequence.//3.9e-47:494:75//AC005544
R-HEMBB1001282//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 184J9, WORKING DRAFT SEQUENCE.//0.0011:97:79//AL031428
R-HEMBB1001288
R-HEMBB1001289//Homo sapiens chromosome 5, BAC clone 343g16 (LBNL H180), complete sequence.//2.0e-

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31:301:78//AC005601
R-HEMBB1001294//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.//0.053:283:60//AC003083
R-HEMBB1001302
R-HEMBB1001304//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27K12, WORKING DRAFT SEQUENCE.//6.3e-15:396:64//AL033397
R-HEMBB1001314//Homo sapiens genomic DNA, 21q region, clone: f30F8SpN6, genomic survey sequence.//3.4e-42:293:86//AG013777
R-HEMBB1001315//Human NFE genomic fragment.//7.5e-30:243:78//M98511
R-HEMBB1001317//Homo sapiens chromosome 17, clone hRPC.1028_K_7, complete sequence.//2.3e-39:301:82//AC004585
R-HEMBB1001326//HS_3054_A1_F12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=23 Row=K, genomic survey sequence.//0.90:117:63//AQ106096
R-HEMBB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//0.037:103:77//D63850
R-HEMBB1001335//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//9.1e-19:229:77//AC003037
R-HEMBB1001337
R-HEMBB1001339//Homo sapiens FSHD-associated repeat DNA, proximal region.//2.9e-45:551:72//U85056
R-HEMBB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//2.7e-59:292:99//AF097441
R-HEMBB1001348//Homo sapiens clone DJ0691F11, WORKING DRAFT SEQUENCE, 11 unordered pieces.//9.1e-41:326:82//AC004859
R-HEMBB1001356//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//1.8e-11:213:67//Z82207
R-HEMBB1001364//HS_3050_A2_F05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=10 Row=K, genomic survey sequence.//1.8e-21:158:91//AQ133940
R-HEMBB1001366//Homo sapiens chromosome 10 clone CIT987SK-1188I5 map 10p11.2-10p12.1, complete sequence.//4.1e-37:419:73//AC005876
R-HEMBB1001367//Human Chromosome 16 BAC clone CIT987SK-A-234F9, complete sequence.//9.5e-15:201:75//U91326
R-HEMBB1001369//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 477J10, WORKING DRAFT SEQUENCE.//1.8e-28:224:83//AL021686
R-HEMBB1001380//HS_2267_B1_F11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2267 Col=21 Row=L, genomic survey sequence.//4.0e-14:100:95//AQ084896
R-HEMBB1001384//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//9.6e-55:312:81//AF071314
R-HEMBB1001387//Homo sapiens chromosome 9, P1 clone 8660 (LBNL H105), complete sequence.//1.0:166:63//AC003953
R-HEMBB1001394//Homo sapiens chromosome 17, clone hRPK.215_E_13, complete sequence.//1.4e-55:494:76//AC005549
R-HEMBB1001410//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence.//0.011:208:63//AC006204
R-HEMBB1001424//Homo sapiens, WORKING DRAFT SEQUENCE, 76 unordered pieces.//1.5e-22:325:69//AC002370
R-HEMBB1001426//Homo sapiens 12q24 PAC RPCI3-424M6 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-46:328:84//AC002350
R-HEMBB1001429//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0481P14; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//6.6e-105:550:95//AC006160
R-HEMBB1001436
R-HEMBB1001443//HS_2228_A1_B05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=9 Row=C, genomic survey sequence.//0.37:173:62//AQ066934
R-HEMBB1001449//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.7e-23:339:69//AC005522
R-HEMBB1001454//Homo sapiens chromosome 5, P1 clone 1307e8 (LBNL H60), complete sequence.//1.1e-39:299:84//AC005355
R-HEMBB1001458//Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence.//6.0e-05:486:59//AE001430

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R-HEMBB1001463//Homo sapiens PAC clone DJ0777O23 from 7p14-p15, complete sequence.//1.2e-50:317:89//AC005154
R-HEMBB1001464//CIT-HSP-2370C10.TF CIT-HSP Homo sapiens genomic clone 2370C10, genomic survey sequence.//0.20:95:71//AQ107941
R-HEMBB1001482//Mus musculus clone OST20235, genomic survey sequence.//4.3e-09:192:70//AF046762
R-HEMBB1001500//Human DNA sequence from PAC 465G10 on chromosome X contains Menkes Disease (ATP7A) putative Cu^{++}-transporting P-type ATPase exons 2 to 21, PGAM-B, ESTs.//1.9e-21:253:70//Z94801
R-HEMBB1001521//Mus musculus clone OST1209, genomic survey sequence.//7.5e-30:332:75//AF046642
R-HEMBB1001527//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//9.5e-55:483:76//AC005000
R-HEMBB1001531//Human BAC clone 7E17 from 12q, complete sequence.//1.3e-08:159:71//AC002070
R-HEMBB1001535//Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-qter contains STS.//4.0e-30:286:79//Z74581
R-HEMBB1001536//Homo sapiens cosmid clone LUCA16 from 3p21.3, complete sequence.//1.6e-39:342:80//U73169
R-HEMBB1001537//Genomic sequence from Human 9q34, complete sequence.//3.7e-41:361:77//AC000394
R-HEMBB1001555//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-485G10, complete sequence.//0.34:212:61//AC003049
R-HEMBB1001562//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-328A3, complete sequence.//8.0e-40:267:88//AC002301
R-HEMBB1001564//Homo sapiens clone DJ0414A15, WORKING DRAFT SEQUENCE, 9 unordered pieces.//5.1e-30:286:76//AC005225
R-HEMBB1001565//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//2.5e-15:194:75//AC004840
R-HEMBB1001585//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//2.6e-33:234:79//AL031677
R-HEMBB1001586//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//2.7e-30:371:74//AC005236
R-HEMBB1001588//Homo sapiens Xp22 GS-524I1 (Genome Systems Human BAC library), complete sequence.//8.0e-32:323:73//AC003106
R-HEMBB1001603//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-59, complete sequence.//0.034:302:59//AL010235
R-HEMBB1001618//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and OpG island.//7.1e-31:503:68//Z93023
R-HEMBB1001619//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//3.7e-50:539:72//AC002368
R-HEMBB1001630//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//1.3e-27:228:82//Z86062
R-HEMBB1001635//Homo Sapiens Chromosome X clone bWXD90, complete sequence.//1.5e-23:407:69//AC004075
R-HEMBB1001637//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//3.9e-54:519:74//AC002368
R-HEMBB1001641//Human DNA sequence from clone 133H11 on chromosome 6p24. Contains STSs, GSSs and genomic marker D6S410, complete sequence.//1.9e-08:464:60//AL024506
R-HEMBB1001653//Homo sapiens chromosome 17, clone HCIT3L16, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.8e-39:318:82//AC002344
R-HEMBB1001665//***ALU WARNING: Human Alu-Sp subfamily consensus sequence.//3.8e-47:283:90//U14572
R-HEMBB1001668
R-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//1.8e-115:573:97//AB014546
R-HEMBB1001684//Sequence 1 from patent US 5700927.//1.9e-40:343:77//I86429
R-HEMBB1001685//Homo sapiens chromosome 17, clone hRPK.721_K_1, complete sequence.//2.6e-43:31:83//AC005411
R-HEMBB1001695
R-HEMBB1001704//CIT-HSP-2324C15.TR CIT-HSP Homo sapiens genomic clone 2324C15, genomic survey sequence.//0.0074:259:58//AQ028704
R-HEMBB1001706//Homo sapiens clone DJ0665P05, WORKING DRAFT SEQUENCE, 5 unordered pieces.//9.1e-34:296:80//AC004851

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R-HEMBB1001707//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//7.7e-32:241:76//AC004020
R-HEMBB1001717//CIT-HSP-2378C19.TF CIT-HSP Homo sapiens genomic clone 2378C19, genomic survey sequence.//4.8e-35:228:89//AQ108992
R-HEMBB1001735//Homo sapiens chromosome 5, BAC clone 114k9 (LBNL H94), complete sequence.//1.8e-10:80:90//AC005613
R-HEMBB1001736//CIT-HSP-2369K6.TF CIT-HSP Homo sapiens genomic clone 2369K6, genomic survey sequence.//9.9e-38:242:90//AQ075221
R-HEMBB1001747//Homo sapiens cosmids Qc14E2, Qc12H12, Qc11F9, Qc10G9, LA1733 and Qc17B8 from Xq28, complete sequence.//3.3e-60:366:80//U82671
R-HEMBB1001749//Homo sapiens chromosome 17, clone hRPK.259_G_18, complete sequence.//1.4e-60:242:92//AC005829
R-HEMBB1001753//RPCI11-59J22.TK RPCI11 Homo sapiens genomic clone R-59J22, genomic survey sequence.//6.2e-08:281:64//AQ200046
R-HEMBB1001756//Homo sapiens BAC clone RG293F17 from 7p15-p21, complete sequence.//3.1e-18:395:67//AC004130
R-HEMBB1001760//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//9.9e-18:416:64//AP000050
R-HEMBB1001762//Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-like (NG10), hypothetical protein (NG8), and butyrophilin-like (NG11) genes, partial cds; NG12 pseudogene, partial sequence; and hypothetical butyrophilin-like protein (NG13) gene, partial cds.//0.21:521:57//AF050157
R-HEMBB1001785//Torulopsis glabrata mitochondrial intergenic region ATPase 6 -ATPase 9 genes.//0.00073:189:65//X02170
R-HEMBB1001797//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0049:322:62//AC005140
R-HEMBB1001802//Human desmin gene, complete cds.//8.1e-95:510:93//M63391
R-HEMBB1001812//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 356B8, WORKING DRAFT SEQUENCE.//1.3e-71:368:96//Z98882
R-HEMBB1001816//Homo sapiens chromosome 21 PAC LLNLP704G1150Q13.//8.4e-21:164:76//AJ006996
R-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//1.7e-104:498:98//AF056209
R-HEMBB1001836//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.2e-44:388:71//AC005328
R-HEMBB1001839
R-HEMBB1001850//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence.//0.00093:488:60//AB005241
R-HEMBB1001863//Human poly(ADP-ribose) polymerase gene, 5' end.//1.2e-16:458:65//M60436
R-HEMBB1001867//Human DNA sequence from cosmid U25D11, between markers DXS366 and DXS87 on chromosome X.//5.0e-31:399:74//Z68327
R-HEMBB1001868//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence.//0.26:303:59//AB020754
R-HEMBB1001869//Homo sapiens chromosome 17, clone hCIT529I10, complete sequence.//7.0e-37:285:85//AC002553
R-HEMBB1001872//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y44F5, WORKING DRAFT SEQUENCE.//0.093:367:58//AL009027
R-HEMBB1001874
R-HEMBB1001875//Lactococcus lactis DPC3147 plasmid pMRC01, complete plasmid sequence.//0.037:406:60//AE001272
R-HEMBB1001880//Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence.//1.3e-49:461:77//AC005922
R-HEMBB1001899//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y116A8, WORKING DRAFT SEQUENCE.//0.56:295:60//Z98858
R-HEMBB1001905//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//1.9e-28:181:75//AL022345
R-HEMBB1001906
R-HEMBB1001908//Genomic sequence from Human 17, complete sequence.//2.9e-36:274:76//AC001231

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R-HEMBB1001910//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence.//3.5e-41:408:76//AC003070
R-HEMBB1001911//Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRAFT SEQUENCE.//6.1e-64:310:89//AJ011929
R-HEMBB1001915//Mouse mRNA for arylhydrocarbon receptor, complete cds.//2.0e-20:220:78//D38417
R-HEMBB1001921//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1141E15, WORKING DRAFT SEQUENCE.//1.9e-47:410:80//AL034422
R-HEMBB1001922//Homo sapiens chromosome 17, clone HCIT421K24, complete sequence.//6.2e-32:378:74//AC004099
R-HEMBB1001925//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//8.2e-41:304:84//AC000406
R-HEMBB1001930//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 10/11.//8.3e-12:202:69//AB020867
R-HEMBB1001944//P.falciparum gene for beta subunit RNA polymerase.//0.00090:264:62//X75544
R-HEMBB1001945//Swietenia humilis DNA for simple tandem repeat (242bp).//0.056:224:62//AJ000408
R-HEMBB1001947//RPCI11-60L13.TJ RPCI11 Homo sapiens genomic clone R-60L13, genomic survey sequence.//7.4e-23:146:94//AQ202335
R-HEMBB1001950//Human DNA sequence from clone 415G2 on chromosome 22 Contains synapsin IIIa exon 1, EST and GSS, complete sequence.//0.57:115:68//Z83846
R-HEMBB1001952//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.6e-36:283:84//AC004676
R-HEMBB1001953//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.9e-60:334:82//AC005037
R-HEMBB1001957//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.9e-56:518:77//AC005077
R-HEMBB1001962//Homo sapiens chromosome 16, BAC clone 462G18 (LANL), complete sequence.//3.2e-19:157:86//AC005736
R-HEMBB1001967//Homo sapiens DNA for amyloid precursor protein, complete cds.//5.7e-68:314:89//D87675
R-HEMBB1001973//Homo sapiens *** SEQUENCING IN PROGRESS *** from PAC E7.1 / cosmid 40M1, WORKING DRAFT SEQUENCE.//1.4e-37:484:70//AJ009617
R-HEMBBI001983//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 215D11, WORKING DRAFT SEQUENCE.//2.1e-28:286:75//AL034417
R-HEMBB1001988//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1112F19, WORKING DRAFT SEQUENCE.//6.9e-29:203:88//AL034420
R-HEMBB1001990//Homo sapiens full-length insert cDNA clone ZC33G03.//7.8e-95:456:99//AF086192
R-HEMBB1001996
R-HEMBB1001997//Homo sapiens clone RG050N15, WORKING DRAFT SEQUENCE, 26 unordered pieces.//6.4e-26:162:83//AC005055
R-HEMBB1002002//Human DNA sequence from PAC 2A2 on chromosome X contains ESTs.//8.2e-83:362:93//Z84816
R-HEMBB1002005//Homo sapiens chromosome 3p clone RPCI5-1034C16, WORKING DRAFT SEQUENCE, 45 unordered pieces.//8.5e-36:291:83//AC005903
R-HEMBB1002009//Homo sapiens clone DJ0828F13, complete sequence.//5.6e-08:307:65//AC004904
R-HEMBB1002015//HS-1039-A1-C10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 821 Col=19 Row=E, genomic survey sequence.//1.9e-05:375:62//B36336
R-HEMBB1002042//CIT-HSP-2313E13.TF CIT-HSP Homo sapiens genomic clone 2313E13, genomic survey sequence.//0.34:241:62//AQ028389
R-HEMBB1002043//Homo sapiens chromosome 21, P1 clone LBL#8 (LBNL H8), complete sequence.//7.4e-35:297:82//AC005612
R-HEMBB1002044//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//5.8e-96:582:90//AC005740
R-HEMBB1002045//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//4.7e-63:575:77//AC005778
R-HEMBB1002049//Human Chromosome X clone bWXD187, complete sequence.1/1.9e-21:384:64//AC004383
R-HEMBB1002050//Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence.//2.5e-37:368:76//AC005553
R-HEMBB1002068//Homo sapiens chromosome 5, BAC clone 205e20 (LBNL H170), complete sequence.//0.30:167:65//AC004782

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R-HEMBB1002069//Homo sapiens chromosome 19, cosmid R33516, complete sequence.//2.3e-73:449:84//AC004799
R-HEMBB1002092//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.//3.8e-45:307:87//AC005828
R-HEMBB1002094//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//3.1e-47:457:76//AC005943
R-HEMBB1002115//HS_2223_B1_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2223 Col=19 Row=N, genomic survey sequence.//3.0e-58:295:98//AQ152279
R-HEMBB1002139//***ALU WARNING: Human Alu-Sq subfamily consensus sequence.//6.6e-49:283:93//U14573
R-HEMBB1002142//Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.1e-45:451:76//AC006006
R-HEMBB1002152//Homo sapiens chromosome 10 clone CIT987SK-1079E16 map 10q25, complete sequence.//1.3e-57:359:81//AC005881
R-HEMBB1002189//Human Chromosome 11 pac pDJ392a17, complete sequence.//4.5e-43:420:77//AC000385
R-HEMBB1002190//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//8.2e-33:340:64//AC004913
R-HEMBB1002193//Sequence 5 from patent US 5709858.//3.2e-23:154:92//I80846
R-HEMBB1002217//Homo sapiens clone HS19.2 Alu-Ya5 sequence.//2.6e-52:415:81//AF015148
R-HEMBB1002218//, complete sequence.//3.4e-17:178:82//AC005300
R-HEMBB1002232//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0052I22; HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-55:292:88//AC004599
R-HEMBB1002247//Homo sapiens chromosome 17, clone hRPK.259_G_18, complete sequence.//2.9e-13:227:70//AC005829
R-HEMBB1002249//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 455J7, WORKING DRAFT SEQUENCE.//1.1e-06:284:64//AL031733
R-HEMBB1002254//Human Chromosome X, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.3e-104:593:91//AC002415
R-HEMBB1002255//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 292E10, WORKING DRAFT SEQUENCE.//2.1e-40:284:85//Z93930
R-HEMBB1002266//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-10, complete sequence.//1.3e-09:371:63//AL010216
R-HEMBB1002280//Homo sapiens PAC clone DJ0545C24 from 7q21-q22, complete sequence.//1.3e-39:247:86//AC004534
R-HEMBB1002300//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//4.1e-84:549:86//U73642
R-HEMBB1002306//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence.//2.5e-10:164:71//AC004129
R-HEMBB1002327//Homo sapiens BAC clone GS539F22 from 7p12-p14, complete sequence.//0.39:365:59//AC005028
R-HEMBB1002329//HS-1049-B1-D05-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 771 Col=9 Row=H, genomic survey sequence.//0.96:180:58//B39313
R-HEMBB1002340//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence.//7.9e-17:258:73//AC004849
R-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.//6.9e-96:479:97//AJ010841
R-HEMBB1002358//Human Xp22 BAC CT-285I15 (from CalTech/Research Genetics) , PAC RPCI1-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//2.3e-53:309:83//AC002366
R-HEMBB1002359//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.9e-27:350:74//AC005038
R-HEMBB1002364//Homo sapiens Xp22 PAC RPCI1-108M6 (Roswell Park Cancer Center PAC library) complete sequence.//8.6e-53:302:79//AC003036
R-HEMBB1002371//Human gene for catalase (EC 1.11.1.6) exon 11 mapping to chromosome 11, band p13.//3.2e-38:199:100//X04094
R-HEMBB1002381//Homo sapiens (JH8) mRNA, partial cds.//3.2e-07:120:78//AF072467
R-HEMBB1002383//Human DNA sequence from cosmid U19H10 on chromosome X. Contains ESTs and CA repeat.//0.98:351:58//AL021182
R-HEMBB1002387//HS-1052-B2-G10-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 774 Col=20 Row=N, genomic survey sequence.//2.0e-07:276:67//B41091
R-HEMBB1002415//Homo sapiens chromosome 17, clone hRPK.209_D_14, complete sequence.//1.4e-25:202:

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79//AC005730
R-HEMBB1002425//Homo sapiens chromosome 19, cosmid R33516, complete sequence.//3.6e-60:401:87//AC004799
R-HEMBB1002442//Homo sapiens clone UWGC:r9a from 6p21, complete sequence.//3.1e-51:358:81//AC006046
R-HEMBB1002453//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 86D1, WORKING DRAFT SEQUENCE.//1.4e-115:557:98//AL034349
R-HEMBB1002457//Human DNA sequence from clone 364I22 on chromosome Xq21.31-22.3. Contains an STS and GSSs, complete sequence.//6.3e-37:338:80//AL031012
R-HEMBB1002458//Homo sapiens T-cell receptor alpha delta locus from bases 250472 to 501670 (section 2 of 5) of the Complete Nucleotide Sequence.//9.7e-09:314:64//AE000659
R-HEMBB1002477//Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSAII project).//0.42:110:74//AL021635
R-HEMBB1002489//Salvelinus fontinalis microsatellite sequence SFO-12.//6.6e-06:167:71//U50302
R-HEMBB1002492//RPCI11-74F21.TK RPCI11 Homo sapiens genomic clone R-74F21, genomic survey sequence.//3.1e-14:410:63//AQ238960
R-HEMBB1002495//HS_3220_A2_F07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220 Col=14 Row=K, genomic survey sequence.//1.3e-24:137:100//AQ180762
R-HEMBB1002502//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//9.6e-81:538:86//AC006120
R-HEMBB1002509//Human DNA sequence from clone 581F12 on chromosome Xq21. Contains Eukaryotic Translation Initiation Factor EIF3 P35 Subunit and 60S Ribosomal protein L22 pseudogenes. Contains ESTs, complete sequence.//0.0061:482:57//AL031313
R-HEMBB1002510//HS_2179_A1_F03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=5 Row=K, genomic survey sequence.//6.9e-35:423:72//AQ298309
R-HEMBB1002520//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27K12, WORKING DRAFT SEQUENCE.//2.0e-62:201:85//AL033397
R-HEMBB1002522//Homo sapiens chromosome 5, Pac clone 61c2 (LBNL H139), complete sequence.//0.99:323:58//AC004225
R-HEMBB1002531
R-HEMBB1002534//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 2/15, WORKING DRAFT SEQUENCE.//1.0e-61:380:79//AP000009
R-HEMBB1002545//RPCI11-2F3.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-2F3, genomic survey sequence.//3.5e-12:414:63//B63283
R-HEMBB1002550
R-HEMBB1002556//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0481P14; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.6e-62:299:85//AC006160
R-HEMBB1002579//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1141E15, WORKING DRAFT SEQUENCE.//1.7e-42:286:88//AL034422
R-HEMBB1002582//Homo sapiens clone DJ1119N05, complete sequence.//3.0e-14:426:60//AC004968
R-HEMBB1002590//Homo sapiens clone RG132J19, complete sequence.//1.1e-30:392:74//AC005163
R-HEMBB1002596//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 508I15, WORKING DRAFT SEQUENCE.//8.5e-44:335:83//AL021707
R-HEMBB1002600//Homo sapiens 12p13.3 PAC RPCI5-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.0e-105:470:96//AC005865
R-HEMBB1002601//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//1.3e-44:445:77//AC004223
R-HEMBB1002603//Homo sapiens clone UWGC:y23c049 from 6p21, complete sequence.//7.0e-40:321:82//AC006162
R-HEMBB1002607//CIT-HSP-2347D7.TF CIT-HSP Homo sapiens genomic clone 2347D7, genomic survey sequence.//1.1e-44:234:98//AQ060197
R-HEMBB1002610//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//7.0e-22:455:65//U91321
R-HEMBB1002613//Homo sapiens 12p13.3 BAC RPCI11-476M19 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//3.0e-72:302:85//AC005908
R-HEMBB1002614//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.8e-10:512:60//AC004801
R-HEMBB1002617//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.8e-24:486:63//AC005520

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R-HEMBB1002623//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//2.4e-41:326:83//AC004953
R-HEMBB1002635//Homo sapiens chromosome 12p13.3 clone RPCI11-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//2.6e-42:360:80//AC005910
R-HEMBB1002664//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence.//9.1e-51:335:87//AF042090
R-HEMBB1002677//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//0.0011:399:59//AF030694
R-HEMBB1002683//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence.//4.1e-55:515:76//AF042090
R-HEMBB1002684//Human BAC clone RG066D11 from 7q22, complete sequence.//1.7e-18:504:62//AC002430
R-HEMBB1002686//Homo sapiens full-length insert cDNA clone ZC65D06.//7.0e-85:413:99//AF086217
R-HEMBB1002692//Homo sapiens 12p13.3 BAC RPCI11-319E16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//9.8e-69:505:82//AC006206
R-HEMBB1002697//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.26:390:58//AC004153
R-HEMBB1002699//Human NFE genomic fragment.//8.0e-32:226:79//M98511
R-HEMBB1002702//CIT-HSP-344K23.TVC CIT-HSP Homo sapiens genomic clone 344K23, genomic survey sequence.//8.6e-43:351:8011859764
R-HEMBB1002705//Plasmodium yoelii rhoptry protein, complete cds.//0.0064:454:59//L27838
R-HEMBB1002712//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//9.6e-09:187:67//Z98052
R-MAMMA1000009//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.1e-21:201:80//AC005037
R-MAMMA1000019//Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence.//4.2e-48:306:82//AF015720
R-MAMMA1000020//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//1.4e-41:306:86//AL022163
R-MAMMA1000025//Human DNA sequence from clone 512B11 on chromosome 6p24-25. Contains the Desmoplakin I (DPI) gene, ESTs, STSs and GSSs, complete sequence.//6.1e-36:281:83//AL031058
R-MAMMA1000043//Homo sapiens Chromosome 22q11.2 Cosmid Clone 8c In DGCR Region, complete sequence.//1.3e-67:321:88//AC000090
R-MAMMA1000045//Homo sapiens chromosome 4 clone B220G8 map 4q21, complete sequence.//6.7e-86:559:86//AC004054
R-MAMMA1000055//Branta canadensis CA dinucleotide repeat locus Bcamicrol.//0.79:63:77//AF025889
R-MAMMA1000057//Homo sapiens DNA sequence from cosmid ICK0721Q on chromosome 6. Contains a 60S Ribosomal Protein L35A LIKE pseudogene, a gene coding for a 60S Ribosomal Protein L12 LIKE protein in an intron of the HSET gene coding for a Kinesin related protein, the PHF1 (PHF2) gene coding for alternative splice products PHD finger proteins 1 and 2, the gene coding for five different alternatively spliced mRNAs coding for a protein similar to CYTA (CYCY) and identical to a polypeptide coded for by a known patented cDNA, and the first two exons of the gene coding for the human homolog of the rat synaptic ras GTPase-activating protein p135 SynGAP. Contains three predicted CpG islands, ESTs and an STS, complete sequence.//1.6e-53:397:83//AL021366
R-MAMMA1000069//Homo sapiens clone RG052H06, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.0e-37:295:83//AC005057
R-MAMMA1000084//Homo sapiens chromosome Xp22-135-136 clone GSHB-5671I, WORKING DRAFT SEQUENCE, 35 unordered pieces.//7.1e-45:296:88//AC005867
R-MAMMA1000085
R-MAMMA1000092//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 774G10, WORKING DRAFT SEQUENCE.//8.2e-34:539:69//AL034410
R-MAMMA1000103//Homo sapiens chromosome 17, clone hCIT.91_J_4, complete sequence.//3.4e-39:297:85//AC003976
R-MAMMA1000117//Homo sapiens p47-phox (NCF1) pseudogene, clone P38, exon 5.//2.6e-07:162:67//U69641
R-MAMMA1000129//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.1e-13:141:80//AC004882
R-MAMMA1000133

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R-MAMMA1000134//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.7e-18:171:80//AC005328

R-MAMMA1000139//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-49:366:75//AC005000

R-MAMMA1000143//Homo sapiens *** SEQUENCING IN PROGRESS *** from PAC D9.2, WORKING DRAFT SEQUENCE.//3.9e-56:318:89//AJ009615

R-MAMMA1000155//Human DNA sequence from clone 323M22 on chromosome 22q13.1-13.2. Contains the 5' part of the human ortholog of chicken P52 and mouse H74, and a novel gene coding for a protein similar to KIAA0173 and worm Tubulin Tyrosine Ligase. Contains ESTs, STSs, GSSs, genomic marker D22S418 and putative CpG islands, complete sequence.//2.1e-68:562:78//AL022476

R-MAMMA1000163//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//5.3e-06:408:58//AC005089

R-MAMMA1000171//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.5e-42:173:89//AQ037381

R-MAMMA1000173

R-MAMMA1000175//H.sapiens CpG island DNA genomic Mse1 fragment, clone 186c5, reverse read cpg186c5.rt1b.//0.072:90:72//Z57594

R-MAMMA1000183//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete sequence.//1.5e-44:445:75//AC004552

R-MAMMA1000198//Homo sapiens clone c102D0968, complete sequence.//1.9e-23:135:85//AF038667

R-MAMMA1000221//HS_3242_B2_H02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=4 Row=P, genomic survey sequence.//0.031:167:67//AQ220385

R-MAMMA1000227//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1071N3, WORKING DRAFT SEQUENCE.//4.5e-36:487:71//AL031728

R-MAMMA1000241//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains ESTs and an STS, complete sequence.//6.2e-07:445:59//AL022401

R-MAMMA1000251//Homo sapiens chromosome 19, cosmid F23465, complete sequence.//1.6e-25:390:69//AC005266

R-MAMMA1000254//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a ggtt repeat polymorphism, complete sequence.//1.1e-37:327:80//AL008715

R-MAMMA1000257//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1125A11, WORKING DRAFT SEQUENCE.//1.3e-22:281:74//AL034549

R-MAMMA1000264//*** SEQUENCING IN PROGRESS *** EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//1.7e-29:337:67//AC003656

R-MAMMA1000266//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 681N20, WORKING DRAFT SEQUENCE.//7.7e-37:339:80//AL031670

R-MAMMA1000270//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//1.2e-40:283:86//AF001549

R-MAMMA1000277//CIT-HSP-516K6.TP CIT-HSP Homo sapiens genomic clone 516K6, genomic survey sequence.//3.0e-29:265:80//B49900

R-MAMMA1000278//Sequence 25 from patent US 5708157.//2.6e-39:282:82//I80056

R-MAMMA1000279//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence.//1.6e-52:295:84//AC004494

R-MAMMA1000284//CITBI-E1-2522B20.TF CITBI-E1 Homo sapiens genomic clone 2522B20, genomic survey sequence.//1.8e-11:288:61//AQ280722

R-MAMMA1000287

R-MAMMA1000302//Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence.//4.1e-16:169:77//AC005553

R-MAMMA1000307//RPCI11-89L1.TV RPCI11 Homo sapiens genomic clone R-89L1, genomic survey sequence.//1.3e-86:429:97//AQ284795

R-MAMMA1000309//Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spliced isoform of Jagged2, complete cds.//0.00020:384:60//AF029779

R-MAMMA1000312//Ichneutes sp. 16S ribosomal RNA gene, partial sequence.//0.0026:310:60//AF003518

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R-MAMMA1000313//Human cosmid Xq28_IA649, complete sequence.//1.5e-26:317:67//U82694
R-MAMMA1000331//Homo sapiens clone DJ1007F24, WORKING DRAFT SEQUENCE, 5 unordered pieces.// 3.1e-39:277:86//AC004947
R-MAMMA1000339//Homo sapiens clone HS19.1 Alu-Ya5 sequence.//3.2e-44:180:89//AF015147
R-MAMMA1000340//Plasmodium falciparum chromosome 2, section 25 of 73 of the complete sequence.//0.97: 293:64//AE001388
R-MAMMA1000348//Homo sapiens BAC129, complete sequence.//4.4e-27:365:72//U85195
R-MAMMA1000356//Drosophila melanogaster DNA sequence (P1 DS02252 (D97)), complete sequence.//0.73: 332:61//AC002493
R-MAMMA1000360//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//4.6e-80:279:89// AC005189
R-MAMMA1000361//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 753D4, WORKING DRAFT SEQUENCE.//7.8e-18:346:63//AL031676
R-MAMMA1000372//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y214H10, WORKING DRAFT SEQUENCE.//5.3e-40:299:83//AL022344
R-MAMMA1000385//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 310013, WORKING DRAFT SEQUENCE.//1.0e-28:225:84//AL031658
R-MAMMA1000388//CIT-HSP-2321D3.TR CIT-HSP Homo sapiens genomic clone 2321D3, genomic survey sequence.//4.7e-60:298:99//AQ038102
R-MAMMA1000395
R-MAMMA1000402//Homo sapiens PAC clone DJ1107K12 from 7p12-p14, complete sequence.//1.4e-84:276:88// AC004692
R-MAMMA1000410//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//6.7e-35:360: 76//AC002394
R-MAMMA1000413//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//3.1e-69:327: 79//AC004662
R-MAMMA1000414//Homo sapiens DNA sequence from PAC 164L12 on chromosome Xq13.1-Xq21.2. Contains GSS (BAC end sequence),STS.//3.6e-41:180:87//AL009028
R-MAMMA1000416//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.// 3.1e-59:478:77//AC005377
R-MAMMA1000421//Human coxVIb gene, last exon and flanking sequence.//5.3e-53:294:82//X58139
R-MAMMA1000422//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 8B22, WORKING DRAFT SEQUENCE.//1.0:252:59//AL031737
R-MAMMA1000423//Homo sapiens clone DA0065G23, complete sequence.//2.0e-50:491:76//AC004816
R-MAMMA1000424//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//3.5e-40:340:80//Z98950
R-MAMMA1000429//Mus musculus SDP8 mRNA, complete cds.//0.0019:87:79//AF062484
R-MAMMA1000431//Homo sapiens clone DJ0098O22, WORKING DRAFT SEQUENCE, 5 unordered pieces.// 2.0e-58:564:77//AC004821
R-MAMMA1000444//Human BAC clone RG126M09 from 7q21-q22, complete sequence.//3.0e-43:328:83// AC002067
R-MAMMA1000446//Human chromosome X clone Qc15B1, complete sequence.//0.95:209:65//U82672
R-MAMMA1000458//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence.// 0.99:182:61//AB019236
R-MAMMA1000468
R-MAMMA1000472//Homo sapiens genomic DNA, 21q region, clone: 655M9N34, genomic survey sequence.// 1.0e-38:142:88//AG010148
R-MAMMA1000478//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 169I5, WORKING DRAFT SEQUENCE.//1.3e-37:286:83//Z93015
R-MAMMA1000483//CIT-HSP-384B14.TR CIT-HSP Homo sapiens genomic clone 384B14, genomic survey sequence.//4.3e-34:158:86//B54637
R-MAMMA1000490//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//4.2e-98:569:90// AC006130
R-MAMMA1000500//Human BRCA1, Rho7 and vatl genes, complete cds, and ipf35 gene, partial cds.//1.2e-41: 334:79//L78833
R-MAMMA1000501//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 153G14, WORKING DRAFT SEQUENCE.//1.4e-38:250:84//AL031118
R-MAMMA1000516//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING

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DRAFT SEQUENCE.//1.3e-43:318:83//Z82207
R-MAMMA1000522//Human DNA sequence from clone 739H11 on chromosome 1p33-34.2 Contains KIAA0237 gene, EST, STS, GSS, complete sequence.//4.4e-13:202:73//AL031289
R-MAMMA1000559//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 169I5, WORKING DRAFT SEQUENCE.//2.2e-30:245:83//Z93015
R-MAMMA1000565//Homo sapiens chromosome 10 clone LA10NC01_183_B_7 map 10q24, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.6e-39:281:80//U82205
R-MAMMA1000567//Rattus norvegicus nonmuscle caldesmon mRNA, complete cds.//9.2e-19:216:76//U18419
R-MAMMA1000576
R-MAMMA1000583//Homo sapiens chromosome 17, clone hRPK.112_H_10, complete sequence.//5.4e-53:297:85//AC005666
R-MAMMA1000585//Homo sapiens clone DJ1015P16, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-35:450:71//AC006018
R-MAMMA1000594//Homo sapiens *** SEQUENCING IN PROGRESS *** from cosmid 5L5, WORKING DRAFT SEQUENCE.//4.3e-26:293:75//AJ009613
R-MAMMA1000597//CIT-HSP-2341F4.TF CIT-HSP Homo sapiens genomic clone 2341F4, genomic survey sequence.//0.83:110:70//AQ057131
R-MAMMA1000605//Homo sapiens clone DJ1090E20, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.6e-50:290:86//AC004956
R-MAMMA1000612//CIT-HSP-2334J18.TF CIT-HSP Homo sapiens genomic clone 2334J18, genomic survey sequence.//0.76:132:65//AQ038364
R-MAMMA1000616//Ibalia leucospoides mitochondrion 16S rRNA gene, partial sequence.//6.8e-06:431:59//U06970
R-MAMMA1000621//Human NBR2 mRNA, complete cds.//5.3e-27:258:80//U88573
R-MAMMA1000623
R-MAMMA1000625//Homo sapiens chromosome 19, cosmid R31665, complete sequence.//3.3e-07:325:63//AC005498
R-MAMMA1000643//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 39B17, WORKING DRAFT SEQUENCE.//1.4e-06:236:68//AL023656
R-MAMMA1000664//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0326F06; HTGS phase 1, WORKING DRAFT SEQUENCE, 16 unordered pieces.//1.4e-40:338:81//AC004555
R-MAMMA1000669//Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.//1.2e-46:327:86//AL021578
R-MAMMA1000670
R-MAMMA1000672//Human DNA sequence from clone 478D8 on chromosome 6p24. Contains STSs and GSSs, complete sequence.//2.2e-29:328:76//AL031785
R-MAMMA1000684//Mus musculus frizzled-1 mRNA, complete cds.//0.21:247:63//AF054623
R-MAMMA1000696//Human Chromosome X clone bWXD173, WORKING DRAFT SEQUENCE, 2 ordered pieces.//2.7e-46:464:71//AC004387
R-MAMMA1000707//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.4e-09:244:66//AC005075
R-MAMMA1000713//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.7e-51:439:74//AC005478
R-MAMMA1000714//Homo sapiens BAC clone RG152H24 from 7p15-p21, complete sequence.//2.8e-29:288:75//AC004694
R-MAMMA1000718//Human Xp22 BAC CT-285I15 (from CalTech/Research Genetics) , PAC RPCI1-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//3.0e-37:231:91//AC002366
R-MAMMA1000720//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//1.4e-35:299:81//AC005781
R-MAMMA1000723//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//3.9e-59:409:79//AL022163
R-MAMMA1000731//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.4e-29:560:66//AC005077
R-MAMMA1000732//Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.4e-14:309:68//AC004832

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R-MAMMA1000733//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 732E4, WORKING DRAFT SEQUENCE.//4.1e-29:377:71//AL008722
R-MAMMA1000734//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191J18, WORKING DRAFT SEQUENCE.//2.0e-108:420:99//AL024507
R-MAMMA1000738//Human V beta T-cell receptor (TCRBV) gene locus.//6.6e-41:347:82//U03115
R-MAMMA1000744//T27O8-T7 TAMU Arabidopsis thaliana genomic clone T27O8, genomic survey sequence.//0.095:367:60//B20150
R-MAMMA1000746//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0135005; HTGS phase 1, WORKING DRAFT SEQUENCE, 23 unordered pieces.//7.4e-95:569:87//AC004661
R-MAMMA1000752//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequense.//1.3e-48:295:84//AC003071
R-MAMMA1000760//Human DNA sequence from clone B79B4 on chromosome 22 Contains CA repeat and GSS, complete sequence.//5.7e-45:347:82//Z82178
R-MAMMA1000761//Homo sapiens cosmid clone LUCA16 from 3p21.3, complete sequence.//1.1e-32:292:80//U73169
R-MAMMA1000775//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//2.5e-50:467:79//AC005412
R-MAMMA1000776//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//1.0e-63:429:79//AC002454
R-MAMMA1000778//Human DNA sequence from 4PTEL, Huntington's Disease Region, chromosome 4p16.3.//3.5e-25:234:81//Z95704
R-MAMMA1000782//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//0.0021:119:74//AL031120
R-MAMMA1000798//Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3.//6.3e-08:269:64//AJ229042
R-MAMMA1000802//Homo sapiens chromosome 19, cosmid R33729, complete sequence.//1.1e-36:261:80//AC005339
R-MAMMA1000831//CIT-HSP-2387J3.TF.1 CIT-HSP Homo sapiens genomic clone 2387J3, genomic survey sequence.//0.68:156:65//AQ240807
R-MAMMA1000839//Homo sapiens chromosome 17, clone hRPK.726_O_12, WORKING DRAFT SEQUENCE, 6 unordered pieces.//4.6e-50:335:86//AC005517
R-MAMMA1000841//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//1.3e-40:322:77//U91323
R-MAMMA1000842//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 341D10, WORKING DRAFT SEQUENCE.//4.1e-44:471:74//Z97985
R-MAMMA1000843//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.85:394:60//AC004815
R-MAMMA1000845//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//0.54:303:63//AL031744
R-MAMMA1000851//Homo sapiens chromosome X, MeCP2 locus, complete sequence.//1.7e-10:115:83//AF030876
R-MAMMA1000855//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//5.0e-44:352:83//AC004263
R-MAMMA1000856//Homo sapiens chromosome 19, cosmid F24200, complete sequence.//1.8e-10:149:74//AC00461
R-MAMMA1000862//Hepatitis C virus genomic RNA, 3' nonstranslated region, partial sequence. clone #16.//8.1e-05:205:66//AF009075
R-MAMMA1000863//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//2.9e-49:421:80//AC002364
R-MAMMA1000865//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-328A3, complete sequence.//9.1e-41:302:83//AC002301
R-MAMMA1000867//Human BRCA1, Rho7 and vatl genes, complete cds, and ipf35 gene, partial cds.//1.9e-17:500:61//L78833
R-MAMMA1000875//Homo sapiens chromosome 16, cosmid clone RT99 (LANL), complete sequenced.//1.2e-17:211:74//AC004653
R-MAMMA1000876//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//4.7e-09:160:65//AC003658
R-MAMMA1000877//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains

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ESTs STS and CpG island.//3.2e-34:354:75//Z93023
R-MAMMA1000880//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.//1.4e-41:411:74//AC002425
R-MAMMA1000883
R-MAMMA1000897
R-MAMMA1000905//Homo sapiens chromosome 5, P1 clone 274A11 (LBNL H66), complete sequence.//1.3e-73:304:91//AC004506
R-MAMMA1000906//Human DNA from chromosome 19-specific cosmid F14150, genomic sequence, complete sequence.//8.4e-23:194:83//AC003110
R-MAMMA1000908//Human Chromosome 15q26.1 PAC clone pDJ416i6, complete sequence.//1.5e-09:170:71//AC003024
R-MAMMA1000914//Homo sapiens PAC clone DJ0740L10 from 7p13-p14, complete sequence.//8.3e-13:323:67//AC005247
R-MAMMA1000921//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//6.8e-28:333:72//AL034379
R-MAMMA1000931//HS_3227_B1_B03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3227 Col=5 Row=D, genomic survey sequence.//1.4e-55:443:79//AQ191777
R-MAMMA1000940//Homo sapiens clone RG013F03, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.0e-43:340:84//AC005046
R-MAMMA1000941//Homo sapiens chromosome 17, clone 297N7, complete sequence.//1.8e-53:330:84//AC002347
R-MAMMA1000942//Human Chromosome X clone bWXD187, complete sequence.//1.2e-39:391:74//AC004383
R-MAMMA1000943//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//4.6e-75:566:81//AC002477
R-MAMMA1000956//Plasmodium falciparum MAL3P7, complete sequence.//0.013:285:59//AL034559
R-MAMMA1000957//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//5.2e-45:288:90//AC005096
R-MAMMA1000962//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.9e-108:561:96//AC006001
R-MAMMA1000968//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//3.9e-41:287:87//AC004263
R-MAMMA1000975//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//9.4e-65:542:79//Z95152
R-MAMMA1000979//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.//3.2e-34:296:80//AJ011930
R-MAMMA1000987//Homo sapiens CC chemokine gene cluster, complete sequence.//1.7e-40:255:87//AF088219
R-MAMMA1000998//Homo sapiens PAC clone DJ1152D16 from Xq23, complete sequence.//2.5e-39:315:73//AC005190
R-MAMMA1001003//Homo sapiens chromosome 10 clone CIT-HSP-1338F24 map 10p11.2-10p12.1, complete sequence.//2.4e-52:296:84//AC006101
R-MAMMA1001008//Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRAFT SEQUENCE.//7.9e-88:432:98//AJ011929
R-MAMMA1001021//Homo sapiens PAC clone DJ0859M06 from 7q11, complete sequence.//3.8e-39:286:87//AC004910
R-MAMMA1001024//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.0e-31:274:80//AC004913
R-MAMMA1001030//Homo sapiens full-length insert cDNA clone ZD96C01.//3.2e-99:469:99//AF088074
R-MAMMA1001035//RPCI-1-46G8Sp6 RPCI-1 Homo sapiens genomic clone RPCI-1-46G8Sp6, genomic survey sequence.//3.5e-49:270:90//AQ275285
R-MAMMA1001038//Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence.//1.1e-41:285:87//AF042089
R-nnnnnnnnnnnn
R-MAMMA1001050//Homo sapiens genomic DNA, 237 kb segment from 6p21.3 region including HLA genes, WORKING DRAFT SEQUENCE.//1.3e-55:334:91//D84394
R-MAMMA1001059//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//1.7e-51:481:77//L25125

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R-MAMMA1001067//CIT-HSP-2371K20.TF CIT-HSP Homo sapiens genomic clone 2371K20, genomic survey sequence.//7.2e-65:946:95//AQ111326
R-MAMMA1001073
R-MAMMA1001074//Homo sapiens BAC clone NH0400O10 from Y, complete sequence.//8.6e-33:457:69//AC006040
R-MAMMA1001075//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//0.15:325:62//AC004605
R-MAMMA1001078//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence.//1.6e-45:344:84//AC005609
R-MAMMA1001082//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//8.5e-15:413:64//Z93403
R-MAMMA1001091//Sequence 7 from patent US 5468610.//0.0027:159:64//I15499
R-MAMMA1001092//Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.//2.0e-51:267:82//AC005951
R-MAMMA1001105//Homo sapiens DNA sequence from PAC 119E23 on chromosome Xq25-q27.1. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2),5'UTR. ESTs, STS.//6.9e-22:178:85//Z99570
R-MAMMA1001110//Homo sapiens chromosome 17, clone HRPC1169K15, complete sequence.//3.0e-19:141:81//AC003963
R-MAMMA1001126//Human DNA from overlapping chromosome 7 PAC and P1 clones containing the XRCC2 gene, genomic sequence, complete sequence.//2.2e-46:462:75//AC003109
R-MAMMA1001133//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 120G22, WORKING DRAFT SEQUENCE.//1.8e-68:455:86//AL031847
R-MAMMA1001139//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//7.1e-09:100:84//AL022345
R-MAMMA1001143//Papio hamadryas lipoprotein lipase (LPL) gene, intron 7.//1.9e-49:362:85//U73684
R-MAMMA1001145//Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence.//9.5e-49:512:74//AC005922
R-MAMMA1001154//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-88D1 ~complete genomic sequence, complete sequence.//1.5e-29:305:76//AC002289
R-MAMMA1001161//Human DNA sequence from clone 681J21 on chromosome 1q23.2-24.3 Contains CpG island, complete sequence.//1.1e-64:339:90//AL031286
R-MAMMA1001162//Human DNA from cosmid DNA MMDB (f10080) and MMDC (f13544) from chromosome 19q13.3 (obtained by automated sequence analysis).//3.4e-09:243:64//M89651
R-MAMMA1001181//Human Chromosome X clone bWXD173, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.7e-29:351:74//AC004387
R-MAMMA1001186//Homo sapiens chromosome 19, cosmid R28778, complete sequence.//2.2e-25:415:68//AC006125
R-MAMMA1001191//Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence.//0.99:243:61//AE000662
R-MAMMA1001198//Mus musculus eps15R mRNA, complete cds.//8.0e-57:223:86//U29156
R-MAMMA1001202//Mus musculus clone OST13722, genomic survey sequence.//1.0e-30:220:85//AF046748
R-MAMMA1001203//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//8.9e-61:567:78//AC005412
R-MAMMA1001206//Homo sapiens chromosome 5, P1 clone 854b11 (LBNL H44), complete sequence.//4.6e-08:442:61//AC004763
R-MAMMA1001215//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence.//1.3e-117:564:97//AC005393
R-MAMMA1001220//HS-1023-A1-G10-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 802 Col=19 Row=M, genomic survey sequence.//6.0e-16:276:68//B33708
R-MAMMA1001222//F17E12TFB IGF Arabidopsis thaliana genomic clone F17E12, genomic survey sequence.//0.041:277:61//B97762
R-MAMMA1001243
R-MAMMA1001244//HS-1058-A2-G01-MF.abi CIT Human Genomic Sperm Library C Homo-sapiens genomic clone Plate=CT 780 Col=2 Row=M, genomic survey sequence.//3.5e-05:104:74//B43862
R-MAMMA1001249//H.sapiens DNA for matrix attachment region.//0.0013:95:75//Z54221
R-MAMMA1001256//Human BAC clone GS188P18, complete sequence.//3.4e-32:356:74//AC000115
R-MAMMA1001259
R-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds.//6.3e-20:226:75//AB014561

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R-MAMMA1001268//Human DNA sequence from PAC 225D2 on chromosome Xq21. Contains ESTs, CA repeat.// 1.1e-47:352:85//Z95124
R-MAMMA1001271
R-MAMMA1001274//H.sapiens DNA for trapped exon (ID HMC07C06), genomic survey sequence.//3.1e-40:232: 93//X88457
R-MAMMA1001280//Homo sapiens full-length insert cDNA clone YW26C09.//1.9e-112:574:95//AF087976
R-MAMMA1001292//Human DNA sequence from clone 1170K4 on chromosome 22q12.2-13.1. Contains three novel genes, one of which codes for a Trypsin family protein with class A LDL receptor domains, and the IL2RB gene for Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen). Contains a putative CpG island, ESTs, and GSSs, complete sequence.//2.9e-114:582:96//AL022314
R-MAMMA1001296//Human DNA sequence from PAC 487J7 on chromosome 6q21-22.1. Contains an unknown gene coding for three alternative mRNAs. Contains ESTs, STSs, a BAC end-sequence (GSS) and a CA repeat polymorphism.//1.9e-64:268:88//AL008730
R-MAMMA1001298//Homo sapiens chromosome 17, clone hRPK.849_N_15, complete sequence.//1.5e-38:306: 83//AC005703
R-MAMMA1001305//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein, ribosomal protein L6 pseudogene, ESTs and CA repeat.// 1.5e-37:306:82//Z83838
R-MAMMA1001322//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//2.4e-15:260:71//AL022398
R-MAMMA1001324//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//4.0e-06:90:83// AC005614
R-MAMMA1001330//Human BAC clone RG066D11 from 7q22, complete sequence.//1.4e-45:439:74//AC002430
R-MAMMA1001341//Human DNA sequence from PAC 211D12 on chromosome 20q12-13.2. Contains Krs-2, K+ channel protein, stress responsive.//1.3e-24:137:81//Z93016
R-MAMMA1001343//Human Chromosome 16 BAC clone CIT987SK-A-17E1, complete sequence.//5.4e-51:197: 89//AC002041
R-MAMMA1001346//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-233A8, complete sequence.//0.99: 182:64//AC004685
R-MAMMA1001383//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.9e-42: 303:86//AC004815
R-MAMMA1001388//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 508I15, WORKING DRAFT SEQUENCE.//1.5e-44:324:83//AL021707
R-MAMMA1001397//Homo sapiens genomic DNA, chromosome 21q11.1, segment 15/28, WORKING DRAFT SEQUENCE.//2.0e-39:254:89//AP000044
R-MAMMA1001408//Homo sapiens chromosome 12q24.1, WORKING DRAFT SEQUENCE, 33 unordered pieces.//9.4e-36:251:88//AC005805
R-MAMMA1001411//T15F1-T7.1 TAMU Arabidopsis thaliana genomic clone T15F1, genomic survey sequence.// 1.0:98:71//AQ248928
R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, complete cds.//4.8e-18:117:96// AF038957
R-MAMMA1001420//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence.//2.8e- 09:377:63//AC005179
R-MAMMA1001435//S.pombe chromosome I cosmid c26H5.//1.0:356:59//Z99126
R-MAMMA1001442//Homo sapiens chromosome 4 clone B150J4 map 4q25, complete sequence.//3.4e-17:259: 72//AC004047
R-MAMMA1001446//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//2.9e-17:231:71// AC004491
R-MAMMA1001452//Human DNA sequence from clone 452M16 on chromosome Xq21.1-21.33 Contains capping protein alpha subunit isoform 1 pseudogene, STS, GSS, and CA repeat, complete sequence.//6.1e-50:558:73// AL024493
R-MAMMA1001465//cSRL-2F3-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-2F3, genomic survey sequence.//3.0e-23:141:96//B04295
R-MAMMA1001476//Mus musculus uridine kinase mRNA, partial cds.//3.4e-09:309:64//L31783
R-MAMMA1001487//Homo sapiens chromosome 17, clone hRPC.1108_L_11, complete sequence.//5.1e-30:286: 79//AC005206

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R-MAMMA1001501
R-MAMMA1001502//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 356B7, WORKING DRAFT SEQUENCE.//4.3e-19:349:64//AL031714
R-MAMMA1001510
R-MAMMA1001522//Homo sapiens chromosome 5, BAC clone 24h24 (LBNL H194), complete sequence.//1.5e-09:136:75//AC005352
R-MAMMA1001547//Human Chromosome X, complete sequence.//3.5e-40:300:84//AC002418
R-MAMMA1001551//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.1e-57:282:89//AL020997
R-MAMMA1001575
R-MAMMA1001576//Human gamma-tubulin mRNA, complete cds.//7.6e-60:530:78//M61764
R-MAMMA1001590//Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds.//1.3e-29:161:86//U78027
R-MAMMA1001600//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.1e-18:390:66//AC004216
R-MAMMA1001604//Human DNA sequence from clone 1042K10 on chromosome 22q13.1-13.2. Contains the ADSL gene for Adenylosuccinate lyase (EC 4.3.2.2, Adenylosuccinase, ASL) and 4 novel genes (one with probable rabGAP domains and Src homology domain 3). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//1.0:227:62//AL022238
R-MAMMA1001606//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING DRAFT SEQUENCE.//1.3e-17:219:69//AL031985
R-MAMMA1001620//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE.//2.1e-51:298:84//AL031650
R-MAMMA1001627//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 229A8, WORKING DRAFT SEQUENCE.//7.8e-45:328:85//Z86090
R-MAMMA1001630//, complete sequence.//2.5e-08:170:72//AC005399
R-MAMMA1001633//Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10q25, complete sequence.//2.2e-21:241:70//AC005386
R-MAMMA1001635//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//1.1e-32:346:74//Z84466
R-MAMMA1001649
R-MAMMA1001663//Homo sapiens clone 162B15, complete sequence.//9.4e-68:267:89//AC004811
R-MAMMA1001670//Human DNA sequence from PAC 75N13 on chromosome Xq21.1. Contains ZNF6 like gene, ESTs, STSs and CpG islands.//1.7e-49:322:88//Z82216
R-MAMMA1001671//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//2.4e-114:575:96//AC005614
R-MAMMA1001679//CIT-HSP-2335N4.TF CIT-HSP Homo sapiens genomic clone 2335N4, genomic survey sequence.//2.4e-82:400:99//AQ037393
R-MAMMA1001683//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces.//5.7e-47:533:72//AC004166
R-MAMMA1001686//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//6.6e-12:194:72//AC005261
R-MAMMA1001692//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//9.6e-44:414:77//AL022345
R-MAMMA1001711//Homo sapiens clone BAC 9H13 chromosome 8 map 8q21, complete sequence.//3.1e-31:436:70//AF110324
R-MAMMA1001715//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 73E16, WORKING DRAFT SEQUENCE.//8.8e-76:524:84//Z95330
R-MAMMA1001730
R-MAMMA1001735//Cricetulus griseus (chinese hamster) mRNA for beta tubulin (clone B9T), partial.//2.7e-13:382:63//X60786
R-MAMMA1001740//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//3.9e-47:318:87//AP000050
R-MAMMA1001743//Homo sapiens clone DJ0981O07, complete sequence.//4.0e-108:566:95//AC006017
R-MAMMA1001744
R-MAMMA1001745//Homo sapiens BAC clone 529F11 from 8q21, complete sequence.//3.5e-113:564:97//AF070718
R-MAMMA1001751//Homo sapiens chromosome 19, cosmid R27328, complete sequence.//3.6e-30:312:75//

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AC005625
R-MAMMA1001754//Bos taurus vacuolar proton pump subunit SFD alpha isoform (SFD) mRNA, complete cds.// 4.7e-34:320:77//AF041338
R-MAMMA1001757//Homo sapiens chromosome 17, clone hRPC.4_G_17, complete sequence.//4.7e-10:244:67// AC003688
R-MAMMA1001760//RPCI11-38L16.TV RPCI-11 Homo sapiens genomic clone RPCI-11-38L16, genomic survey sequence.//1.3e-10:236:64//AQ029432
R-MAMMA1001764//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.74:361:60//AC005140
R-MAMMA1001768//Homo sapiens chromosome 17, clone hRPK.147_L_13, complete sequence.//1.6e-42:416: 76//AC005332
R-MAMMA1001769//Homo sapiens chromosome 17, clone hRPC.1073_F_15, complete sequence.//1.4e-13:129: 83//AC004686
R-MAMMA1001771//M.musculus mRNA for semaphorin B.//1.1e-34:530:69//X85991
R-MAMMA1001783//Homo sapiens Chromosome 2 BAC Clone 376a1, WORKING DRAFT SEQUENCE, 17 unordered pieces.//1.1e-42:282:85//AC000360
R-MAMMA1001785//Human chromosome 16p13.11 BAC clone CIT987SK-98H8 complete sequence.//3.0e-49: 282:86//U91319
R-MAMMA1001788
R-MAMMA1001790//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.// 9.8e-43:530:71//AC004913
R-MAMMA1001806//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//1.8e-43:324:79//AC004020
R-MAMMA1001812//Plasmodium falciparum chromosome 2, section 69 of 73 of the complete sequence.//0.65: 183:63//AE001432
R-MAMMA1001815//Homo sapiens clone GS223D04, WORKING DRAFT SEQUENCE, 3 unordered pieces.// 1.1e-10:417:62//AC005018
R-MAMMA1001817//Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) complete sequence.//2.6e-40:313:84//AC005859
R-MAMMA1001818
R-MAMMA1001820//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//2.2e-45:340:82// AC004086
R-MAMMA1001824//Homo sapiens clone DJ1107K15, WORKING DRAFT SEQUENCE, 8 unordered pieces.// 1.9e-53:291:85//AC004966
R-MAMMA1001836//HS_3164_B1_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3164 Col=3 Row=B, genomic survey sequence.//6.5e-08:79:89//AQ185484
R-MAMMA1001837//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//8.4e-55:309:85//AC003682
R-MAMMA1001848//Homo sapiens PAC clone DJ0296G17 from Xq23, complete sequence.//1.6e-16:125:90// AC006144
R-MAMMA1001851//Genomic sequence from Human 9q34, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.4e-50:516:74//AC002099
R-MAMMA1001854//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.//1.7e-38:308:82//AC002425
R-MAMMA1001858//Human Xq13 3' end of PAC 92E23 containing the X inactivation transcipt (XIST) gene, complete sequence.//6.5e-50:283:86//U80460
R-MAMMA1001864//Human Chromosome 15q26.1 PAC clone pDJ398g19, WORKING DRAFT SEQUENCE, 21 unordered pieces.//3.4e-36:224:86//AC005143
R-nnnnnnnnnnnn//Plasmodium falciparum chromosome 2, section 54 of 73 of the complete sequence.//1.4e-11: 495:63//AE001417
R-MAMMA1001874//Human chromosome 1 BAC 308G1 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.2e-42:446:76//AC003117
R-MAMMA1001878//Human DNA sequence from PAC 431A14 on chromosome 6p21. Contains CYCLOPHILIN (PEPTIDYLPROLYL ISOMERASE) like and CIP1 (WAF1, CDKNA1, CDKN1, MDA-6, SDI1, PIC1, CAP20) genes. Contains probable GTPase and receptor genes and ESTs, STSs and CpG islands.//6.9e-44:391:78//Z85996
R-MAMMA1001880//Human DNA sequence from fosmid F77D12 on chromosome 22q12-qter contains ESTs, tRNA.//1.3e-15:181:76//Z82097
R-MAMMA1001890//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-670B5 ~complete genomic se-

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quence, complete sequence.//1.7e-43:283:86//AC002303
R-MAMMA1001907//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 385E7, WORKING DRAFT SEQUENCE.//1.4e-48:420:79//AL031720
R-nnnnnnnnnnnn//Saccharomyces cerevisiae chromosome IV cosmid 9481.//2.9e-14:505:60//U28373
R-MAMMA1001931//Homo sapiens NACP/alpha-synuclein gene, allele A0, intron 4, partial sequence.//0.51:162:63//AF041008
R-MAMMA1001956//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50O24, WORKING DRAFT SEQUENCE.//1.4e-51:422:79//AL034380
R-MAMMA1001963//Homo sapiens clone HS19.3 Alu-Ya5 sequence.//1.9e-31:163:91//AF015149
R-MAMMA1001969//Human DNA from chromosome 19 cosmid F19410, genomic sequence, complete sequence.//8.7e-10:186:76//AC002128
R-MAMMA1001970//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.0e-62:298:86//AC003071
R-MAMMA1001992//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-44:525:72//AC004581
R-MAMMA1002009//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 109G6, WORKING DRAFT SEQUENCE.//1.4e-43:282:79//AL023879
R-MAMMA1002011
R-MAMMA1002032//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469D22, WORKING DRAFT SEQUENCE.//1.1e-39:310:84//AL031284
R-MAMMA1002033//Homo sapiens chromosome 5, Pac clone 162o17 (LBNL H147), complete sequence.//2.5e-17:170:81//AC003954
R-MAMMA1002041//Homo sapiens PAC clone DJ0728D04, complete sequence.//8.7e-79:296:85//AC004865
R-MAMMA1002042//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//8.8e-46:386:80//U91318
R-MAMMA1002047//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//1.9e-32:326:75//U91318
R-MAMMA1002056//Homo sapiens chromosome 17, clone hRPK.506_H_21, complete sequence.//6.6e-48:367:82//AC005962
R-MAMMA1002058//Homo sapiens clone RG038K21, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.25:139:69//AC005052
R-MAMMA1002068//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.2e-45:406:78//AC004676
R-MAMMA1002078//Homo sapiens chromosome 17, clone hRPK.401_O_9, complete sequence.//2.3e-22:357:64//AC005291
R-MAMMA1002082//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//2.5e-38:304:82//AC004263
R-MAMMA1002084//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1174N9, WORKING DRAFT SEQUENCE.//8.9e-41:319:83//AL031602
R-MAMMA1002093//CIT-HSP-2060J9.TF CIT-HSP Homo sapiens genomic clone 2060J9, genomic survey sequence.//9.7e-17:129:88//B69983
R-MAMMA1002108
R-MAMMA1002118//Human DNA sequence from cosmid E116C6, on chromosome 22 Contains ESTs, complete sequence.//0.94:168:64//Z73495
R-MAMMA1002125//Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.//4.8e-40:313:83//AC005670
R-MAMMA1002132//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//2.0e-70:461:83//AC004953
R-MAMMA1002140//Human DNA sequence from PAC 465G10 on chromosome X contains Menkes Disease (ATP7A) putative Cu^{++}-transporting P-type ATPase exons 2 to 21, PGAM-B, ESTs.//1.1e-32:477:73//Z94801
R-MAMMA1002143//Homo sapiens platelet-activating factor acetylhydrolase gene, promoter region and exon 1.//6.6e-06:130:73//AF027357
R-MAMMA1002145//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE.//6.0e-19:242:73//AL031447
R-MAMMA1002153//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0281M17; HTGS phase 1, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.1e-51:291:75//AC006052
R-MAMMA1002155//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 608E8, WORKING DRAFT SEQUENCE.//1.2e-53:461:79//AL022343

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R-MAMMA1002156//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.//5.1e-37:305:82//AC004997

R-MAMMA1002158//Human DNA sequence from clone 1049G16 on chromosome 20q12-13.2 Contains gene similar to GLUCOSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete sequence.//8.1e-34:296:81//AL034418

R-MAMMA1002170//Human DNA sequence from clone 1163J1 on chromosome 22q13.2-13.33. Contains the 3' part of a gene for the ortholog of mouse transmembrane receptor Celsr1, a novel gene for a protein similar to C. elegans B0035.16 and bacterial tRNA (5-Methylaminomethyl-2-thiouridylate)-Methyltransferases, and the 3' part of a novel gene for a protein similar to mouse B99. Contains ESTs, GSSs and putative CpG islands, complete sequence.//7.9e-39:332:82//AL031588

R-MAMMA1002174//Homo sapiens chromosome 10 clone CIT987SK-1109P11, complete sequence.//4.4e-12:189:72//AC005871

R-MAMMA1002198//Homo sapiens clone DJ0800G07, complete sequence.//1.1e-48:338:81//AC004890

R-MAMMA1002209//Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence.//1.2e-23:269:74//AC005821

R-MAMMA1002215//Homo sapiens clone GS250N06, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-12:243:68//AC005158

R-MAMMA1002219//Homo sapiens 12p13.3 RPCI4-773N5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.3e-45:295:88//AC004802

R-MAMMA1002230//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//7.3e-41:385:78//AL034379

R-MAMMA1002236//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//7.3e-45:363:79//U38253

R-MAMMA1002243//Homo sapiens chromosome 17, clone hRPK.112_H_10, complete sequence.//2.8e-119:582:98//AC005666

R-MAMMA1002250//Homo sapiens chromosome 16, P1 clone 109-9G (LANL), complete sequence.//4.7e-42:319:84//AC005600

R-MAMMA1002267//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//1.5e-33:571:67//AC006120

R-MAMMA1002268//Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds.//2.3e-35:462:70//AF068749

R-MAMMA1002269//345I17.TV CIT978SKA1 Homo sapiens genomic clone A-345I17, genomic survey sequence.//4.7e-05:153:69//B15590

R-MAMMA1002282//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 112K5, WORKING DRAFT SEQUENCE.//8.5e-37:467:71//Z85987

R-MAMMA1002292//Hordeum vulgare lipoxygenase 2 (LoxC) mRNA, complete cds.//0.074:178:61//L37358

R-MAMMA1002293//Homo sapiens chromosome 16, cosmid clone RT167 (LANL), complete sequence.//5.8e-26:355:71//AC005568

R-MAMMA1002294//Homo sapiens chromosome 17, clone hRPC.1110_E_20, complete sequence.//1.2e-35:281:82//AC004231

R-MAMMA1002297//Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome 4p16.3.//6.7e-48:381:80//Z69375

R-MAMMA1002298//Homo sapiens BAC clone RG208H19 from 7q11.23, complete sequence.//.8e-17:296:70//AC005074

R-MAMMA1002299//HS_3116_A2_F07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3116 Col=14 Row=K, genomic survey sequence.//4.1e-60:354:91//AQ140526

R-MAMMA1002308

R-MAMMA1002310//Human DNA sequence from cosmid B10B1 on chromosome 22 Contains ESTs, CA repeat and STS, complete sequence.//9.9e-35:283:83//Z73979

R-MAMMA1002311//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.3e-86:503:90//AC006210

R-MAMMA1002312//H.sapiens gene encoding La autoantigen.//1.3e-23:382:67//X97869

R-MAMMA1002317//Human DNA sequence from clone 48G12 on chromosome Xq27.1-27.3. Contains STSs and GSSs, complete sequence.//1.3e-59:323:87//AL031054

R-MAMMA1002319//Homo sapiens chromosome 19, fosmid 39347, complete sequence.//2.2e-106:522:98//AC005756

R-MAMMA1002322//Homo sapiens genomic DNA, chromosome 21q11.1, segment 13/28, WORKING DRAFT SEQUENCE.//2.3e-48:452:76//AP000042

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R-MAMMA1002329//M.musculus mRNA for semaphorin B.//2.0e-12:210:73//X85991
R-MAMMA1002332//Homo sapiens PAC clone DJ1139I01 from Xq23, complete sequence.//3.4e-46:393:71//AC004973
R-MAMMA1002333//HS_3245_A1_B04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3245 Col=7 Row=C, genomic survey sequence.//3.1e-21:146:92//AQ205759
R-MAMMA1002339//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//9.7e-39:310:79//AF001549
R-MAMMA1002347//Homo sapiens 12q24.1 PAC RPCI3-305I20 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.2e-46:443:76//AC006088
R-MAMMA1002351//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1059H15, WORKING DRAFT SEQUENCE.//1.1e-90:553:89//AL022100
R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2.//8.8e-81:388:92//Y15228
R-MAMMA1002353//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//5.5e-35:302:80//AC002996
R-MAMMA1002355//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 222E13, WORKING DRAFT SEQUENCE.//5.4e-52:361:76//Z93241
R-MAMMA1002356//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//8.3e-28:187:91//AC004662
R-MAMMA1002359//Human DNA sequence from cosmid L118D5, Huntington's Disease Region, chromosome 4p16.3 contains CpG islands.//6.3e-47:297:85//268869
R-MAMMA1002360//HS_2163_B2_C08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2163 Col=16 Row=F, genomic survey sequence.//1.5e-20:374:66//AQ125213
R-MAMMA1002361//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 349A12, WORKING DRAFT SEQUENCE.//2.2e-35:264:85//AL033520
R-MAMMA1002362//H.sapiens PEX gene.//1.8e-40:243:86//Y10196
R-MAMMA1002380//RPCI11-73J4.TJ RPCI11 Homo sapiens genomic clone R-73J4, genomic survey sequence.//1.7e-38:295:77//AQ268168
R-MAMMA1002384//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.5e-37:311:81//AC004801
R-MAMMA1002385
R-MAMMA1002392//Human BAC clone RG066D11 from 7q22, complete sequence.//2.0e-37:365:77//AC002430
R-MAMMA1002411//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 64K7, WORKING DRAFT SEQUENCE.//9.4e-22:496:65//AL031668
R-MAMMA1002413//Homo sapient 12q24.2 PAC RPCI1-157K6 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.3e-15:153:77//AC005146
R-MAMMA1002417//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.8e-23:508:62//AL020997
R-MAMMA1002427//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//2.5e-37:288:84//U91321
R-MAMMA1002428//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE.//6.0e-05:130:75//AL034423
R-MAMMA1002434//Homo sapiens DNA sequence from PAC 380E11 on chromosome 6p22.3-p24. Contains HB15 gene, ESTs, CA repeat, STS and GSS.//4.8e-18:205:78//AL022396
R-MAMMA1002446//CIT-HSP-2021L14.TR CIT-HSP Homo sapiens genomic clone 2021L14, genomic survey sequence.//4.6e-41:387:72//B65379
R-MAMMA1002454//Homo sapiens chromosome 19, cosmid F23259, complete sequence.//1.2e-67:491:82//AC005512
R-MAMMA1002461//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//1.4e-28:188:85//AC003982
R-MAMMA1002470//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//6.3e-09:280:61//U10556
R-MAMMA1002475//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//1.5e-25:310:74//Z83822
R-MAMMA1002480//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.2e-98:533:93//AC005077
R-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//2.7e-114:560:97//AF055460
R-MAMMA1002494//Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome 4p16.3.//2.1e-46:329:84//Z69375
R-MAMMA1002498//Rat mRNA.//0.0068:223:64//M59859
R-MAMMA1002524//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING

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DRAFT SEQUENCE, 5 unordered pieces.//0.012:460:60//AC005139
R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.// 1.2e-101:529:95//AF065214
R-MAMMA1002545//Homo sapiens ribosomal protein s4 Y isoform gene, complete cds.//6.6e-50:471:77// AF041427
R-MAMMA1002554//Homo sapiens chromosome 4 clone B227H22 map 4q25, complete sequence.//5.7e-38:279: 84//AC004056
R-MAMMA1002556//Homo sapiens chromosome 10 clone CIT-HSP-1255F20 map 10p11.2-10p12.1, complete sequence.//9.6e-13:237:67//AC005878
R-MAMMA1002566//CITBI-E1-2509P21.TR CITBI-E1 Homo sapiens genomic clone 2509P21, genomic survey sequence.//9.7e-14:216:73//AQ261427
R-MAMMA1002571//CITBI-E1-2516L21.TF CITBI-E1 Homo sapiens genomic clone 2516L21, genomic survey sequence.//4.6e-25:142:99//AQ279542
R-MAMMA1002573//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 811H13, WORKING DRAFT SEQUENCE.//1.1e-30:250:82//AL023805
R-MAMMA1002585//Rabbit angiotensin-converting enzyme (ACE) gene, 5' end.//1.0:196:61//M58580
R-MAMMA1002590//H.sapiens CpG island DNA genomic Mse1 fragment, clone 8d5, forward read cpg8d5.f1g.// 1.0:114:64//Z63758
R-MAMMA1002597//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1103G7, WORKING DRAFT SEQUENCE.//9.0e-96:459:98//AL034548
R-MAMMA1002598//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 120G22, WORKING DRAFTSEQUENCE.//0.79:362:58//AL031847
R-MAMMA1002603//Homo sapiens chromosome 17, clone hRPK.214_C_8, complete sequence.//1.3e-46:333: 80//AC005803
R-MAMMA1002612//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 269M15, WORKING DRAFT SEQUENCE.//7.4e-41:283:86//AL021395
R-MAMMA1002617//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 591N18, WORKING DRAFT SEQUENCE.//1.7e-20:308:71//AL031594
R-MAMMA1002618//Homo sapiens clone RG122E10, complete sequence.//1.2e-31:230:76//AC005067
R-MAMMA1002619//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2.//9.0e-113:551:98//AJ010598
R-MAMMA1002622//Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.//2.8e-43:324: 83//AC004050
R-MAMMA1002623//Homo sapiens chromosome 17, clone hRPC.1171_I_10, complete sequence.//2.7e-80:344: 84//AC004687
R-MAMMA1002625//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1056L3, WORKING DRAFT SEQUENCE.//2.6e-34:391:72//AL031727
R-MAMMA1002629//Human DNA from overlapping chromosome 19-specific cosmids R32543,, and F15613 containing ZNF gene family member, genomic sequence, complete sequence.//5.5e-58:346:81//AC003006
R-MAMMA1002636//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.// 1.1e-52:285:92//AC004895
R-MAMMA1002637//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//2.1e-13:359:64//AF055666
R-MAMMA1002646//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 394I7, WORKING DRAFT SEQUENCE.//2.5e-24:285:68//AL023585
R-MAMMA1002650//Human IGF-II gene exon 2 for insulin-like growth factor II located on chromosome 11.//0.64: 237:61//X03424
R-MAMMA1002655//Homo sapiens mini satellite cebl repeat region.//0.18:152:65//AF048727
R-MAMMA1002662//Homo sapiens clone DJ0739M23, complete sequence.//2.5e-46:370:82//AC004870
R-MAMMA1002665//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//7.4e-55:298: 92//Z92844
R-MAMMA1002671//RPCI11-45M10.TK RPCI11 Homo sapiens genomic clone R-45M10, genomic survey sequence.//0.99:151:66//AQ194411
R-MAMMA1002673//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//3.1e-38:410:76//AL022162
R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds.//1.4e-107:544:96//D86987
R-MAMMA1002685//HS_2052_A1_H02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=3 Row=O, genomic survey sequence.//1.2e-23:255:75//AQ231087
R-MAMMA1002698//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library)

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complete sequence.//1.1e-38:299:83//AC004673
R-MAMMA1002699//Mus musculus intersectin-EH binding protein Ibp1 mRNA, partial cds.//3.3e-05:61:93//AF057285
R-MAMMA1002701//Homo sapiens gene for AF-6, complete cds.//3.5e-39:317:81//AB011399
R-MAMMA1002708//Homo sapiens 12p13.3 PAC RPCI5-977L1 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.26:365:62//AC005293
R-MAMMA1002711//Homo sapiens chromosome 21 PAC LLNLP704F18108Q13.//2.5e-31:304:77//AJ006995
R-MAMMA1002721//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 473B4, WORKING DRAFT SEQUENCE.//2.3e-40:279:87//Z83826
R-MAMMA1002727//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.45:183:64//AC004710
R-MAMMA1002728//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.//1.1e-42:410:74//AC002037
R-MAMMA1002744//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//1.6e-19:473:63//U96629
R-MAMMA1002746//Homo sapiens chromosome 17, clone hRPK.136_H_19, complete sequence.//2.2e-108:544:97//AC005856
R-MAMMA1002748//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.9e-106:551:95//AC006055
R-MAMMA1002754//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.7e-34:305:79//AC005020
R-MAMMA1002758//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//0.00014:130:74//U95626
R-MAMMA1002764//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//8.7e-10:118:81//AC005781
R-MAMMA1002765//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//1.2e-31:290:78//AC006128
R-MAMMA1002769//Human DNA sequence from PAC 36J3, between markers DXS1192 and DXS102 on chromosome X.//0.94:260:62//Z82975
R-MAMMA1002780//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 620E11, WORKING DRAFT SEQUENCE.//2.6e-21:529:62//AL031667
R-MAMMA1002782//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 199H16, WORKING DRAFT SEQUENCE.//2.8e-30:234:72//AL022320
R-MAMMA1002796//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 237J2, WORKING DRAFT SEQUENCE.//1.0:155:66//AL021394
R-MAMMA1002807//Human DNA sequence from BAC 941F9 on chromosome 22q11.2-qter. Contains ESTs, STSs and 3' part of FIBULIN-1 D PRECURSOR like gene, part of a Brain Protein E46 like gene and a CpG island, complete sequence.//5.0e-42:443:75//Z95331
R-MAMMA1002820//345M16.TVB CIT978SKA1 Homo sapiens genomic clone A-345M16, genomic survey sequence.//1.3e-14:95:87//B17487
R-MAMMA1002830//Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.//4.1 e-20:223:74//AC002073
R-MAMMA1002833//Homo sapiens Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//1.8e-37:295:84//AC005295
R-MAMMA1002835
R-MAMMA1002838//Human gene hY3 encoding a cytoplasmic Ro RNA.//4.4e-14:108:92//V00585
R-MAMMA1002842//CIT-HSP-2017022.TRB CIT-HSP Homo sapiens genomic clone 2017022, genomic survey sequence.//5.2e-43:168:85//B67141
R-MAMMA1002843//Homo sapiens clone GS051M12, complete sequence.//8.7e-44:525:71//AC005007
R-MAMMA1002844
R-MAMMA1002858//H.sapiens ERF-1 mRNA 3' end.//2.8e-99:361:91//X79067
R-MAMMA1002868//Homo sapiens clone DJ0852O24, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.6e-39:288:81//AC004906
R-MAMMA1002871//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.//0.0022:490:57//AC006044
R-MAMMA1002880//Homo sapiens Xp22 Bins 35-37 BAC GSHB-214D18 (Genome Systems Human BAC Library) complete sequence.//1.3e-09:143:76//AC005296
R-MAMMA1002881//Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial

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cds for thymopoietin beta.//5.1e-41:264:87//U18271
R-MAMMA1002886//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//4.7e-32:216:90//AL022069
R-MAMMA1002887
R-MAMMA1002890
3.4e-49:376:81//AG006257
R-MAMMA1002892//Homo sapiens PAC clone DJ0765G07 from 7q11, complete sequence.//6.0e-60:344:79//AC004881
R-MAMMA1002895//RPCI11-90K13.TV RPCI11 Homo sapiens genomic clone R-90K13, genomic survey sequence.//2.1e-34:300:77//AQ283502
R-MAMMA1002908//Human Chromosome X, complete sequence.//4.2e-39:297:85//AC004070
R-MAMMA1002909//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0442P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.4e-23:344:74//AC005798
R-MAMMA1002930//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//5.2e-39:261:88//AC006019
R-MAMMA1002938//C.pasteurianum gap gene.//1.0:343:59//X72219
R-MAMMA1002941//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//6.3e-88:556:87//AC006120
R-MAMMA1002947
0.48:156:69//AC005469
R-MAMMA1002964//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.2e-39:473:73//AL020997
R-MAMMA1002970//Homo sapiens chromosome 5, P1 clone 793c5 (LBNL H57), complete sequence.//4.7e-47:420:77//AC005200
R-MAMMA1002972//alpha 1 syntrophin [human, mRNA Partial, 1771 nt] .//0.97:305:62//S81737
R-MAMMA1002973//Human DNA sequence from cosmid V210E9, between markers DXS366 and DXS87 on chromosome X.//2.6e-35:256:85//Z70280
R-MAMMA1002982 1.0e-27:110:85//AG005524
R-MAMMA1002987//Homo sapiens PAC clone DJ1086D14, complete sequence.//1.4e-28:527:66//AC004460
R-MAMMA1003003//Homo sapiens chromosome 10 clone CRI-JC2059 map 10q24.1-10q24.2, WORKING DRAFT SEQUENCE, 1 ordered pieces.//7.9e-48:418:78//AC006109
R-MAMMA1003004//, complete sequence.//2.0e-12:442:61//AC005406
R-MAMMA1003007//Homo sapiens chromosome 10 clone CRI-JC2059 map 10q24.1-10q24.2, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.7e-48:293:91//AC006109
R-MAMMA1003011//A-306G8.TP CIT978SK Homo sapiens genomic clone A-306G8, genomic survey sequence.//0.45:168:64//B18092
R-MAMMA1003015//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.9e-44:399:77//AC005740
R-MAMMA1003019//RPCI11-9J9.TV RPCI-11 Homo sapiens genomic clone RPCI-11-9J9, genomic survey sequence.//2.7e-14:294:68//B71583
R-MAMMA1003026//HS_2166_B2_C12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2166 Col=24 Row=F, genomic survey sequence.//0.021:189:64//AQ125639
R-MAMMA1003031//Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.//1.8e-98:525:95//AC005214
R-MAMMA1003035//Homo sapiens 12q13.1 Cosmid C174F5 (Lawrence Livermore LL12NC01 or LL12NC02 human cosmid libraries) complete sequence.//6.7e-06:297:63//AC004550
R-MAMMA1003039//RPCI11-56J17.TJ RPCI11 Homo sapiens genomic clone R-56J17, genomic survey sequence.//0.21:375:59//AQ081889
R-MAMMA1003040//Human DNA sequence from cosmid L108f12, Huntington's Disease Region, chromosome 4p16.3.//2.7e-29:298:67//Z49235
R-MAMMA1003044//Homo sapiens chromosome 19, cosmid R30676, complete sequence.//2.9e-14:113:91//AC004560
R-MAMMA1003047
R-MAMMA1003049
R-MAMMA1003055//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 377F16, WORKING DRAFT SEQUENCE.//2.3e-45:317:86//Z93783
R-MAMMA1003056//Homo sapiens chromosome 19, cosmid R34275, complete sequence.//1.0:229:63//AC005305

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R-MAMMA1003057//M.domesticus MD6 mRNA.//6.2e-42:326:82//X54352
R-MAMMA1003066//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 473B4, WORKING DRAFT SEQUENCE.//3.1e-49:299:87//Z83826
R-MAMMA1003089//Homo sapiens BAC clone RG298G08 from 7p15-p21, complete sequence.//2.7e-30:520:67//AC005084
R-MAMMA1003099//RPCI11-8N9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-8N9, genomic survey sequence.//4.2e-44:338:82//B71494
R-MAMMA1003104//Mus musculus rostral cerebellar malformation protein (rcm) mRNA, complete cds.//3.4e-48:423:79//U72634
R-MAMMA1003113//Homo sapiens chromosome 12p13.3 clone RPCI11-433J6, WORKING DRAFT SEQUENCE, 100 unordered pieces.//4.8e-114:567:97//AC006087
R-MAMMA1003127//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 250D10, WORKING DRAFT SEQUENCE.//1.4e-34:283:83//Z99716
R-MAMMA1003135//P.knowlesi Mbn-cutting sites in lambda KBS50.//0.010:243:62//M38776
R-MAMMA1003140//Homo sapiens chromosome 17, clone HCIT87G17, complete sequence.//6.7e-34:288:81//AC003663
R-MAMMA1003146//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//4.8e-08:438:59//M97514
R-nnnnnnnnnnnn//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 598F2, WORKING DRAFT SEQUENCE.//1.7e-63:149:94//AL021579
R-MAMMA1003166//HS_3128_A1_B01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3128 Col=1 Row=C, genomic survey sequence.//3.0e-17:261:70//AQ140766
R-NT2RM2002580//Homo sapiens clone 24781 mRNA sequence.//2.6e-111:593:94//AF070640
R-NT2RM4000024
R-NT2RM4000027//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence.//0.026:476:56//AC004993
R-NT2RM4000030//Mus musculus musculus sex determining protein (Sry) gene, complete cds.//0.00044:378:59//U70653
R-NT2RM4000046//M.mulatta MHC DR beta 6 gene encoding major histocompatibility complex.//0.27:130:64//Z26239
R-NT2RM4000061
R-NT2RM4000085//Homo sapiens clone 24700 unknown mRNA, partial cds.//7.2e-112:550:97//AF070639
R-NT2RM4000086//RPCI11-6J23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-6J23, genomic survey sequence.//7.2e-18:277:71//B49463
R-NT2RM4000104//F.rubripes GSS sequence, clone 063K10aG5, genomic survey sequence.//3.6e-08:287:61//Z88817
R-NT2RM4000139//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence.//9.4e-08:336:65//AC005199
R-NT2RM4000155
R-NT2RM4000156//Homo sapiens chromosome 17, clone hRPK.136_H_19, complete sequence.//3.4e-23:335:72//AC005856
R-nnnnnnnnnnnn//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//1.6e-87:551:87//D12646
R-NT2RM4000169//Human ribosomal protein L37a mRNA sequence.//5.9e-14:122:88//L22154
R-NT2RM4000191
R-NT2RM4000197//HS_3241_A2_H05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=10 Row=O, genomic survey sequence.//2.8e-86:430:97//AQ206812
R-NT2RM4000199//Mus musculus Yp BAC GSMB-368G7 (Genome Systems Mouse BAC Library) complete sequence.//0.0047:193:63//AC006056
R-NT2RM4000200
R-NT2RM4000202//Homo sapiens chromosome 16, cosmid clone 378E2 (LANL), complete sequence.//2.1e-40:334:76//AC004035
R-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//5.2e-102:546:94//AB018255
R-NT2RM4000215
R-nnnnnnnnnnnn//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//2.1e-55:303:86//AC005383
R-NT2RM4000233//Struthio camelus microsatellite sequence OSM 7.//1.2e-07:198:67//AF003735
R-NT2RM4000244//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.7e-

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49:322:88//AC006116
R-NT2RM4000251//Homo sapiens Chromosome 22q11.2 BAC Clone 72f8 In DGCR Region, complete sequence.// 0.97:184:66//AC000085
R-NT2RM4000265//Human PAC clone DJ073F11 from Xq23, complete sequence.//6.2e-66:552:78//AC000055
R-NT2RM4000290//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 394I7, WORKING DRAFT SEQUENCE.//1.4e-05:229:65//AL023585
R-NT2RM4000324
R-NT2RM4000327//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 75N14, WORKING DRAFT SEQUENCE.//3.3e-42:443:75//Z97199
R-NT2RM4000344//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.// 6.4e-64:433:84//AC004826
R-NT2RM4000349//Human mRNA for KIAA0005 gene, complete cds.//7.7e-11:210:69//D13630
R-NT2RM4000354//Caenorhabditis elegans cosmid T14A8.//0.084:257:60//U50066
R-NT2RM4000356
R-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds.//8.7e-112:577:95//AB014542
R-NT2RM4000368
1.6e-48:348:85//AG006257
R-NT2RM4000386//Rat mRNA for growth potentiating factor, complete cds.//4.4e-35:141:87//D42148
R-NT2RM4000395//RPCI11-8N9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-8N9, genomic survey sequence.//1.4e-25:207:75//871494
R-NT2RM4000414//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING DRAFT SEQUENCE.//7.1e-17:492:64//AL031985
R-NT2RM4000421//RPCI11-66B1.TK RPCI11 Homo sapiens genomic clone R-66B1, genomic survey sequence.// 1.8e-40:311:82//AQ241167
R-NT2RM4000425//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SEQUENCE, 35 unordered pieces.//2.5e-47:316:87//AC005867
R-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.//1.6e-17:133: 78//AF062476
R-NT2RM4000457
R-NT2RM4000471//Homo sapiens mRNA for putative tRNA splicing protein, partial.//4.6e-113:559:96//AJ010952
R-NT2RM4000486//Homo sapiens mRNA, complete cds, clone:RES4-22C.//0.00015:170:67//AB000461
R-NT2RM4000496
R-NT2RM4000511//Rat troponin T cardiac isoform gene, complete cds.//0.21:290:58//M80829
R-NT2RM4000514//CIT-HSP-2169K4.TR CIT-HSP Homo sapiens genomic clone 2169K4, genomic survey sequence.//1.5e-20:150:89//B95717
R-nnnnnnnnnnnn//HS-1024-B2-G01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 803 Col=2 Row=N, genomic survey sequence.//6.3e-10:74:98//B34556
R-NT2RM4000520//Caenorhabditis elegans cosmid F36H12.//0.15:406:61//AF078790
R-NT2RM4000531
R-NT2RM4000532//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence.//1.0:119: 66//AE001391
R-NT2RM4000534//paramecium species 4.51er mt dna dimer: replication init. region, clone 2.//9.8e-05:326:60// K00909
R-NT2RM4000585//HS_3252_A2_G08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=16 Row=M, genomic survey sequence.//1.9e-69:376:93//AQ219890
R-NT2RM4000590//CIT-HSP-539O24.TV CIT-HSP Homo sapiens genomic clone 539O24, genomic survey sequence.//1.7e-38:226:93//B50657
R-NT2RM4000595//Human Chromosome X clone bWXD342, complete sequence.//1.0:239:61//AC004072
R-NT2RM4000603//RPCI11-49P13.TK RPCI11 Homo sapiens genomic clone R-49P13, genomic survey sequence.//0.77:139:64//AQ051950
R-nnnnnnnnnnn
R-NT2RM4000616//HS_3107_A2_B03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3107 Col=6 Row=C, genomic survey sequence.//1.3e-54:272:99//AQ210034
R-NT2RM4000674
R-NT2RM4000689//Mus musculus pericentrin mRNA, complete cds.//3.5e-70:551:80//U05823
R-NT2RM4000698
R-nnnnnnnnnnn
R-NT2RM4000712//Homo sapiens clone NH0512E16, complete sequence.//0.54:294:58//AC005039

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R-NT2RM4000717//Plasmodium falciparum MAL3P8, complete sequence.//0.050:387:58//AL034560
R-NT2RM4000733//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//1.0e-107:566:95//AL034379
R-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds.//1.1e-103:536:95//AB018303
R-NT2RM4000741//CIT-HSP-2294N4.TR CIT-HSP Homo sapiens genomic clone 2294N4, genomic survey sequence.//5.2e-41:244:93//AQ006361
R-NT2RM4000751//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SEQUENCE.//2.7e-28:416:67//AL034405
R-NT2RM4000764//Human HepG2 3' region MboI cDNA, clone hmd3g01m3.//2.1e-33:199:96//D17217
R-NT2RM4000778//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//0.00060:241:62//AC002980
R-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds.//2.9e-104:546:94//AB007920
R-NT2RM4000787//Homo sapiens, clone hRPK.3_A_1, complete sequence.//5.3e-32:321:77//AC006198
R-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216, complete sequence.//1.9e-111:552:97//AC005306
R-NT2RM4000795//Homo sapiens Chromosome 17p13 Cosmid Clone cos39, complete sequence.//0.74:364:57//U58675
R-NT2RM4000796//Homo sapiens full-length insert cDNA clone ZD62D10.//2.7e-105:510:98//AF086348
R-NT2RM4000798//Human polymorphic epithelial mucin core protein mRNA, 3' end.//7.7e-27:158:96//M21868
R-NT2RM4000813
R-NT2RM4000820//, complete sequence.//2.0e-104:432:97//AC005406
R-NT2RM4000833//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence.//2.0e-07:166:68//AB012248
R-NT2RM4000848//Rabies virus matrix (M) protein mRNA, complete cds.//0.073:70:84//M22013
R-NT2RM4000852//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:237:62//AC004709
R-NT2RM4000855
R-nnnnnnnnnnnn//HS_3189_B2_B08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3189 Col=16 Row=D, genomic survey sequence.//2.1e-06:114:73//AQ300597
R-NT2RM4000895//Pan troglodytes HS19.8-similar locus and Y Alu element, genomic survey sequence.//3.8e-46:207:91//AF077058
R-NT2RM4000950//Human BAC clone RG341D10 from 7p15-p21, complete sequence.//1.0:336:60//AC002530
R-NT2RM4000971//Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence.//7.1e-09:259:64//AF011889
R-NT2RM4000979
R-NT2RM4000996//HS_3164_A1_E02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3164 Col=3 Row=I, genomic survey sequence.//2.0e-82:443:94//AQ141622
R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds.//1.2e-112:545:97//AB018272
R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds.//7.9e-113:556:97//AB014539
R-NT2RM4001032//Homo sapiens Surf-5 and Surf-6 genes.//1.2e-10:120:82//AJ224639
R-NT2RM4001047//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 163G9, WORKING DRAFT SEQUENCE.//1.0:158:67//AL008733
R-NT2RM4001054//CIT-HSP-2292N8.TR CIT-HSP Homo sapiens genomic clone 2292N8, genomic survey sequence.//5.8e-19:118:97//AQ004096
R-nnnnnnnnnnnn//Mouse DNA with homology to EBV IR3 repeat, segment 1, clone Mu2.//1.0e-05:271:64//M10296
R-NT2RM4001092//CITBI-E1-2524J20.TR CITBI-E1 Homo sapiens genomic clone 2524J20, genomic survey sequence.//1.0:186:63//AQ277294
R-NT2RM4001116
R-NT2RM4001140//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.//3.6e-79:468:90//AC004593
R-NT2RM4001151//HS_2270_B1_E05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=9 Row=J, genomic survey sequence.//5.5e-62:312:98//AQ163739
R-NT2RM4001155//Homo sapiens chromosome 12p13.3 clone RPCI4-816N1, WORKING DRAFT SEQUENCE, 31 unordered pieces.//1.4e-107:536:97//AC005841
R-NT2RM4001160//HS_3015_B1_H10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3015 Col=19 Row=P, genomic survey sequence.//7.1e-35:201:95//AQ118712

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R-NT2RM4001187//X.laevis xUBFbeta2 mRNA for upstream binding factor 1.//0.019:177:63//X57201
R-NT2RM4001191//HS_3002_A1_F05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=9 Row=K, genomic survey sequence.//3.9e-33:230:75//AQ088791
R-NT2RM4001200//Homo sapiens full-length insert cDNA clone YL35H03.//7.5e-69:335:99//AF085857
R-NT2RM4001203
R-NT2RM4001204
R-NT2RM4001217
R-NT2RM4001256
R-NT2RM4001258
R-NT2RM4001309
R-NT2RM4001313//Homo sapiens 12q24.1 PAC RPCI1-71H24 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.00055:183:63//AC004551
R-NT2RM4001316//Homo sapiens chromosome 17, clone hCIT.117_K_16, complete sequence.//4.5e-21:212:79//AC004757
R-NT2RM4001320//CIT-HSP-2303E22.TR CIT-HSP Homo sapiens genomic clone 2303E22, genomic survey sequence.//3.8e-30:86:89//AQ021084
R-NT2RM4001340
0.0027:493:60//AC005133
R-NT2RM4001344
R-NT2RM4001347//CITBI-E1-2506I20.TR CITBI-E1 Homo sapiens genomic clone 2506I20, genomic survey sequence.//6.5e-16:1.01:99//AQ262797
R-NT2RM4001371//CITBI-E1-2503G21.TR CITBI-E1 Homo sapiens genomic clone 2503G21, genomic survey sequence.//0.063:140:65//AQ265776
R-NT2RM4001382//HS_3044_A1_F02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3044 Col=3 Row=K, genomic survey sequence.//0.96:103:66//AQ098668
R-NT2RM4001384//R.norvegicus mRNA for dendrin.//8.5e-07:120:75//Y09000
R-NT2RM4001410//Bovine cytochrome P450-scc mRNA fragment.//2.3e-15:199:75//M25920
R-NT2RM4001411//Rattus norvegicus FceRI gamma-chain interacting protein SH2-B (SH2-B) mRNA, complete cds.//1.7e-55:235:83//U57391
R-NT2RM4001412
R-NT2RM4001414//Homo sapiens Xp22 Cosmids U98B4 and U24F2 (Lawrence Livermore human cosmid library) complete sequence.//1.7e-80:489:89//U69730
R-NT2RM4001437//RPCI11-56D2.TJ RPCI11 Homo sapiens genomic clone R-56D2, genomic survey sequence.//3.8e-43:250:93//AQ081969
R-NT2RM4001444//Homo sapiens Xp22-171-173 BAC GSHB-312I4 (Genome Systems Human BAC Library) complete sequence.//0.0034:224:63//AC005926
R-NT2RM4001454//Homo Sapiens Chromosome X clone bWXD90, complete sequence.//2.4e-33:360:68//AC004075
R-NT2RM4001455//HS_3229_B1_E04_MR CIT Approved-Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 Col=7 Row=J, genomic survey sequence//1.0:183:61//AQ191289
R-NT2RM4001483//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.2e-51:451:79//AC005282
R-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds.//2.2e-102:547:93//AB014585
R-NT2RM4001519//HS_2208_A1_F07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=13 Row=K, genomic survey sequence.//0.25:214:63//AQ091836
R-NT2RM4001522//H.sapiens gene for Cu/Zn-superoxide dismutase.//3.6e-13:246:70//Z29336
R-NT2RM4001557//Plasmodium falciparum MAL3P4, complete sequence.//0.055:320:58//AL008970
R-NT2RM4001565//Homo sapiens chromosome 12p13.3 clone RPCI11-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//3.9e-26:329:72//AC005910
R-NT2RM4001566//Human trophinin mRNA, complete cds.//6.3e-38:296:86//U04811
R-NT2RM4001569//Human DNA sequence from clone 461P17 on chromosome 20q12-13.2. Contains four novel (pseudo)genes for proteins with Kunitz/Bovine pancreatic trypsin inhibitor and/or WAP-type (Whey Acidic Protein) 'four-disulfide core' domains, COX6C (Cytochrome C Oxidase Polypeptide VIC, EC 1.9.3.1) and RPL5 (60S Ribosomal Protein L5) pseudogenes, a pseudogene similar to part of the HSPD1 (HSP60, Mitochondrial Matrix Protein P1 precursor, Heat Shock Protein 60, GROEL protein, HUCHA60) gene, and the Major Epididymis-specific protein E4 precursor (HE4, Epididymis Secretory protein E4, WAP-type (Whey Acidic Protein) 'four-disulfide core' domain) gene. Contains ESTs, an STS, GSSs and a putative CpG island, complete sequence.//2.0e-35:213:89//AL031663

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R-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//5.4e-60:558:77//AF071317
R-nnnnnnnnnnn//M.musculus mRNA of enhancer-trap-locus 1.//4.8e-86:565:85//X69942
R-NT2RM4001594//Human interleukin-13 (IL-13) precursor gene, complete cds.//0.083:283:61//U31120
R-NT2RM4001597//HS_2059_A1_G11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2059 Col=21 Row=M, genomic survey sequence.//4.4e-09:105:83//AQ245136
R-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds.//6.7e-111:565:95//AB018334
R-NT2RM4001611//Homarus americanus ryanodine receptor (RyR) mRNA, partial cds.//1.0:364:61//AF051936
R-NT2RM4001629//RPCI11-54G14.TJ RPCI11 Homo sapiens genomic clone R-54G14, genomic survey sequence.//0.0018:347:61//AQ083173
R-NT2RM4001650
R-NT2RM4001662//Homo sapiens DNA sequence from PAC 159A15 on chromosome Xp11.21-p11.23. Contains inter-alpha-trypsin inhibitor heavy chain H3 precursor-like protein.//0.75:212:62//AL022575
R-NT2RM4001666//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-233A8, complete sequence.//2.6e-26:461:65//AC004685
R-NT2RM4001682//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//1.5e-107:544:96//AL031775
R-NT2RM4001710//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE.//1.8e-110:580:95//AL031447
R-NT2RM4001714//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.1e-10:543:59//AC004153
R-nnnnnnnnnnn//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//8.7e-111:577:94//AL034430
R-NT2RM4001731//Ovis aries dinucleotide repeat polymorphism at MAF92 locus.//0.017:93:73//M80527
R-NT2RM4001741//Mouse mRNA for talin.//2.4e-34:273:83//X56123
R-NT2RM4001746//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 316G12, WORKING DRAFT SEQUENCE.//1.7e-112:567:96//AL031709
R-NT2RM4001754//Homo sapiens PAC clone 248O15 from 13q12-q13, complete sequence.//1.4e-64:475:83//AC002483
R-NT2RM4001758//R.norvegicus mRNA for serine/threonine kinase MARK1.//1.9e-18:202:78//Z83868
R-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds.//2.0e-22:236:80//AB018270
R-NT2RM4001783//Homo sapiens clone DJ0981O07, complete sequence.//4.4e-106:551:95//AC006017
R-NT2RM4001810//T28D3TF TAMU Arabidopsis thaliana genomic clone T28D3, genomic survey sequence.//0.76:279:60//B27099
R-NT2RM4001813
R-NT2RM4001823
R-NT2RM4001828//HS_3073_A2_E01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3073 Col=2 Row=I, genomic survey sequence.//1.6e-46:255:96//AQ121030
R-NT2RM4001836//Sus scrofa microsatellite S0398 sequence.//9.4e-06:141:69//U78024
R-NT2RM4001841//Salmo salar microsatellite Ssa65 DNA.//1.5e-06:175:65//AF019184
R-NT2RM4001842//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.0e-07:332:61//AC005077
R-NT2RM4001856//Mus musculus clone OST16642, genomic survey sequence.//4.8e-30:235:85//AF046633
R-nnnnnnnnnnn//Hs_3244_B1_F10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=19 Row=L, genomic survey sequence.//3.0e-40:263:89//AQ252798
R-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//5.0e-119:592:97//Y17711
R-NT2RM4001876//Megastigmus wachtli dinucleotide microsatellite, clone MWA47CT.//0.13:134:64//AJ001069
R-NT2RM4001880
R-NT2RM4001905//HS_2016_B1_H11 _T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=21 Row=P, genomic survey sequence.//0.0066:264:59//AQ226877
R-NT2RM4001922//HS_2228_B2_B07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=14 Row=D, genomic survey sequence.//2.5e-35:205:96//AQ065498
R-NT2RM4001930//Homo sapiens chromosome 17, clone hRPC.34_M_24, complete sequence.//0.26:325:63//AC004562
R-NT2RM4001938//Homo sapiens chromosome 17, clone hRPC.1081_P_3, complete sequence.//2.9e-85:421:

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98//AC005207
R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//6.2e-109:556:95//AF098162
R-NT2RM4001953//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 473B4, WORKING DRAFT SEQUENCE.//1.3e-08:175:70//Z83826
R-NT2RM4001965//CIT-HSP-385N14.TR CIT-HSP Homo sapiens genomic clone 385N14, genomic survey sequence.//5.7e-69:532:81//B55044
R-nnnnnnnnnnnn//R.norvegicus mRNA for IP63 protein.//1.9e-61:352:83//X99330
R-NT2RM4001979//Homo sapiens full-length insert cDNA clone ZD29F04.//1.1e-98:465:100//AF086241
R-NT2RM4001984//Borrelia burgdorferi (section 47 of 70) of the complete genome.//0.14:461:60//AE001161
R-NT2RM4001987
R-NT2RM4002013
R-NT2RM4002018
R-NT2RM4002034//Homo sapiens chromosome 5, BAC clone 24p24 (LBNL H195), complete sequence.//3.6e-42:277:89//AC005353
R-NT2RM4002044//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence.//0.83:476:57//AC006204
R-NT2RM4002054
R-NT2RM4002062//Human microsomal epoxide hydrolase gene, exons 5 and 6.//0.11:136:67//U06659
R-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//2.9e-99:503:96//U82267
R-nnnnnnnnnnnn//Homo sapiens CAGH45 mRNA, complete cds.//9.6e-41:554:68//U80742
R-NT2RM4002067//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 329A5, WORKING DRAFT SEQUENCE.//7.7e-64:476:81//Z97832
R-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//1.1e-33:238:85//AF072758
R-NT2RM4002075//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0031:403:57//AC005504
R-NT2RM4002093//Human Chromosome 11 pac pDJ227b23, WORKING DRAFT SEQUENCE, 19 unordered pieces.//9.4e-07:322:62//AC000383
R-nnnnnnnnnnnn//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//5.6e-44:432:74//D12646
R-NT2RM4002128//Human HepG2 partial cDNA, clone hmd2e12m5.//2.0e-26:186:90//D17000
R-NT2RM4002140
R-NT2RM4002145//Homo sapiens full-length insert cDNA clone ZD38E12.//1.4e-15:193:76//AF086247
R-NT2RM4002146//Human ABL gene, intron 1b, partial sequence.//0.66:170:63//U07562
R-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds.//4.5e-110:560:96//AF084535
R-NT2RM4002174//Homo sapiens chromosome 17, clone hRPK.74_E_22, complete sequence.//8.0e-43:302:85//AC005696
R-NT2RM4002189
R-NT2RM4002194//Human Cosmid g5129g129 from 7q31.3, complete sequence.//0.29:382:60//AC003960
R-NT2RM4002205//Spiroplasma virus (SpV1-R8A2 B) complete genome.//3.5e-05:432:56//X51344
R-NT2RM4002213
R-NT2RM4002226//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//0.94:198:61//AC004448
R-NT2RM4002251
R-NT2RM4002256//Homo sapiens PAC clone DJ0570D02 from 7p13-p14, complete sequence.//2.3e-58:299:85//AC004837
R-NT2RM4002266//H.sapiens CpG island DNA genomic Mse1 fragment, clone 179f11, forward read cpg179f11.ft1a.//0.72:97:69//Z57487
R-NT2RM4002278//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//7.5e-49:405:84//AC005069
R-NT2RM4002281//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 702J19, WORKING DRAFT SEQUENCE.//1.7e-13:168:77//AL033531
R-NT2RM4002287
R-NT2RM4002294//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.98:208:65//AC004676
R-NT2RM4002301//HS_2028_A1_E10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2028 Col=19 Row=I, genomic survey sequence.//0.94:321:57//AQ233262
R-NT2RM4002323//Human DNA sequence from clone 59B16 on chromosome 6p22.1-22.3. Contains a pseudo-

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gene similar to GPISG20 and other exonucleases). Contains ESTs, STSs, GSSs, genomic markers D6S1691 and D6S299 and a ca repeat polymorphism, complete sequence.//1.9e-35:265:84//AL032822
R-nnnnnnnnnnnn//Human mRNA for KIAA0319 gene, complete cds.//2.4e-42:569:68//AB002317
R-NT2RM4002344//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.013:391:59//AC004709
R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds.//8.6e-121:593:97//AB014549
R-NT2RM4002374//Human DNA sequence from cosmid U131B10, between markers DXS366 and DXS87 on chromosome X contains XK membrane transport protein, ESTs and STS.//3.8e-44:258:86//Z73417
R-NT2RM4002383//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence.//0.00084:345:60//AC005316
R-NT2RM4002390
R-NT2RM4002409//RPCI11-45M10.TK RPCI11 Homo sapiens genomic clone R-45M10, genomic survey sequence.//0.99:151:66//AQ194411
R-NT2RM4002438
R-NT2RM4002446//Human DNA sequence from clone 360A4 on chromosome 16. Contains ESTs, complete sequence.//2.8e-103:533:95//AL031008
R-NT2RM4002452
R-NT2RM4002457//Homo sapiens chromosome 16, cosmid clone 321D4 (LANL), complete sequence.//0.99:171:64//AC004034
R-NT2RM4002460//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//0.96:94:71//Z92545
R-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds.//2.9e-102:508:97//AF083255
R-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds.//7.0e-31:172:98//AB014591
R-NT2RM4002493//CIT-HSP-2296C24.TF CIT-HSP Homo sapiens genomic clone 2296C24, genomic survey sequence.//0.46:182:62//AQ006882
R-NT2RM4002499//Human v-fos transformation effector protein (Fte-1), mRNA complete cds.//7.3e-24:134:99//M84711
R-NT2RM4002504//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 geneexons 1,2, and 3, complete sequence.//3.9e-11:334:63//AC002368
R-nnnnnnnnnnnn
R-NT2RM4002532//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 341D10, WORKING DRAFT SEQUENCE.//3.4e-17:171:79//Z97985
R-NT2RM4002534
R-NT2RM4002567//Homo sapiens chromosome 7 clone UWGC:g1564a040 from 7p14-15, complete sequence.//2.2e-26:181:76//AC005271
R-NT2RM4002571
R-NT2RM4002593//CIT-HSP-2303L15.TF CIT-HSP Homo sapiens genomic clone 2303L15, genomic survey sequence.//0.034:73:82//AQ015579
R-NT2RM4002623//Homo sapiens clone UWGC:g1564a209 from 7p14-15, complete sequence.//0.0014:670:55//AC005862
R-NT2RP2000001//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.00087:251:59//AE001422
R-NT2RP2000006//Human DNA sequence from PAC 155D22 on chromosome 6q27. Contains EST, STSs and a GSS.//2.7e-37:259:86//Z97205
R-NT2RP2000008//RPCI11-41G16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41G16, genomic survey sequence.//4.1e-25:365:70//AQ029090
R-NT2RP2000027//Homo sapiens chromosome 17, clone HCIT305D20, complete sequence.//6.0e-05:307:62//AC004098
R-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds.//8.4e-41:223:96//AB018290
R-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//5.8e-63:325:96//AF061749
R-NT2RP2000054//Human tyrosinase gene, 5'-flanking region (containing enhancer element resposible for pigment cell-specific transcription).//0.88:210:60//D26163
R-NT2RP2000056//Mus musculus epsilon tyrosine phosphatase cytoplasmic isoform (Ptpre) mRNA, complete cds.//4.7e-38:377:78//U36758
R-NT2RP2000067//Rat mRNA for growth potentiating factor, complete cds.//6.0e-10:137:79//D42148

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R-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//3.1e-76:381:98//AC005754
R-NT2RP2000076//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.3e-06:380:60//AE001372
R-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds.//3.5e-77:379:97+++F050079
R-NT2RP2000079//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1125A11, WORKING DRAFT SEQUENCE.//6.5e-32:314:78//AL034549
R-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//5.6e-74:378:96//AB018338
R-NT2RP2000091//Homo sapiens clone RG015P03, complete sequence.//9.3e-21:226:76//AC005048
R-NT2RP2000097//Human DNA sequence from cosmid U209G1 on chromosome X.//9.2e-40:278:81//Z68873
R-NT2RP2000098//Human BAC clone RG333F24 from 7q11.2-q21, complete sequence.//0.34:132:65//AC004015
R-NT2RP2000108//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//3.1e-09:259:67//AC003973
R-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//1.8e-74:386:95//AB018356
R-NT2RP2000120//CITBI-E1-2503M8.TR CITBI-E1 Homo sapiens genomic clone 2503M8, genomic survey sequence.//5.1e-05:87:77//AQ263909
R-nnnnnnnnnnn
R-nnnnnnnnnnn//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//4.9e-11:153:69//AC004827
R-NT2RP2000147
R-NT2RP2000153//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//0.0058:261:57//U95626
R-NT2RP2000157//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.5e-119:603:96//AC005924
R-NT2RP2000161//CIT-HSP-2045P7.TR CIT-HSP Homo sapiens genomic clone 2045P7, genomic survey sequence.//0.89:173:63//B79728
R-NT2RP2000175
R-NT2RP2000183
R-NT2RP2000195//Homo sapiens chromosome 17, clone hRPK.60_A_24, complete sequence.//4.3e-39:306:83//AC005325
R-NT2RP2000205//Human DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155
R-NT2RP2000224//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//7.3e-55:306:94//AC004382
R-NT2RP2000232
R-NT2RP2000233//Mus musculus tumor metastasis associated gene product (MAG) mRNA, complete cds.//7.6e-13:144:75//U88401
R-NT2RP2000239//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//9.6e-63:410:86//AC004066
R-NT2RP2000248//Caenorhabditis elegans cosmid T01C8.//1.0:282:58//U58726
R-NT2RP2000257//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence.//2.5e-11:163:72//AC004894
R-NT2RP2000258//Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence.//0.58:442:58//AC004077
R-NT2RP2000270//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence.//1.1e-39:292:84//AL009179
R-NT2RP2000274//CIT-HSP-237901.TR CIT-HSP Homo sapiens genomic clone 237901, genomic survey sequence.//6.9e-10:121:81//AQ109409
R-NT2RP2000288
R-NT2RP2000289
R-NT2RP2000297//Homo sapiens full-length insert cDNA clone ZB81C03.//7.7e-109:519:99//AF086165
R-NT2RP2000298
R-NT2RP2000310//Homo sapiens p53 induced protein mRNA, partial cds.//1.5e-38:224:93//AF010310
R-NT2RP2000327//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE

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pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//4.3e-113:580:96//AL022398
R-NT2RP2000329//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.// 7.4e-47:367:77//AC006039
R-NT2RP2000337//Anopheles quadrimaculatus NADH dehydrogenase subunits (1-4, 4L, 5-6); cytochrome oxidase subunits (1-3); adenosine triphosphatase subunits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large and small subunits).//4.9e-08:494:58//L04272

R-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds.//3.4e-46:262: 94//U83981
R-NT2RP2000369//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.0e-07:334:61//AC002993
R-NT2RP2000414//Mouse DNA sequence *** SEQUENCING IN PROGRESS *** from clone BAC394, WORKING DRAFT SEQUENCE.//7.0e-08:98:83//AJ004828
R-NT2RP2000420//Homo sapiens chromosome 17, clone hRPK.640_I_15, complete sequence.//0.99:150:62// AC005324
R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//4.6e-19:142: 90//AF102265
R-NT2RP2000438//RPCI11-62I13.TK RPCI11 Homo sapiens genomic clone R-62I13, genomic survey sequence.// 3.1e-06:103:79//AQ199572
R-NT2RP2000448//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//2.0e-22:276:73// AC004691
R-NT2RP2000459//CIT-HSP-2013N9.TR CIT-HSP Homo sapiens genomic clone 2013N9, genomic survey sequence.//5.5e-27:205:87//853940
R-NT2RP2000498//Homo sapiens Chromosome 11q23 PAC clone pDJ149k2 containing PLZF gene encoding kruppel-like zinc finger protein, complete sequence.//6.0e-12:119:84//AC001234
R-NT2RP2000503//Human CYP11B2 gene for steroid 18-hydroxylase (P-450 C18), 5'-flanking region and exon 1.//0.48:201:64//D10170
R-NT2RP2000510//Bactrocera dorsalis strain Tahiti mitochondrial D-loop region, complete sequence.//3.6e-07: 472:59//AF033929
R-nnnnnnnnnnn
R-NT2RP2000523//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 150C2, WORKING DRAFT SEQUENCE.//2.3e-61:317:97//AL022318
R-NT2RP2000603//Homo sapiens mRNA for MCM3 import factor, complete cds.//6.6e-29:167:97//AB005543
R-NT2RP2000617
R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//2.5e-64:335:96//AB014514
R-NT2RP2000644//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//1.8e-28:383:70//Z92545
R-NT2RP2000656//Homo sapiens DNA sequence from PAC 874C20 on chromosome 6p22.1-22.3. Contains a Zinc Finger Protein ZFP47 LIKE gene, a Zinc Finger Protein pseudogene and a Zinc Finger Protein SRE-ZBP pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.0093:110:70//AL021997
R-NT2RP2000658//Bacillus thuringiensis chitinase (chi) gene, complete cds.//0.73:301:60//U89796
R-NT2RP2000668
R-NT2RP2000678//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 8/15, WORKING DRAFT SEQUENCE.//2.8e-11:256:66//AP000015
R-NT2RP2000710//Genomic sequence from Human 17, WORKING DRAFT SEQUENCE, 9 unordered pieces.// 0.036:176:69//AC002346
R-NT2RP2000715//Homo sapiens PAC clone DJ1066K24 from 7p15, complete sequence.//2.7e-110:555:96// AC004540
R-NT2RP2000731//Human DNA sequence from clone 497J21 on chromosome 6q26-27. Contains a KOC (KH-domain containg transcript overexpressed in cancer) pseudogene, genomic marker D6S193, ESTs, STSs and GSSs, and a ca repeat polymorphism, complete sequence.//2.6e-18:319:68//AL023775
R-NT2RP2000758//CIT-HSP-507A14.TP CIT-HSP Homo sapiens genomic clone 507A14, genomic survey sequence.//1.0:189:60//B50590
R-NT2RP2000764
R-NT2RP2000809//Human BAC clone RG356F09 from 7p21, complete sequence.//1.7e-24:215:81//AC004002
R-NT2RP2000812//CIT-HSP-2281C3.TR CIT-HSP Homo sapiens genomic clone 2281C3, genomic survey se-

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quence.//9.5e-32:176:97//B99575
R-nnnnnnnnnnnn//paramecium species 5.87 mt dna dimer: replication init. region.//0.0077:418:57//K00916
R-NT2RP2000816//F.rubripes GSS sequence, clone 011H02aA6, genomic survey sequence.//0.61:52:73//AL011013
R-NT2RP2000819
R-NT2RP2000841//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 43408, WORKING DRAFT SEQUENCE.//0.00012:181:70//AL033504
R-NT2RP2000842//Mus musculus (C57BL/10 X C3H)F2 clone 4.9 novel mRNA from reninexpressing kidney tumor cell line, partial sequence.//3.7e-27:388:72//U13370
R-NT2RP2000845//Homo sapiens chromosome 17, clone hRPK.849_N_15, complete sequence.//0.0022:200:68//AC005703
R-NT2RP2000863
R-NT2RP2000880//Homo sapiens mRNA for putative GTP-binding protein, partial.//2.3e-43:279:89//AJ006412
R-NT2RP2000892//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epitherium cancer, segment 7/10.//0.0028:221:62//AB020875
R-NT2RP2000931//Homo sapiens mRNA for KIAA0723 protein, complete cds.//2.2e-55:290:96//AB018266
R-NT2RP2000938//Homo sapiens full-length insert cDNA clone ZD55G12.//2.1e-37:215:93//AF086336
R-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//3.0e-96:494:96//AB018298
R-NT2RP2000965
R-NT2RP2000970//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence.//4.5e-87:440:97//AL021393
R-NT2RP2000985//Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence.//5.4e-93:484:95//AC005277
R-NT2RP2000987//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.1e-06:318:62//AE001372
R-NT2RP2001036//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 410I8, WORKING DRAFT SEQUENCE.//2.0e-24:273:73//AL031732
R-NT2RP2001044//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//3.3e-07:365:65//AC005140
R-NT2RP2001065//Caenorhabditis elegans cosmid F10G7.//9.2e-06:273:59//U40029
R-NT2RP2001070//CITBI-E1-2503F4.TF CITBI-E1 Homo sapiens genomic clone 2503F4, genomic survey sequence.//0.13:97:72//AQ265973
R-NT2RP2001094//Mycoplasma mycoides mycoides SC immunodominant protein P72 (p72) gene, complete cds, mannitol-1-phosphate dehydrogenase (mt1D) gene, partial cds and insertion sequence IS1296, complete sequence.//0.018:373:57//U61140
R-NT2RP2001119
R-NT2RP2001127//Homo sapiens HRIHFB2060 mRNA, partial cds.//4.5e-55:304:94//AB015348
R-NT2RP2001137//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//0.69:129:65//AL022394
R-NT2RP2001149//Sequence 5 from Patent US 4798885.//8.5e-28:322:77//I01838
R-NT2RP2001168
R-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds.//4.8e-95:490:96//AB 007949
R-NT2RP2001174//CIT-HSP-2170B18.TR CIT-HSP Homo sapiens genomic clone 2170B18, genomic survey sequence.//1.3e-33:204:93//B89680
R-NT2RP2001196//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-65, complete sequence.//1.7e-06:413:61//AL010134
R-NT2RP2001218//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//8.5e-15:278:68//AL022153
R-NT2RP2001226//Human DNA sequence from clone 1170D6 on chromosome Xq22.3-23. Contains a pseudogene similar to U-SNRNP associated Cyclophilin (USA-CYP, EC 5.2.1.8), ESTs, an STS and a GSS, complete sequence.//0.0020:462:57//AL030995
R-NT2RP2001233//CIT-HSP-2356P23.TR CIT-HSP Homo sapiens genomic clone 2356P23, genomic survey sequence.//8.0e-108:547:96//AQ081110
R-NT2RP2001245//Spodoptera frugiperda 16S rRNA gene, Val-tRNA, and Leu-tRNA genes, and ND-1 protein gene, 5' end.//0.0052:350:58//M76713

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R-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds.//4.6e-111:544:97//AB018353
R-NT2RP2001277//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y59A8, WORKING DRAFT SEQUENCE.//0.0058:327:59//Z98870
R-NT2RP2001290//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.96:187:65//AC004709
R-NT2RP2001295//Homo sapiens BAC clone NH0491B03 from 7p21-p15, complete sequence.//0.59:218:62//AC006041
R-NT2RP2001312//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 349A12, WORKING DRAFT SEQUENCE.//0.12:117:64//AL033520
R-NT2RP2001327//Caenorhabditis elegans cosmid R04D3, complete sequence.//0.31:119:66//Z70212
R-NT2RP2001328//HS_2213_A1_D07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=13 Row=G, genomic survey sequence.//1.7e-22:200:83//AQ136874
R-NT2RP2001347//Plasmodium falciparum MAL3P8, complete sequence.//0.81:509:56//AL034560
R-NT2RP2001378//H.sapiens DNA sequence.//0.94:147:63//Z22404
R-NT2RP2001381//Homo sapiens cyclin E2 mRNA, complete cds.//3.2e-09:75:97//AF091433
R-NT2RP2001392//Myxococcus xanthus ATP-dependent protease (bsgA) gene, complete cds.//0.079:178:62//L19301
R-NT2RP2001394//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//3.4e-60:351:90//Z93242
R-NT2RP2001397//Hamster mRNA for cyclinB2, complete cds.//5.4e-55:320:83//D17294
R-NT2RP2001420//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1108D11, WORKING DRAFT SEQUENCE.//1.0e-44:246:85//AL034419
R-NT2RP2001423//Human DNA sequence from clone 726F20 on chromosome 1p36.11-36.23. Contains ESTs and a GSS, complete sequence.//3.7e-05:417:61//AL031273 R-NT2RP2001427//Human Chromosome 11 Cosmid cSRL34e5, complete sequence.//0.94:287:59//U73643
R-NT2RP2001436//Mus musculus clone OST1784, genomic survey sequence.//5.2e-31:299:77//AF046702
R-NT2RP2001440//Rattus norvegicus mRNA for 14-3-3 protein gamma-subtype, complete cds.//7.8e-75:548:83//D17447
R-NT2RP2001445//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0e-06:452:59//AC004801
R-NT2RP2001449//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//5.1e-08:218:67//AC004846
R-NT2RP2001450
R-NT2RP2001467//Human BAC clone RG343P13 from 7q31, complete sequence.//3.8e-31:254:83//AC002465
R-NT2RP2001506//C.barati p-47, ntnh, bonT genes.//1.2e-06:415:60//Y12091
R-NT2RP2001511//Plasmodium falciparum MAL3P7, complete sequence.//0.11:155:63//AL034559
R-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1.//2.1e-104:545:95//Y14494
R-NT2RP2001526//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence.//7.0e-16:283:68//AC004596
R-NT2RP2001536//Human DNA from chromosome 14-specific cosmid containing XRCC3 DNA repair gene, genomic sequence, complete sequence.//7.7e-16:108:96//AF037222
R-NT2RP2001560//CIT978SK-A-56H4.TP CIT978SK Homo sapiens genomic clone A-56H4, genomic survey sequence.//0.052:112:66//B73597
R-NT2RP2001569//CIT-HSP-2335F8.TF CIT-HSP Homo sapiens genomic clone 2335F8, genomic survey sequence.//6.0e-78:383:98//AQ042029
R-NT2RP2001576//Homo sapiens sulfonylurea receptor (SUR2) gene, exon 37.//0.33:135:66//AF061322
R-NT2RP2001581//Homo sapiens (clone MFD220) PCR primer.//2.7e-07:240:63//L15407
R-NT2RP2001597//HS_3016_B2_F06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3016 Col=12 Row=L, genomic survey sequence.//5.3e-45:310:87//AQ118854
R-NT2RP2001601//Homo sapiens chromosome 17, clone hRPK.855_D_21, complete sequence.//0.015:445:58//AC006079
R-NT2RP2001613//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence.//3.5e-16:413:63//AF009326
R-NT2RP2001628//Phytomonas serpens kinetoplast maxicircle ribosomal protein S12 (G6) edited mRNA, complete cds.//0.11:190:63//AF034626
R-NT2RP2001663//Homo sapiens Chromosome 16 BAC clone CIT987SK-625P11, complete sequence.//3.0e-26:157:81//AC004125
R-NT2RP2001677//Homo sapiens chromosome 9, P1 clone 11659, complete sequence.//3.0e-58:305:96//

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AC004472
R-NT2RP2001678//Human BAC clone RG222A16 from 7q31, complete sequence.//0.95:107:66//AC002385
R-NT2RP2001699//Mus musculus erythroid ankyrin and two alternatively spliced erythroid ankyrins (Ank1) gene, putative exon 41 and partial cds.//8.8e-05:211:63//U76758
R-NT2RP2001720//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//4.7e-68:352:97//AC004079
R-NT2RP2001721//HS-1052-B1-G06-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 774 Col=11 Row=N, genomic survey sequence.//7.7e-05:346:59//B40914
R-NT2RP2001740//HS_3213_A2_D02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=4 Row=G, genomic survey sequence.//1.1e-16:162:82//AQ175104
R-NT2RP2001748//Human gene for L-histidine decarboxylase, complete cds.//2.0e-33:312:77//D16583
R-NT2RP2001762//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//2.3e-100:435:97//AC004783
R-NT2RP2001813//Human leukocyte common antigen T200 (CD45, LCA) gene, exon 9.//0.031:261:60//M23468
R-NT2RP2001861
R-NT2RP2001869//Sequence 5 from patent US 5595900.//4.2e-21:194:77//I34189
R-NT2RP2001876
R-NT2RP2001883//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//5.0e-111:485:97//AL031864
R-NT2RP2001900
R-NT2RP2001907//Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.//5.4e-42:382:77//U07563
R-NT2RP2001926//HS_3180_B2_F02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3180 Col=4 Row=L, genomic survey sequence.//2.8e-25:138:80//AQ185415
R-NT2RP2001936//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:320:60//AC005504
R-NT2RP2001943//Dictyostelium discoideum PkgA (pkgA) gene, partial cds.//1.4e-08:378:59//AF020280
R-NT2RP2001946//Homo sapiens clone NH0140K04, complete sequence.//3.6e-85:409:100//AC005033
R-NT2RP2001947//Human mRNA for KIAA0390 gene, complete cds.//0.85:140:64//AB002388
R-NT2RP2001969
R-NT2RP2001976//CIT-HSP-2281C3.TR CIT-HSP Homo sapiens genomic clone 2281C3, genomic survey sequence.//2.0e-60:307:98//B99575
R-NT2RP2001985//Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20 (ESSAII project).//0.031:282:61//AL022140
R-NT2RP2002025
R-NT2RP2002032//CITBI-E1-2502C19.TF CITBI-E1 Homo sapiens genomic clone 2502C19, genomic survey sequence.//1.2e-52:285:95//AQ264715
R-NT2RP2002033//Human (lambda) DNA for immunoglobin light chain.//1.1e-08:389:61//D88270
R-NT2RP2002041//Homo sapiens 12p13.3 BAC RPCI11-319E16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.1e-49:264:97//AC006206
R-NT2RP2002046//Human BAC clone GS119P05 from 7q21, complete sequence.//0.0023:429:61//AC004011
R-NT2RP2002047//P.falciparum PK1 gene.//0.00015:239:62//X83707
R-NT2RP2002058//HS_2183_A1_G01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=1 Row=M, genomic survey sequence.//1.2e-21:185:84//AQ022560
R-NT2RP2002066//G.gallus microsatellite DNA (LEI0222 (=T15ivD04)).//0.18:102:70//Z83792
R-NT2RP2002070//P.falciparum major merozoite surface antigen (PMMSA) mRNA, complete cds, isolate FC27.//0.95:192:61//M19143
R-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.//3.8e-25:182:86//AF052183
R-NT2RP2002079//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STss, GSSs, and a putative CpG island, complete sequence.//1.7e-10:97:90//AL009178
R-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//4.6e-59:376:89//AJ007509
R-NT2RP2002105
R-NT2RP2002124//RPCI11-75J16.TJ RPCI11 Homo sapiens genomic clone R-75J16, genomic survey sequence.//0.58:191:64//AQ266779

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R-NT2RP2002137//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//0.0065:294:61//AC005913
R-NT2RP2002154
R-NT2RP2002172//RPCI11-90C20.TJ RPCI11 Homo sapiens genomic clone R-90C20, genomic survey sequence.//0.049:160:65//AQ282591
R-NT2RP2002185//CIT-HSP-2341I15.TF CIT-HSP Homo sapiens genomic clone 2341I15, genomic survey sequence.//6.0e-36:230:90//AQ053355
R-NT2RP2002192//HS_2222_B1_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=15 Row=L, genomic survey sequence.//1.9e-15:249:71//AQ178491
R-NT2RP2002193//Rattus norvegicus potassium channel regulatory protein KChAP mRNA, complete cds.//4.7e-35:438:73//AF032872
R-NT2RP2002208//Hansenula wingei mitochondrial DNA, complete sequence.//0.00057:468:57//D31785
R-NT2RP2002219//HS_2058_A1_C09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=17 Row=E, genomic survey sequence.//3.4e-55:512:77//AQ234380
R-NT2RP2002231//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-31, complete sequence.//1.5e-06:398:61//Z98557
R-nnnnnnnnnnnn//Sequence 11 from patent US 5624818.//3.3e-91:553:87//I41141
R-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//3.0e14:132:84//AF005418
R-NT2RP2002259//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 118J21, WORKING DRAFT SEQUENCE.//1.6e-96:548:91//AL033527
R-NT2RP2002270//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//5.1e-06:391:60//AC004605
R-NT2RP2002292//Genomic sequence from Human 13, complete sequence.//0.91:159:64//AC001226
R-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//1.3e-101:527:94//AF069532
R-NT2RP2002316//Plasmodium falciparum chromosome 2, section 45 of 73 of the complete sequence.//0.00052:389:59//AE001408
R-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds.//2.3e-112:567:95//AF093668
R-NT2RP2002333//Rat POU domain factor (Brn-5) mRNA.//1.5e-22:323:73//L23204
R-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//3.7e-102:600:89//AF038958
R-NT2RP2002394//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.039:399:59//AC005308
R-NT2RP2002408//HS_2212_A1_E09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2212 Col=17 Row=I, genomic survey sequence.//9.6e-35:231:88//AQ184632
R-NT2RP2002426//Human DNA sequence from clone 101G11 on chromosome 22q12. Contains an ACO2 (Mitochondrial Aconitate Hydratase (Aconitase, Citrate Hydro-Lyase, EC 4.2.1.3)) pseudogene, ESTs, STSs, GSSs and a putative CpG island, complete sequence.//2.8e-39:308:82//AL021877
R-NT2RP2002439//Leishmania tarentolae mitochondrial electron transport chain component mRNA.//0.022:102:71//M74225
R-NT2RP2002457//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence.//0.00099:354:59//Z99289
R-NT2RP2002464//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 6/15, WORKING DRAFT SEQUENCE.//0.0015:219:67//AP000013
R-NT2RP2002475
R-nnnnnnnnnnnn//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//3.1e-113:605:92//AB005289
R-NT2RP2002498//Human DNA sequence from PAC 162H14 on chromosome 22. Contains 3' part of a FIBULIN 1 like gene and ESTs, complete sequence.//0.32:210:64//Z98047
R-NT2RP2002503//Homo sapiens, clone hRPK.15_A_1, complete sequence.//4.0e-86:429:98//AC006213
R-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds.//2.7e-105:583:91//AB018334
R-NT2RP2002520//Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & amp; tRNA-Met genes.//0.14:406:58//AJ223323
R-NT2RP2002537//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 500L14, WORKING DRAFT SEQUENCE.//2.8e-16:188:78//AL023583

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R-NT2RP2002546//Homo sapiens clone TUA8 Cri-du-chat region mRNA.//4.7e-108:571:93//AF009314
R-NT2RP2002549//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence.//1.1e-103:422:95//AC005316
R-NT2RP2002591//Human DNA binding protein (HPF2) mRNA, complete cds.//1.8e-36:526:67//M27878
R-NT2RP2002595
R-NT2RP2002606//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 2705, WORKING DRAFT SEQUENCE.//7.2e-10:211:71//AL033529
R-NT2RP2002609
R-NT2RP2002618//Plasmodium falciparum MAL3P6, complete sequence.//2.9e-05:566:60//Z98551
R-NT2RP2002621//Human DNA sequence from PAC 341I10 on chromosome 6q22.2-22.33. Contains 60S ribosomal protein L5 like (pseudo)gene, ESTs and STSs.//1.1e-38:348:78//Z97352
R-NT2RP2002643//Homo sapiens chromosome 11 clone pTWB15.28 map 11p15.4-p15.5, genomic survey sequence.//1.2e-35:414:66//AF074030
R-NT2RP2002672//Homo sapiens chromosome 10 clone CIT-HSP-1326H7 map 10q24.3-10q25.1, complete sequence.//1.3e-77:403:95//AC005384
R-NT2RP2002701
R-NT2RP2002706//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//4.0e-42:147:90//AC005778
R-NT2RP2002710//P.falciparum serine rich protein (SERP I) gene.//0.84:135:67//J03983
R-NT2RP2002727//, complete sequence.//1.0:363:59//AC005815
R-NT2RP2002736//Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence.//0.44:267:60//AC004138
R-NT2RP2002740//Homo sapiens Xp22 BAC GSHB-600G8 (Genome Systems Human BAC library) complete sequence.//0.0016:474:60//AC004674
R-NT2RP2002741//HS_3051_B1_H11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=21 Row=P, genomic survey sequence.//1.1e-38:217:86//AQ106283
R-NT2RP2002750//Homo sapiens 12q24.1 PAC RPCI1-315L5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.0e-36:430:75//AC002395
R-NT2RP2002752//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 366L4, WORKING DRAFT SEQUENCE.//8.2e-41:437:76//AL023494
R-NT2RP2002753//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.8e-100:496:97//AC004882
R-NT2RP2002769//paramecium species 5,311 mt dna dimer: replication init. region.//7.4e-10:404:60//K00917
R-NT2RP2002778//Homo sapiens clone 24606 mRNA sequence.//1.2e-63:341:94//AF070537
R-NT2RP2002800//RPCI11-37G8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-37G8, genomic survey sequence.//4.9e-60:321:95//AQ029850
R-NT2RP2002839//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.9e-100:492:98//AC006078
R-NT2RP2002857//HS_3026_B2_H07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=14 Row=P, genomic survey sequence.//8.9e-06:242:62//AQ 128697
R-NT2RP2002862//RPCI11-42I15.TJ RPCI11 Homo sapiens genomic clone R-42I15, genomic survey sequence.//1.5e-44:270:85//AQ052700
R-NT2RP2002880//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 150C2, WORKING DRAFT SEQUENCE.//1.0:295:58//AL022318
R-NT2RP2002891
R-NT2RP2002925//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 243L18, WORKING DRAFT SEQUENCE.//2.0e-24:395:67//AL034395
R-NT2RP2002928//Plasmodium falciparum MAL3P5, complete sequence.//0.044:461:55//AL034556
R-NT2RP2002929//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.35:491:56//AC005140
R-NT2RP2002954//Homo sapiens chromosome 17, clone hRPK.628_E_12, complete sequence.//1.0:275:61//AC005701
R-NT2RP2002959//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//2.7e-61:508:79//U62483
R-NT2RP2002979//RPCI11-20F13.TPK RPCI-11 Homo sapiens genomic clone RPCI-11-20F13, genomic survey sequence.//0.88:110:72//AQ008132
R-NT2RP2002980//Homo sapiens PAC clone DJ0841B21 from 7q21.1-q31.1, complete sequence.//1.1e-102:433:95//AC004140

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R-NT2RP2002986//Human DNA sequence from clone 1147O16 on chromosome Xp21.1-21.3. Contains 13 exons of the DMD muscular dystrophy gene. Contains an STS and GSSs, complete sequence.//0.31:219:62//AL031542
R-NT2RP2002987//Homo sapiens chromosome 18, clone hRPK.24_A_23, complete sequence.//1.3e-51:283:88//AC005968
R-NT2RP2002993//Human DNA sequence from PAC 106B9 on chromosome Xq21://4.3e-11:430:63//AL021307
R-NT2RP2003000//Saccharomyces cerevisiae mitochondrion transfer RNA- Leu, Gln, Lys, Arg, Gly, Asp, Ser2, Arg2, Ala, Ile, Tyr, Asn genes.//0.00088:347:62//L36887
R-NT2RP2003034//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epitherium cancer, segment 2/10.//3.5e-33:271:82//AB020870
R-NT2RP2003073
R-NT2RP2003099//Homo sapiens PAC clone DJ0886O08 from 7q32-q35, complete sequence.//1.5e-45:548:69//AC004914
R-NT2RP2003108
R-NT2RP2003117//Homo sapiens clone DJ1137M13, complete sequence.//2.0e-51:323:88//AC005378
R-NT2RP2003121//HS_2238_A1_E08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=15 Row=I, genomic survey sequence.//0.00055:324:61//AQ293058
R-NT2RP2003125
R-NT2RP2003129
R-NT2RP2003137//Human BAC clone RG084D04 from 7q31, complete sequence.//1.1e-46:521:74//AC003084
R-NT2RP2003161//Homo sapiens chromosome 10 clone CIT-HSP-1287C20, complete sequence.//1.0:368:59//AC005879
R-NT2RP2003164//Dictyostelium discoideum actin 4 gene, 3' UTR.//1.0:120:64//M25581
R-NT2RP2003165//Homo sapiens chromosome 17, clone hRPK.1018_N_14, complete sequence.//2.2e-71:467:86//AC005823
R-NT2RP2003177
R-NT2RP2003194//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 996D20, WORKING DRAFT SEQUENCE.//1.1e-95:585:88//AL031597
R-NT2RP2003206//P.falciparum interspersed repeat antigen (FIRA) gene.//0.039:338:60//M17877
R-NT2RP2003230//Plasmodium falciparum MAL3P6, complete sequence.//1.9e-11:542:60//Z98551
R-NT2RP2003237//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence.//1.0:311:60//AB016888
R-NT2RP2003243//CIT-HSP-2368D12.TR CIT-HSP Homo sapiens genomic clone 2368D12, genomic survey sequence.//0.39:112:66//AQ077738
R-NT2RP2003265//Muridae sp. (mouse-rat, neuroblastoma-glioma hybrid cell line NGD5) mRNA, complete cds.//1.3e-38:273:83//L38481
R-NT2RP2003272//Homo sapiens clone UWGC:y17c131 from 6p21, complete sequence.//4.4e-15:181:66//AC004187
R-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds.//4.2e-110:565:95//AB014525
R-NT2RP2003280//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.2e-12:221:70//AC005831
R-NT2RP2003286//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//0.86:379:60//AC005261
R-NT2RP2003293//Homo sapiens clone RG252P22, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0e-39:418:74//AC005079
R-NT2RP2003295//HS_2053_B1_A10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2053 Col=19 Row=B, genomic survey sequence.//0.0016:346:61//AQ235251
R-NT2RP2003297//Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence.//0.74:397:56//AC002332
R-NT2RP2003308//Homo sapiens PAC clone DJ1098B01 from 7q11.23-q21, complete sequence.//0.99:447:60//AC004960
R-NT2RP2003329//C.reinhartii psbB 5' flanking region.//0.79:161:59//X59731
R-NT2RP2003339//RPCI11-57H15.TK RPCI11 Homo sapiens genomic clone R-57H15, genomic survey sequence.//0.13:184:64//AQ116039
R-NT2RP2003347//RPCI11-15B19.TV RPCI-11 Homo sapiens genomic clone RPCI-11-15B19, genomic survey sequence.//6.4e-31:218:89//B76357
R-NT2RP2003367//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//9.0e-11:101:84/U91321
R-NT2RP2003391//HS_2255_B2_B04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-

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nomic clone Plate=2255 Col=8 Row=D, genomic survey sequence.//1.6e-38:247:90//AQ068937
R-NT2RP2003393//RPCI11-44K6.TJ RPCI11 Homo sapiens genomic clone R-44K6, genomic survey sequence.//3.9e-31:290:79//AQ202481
R-NT2RP2003394//Yeast mitochondrial oxi3 gene exon 1 for cytochrome c oxidase subunit I.//5.1e-14:579:61//X14910
R-NT2RP2003401//Caprine arthritis-encephalitis virus tat protein (tat) and envelope glycoprotein (env) gene, partial cds.//0.32:174:66//U81429
R-NT2RP2003433//Ascidian mRNA for HRSec61, complete cds.//1.5e-10:193:69//D25536
R-NT2RP2003445//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//4.4e-99:585:89//AL023808
R-NT2RP2003446
R-NT2RP2003456//Plasmodium falciparum MAL3P7, complete sequence.//0.98:399:57//AL034559
R-NT2RP2003480//Homo sapiens full-length insert cDNA clone ZE09A11.//4.7e-111:540:98//AF086540
R-NT2RP2003499
R-NT2RP2003506
R-NT2RP2003511
R-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds.//4.1e-107:566:93//D87460
R-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/PDGF2) mRNA, complete cds.//1.5e-60:518:79//M12783
R-NT2RP2003522//HS_2182_A1_D05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=9 Row=G, genomic survey sequence.//0.053:251:60//AQ024304
R-NT2RP2003533//Homo sapiens chromosome 12p13.3 clone RPCI4-816N1, WORKING DRAFT SEQUENCE, 31 unordered pieces.//1.5e-37:328:80//AC005841
R-NT2RP2003543//HS_3028_A2_C12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3028 Col=24 Row=E, genomic survey sequence.//2.0e-39:203:100//AQ094957
R-NT2RP2003559//Homo sapiens full-length insert cDNA clone ZD65E09.//2.3e-59:325:95//AF088055
R-NT2RP2003564
R-NT2RP2003581
R-NT2RP2003596//HS_2163_B1_D11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2163 Col=21 Row=H, genomic survey sequence.//0.0011:212:67//AQ125143
R-NT2RP2003604//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//5.4e-102:501:97//U97067
R-NT2RP2003629//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0012:363:61//AC005507
R-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.//5.1e-37:561:68//AJ006215
R-NT2RP2003668//Human DNA sequence from PAC 24608, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//0.0053:395:58//Z76735
R-NT2RP2003687//Human BAC clone RG222A16 from 7q31, complete sequence.//8.0e-10:205:67//AC002385
R-NT2RP2003691//HS_3252_A2_A11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=22 Row=A, genomic survey sequence.//5.3e-05:332:60//AQ219783
R-NT2RP2003702//CIT-HSP-2333P5.TF CIT-HSP Homo sapiens genomic clone 2333P5, genomic survey sequence.//3.9e-43:431:75//AQ035000
R-NT2RP2003704
R-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds.//2.6e-45:265:93//AB011097
R-NT2RP2003713//Human DNA sequence from PAC 411B6 on chromosome X './/0.64:169:67//Z84470
R-NT2RP2003714//Human DNA sequence from 4PTEL, Huntington's Disease Region, chromosome 4p16.3.//4.6e-11:152:73//295704
R-nnnnnnnnnnnn//H.sapiens mRNA for PIBF1 protein, complete.//0.94:443:59//Y09631
R-NT2RP2003737//Homo sapiens clone DJ1022I14, WORKING DRAFT SEQUENCE, 14 unordered pieces.//2.2e-109:547:96//AC004951
R-NT2RP2003751//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-427H10, complete sequence.//4.1e-109:545:97//AC004626
R-NT2RP2003760//B. taurus mRNA for gamma-COP.//6.3e-28:400:69//X70019
R-NT2RP2003764//Mouse preprosomatostatin gene.//0.90:285:62//X51468
R-NT2RP2003769//Schizosaccharomyces pombe gene for protein involved in sexual development, complete cds.//0.96:446:58//D87956
R-NT2RP2003770//Homo sapiens sperm acrosomal protein mRNA, complete cds.//1.8e-104:531:96//AF047437
R-NT2RP2003777

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R-NT2RP2003781//HS_3109_B1_B04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3109 Col=7 Row=D, genomic survey sequence.//1.3e-60:346:92//AQ186749
R-NT2RP2003793
R-NT2RP2003840
R-NT2RP2003857//HS_2205_A2_H12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2205 Col=24 Row=O, genomic survey sequence.//8.1e-22:127:99//AQ151299
R-NT2RP2003859//RPCI11-37G8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-37G8, genomic survey sequence.//8.3e-60:320:95//AQ029850
R-NT2RP2003871//HS_3210_A1_C08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3210 Col=15 Row=E, genomic survey sequence.//8.6e-09:322:61//AQ175028
R-NT2RP2003885//RPCI11-7M10.TP RPCI-11 Homo sapiens genomic clone RPCI-11-7M10, genomic survey sequence.//4.7e-67:380:92//B72214
R-NT2RP2003912//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32B1, WORKING DRAFT SEQUENCE.//1.2e-33:379:75//AL023693
R-NT2RP2003952
R-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds.//2.3e-114:568:97//AB014458
R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds.//1.1e-107:540:97//AB007916
R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds.//7.7e-114:568:96//AB018347
R-NT2RP2003984
R-NT2RP2003986//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//6.6e-99:551:92//AC0003 82
R-NT2RP2003988
R-NT2RP2004014
R-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127, complete sequence.//4.9e-114:568:97//AC004780
R-NT2RP2004042//nbxb0020F03r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0020F03r, genomic survey sequence.//0.11:195:64//AQ258389
R-nnnnnnnnnnnn//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 134019, WORKING DRAFT SEQUENCE.//7.6e-110:564:95//AL034555
R-NT2RP2004081//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.012:503:57//AC005308
R-NT2RP2004098//H.sapiens CpG island DNA genomic Mse1 fragment, clone 133h3, reverse read cpg133h3.rt1a.//7.9e-25:140:100//Z64530
R-NT2RP2004124
R-NT2RP2004142//CIT-HSP-2316F21.TR CIT-HSP Homo sapiens genomic clone 2316F21, genomic survey sequence.//2.8e-83:409:98//AQ034964
R-NT2RP2004152//HS_3065_A2_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3065 Col=8 Row=G, genomic survey sequence.//2.5e-62:304:100//AQ137776
R-NT2RP2004165//Anthocidaris crassispina mRNA for dynein beta-heavy chain, complete cds.//3.4e-20:343:65//D01021
R-NT2RP2004170//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B33108; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.5e-89:587:86//AC004064
R-NT2RP2004172//Dictyostelium discoideum LTR-retrotransposon Skipper, partial genomic sequence, 3' end.//0.24:440:60//AF017047
R-NT2RP2004187//RPCI11-59E12.TK RPCI11 Homo sapiens genomic clone R-59E12, genomic survey sequence.//3.1e-05:175:66//AQ198120
R-NT2RP2004194
R-NT2RP2004196//Fugu rubripes GSS sequence, clone 076D01bE2, genomic survey sequence.//1.6e-22:178:71//AL026601
R-NT2RP2004207//Homo sapiens BAC clone GS421I03 from Xq25-q26, complete sequence.//0.19:175:64//AC005023
R-NT2RP2004226//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//6.1e-17:445:64//AL023808
R-NT2RP2004232//M.musculus (Balb/c) mRNA for serine/threonine protein kinase.//3.2e-25:326:71//Z34524
R-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds.//8.7e-108:563:94//AB015718
R-NT2RP2004240//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cds.//1.1e-101:530:93//AF039687

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R-NT2RP2004242
R-NT2RP2004245//Homo sapiens DNA sequence from PAC 455H14 on chromosome Xq21.3-22.3. Contains genomic marker DXS1203 with a CA repeat polymorphism, STSs and GSSs, complete sequence.//5.1e-08:236:65//AL023280
R-NT2RP2004270//Lycopersicon esculentum ldh2 gene.//0.98:259:61//Y10603
R-NT2RP2004300//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1068F16, WORKING DRAFT SEQUENCE.//5.0e-14:396:65//AL023913
R-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds.//1.5e-108:544:96//AF000416
R-NT2RP2004321//Caenorhabditis elegans cosmid F47B8, complete sequence.//0.0078:333:61//Z77662
R-NT2RP2004339//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.4e-75:306:86//AC005229
R-NT2RP2004347//RPCI11-90N11.TJ RPCI11 Homo sapiens genomic clone R-90N11, genomic survey sequence.//2.9e-87:494:92//AQ284548
R-NT2RP2004364//Human DNA sequence from clone 422F24 on chromosome 6q24.1-25.2. Contains a novel gene similar to C. elegans C02C2.5. Contains ESTs, STSs and GSSs, complete sequence.//4.2e-10:161:76//AL031010
R-NT2RP2004365//Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence.//3.6e-08:483:57//AE001433
R-NT2RP2004366//F.rubripes GSS sequence, clone 013B16aF3, genomic survey sequence.//2.1e-05:128:67//AL000528
R-NT2RP2004373//Homo sapiens 12q24.2 BAC RPCI11-407A16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.81:205:62//AC006065
R-NT2RP2004389//HS_2183_B2_H04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=8 Row=P, genomic survey sequence.//3.9e-06:82:84//AQ063969
R-NT2RP2004392//Ceratovacuna sp. mitochondrial cytochrome oxidase I (3' end), cytochrome oxidase II (complete cds) and transfer RNA-Leu gene.//2.7e-06:495:58//L39993
R-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21, complete sequence.//6.4e-111:572:96//AC005164
R-NT2RP2004399//Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence.//0.13:253:64//AC006085
R-NT2RP2004400//HS_3238_A2_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=22 Row=O, genomic survey sequence.//5.1e-23:162:89//AQ211412
R-NT2RP2004412//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//2.6e-09:458:60//M97514
R-NT2RP2004425//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs, complete sequence.//0.99:481:56//AL022718
R-NT2RP2004476//Rattus norvegicus activity and neurotransmitter-induced early gene 6 (ania-6) mRNA, 3'UTR.//5.3e-99:600:90//AF030091
R-NT2RP2004490//Homo sapiens chromosome 16, P1 clone 94-10H (LANL), complete sequence.//3.9e-115:575:97//AC005591
R-NT2RP2004512//Plasmodium falciparum MAL3P3, complete sequence.//0.00034:517:58//Z98547
R-NT2RP2004523//Homo sapiens clone DJ0800G07, complete sequence.//1.8e-115:571:97//AC004890
R-NT2RP2004538//Homo sapiens BAC clone RG318C11 from 7p14-p15, complete sequence.//1.7e-47:322:87//AC005091
R-NT2RP2004551//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//0.035:511:58//AC005184
R-NT2RP2004568//T7C20-Sp6 TAMU Arabidopsis thaliana genomic clone T7C20, genomic survey sequence.//0.70:446:54//B08766
R-NT2RP2004580//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 136B1, WORKING DRAFT SEQUENCE.//2.2e-53:397:74//AL031768
R-NT2RP2004587//CIT-HSP-2376P22.TF CIT-HSP Homo sapiens genomic clone 2376P22, genomic survey sequence.//0.0079:223:63//AQ108976
R-NT2RP2004594//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//5.3e-10:493:62//AC004605
R-NT2RP2004600//Homo sapiens full-length insert cDNA clone ZE04E06.//2.1e-70:343:99//AF086522
R-NT2RP2004602//Homo sapiens full-length insert cDNA clone YW26E09.//2.0e-96:528:93//AF086033

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R-NT2RP2004614
R-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//7.3e-117:587:96//AJ006291
R-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds.//1.8e-105:520:96//AB007929
R-NT2RP2004675//Human elastin (ELN) gene, partial cds, and LIM-kinase (LIMK1) gene, complete cds.//3.4e-22:197:79//U63721
R-NT2RP2004681//Rat notch 2 mRNA.//8.0e-30:276:78//M93661
R-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.6e-118:600:96//AB014525
R-NT2RP2004709//Homo sapiens full-length insert cDNA clone ZD42A08.//3.5e-14:139:86//AF086259
R-NT2RP2004710//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE.//6.9e-117:592:96//AL031447
R-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds.//4.2e-117:594:96//AB007947
R-NT2RP2004743//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.53:403:59//AC005505
R-NT2RP2004767//Human DNA sequence from PAC 491M17 on chromosome 1p36.2-1p36.3.//2.0e-81:568:84//Z97988
R-NT2RP2004775//Anopheles quadrimaculatus NADH dehydrogenase subunits (1-4, 4L, 5-6); cytochrome oxidase subunits (1-3); adenosine triphosphatase subunits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large and small subunits).//4.0e-08:365:62//L04272

R-NT2RP2004791//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//7.8e-111:541:98//AC005216
R-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//2.5e-114:564:96//AF058953
R-NT2RP2004802
R-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds.//2.7e-118:584:97//AF054179
R-NT2RP2004841//Human BAC clone RG308B22 from 7q22-q31, complete sequence.//4.0e-46:447:72//AC002089
R-NT2RP2004861//Plasmodium"falciparum MAL3P5, complete sequence.//0.19:189:66//AL034556
R-NT2RP2004897//Human Chromosome X clone bWXD187, complete sequence.//1.1e-08:330:61//AC004383
R-NT2RP2004936//CIT-HSP-2374L4.TF CIT-HSP Homo sapiens genomic clone 2374L4, genomic survey sequence.//0.99:129:65//AQ110571
R-nnnnnnnnnnnn//Plasmodium falciparum MAL3P6, complete sequence.//0.014:402:61//Z98551
R-NT2RP2004961//RPCI11-45P2.TK RPCI11 Homo sapiens genomic clone R-45P2, genomic survey sequence.//9.3e-90:453:97//AQ202282
R-NT2RP2004962//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y40H4, WORKING DRAFT SEQUENCE.//0.017:291:61//AL022573
R-NT2RP2004967//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.6e-52:496:77//AC005077
R-NT2RP2004978//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//0.088:322:63//AC005614
R-NT2RP2004982//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//0.025:339:61//AC003071
R-NT2RP2004985//T31H24TF TAMU Arabidopsis thaliana genomic clone T31H24, genomic survey sequence.//0.40:111:70//B78148
R-NT2RP2004999//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces.//0.23:157:68//AC005682
R-NT2RP2005000
R-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//3.0e-111:577:95//AB014515
R-NT2RP2005003//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//2.4e-21:246:77//AC004673
R-nnnnnnnnnnnn//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//9.5e-115:568:97//AF100141
R-NT2RP2005018//HS_3108_B1_E09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=17 Row=J, genomic survey sequence.//1.9e-31:222:89//AQ104050
R-NT2RP2005020//Rattus norvegicus cationic amino acid transporter-1 (CAT-1) mRNA, complete cds.//6.6e-41:566:73//U70476
R-NT2RP2005031//CIT-HSP-516A2.TV CIT-HSP Homo sapiens genomic clone 516A2, genomic survey sequence.//4.1e-31:357:75//B49897
R-NT2RP2005037

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R-NT2RP2005038//Sequence 5 from patent US 5552281.//2.2e-32:178:98//I25644
R-NT2RP2005108//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence.//3.7e-23:475:67//AF009326
R-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds.//8.4e-104:518:97//AB014564
R-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//1.4e-67:464:85//X98743
R-NT2RP2005139
R-NT2RP2005140//Leishmania mexicana amazonensis kinetoplast (clone 29) maxicircle A+T-rich repetitive DNA sequence.//7.9e-08:460:60//U00101
R-NT2RP2005144//Homo sapiens chromosome 12p13.3 clone RPCI11-372B4, WORKING DRAFT SEQUENCE, 129 ordered pieces.//2.5e-103:519:96//AC005911
R-NT2RP2005147//Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces.//0.068:100:75//AC004971
R-NT2RP2005159//CITBI-E1-2506A8.TF CITBI-E1 Homo sapiens genomic clone 2506A8, genomic survey sequence.//0.90:113:71//AQ262104
R-NT2RP2005162//Homo sapiens chromosome 17, clone HCIT307A16, complete sequence.//5.0e-14:183:75//AC003041
R-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.5e-100:513:95//AJ007509
R-NT2RP2005204
R-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//7.2e-119:583:97//AC005189
R-NT2RP2005239//Homo sapiens mRNA for putative tRNA splicing protein, partial.//8.4e-62:312:98//AJ010952
R-NT2RP2005254//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceeded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//5.7e-09:328:62//Z99297
R-NT2RP2005270//Plasmodium falciparum MAL3P8, complete sequence.//2.3e-05:355:61//AL034560
R-NT2RP2005276//Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence.//0.0014:541:58//AC000107
R-NT2RP2005287//Cavia porcellus zinc finger protein (zfoC1) mRNA, complete cds.//4.4e-69:459:86//L26335
R-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//7.4e-124:594:98//AF060219
R-NT2RP2005289//Homo sapiens mRNA for XRP2 protein.//1.5e-110:545:96//AJ007590
R-NT2RP2005293//Leishmania mexicana amazonensis kinetoplast (clone 29) maxicircle A+T-rich repetitive DNA sequence.//1.1e-12:554:61//U00101
R-NT2RP2005315//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//9.5e-15:218:77//AL022069
R-NT2RP2005325//Rattus norvegicus LIM homeodomain protein (LH-2) mRNA sequence.//2.0e-72:478:88//L06804
R-NT2RP2005336//***ALU WARNING: Human Alu-J subfamily consensus sequence.//7.3e-33:139:82//U14567
R-NT2RP2005344//Human DNA sequence from PAC 128N22 on chromosome Xq25-Xq26.3. contains STS.//0.094:451:60//297629
R-NT2RP2005354//Homo sapiens mRNA for putative thioredoxin-like protein.//1.3e-11:89:96//AJ010841
R-NT2RP2005360//Homo sapiens clone RG023I15, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.046:266:60//AC005049
R-NT2RP2005393//Homo sapiens chromosome 17, clone hRPK.85_B_7, complete sequence.//6.0e-41:226:86//AC005695
R-NT2RP2005407
R-NT2RP2005436//Polistes annularis (clone pan117AAT) tandem repeat region.//0.039:169:63//L10835
R-NT2RP2005441//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//3.0e-38:263:88//AQ055548
R-NT2RP2005453//CIT-HSP-2367N1.TR CIT-HSP Homo sapiens genomic clone 2367N1, genomic survey sequence.//0.67:409:59//AQ079845
R-NT2RP2005457//Homo sapiens partial XPGC gene, exon 2.//2.0e-42:315:82//X71342
R-NT2RP2005464//CIT-HSP-2359C16.TF CIT-HSP Homo sapiens genomic clone 2359C16, genomic survey sequence.//1.0:251:60//AQ075816
R-NT2RP2005465//Drosophila melanogaster, chromosome 2R, region 44D1-44D2, P1 clone DS08616, complete sequence.//01251288:62//AC005457

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R-NT2RP2005472//Chlorarachnion CCMP621 small subunit ribosomal RNA, 5.8S ribosomal RNA, large subunit ribosomal RNA, U6 small nuclear RNA, small subunit ribosomal protein S13 (RPS13), pre-mRNA splicing factor PRP 6 homolog, small subunit ribosomal protein 4 (RPS4), small nucleolar ribonucleoprotein E homolog (snRNPE), ATP-dependent clp protease proteolytic subunit homolog (CLPP), putative RNA polymerase II subunit (RNA POLII), and RNA helicase homolog (RNAHEL) genes, complete cds.//1.0:356:59//U58510

R-NT2RP2005476//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P3, WORKING DRAFT SEQUENCE.//0.00092:421:60//AL031746

R-NT2RP2005490//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.// 6.2e-71:187:100//AC006030

R-NT2RP2005491//paramecium species 5,311 mt dna dimer: replication init. region.//1.6e-10:403:62//K00917

R-NT2RP2005495//Homo sapiens clone RG037F03, WORKING DRAFT SEQUENCE, 12 unordered pieces.// 1.3e-25:208:82//AC005051

R-NT2RP2005496//Human DNA sequence from clone 354N19 on chromosome 6q22. Contains the 3' part of the gene for Mannosyl-Oligosaccharide Alpha-1,2-Mannosidase (Man(9)-alpha-mannosidase, EC 3.2.1.113), a Cytochrome C Oxidase Polypeptide I (EC 1.9.3.1) pseudogene and a pseudogene similar to 60S Ribosomal Protein L13A. Contains genomic markers D6S287 and D6S1696, ESTs, STSs, GSSs and two CA repeat polymorphisms, complete sequence.//1.5e-22:196:84//AL022722

R-NT2RP2005498

R-NT2RP2005501//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.//.7e-29:252:76// AC005828

R-NT2RP2005509//CIT-HSP-2060J6.TR CIT-HSP Homo sapiens genomic clone 2060J6, genomic survey sequence.//3.1e-53:402:84//B69979

R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//9.9e-109: 570:94//AF092563

R-NT2RP2005525//Human clone JkA2 mRNA induced upon T-cell activation, 3' end.//5.1e-32:175:98//U38432

R-NT2RP2005531//Homo sapiens PAC clone DJ0870F17 from 7q33-q36, complete sequence.//0.94:288:61// AC004911

R-NT2RP2005539//Homo sapiens mRNA for NSI-binding protein (NS1-BP).//2.7e-106:560:94//AJ012449

R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//5.3e-114:583:96//AB007963

R-NT2RP2005549//Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRAFT SEQUENCE.//0.91: 287:58//AJ011929

R-NT2RP2005555//Homo sapiens 12p13.3 PAC RPCIS-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.6e-05:222:66//AC004804

R-NT2RP2005557//Homo sapiens PAC clone DJ1200I23 from 7p15, complete sequence.//8.2e-22:236:76// AC004996

R-NT2RP2005581//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.// 7.2e-45:286:85//AC006146

R-NT2RP2005600//Human polymorphic microsatellite DNA.//0.043:304:58//M99148

R-NT2RP2005605//Human Cosmid g1572c190, complete sequence.//2.4e-17:163:77//AC000126

R-NT2RP2005620

R-NT2RP2005622//jd432 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 11B7, genomic survey sequence.//0.010:308:58//B13538

R-NT2RP2005637//Homo sapiens PAC clone DJ0555L14 from 7q34-q36, complete sequence.//2.5e-26:322:72// AC005996

R-NT2RP2005640//Mus musculus squamous cell carcinoma antigen 2 (Scca2) gene, complete cds.//0.030:370: 60//AF063937

R-NT2RP2005645//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//3.2e-08: 355:62//AE001398

R-NT2RP2005651

R-NT2RP2005654//Leishmania major Friedlin cosmid L5769, complete sequence.//0.96:216:66//AL031908

R-NT2RP2005669//Homo sapiens nitrilase homolog 1 (NIT1) gene, alternatively spliced product, complete cds.// 6.7e-117:594:95//AF069984

R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//1.8e-89:434:98// AF089814

R-NT2RP2005683//jd432 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 11B7, genomic survey sequence.//0.037:283:58//B13538

R-NT2RP2005690//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.5e-38:295:83//AC005478

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R-NT2RP2005694//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-106, complete sequence.//0.0026:414:57//AL010210
R-NT2RP2005701
R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//4.1e-104:503:98//AB018342
R-NT2RP2005719//Caenorhabditis elegans cosmid LLC1, complete sequence.//0.83:275:61//Z82277
R-NT2RP2005722//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING DRAFT SEQUENCE.//1.2e-21:199:75//AL031985
R-NT2RP2005723
R-NT2RP2005726//Homo sapiens clone DJ0609N19, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.6e-64:503:82//AC004842
R-NT2RP2005741//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.5e-09:261:64//AC000384
R-NT2RP2005748//RPCI11-64K11.TK RPCI11 Homo sapiens genomic clone R-64K11, genomic survey sequence.//0.00039:215:66//AQ239313
R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//1.3e-40:223:96//AF068868
R-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//3.7e-103:494:98//AF082516
R-NT2RP2005763//Homo sapiens DNA sequence from PAC 510L9 on chromosome 6p24.1-p25.3.//9.7e-34:172:86//AL022098
R-NT2RP2005767//Human clone H3 mRNA.//2.5e-21:179:87//U03672
R-NT2RP2005773//HS_2168_B1_G12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=23 Row=N, genomic survey sequence.//0.99:212:63//AQ086414
R-NT2RP2005775//Rabbit mRNA for endopeptidase, complete cds.//4.8e-98:591:88//D13310
R-NT2RP2005781//Streptomyces sp. genomic DNA for sarcosine oxidase.//0.019:384:59//D10623
R-NT2RP2005784//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE.//1.8e-102:490:99//AL034423
R-NT2RP2005804//Homo sapiens chromosome 17, clone hRPK.147_L_13, complete sequence.//6.3e-16:481:63//AC005332
R-NT2RP2005812//Caenorhabditis elegans cosmid F15810.//0.81:147:63//AF036696
R-NT2RP2005815
R-NT2RP2005835
R-NT2RP2005841//Human DNA sequence from cosmid U209G1 on chromosome X.//1.5e-26:512:64//Z68873
R-NT2RP2005853//Human DNA sequence from clone 1156N12 on chromosome X. Contains an STS and GSSs, complete sequence.//3.7e-16:340:64//AL009047
R-NT2RP2005857//Human DNA sequence from cosmid U246D9 on chromosome X. Contains a histone H2B like pseudogene.//1.3e-09:331:65//AL021308
R-NT2RP2005859//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-83, complete sequence.//0.0097:363:59//AL010152
R-NT2RP2005868//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-18, complete sequence.//1.1e-07:508:60//AL008971
R-NT2RP2005890//Mouse oncogene (ect2) mRNA, complete cds.//2.7e-31:500:67//AL11316
R-NT2RP2005901//Homo sapiens T-cell receptor alpha delta locus from bases 752679 to 1000555 (section 4 of 5) of the Complete Nucleotide Sequence.//0.89:276:60//AE000661
R-NT2RP2005908
R-NT2RP2005933//Rattus norvegicus nucleoporin p54 mRNA, complete cds.//1.2e-40:285:80//U63840
R-NT2RP2005942//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence.//0.0011:480:58//Z99289
R-NT2RP2005980//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//8.9e-21:136:78//AC004616
R-NT2RP2006023//HS_2176_B1_C10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2176 Col=19 Row=F, genomic survey sequence.//2.5e-66:369:95//AQ023148
R-NT2RP2006038//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence.//0.00029:408:58//AE001369
R-NT2RP2006043//Polistes annularis (clone pan117AAT) tandem repeat region.//0.032:195:62//L10835
R-NT2RP2006052//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING

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DRAFT SEQUENCE, 14 unordered pieces.//0.11:263:61//AC005140
R-NT2RP2006069
R-NT2RP2006071//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00044:333:61//AC004709
R-NT2RP2006098//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-77, complete sequence.//4.1e-09:393:62//AL010151
R-NT2RP2006100//HS_2020_A2_H02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2020 Col=4 Row=O, genomic survey sequence.//8.3e-53:304:92//AQ228761
R-NT2RP2006103//Rat sodium-hydrogen exchange protein-isoform 3 (NHE-3) mRNA, complete cds.//1.5e-16:199:79//M85300
R-NT2RP2006141
R-NT2RP2006166//Human Chromosome 16 BAC clone CIT987SK-A-589H1, complete sequence.//8.2e-48:329:76//AC002045
R-NT2RP2006184//RPCI11-6O16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-6O16, genomic survey sequence.//0.52:273:61//B49539
R-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//1.9e-108:553:95//AB014554
R-NT2RP2006196//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-57, complete sequence.//4.2e-05:420:59//AL008981
R-NT2RP2006200//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//2.1e-100:409:96//AC006057
R-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//3.8e-93:532:90//X96484
R-NT2RP2006237//P.falciparum PK1 gene.//2.9e-08:481:59//X83707
R-NT2RP2006238//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//3.5e-79:405:89//U91318
R-NT2RP2006258//Human PAC clone DJ0899B21 from 7p15-p21, complete sequence.//2.2e-08:283:63//AC004008
R-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK.//6.2e-13:234:68//X97630
R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.0e-108:542:97//AF035262
R-NT2RP2006320//347J16.TVB CIT978SKA1 Homo sapiens genomic clone A-347J16, genomic survey sequence.//1.2e-27:215:65//B17768
R-NT2RP2006321//Human karyopherin beta 3 mRNA, complete cds.//1.7e-48:298:90//U72761
R-NT2RP2006323//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 702J19, WORKING DRAFT SEQUENCE.//2.8e-104:524:96//AL033531
R-NT2RP2006333//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//3.9e-33:298:78//AC004893
R-NT2RP2006334
R-NT2RP2006365//RPCI11-72I15.TK RPCI11 Homo sapiens genomic clone R-72I15, genomic survey sequence.//2.6e-35:217:92//AQ267043
R-NT2RP2006393//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B13E4; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//8.0e-40:317:81//AC004046
R-NT2RP2006436//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//3.2e-42:184:86//AL022345
R-NT2RP2006441//Plasmodium falciparum microsatellite TA80 sequence.//0.00021:188:68//AF010568
R-NT2RP2006454//Plasmodium falciparum chromosome 2, section 60 of 73 of the complete sequence.//0.30:265:60//AE001423
R-NT2RP2006456//Homo sapiens clone 23566 mRNA sequence.//2.5e-104:532:96//AF052098
R-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//6.6e-108:524:97//AJ006266
R-NT2RP2006467//Sequence 50 from patent US 5691147.//8.3e-22:235:74//I76222
R-NT2RP2006472//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1172A22, WORKING DRAFT SEQUENCE.//5.4e-12:407:62//AL034386
R-NT2RP2006534//Dictyostelium discoideum actin 8 gene, 3' UTR.//0.44:111:65//M25216
R-NT2RP2006554//Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence.//0.19:392:58//AE001370
R-NT2RP2006565//Sus scrofa SCAMP 1 gene, exon 9.//1.5e-13:292:68//AJ223742
R-NT2RP2006571//Homo sapiens chromosome 19, cosmid F17972, complete sequence.//0.0024:409:58//AC004660
R-nnnnnnnnnnn//Human BRCA2 region, mRNA sequence CG005.//3.3e-16:334:64//U50532
R-NT2RP2006598//Mus musculus retinoid X receptor interacting protein (RIP110) mRNA, partial cds.//1.6e-19:

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448:64//U22015
R-NT2RP3000002//Human DNA sequence from cosmid N104C7 on chromosome 22, complete sequence.//4.4e-14:501:63//Z82246
R-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//5.9e-115:560:97//AJ011972
R-NT2RP3000046//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.//3.9e-57:402:83//AC005995
R-NT2RP3000047//Homo sapiens chromosome 17, clone hRPK.138_P_22, complete sequence.//1.0:158:66//AC005697
R-NT2RP3000050//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 451B21, WORKING DRAFT SEQUENCE.//2.7e-32:411:69//AL033522
R-NT2RP3000055//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1000N6, WORKING DRAFT SEQUENCE.//7.9e-17:309:69//AL034378
R-NT2RP3000072//Brassica rapa DNA for S-locus glycoprotein, complete cds.//2.9e-07:516:60//D88192
R-NT2RP3000080//Homo sapiens clone DJ1129D05, complete sequence.//1.7e-27:186:90//AC005630
R-NT2RP3000085//Arabidopsis thaliana acetyl-CoA carboxylase biotin-containing subunit mRNA, nuclear gene encoding chloroplast protein, complete cds.//0.0051:289:59//U-23155
R-NT2RP3000109//HS_3065_A2_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3065 Col=8 Row=G, genomic survey sequence.//2.5e-62:304:100//AQ137776
R-NT2RP3000134//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P3, WORKING DRAFT SEQUENCE.//0.027:414:57//AL031746
R-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//3.8e-115:578:96//AB011164
R-NT2RP3000149//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence.//1.3e-67:354:95//AC005746
R-NT2RP3000186
R-NT2RP3000197//Human DNA sequence from PAC 181N1 on chromosome X contains ESTs, STS polymorphic CA repeat*.//2.5e-31:295:78//Z82899
R-NT2RP3000207//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-954B10, complete sequence.//0.016:305:61//AC004514
R-NT2RP3000220//RPCI11-63O7.TJ RPCI11 Homo sapiens genomic clone R-63O7, genomic survey sequence.//0.25:118:66//AQ201832
R-NT2RP3000233//Plasmodium falciparum mRNA for major merozoite surface antigen gp195.//3.2e-11:440:59//X15063
R-NT2RP3000235//Mus musculus chromosome 6 clone TB6 subclone TB6pD1//0.81:114:64//U19530
R-NT2RP3000247//Homo sapiens DNA sequence from clone 326L12 on chromosome Xq27.1 27.3. Contains the cancer/testis antigen CT7 (melanoma-associated antigen MAGE-C1) gene, two MAGE family pseudogenes, STSs and a CA repeat polymorphism, complete sequence.//4.8e-73:362:86//AL023279
R-NT2RP3000251//Homo sapiens chromosome 17, clone hRPK.192_H_23, complete sequence.//0.025:131:66//AC005726
R-NT2RP3000252
R-NT2RP3000255//HS-1025-B2-F08-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 804 Col=16 Row=L, genomic survey sequence.//0.67:119:66//B34879
R-NT2RP3000267
R-NT2RP3000299//Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds.//1.2e-23:424:69//D29766
R-NT2RP3000312//Plasmodium falciparum MAL3P4, complete sequence.//0.55:414:59//AL008970
R-NT2RP3000320//HS_3056_A1_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3056 Col=5 Row=E, genomic survey sequence.//4.1e-32:214:89//AQ134064
R-NT2RP3000324//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//1.5e-22:265:75//U78090
R-NT2RP3000333//Plasmodium falciparum MAL3P6, complete sequence.//0.68:460:57//Z98551
R-NT2RP3000341//H.sapiens mRNA for TIM17 preprotein translocase.//1.4e-19:137:90//X97544
R-NT2RP3000348//CITBI-E1-2513C11.TF CITBI-E1 Homo sapiens genomic clone 2513C11, genomic survey sequence.//0.0014:118:72//AQ278177
R-NT2RP3000350
R-NT2RP3000359//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.8e-55:320:75//AC006039
R-NT2RP3000361//Homo sapiens mRNA for KIAA0552 protein, complete cds.//0.18:275:61//AB011124

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R-NT2RP3000366//CIT-HSP-2317H13.TF CIT-HSP Homo sapiens genomic clone 2317H13, genomic survey sequence.//6.7e-42:214:100//AQ041634
R-NT2RP3000397//HS-1012-B1-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 787 Col=1 Row=L, genomic survey sequence//0.015:184:63//B31814
R-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//1.3e-109:529:98//AF071185
R-NT2RP3000418//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 510B21, WORKING DRAFT SEQUENCE.//6.2e-15:445:65//AL031885
R-NT2RP3000433
R-NT2RP3000439
R-NT2RP3000441
R-NT2RP3000449//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE.//1.6e-43:300:76//AL031650 R-NT2RP3000451//3'untranslated region of human mRNA for a K^+ channel protein.//0.71:101:66//E13519
R-NT2RP3000456//Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence.//5.2e-16:376:65//AF011889
R-NT2RP3000484//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 120G22, WORKING DRAFT SEQUENCE.//0.61:326:58//AL031847
R-NT2RP3000487//Sequence 32 from patent US 5476781.//8.6e-08:409:61//I16692
R-NT2RP3000512//RPCI11-60F15.TK RPCI11 Homo sapiens genomic clone R-60F15, genomic survey sequence.//2.2e-68:379:93//AQ201516
R-NT2RP3000526//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 377F16, WORKING DRAFT SEQUENCE.//4.1e-07:224:65//Z93783
R-NT2RP3000527//HS_3228_A1_H07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3228 Col=13 Row=O, genomic survey sequence.//4.5e-30:184:93//AQ209131
R-NT2RP3000531//T6M24-Sp6 TAMU Arabidopsis thaliana genomic clone T6M24, genomic survey sequence.//0.67:88:68//AQ248538
R-NT2RP3000542//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126B4, WORKING DRAFT SEQUENCE.//2.0e-24:145:82//AL022316
R-NT2RP3000561//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//6.1e-107:548:95//AC006012
R-NT2RP3000562//HS_2041_B1_E08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2041 Col=15 Row=J, genomic survey sequence.//9.6e-55:279:98//AQ230207
R-NT2RP3000578//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-105, complete sequence.//0.00060:356:58//AL010212,
R-NT2RP3000582//Homo sapiens chromosome 17, clone hCIT.468_F_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.2e-29:282:67//AC004666
R-NT2RP3000584//Human PAC clone DJ222H05 from Xq25-q26, complete sequence.//7.4e-44:245:78//AC002377
R-NT2RP3000590//Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence.//0.66:341:59//AC004077
R-NT2RP3000592//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.022:491:56//AC005505
R-nnnnnnnnnnnn//HS_3025_A1_D11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3025 Col=21 Row=G, genomic survey sequence.//2.6e-21:161:88//AQ101452
R-NT2RP3000599//Plasmodium falciparum MAL3P8, complete sequence.//1.3e-09:543:58//AL034560
R-NT2RP3000605//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//5.6e-115:554:98//AC006128
R-NT2RP3000622//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 27 unordered pieces.//0.15:233:63//AC005414
R-NT2RP3000624//CIT-HSP-2022D4.TR CIT-HSP Homo sapiens genomic clone 2022D4, genomic survey sequence.//1.0:166:66//B64262
R-NT2RP3000628//Human BAC clone GS188P18, complete sequence.//5.3e-56:384:83//AC000115
R-NT2RP3000632//Human cyclin-selective ubiquitin carrier protein mRNA, complete cds.//4.0e-61:438:85//U73379
R-NT2RP3000644//Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTC, and RAD23A genes, genomic sequence.//1.0e-43:408:77//AD000092
R-NT2RP3000661//F.rubripes GSS sequence, clone 148D22bB9, genomic survey sequence.//2.7e-17:234:69//

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AL005927
R-NT2RP3000665//Human chromosome 11 46b2 cosmid, complete sequence.//2.1e-42:526:72//U73645
R-NT2RP3000685//HS_3007_A2_F02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=4 Row=K, genomic survey sequence.//1.6e-101:506:97//AQ118425
R-NT2RP3000690//Plasmodium falciparum MAL3P6, complete sequence.//1.3e-13:411:61//Z98551
R-NT2RP3000736
R-NT2RP3000742//Rattus norvegicus phospholipase C delta-4 mRNA, complete cds.//0.0071:231:65//U16655
R-NT2RP3000753//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucoronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//0.88:366:56//AL021368
R-NT2RP3000759//HS_2055_A2_D09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=18 Row=G, genomic survey sequence.//0.45:251:60//AQ234828
R-NT2RP3000815//Homo sapiens chromosome 17, clone hRPK.209_J_20, complete sequence.//2.0e-20:293:72//AC005822
R-NT2RP3000825//Plasmodium falciparum MAL3P6, complete sequence.//0.0044:325:62//Z98551
R-NT2RP3000826//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 117I5, WORKING DRAFT SEQUENCE.//5.3e-25:375:72//AL022315
R-NT2RP3000836//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y214H10, WORKING DRAFT SEQUENCE.//1.3e-19:181:81//AL022344
R-NT2RP3000841//Homo sapiens, clone hRPK.1_A_1, complete sequence.//0.20:226:61//AC006196
R-NT2RP3000845//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//6.8e-91:512:92//AC005781
R-NT2RP3000847//***ALU WARNING: Human Alu-Sp subfamily consensus sequence.//7.9e-38:179:86//U14572
R-NT2RP3000850//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//4.4e-48:505:76//AC005014
R-NT2RP3000852//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//2.9e-82:311:98//AL031297
R-NT2RP3000859
R-NT2RP3000865//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//1.2e-15:482:63//AL022153 R-NT2RP3000868//Fruitfly strain g20 mitochondrial DNA, A+T-rich region, partial sequence.//0.00045:260:59//AB003097
R-NT2RP3000869//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 330012, WORKING DRAFT SEQUENCE.//0.0058:172:64//AL031731
R-NT2RP3000875//H.sapiens /Hepatitis B virus fusion mRNA for mevalonate kinase.//1.4e-99:531:93//X75311
R-NT2RP3000901
R-NT2RP3000904//Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence.//0.32:261:57//AC000348
R-NT2RP3000917//Plasmodium falciparum MAL3P7, complete sequence.//0.00092:456:58//AL034559
R-NT2RP3000919
R-NT2RP3000968//H.sapiens mRNA for ribosomal protein S15a.//4.5e-24:375:71//X84407
R-NT2RP3000980//Homo sapiens chromosome 17, clone hRPK.855_D_21, complete sequence.//0.36:186:62//AC006079
R-NT2RP3000994//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.00052:413:60//AC005140
R-NT2RP3001004//Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence.//1.1e-07:330:64//U32857
R-NT2RP3001007//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-82, complete sequence.//0.045:286:61//AL010255
R-NT2RP3001055//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monoamine oxidase B (MAOB), ESTs and polymorphic CA repeats.//2.3e-56:348:91//Z95125
R-NT2RP3001057//H.sapiens HZF4 mRNA for zinc finger protein.//8.2e-84:531:86//X78927
R-NT2RP3001081//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P3, WORKING DRAFT SEQUENCE.//1.1e-08:537:60//AL031746
R-NT2RP3001084
R-NT2RP3001096
R-NT2RP3001107

BNSDOCID: <EP___1074617A2_I_>

R-nnnnnnnnnnnn//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence.//7.4e-62:272:73//AC005316
R-NT2RP3001111
R-NT2RP3001113
R-NT2RP3001115//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//7.2e-112:550:97//AC005189
R-NT2RP3001116//CIT-HSP-2282K23.TR CIT-HSP Homo sapiens genomic clone 2282K23, genomic survey sequence.//0.000.13.160:69//AQ002011
R-NT2RP3001119//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//5.9e-99:497:96//AL031864
R-NT2RP3001120
R-NT2RP3001126//Plasmodium falciparum MAL3P7, complete sequence.//0.035:266:56//AL034559
R-NT2RP3001133
R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//8.1e-114:549:97//AB018305
R-NT2RP3001147//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//0.69:198:63//AC004448
R-NT2RP3001150//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//2.4e-108:542:97//AL034379
R-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//2.9e-116:563:98//AJ006266
R-NT2RP3001176//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.44:227:62//AC004688
R-NT2RP3001214//Borrelia burgdorferi plasmid lp25, complete plasmid sequence.//0.0023:381:61//AE000785
R-NT2RP3001216//RPCI11-18C15.TPC RPCI-11 Homo sapiens genomic clone RPCI-11-18C15, genomic survey sequence.//7.0e-29:167:97//B88077
R-NT2RP3001221//Homo sapiens clone 14503, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.020:211:63//AC005827
R-NT2RP3001232//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.7e-08:390:62//AL021326
R-NT2RP3001236//RPCI11-25C17.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-25C17, genomic survey sequence.//9.5e-41:217:88//AQ014003
R-NT2RP3001239//Human microtubule-associated protein 1B (MAP1B) gene, complete cds.//2.9e-21:438:63//L06237
R-NT2RP3001245//Homo sapiens DNA sequence from PAC 964D12 on chromosome 1q24-q25. Contains EST, GSS.//0.00026:439:59//AL021398
R-NT2RP3001253//HS_3002_A2_H12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=24 Row=O, genomic survey sequence.//0.98:190:63//AQ251982
R-NT2RP3001260
R-NT2RP3001268//Homo sapiens clone DJ0959C21, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.012:509:57//AC004936
R-NT2RP3001272//Homo sapiens BAC clone NH0161H12 from 7p14-p15, complete sequence.//2.2e-22:134:87//AC005589
R-NT2RP3001274//Sequence 11 from Patent WO9517522.//0.0058:133:66//A45341
R-NT2RP3001281//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.//4.4e-55:558:76//Z96811
R-NT2RP3001307//HS_2058_A1_C06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=11 Row=E, genomic survey sequence.//7.2e-33:260:86//AQ305868
R-NT2RP3001318//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence.//0.27:210:65//AC004848
R-NT2RP3001325
R-NT2RP3001338//Rat tropoelastin gene, intron 17 (partial).//1.0:184:64//M86367
R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds.//1.2e-112:566:96//AB007920
R-NT2RP30%1340//Homo sapiens HMG box factor SOX-13 mRNA, complete cds.//3.2e-86:450:95//AF083105
R-NT2RP3001355
R-NT2RP3001374//HS_2184_A2_G04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2184 Col=8 Row=M, genomic survey sequence.//3.7e-10:101:84//AQ024647
R-NT2RP3001383//Plasmodium falciparum chromosome 2, section 34 of 73 of the complete sequence.//7.4e-07:

BNSDOCID: <EP___1074617A2_I_>

279:63//AE001397
R-NT2RP3001384//Homo sapiens chromosome 19, cosmid R33907, complete sequence.//4.4e-75:382:97//AC005785
R-NT2RP3001392//HS_3078_B2_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=10 Row=H, genomic survey sequence.//1.0:164:64//AQ140587
R-NT2RP3001396//RPCI11-63N18.TJ RPCI11 Homo sapiens genomic clone R-63N18, genomic survey sequence.//0.14:242:61//AQ238544
R-NT2RP3001398//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//1.8e-10:193:72//U49046
R-NT2RP3001399
R-NT2RP3001407//Caenorhabditis elegans cosmid D1046, complete sequence.//0.0011:392:60//Z68160
R-NT2RP3001420//Human BAC clone GS165I04 from 7q21, complete sequence.//3.7e-29:412:74//AC002379
R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequence.//1.1e-104:550:94//AF052158
R-NT2RP3001427//Caenorhabditis elegans cosmid K11D5.//0.39:174:64//U53152
R-nnnnnnnnnnnn//Human nuclear pore complex-associated protein TPR (tpr) mRNA, complete cds.//1.4e-94:533:91//U69668
R-NT2RP3001432//Homo sapiens DNA sequence from PAC 164C20 on chromosome 6q16.1-22.1. Contains ESTs and GSSs (BAC end sequences), complete sequence.//2.5e-12:415:61//AL009029
R-NT2RP3001447//Homo sapiens PAC clone DJ0828B12 from 7q11.23-q21.1, complete sequence.//5.6e-36:358:77//AC004903
R-NT2RP3001449//Homo sapiens clone 24497 mRNA sequence.//1.5e-100:499:97//AF070630
R-NT2RP3001453//Homo sapiens clone DJ0852024, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.0e-47:295:86//AC004906
R-NT2RP3001457
R-NT2RP3001459
R-NT2RP3001472//Crithidia fasciculata kinetoplast apocytochrome b gRNA-mRNA chimera, clone:24.//0.33:150:66//D13030
R-NT2RP3001490//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-103, complete sequence.//2.3e-08:483:60//AL010208
R-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//4.4e-60:338:93//U13395
R-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//2.1e-110:549:97//AF064801
R-NT2RP3001527//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1125A11, WORKING DRAFT SEQUENCE.//5.3e-32:310:78//AL034549
R-NT2RP3001529//Human Chromosome X, complete sequence.//5.5e-67:280:93//AC002420
R-NT2RP3001538
R-NT2RP3001554//Human microtubule-associated protein la (MAP1A) mRNA, complete cds.//7.8e-16:391:62//U38292
R-NT2RP3001580//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.00026:456:58//AC004688
R-NT2RP3001587//Homo sapiens HRIHFB2115 mRNA, partial cds.//5.6e-08:86:88//AB015337
R-NT2RP3001589//Homo sapiens chromosome 17, clone hRPK.1096_G_20, complete sequence.//0.066:360:60//AC005410
R-NT2RP3001607//CIT-HSP-2010M8.TR CIT-HSP Homo sapiens genomic clone 2010M8, genomic survey sequence.//0.041:194:67//B53490
R-NT2RP3001608//Human DNA sequence from PAC 296K21 on chromosome X contains cytokeratin exon, delta-aminolevulinate synthase (erythroid); 5-aminolevulinic acid synthase.(EC 2.3.1.37). 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//0.69:151:64//Z83821
R-NT2RP3001621//Human DNA sequence from clone 24o18 on chromosome 6p21:31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.//1.4e-46:354:83//AL021808
R-NT2RP3001629//H.sapiens simple DNA sequence region clone wg1a10.//0.99:137:63//X76572
R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds.//8.5e-108:541:96//AF099149
R-NT2RP3001642
R-NT2RP3001646//HS_3218_A2_A01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=2 Row=A, genomic survey sequence.//2.6e-32:215:91//AQ303003
R-NT2RP3001671//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-88, complete sequence.//0.018:262:61//AL010157
R-NT2RP3001672

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R-NT2RP3001676//Homo sapiens cosmid Q95D4, chromosome 21 5' of IFNAR2.//2.1e-48:413:77//AF039905
R-NT2RP3001678//RPCI11-50C17.TK RPCI11 Homo sapiens genomic clone R-50C17, genomic survey sequence.//0.15:232:62//AQ116359
R-NT2RP3001679//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11.//7.8e-104:549:95//AB020860
R-NT2RP3001688//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//6.6e-41:291:86//AC006019
R-NT2RP3001690//Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence.//3.1e-07:433:59//AE001415
R-NT2RP3001708//Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite sequence.//6.0e-06:237:64//AF053523
R-NT2RP3001712//CITBI-E1-2516N9.TF CITBI-E1 Homo sapiens genomic clone 2516N9, genomic survey sequence.//1.5e-95:456:99//AQ279562
R-NT2RP3001716//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//0.0012:346:58//AC004617
R-NT2RP3001724//Human HepG2 3' region MboI cDNA, clone hmd6a06m3.//1.3e-27:163:95//D17273
R-NT2RP3001730//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 111B22, WORKING DRAFT SEQUENCE.//7.6e-43:409:76//Z98200
R-NT2RP3001739
R-NT2RP3001752//Human clone 23774 mRNA sequence.//1.9e-08:104:84//U79279
R-NT2RP3001753//CIT-HSP-2379P21.TF CIT-HSP Homo sapiens genomic clone 2379P21, genomic survey sequence.//8.8e-06:102:78//AQ113378
R-NT2RP3001764
R-NT2RP3001777//Human mRNA for heparan sulfate proteaglycan (glypican).//0.99:166:66//X54232
R-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds.//1.3e-111:549:97//AB007928
R-NT2RP3001792//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//1.6e-32:266:83//U13262
R-NT2RP3001799//H.sapiens mRNA for OX40 homologue.//8.5e-44:374:79//X75962
R-NT2RP3001819
R-NT2RP3001844//Caenorhabditis elegans cosmid C54G7.//0.0042:231:63//U40410
R-NT2RP3001854//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//1.0:404:59//AF030694
R-NT2RP3001855
R-NT2RP3001896//CIT978SK-A-686F10.TV CIT978SK Homo sapiens genomic clone A-636F10, genomic survey sequence.//0.0012:68:82//AQ116409
R-NT2RP3001898//Homo sapiens Chromsome 11p15.5 PAC clone pDJ754h15 containing cdk-inhibitor p57/KIP2 (CDKN1C) gene, complete sequence.//0.37:266:65//AC005950
R-NT2RP3001915//Human BAC clone RG367O17 from 7p15-p21, complete sequence.//0.018:144:66//AC002486
R-NT2RP3001926//Human polyadenylate binding protein (TIA-1) mRNA, complete cds.//2.4e-10:77:100//M77142
R-NT2RP3001929
R-NT2RP3001931//Homo sapiens full-length insert cDNA clone YU73B11.//1.0e-110:562:96//AF087969
R-NT2RP3001938//Human DNA sequence from PAC 447B16 on chromosome Xq13.1-Xq13.3.//0.38:386:56//Z95328
R-NT2RP3001943//Homo sapiens chromosome 5, P1 clone 1076B9 (LBNL H14), complete sequence.//0.87:298:61//AC004500
R-NT2RP3001944//Bos taurus clone CSSM056 satellite DNA sequence.//0.0095:76:78//U03836
R-NT2RP3001969//Homo sapiens chromosome 12p13.3 clone RPCI11-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.//7.0e-109:552:96//AC005844
R-NT2RP3001989//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.15:111:68//Z81029
R-NT2RP3002002//Plasmodium falciparum 14-3-3 protein gene, partial cds.//0.016:286:60//AF065987
R-NT2RP3002004//H.sapiens mRNA for FAST kinase.//5.1e-41:335:82//X86779
R-NT2RP3002007
R-NT2RP3002014//Human DNA sequence from clone 228A9 on chromosome 22q12.3-13.32 Contains 85 KDA CALCIUM-INDEPENDENT PHOSPHOLIPASE A2, EST, GSS, CpG island, complete sequence.//6.6e-41:297:86//AL022322
R-NT2RP3002033
R-NT2RP3002045//Drosophila melanogaster fat protein (fat) gene, complete cds.//0.77:320:60//M80537

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R-NT2RP3002054//Caenorhabditis elegans cosmid Y69H2, complete sequence.//0.82:362:57//Z98877
R-NT2RP3002056//F.rubripes GSS sequence, clone 020E22bF7, genomic survey sequence.//0.010:185:63//Z87006
R-NT2RP3002057
R-NT2RP3002062//Human BAC clone RG356F09 from 7p21, complete sequence.//1.7e-17:164:81//AC004002
R-nnnnnnnnnnn
R-NT2RP3002081//HS_3082_A1_G09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3082 Col=17 Row=M, genomic survey sequence.//4.2e-25 :344:73//AQ122260
R-NT2RP3002097//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//2.6e-23:212:80//AC006210
R-NT2RP3002102//Homo sapiens BAC clone RG290G13 from 7q21, complete sequence.//0.43:168:64//AC004746
R-NT2RP3002108//CIT-HSP-2346P16.TF CIT-HSP Homo sapiens genomic clone 2346P16, genomic survey sequence.//3.5e-08:110:78//AQ059071
R-NT2RP3002146//Streptococcus gordonii competence factor (comC) and histidine protein kinase (comD) genes, complete cds, and response regulator (comE) gene, partial cds.//0.11:534:55//U80077
R-NT2RP3002147//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 329F2, WORKING DRAFT SEQUENCE.//4.1e-108:551:96//AL031710
R-NT2RP3002151//Mus musculus mRNA for Guanine Nucleotide Regulatory Protein, complete cds.//6.8e-62:347:80//AB003503
R-NT2RP3002163//Anolis pulchellus vitellogenin mRNA, partial cds.//0.77:281:63//U46857
R-NT2RP3002165
R-NT2RP3002166//D.sargus satellite DNA (clone PSE3).//0.81:124:62//Z48711
R-NT2RP3002173
R-NT2RP3002181//HS-1042-A2-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 824 Col=2 Row=K, genomic survey sequence.//1.3e-35:305:81//B36980
R-NT2RP3002244//Caenorhabditis elegans cosmid R11E3.//0.0024:393:61//AF100669
R-NT2RP3002248//Human DNA sequence from PAC 170A21 on chromosome 22q12-qter contains ESTs.//0.30:217:63//Z82189
R-NT2RP3002255
R-NT2RP3002273//Homo sapiens BAC clone 393I22 from 8q21, complete sequence.//0.84:463:57//AF070717
R-NT2RP3002276//HS_2260_A1_MF_E07 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2260 Col=13 Row=I, genomic survey sequence.//0.0017:198:63//AQ292491
R-NT2RP3002303//Human HMG-17 gene for non-histone chromosomal protein HMG-17.//7.4e-93:510:93//X13546
R-NT2RP3002304//Human BAC clone GS188P18, complete sequence.//6.3e-09:477:59//AC000115
R-NT2RP3002330//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.087:388:58//AC004688
R-NT2RP3002343
R-NT2RP3002351//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//0.20:489:56//AC004617
R-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene.//2.4e-104:516:94//Y15164
R-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds.//4.7e-102:524:95//AB014578
R-NT2RP3002484
R-NT2RP3002501//Human DNA sequence from PAC 92M18, BRCA2 gene region chromosome 13q12-13 contains BRCA2 exons 25, 26 and 27 ESTs and STS.//5.2e-17:232:75//Z73359
R-NT2RP3002512
R-NT2RP3002529//CIT-HSP-2340H2.TR CIT-HSP Homo sapiens genomic clone 2340H2, genomic survey sequence.//0.81:266:58//AQ057387
R-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds.//3.3e-82:438:94//AB018272
R-NT2RP3002549//Medicago truncatula ENBP1 gene, exons 1 to 12.//0.95:381:56//AJ002479
R-NT2RP3002566//HS_2036_A1_D08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2036 Col=15 Row=G, genomic survey sequence.//0.18:162:64//AQ230627
R-NT2RP3002587//Homo sapiens clone DJ1090E20, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-15:213:73//AC004956
R-NT2RP3002590//Arabidopsis thaliana genomic DNA; chromosome 5, P1 clone: MXK3, complete sequence.//0.00010:431:59//AB019236
R-NT2RP3002602//Mus musculus stannin gene, complete cds.//1.6e-20:339:70//AF030522
R-NT2RP3002603

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R-NT2RP3002631//Homo sapiens chromosome 21 PAC RPCIP704A9190Q2.//1.0:241:59//AJ006997
R-NT2RP3002659//Rat sodium-hydrogen exchange protein-isoform 3 (NHE-3) mRNA, complete cds.//6.8e-24:331:76//M85300
R-NT2RP3002660//H.sapiens partial gene for progesterone receptor and Alu element DNA.//9.8e-43:273:82//Z49816
R-NT2RP3002663//Lymnaea stagnalis 16S ribosomal RNA gene, mitochondrial gene encoding ribosomal RNA, partial sequence.//0.60:300:59//U82072
R-NT2RP3002671//S.pombe chromosome III cosmid c553.//1.2e-20:399:66//AL023704
R-NT2RP3002682//RPCI11-44K6.TJ RPCI11 Homo sapiens genomic clone R-44K6, genomic survey sequence.//4.7e-09:122:77//AQ202481
R-NT2RP3002687//P.falciparum complete gene map of plastid-like DNA (IR-B).//1.1e-07:494:59//X95276
R-NT2RP3002688//Human 7SL RNA sequence.//2.7e-32:290:79//X01037
R-NT2RP3002701
R-NT2RP3002713//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SEQUENCE.//0.95:334:59//AL031427
R-NT2RP3002763//***ALU WARNING: Human Alu-J subfamily consensus sequence.//3.9e-40:288:85//U14567
R-NT2RP3002770//R.prowazekii genomic DNA fragment (clone A615F).//0.21:174:63//Z82710
R-NT2RP3002785//Homo sapiens PAC clone DJ0170D19 from Xq23, complete sequence.//0.78:354:59//AC004822
R-NT2RP3002799//Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions.//1.1e-20:161:77//AF003528
R-NT2RP3002810//Caenorhabditis elegans cosmid F10D2.//0.28:441:56//AF022972
R-NT2RP3002818//HS_3053_A2_A08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3053 Col=16 Row=A, genomic survey sequence.//0.19:220:60//AQ135025
R-NT2RP3002861//P.falciparum complete gene map of plastid-like DNA (IR-B).//9.3e-05:414:60//X95276
R-NT2RP3002869//Homo sapiens chromosome 19, cosmid F21967, complete sequence.//0.14:165 :64//AC005256
R-NT2RP3002876//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.//2.6e-59:311:96//AL034380
R-NT2RP3002877//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//4.6e-24:422:63//AC003035
R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//4.7e-109:570:95//AB018314
R-NT2RP3002911//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//3.1e-16:471:64//AC005014
R-NT2RP3002948//, complete sequence.//4.5e-94:516:93//AC005500
R-NT2RP3002953//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//3.4e-111:566:96//AC005754
R-NT2RP3002955//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence.//0.19:424:58//AE001391
R-NT2RP3002969//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//1.1e-89:562:88//D30666
R-NT2RP3002972//Stealth virus 5 clone C1311 T7 genomic sequence.//1.0:122:67//AF067482
R-NT2RP3002978//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 455J7, WORKING DRAFT SEQUENCE.//4.8e-05:249:63//AL031733
R-NT2RP3002988//Human DNA sequence from PAC 106H8 on chromosome 1q24. Contains PHOSPHATIDYLINISITOL-GLYCAN class C (PIG-C) and DYNAMIN-3 genes. Contains ESTs and STSs and a CpG island.//0.0097:246:67//Z97195
R-NT2RP3003008//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//1.9e-24:188:78//AF109905
R-NT2RP3003032//Arabidopsis thaliana (clone DW1) DNA retrotransposon Ta11-1 integration site.//5.3e-07:376:63//L47211
R-NT2RP3003059//Homo sapiens chromosome 3, clone hRPK.165_I_16, complete sequence//1.4e-13:323:66//AC005669
R-NT2RP3003061//Homo sapiens mRNA from HIV associated non-Hodgkin's lymphoma (clone hll-10).//3.8e-42:265:91//Y16708
R-NT2RP3003068//HS_3214_B2_G09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3214 Col=18 Row=N, genomic survey sequence.//0.025:207:64//AQ181894

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R-NT2RP3003071//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 510D11, WORKING DRAFT SEQUENCE.//0.00014:329:60//Z98044
R-NT2RP3003078//T26A1TF TAMU Arabidopsis thaliana genomic clone T26A1, genomic survey sequence.//0.95:219:63//B27013
R-NT2RP3003101//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.4e-05:285:62//AC004153
R-NT2RP3003121//Homo sapiens full-length insert cDNA clone ZD62D10.//2.1e-47:242:98//AF086348
R-NT2RP3003133//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING DRAFT SEQUENCE.//1.4e-21:199:75//AL031985
R-NT2RP3003138//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//5.1e-14:287:68//D12646
R-NT2RP3003139//Rattus norvegicus kappa opioid receptor gene, exon 4 and complete cds.//1.5e-13:122:80//U17995
R-NT2RP3003150
R-NT2RP3003157//Homo sapiens 12q15 BAC GSHB-410F4 (Genome Systems Human Bac Library) complete sequence.//5.5e-42:289:74//AC005294
R-NT2RP3003185//HS_2058_A1_H03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=5 Row=O, genomic survey sequence.//0.025:52:94//AQ231298
R-NT2RP3003193//Homo sapiens chromosome 17, clone hRPK.628_E_12, complete sequence.//4.8e-40:349:79//AC005701
R-NT2RP3003197//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 364I1, WORKING DRAFT SEQUENCE.//5.2e-10:180:71//AL031319
R-NT2RP3003203//Mus musculus IFN alpha-treated embryonic fibroblast mRNA.//1.8e-11:148:77//U51904
R-NT2RP3003204//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 892F13, WORKING DRAFT SEQUENCE.//6.6e-41:282:86//AL009183
R-NT2RP3003212//Homo sapiens full-length insert cDNA clone ZB91B11.//1.7e-68:363:95//AF086173
R-NT2RP3003230//Caenorhabditis elegans cosmid T12B5.//0.0018:279:64//AF100307
R-NT2RP3003242//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence.//1.0:346:57//AC005272
R-NT2RP3003251//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.//2.5e-10:436:62//AC003083
R-NT2RP3003264//CIT-HSP-2296M7.TR CIT-HSP Homo sapiens genomic clone 2296M7, genomic survey sequence.//5.8e-05:308:61//AQ005862
R-NT2RP3003278//Human HepG2 partial cDNA, clone hmd3b11m5.//9.4e-47:302:89//D17022
R-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//7.4e-101:550:93//L36983
R-NT2RP3003290//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE.//3.0e-22:228:78//AL031662
R-NT2RP3003301
R-NT2RP3003302//CIT-HSP-2319H19.TF CIT-HSP Homo sapiens genomic clone 2319H19, genomic survey sequence.//1.5e-69:367:95//AQ034950
R-NT2RP3003311//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//5.1e-08:398:64//AC005505
R-NT2RP3003313//Caenorhabditis elegans cosmid F39B1, complete sequence.//0.00022:436:58//Z69660
R-NT2RP3003327//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-237H1 ~complete genomic sequence, complete sequence.//1.5e-16:334:70//AC002287
R-NT2RP3003330//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
R-NT2RP3003344//HS_3235_B2_H09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=18 Row=P, genomic survey sequence.//4.1e-18:197:80//AQ303203
R-NT2RP3003346
R-NT2RP3003353//CITBI-E1-2523B18.TR CITBI-E1 Homo sapiens genomic clone 2523B18, genomic survey sequence.//8.3e-06:130:73//AQ278834
R-NT2RP3003377//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//1.9e-97:481:94//AC005519
R-NT2RP3003384//Homo sapiens clone DJ0038I10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.3e-10:226:71//AC004820
R-NT2RP3003385
R-NT2RP3003403//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin, Type 1 Cytoskeletal 18 (KRT18, CYK18, K18, CK18) pseudogene and an STS, complete sequence.//2.8e-40:496:

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72//AL031585
R-NT2RP3003409//Rat POU domain factor (Brn-5) mRNA.//1.5e-20:375:68//L23204
R-NT2RP3003411//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 438L4, WORKING DRAFT SEQUENCE.//1.0:180:61//Z97635
R-NT2RP3003427//RPCI11-45J23.TJ RPCI11 Homo sapiens genomic clone R-45J23, genomic survey sequence.//0.82:162:69//AQ195566
R-NT2RP3003433//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence.//1.1e-10:379:61//AC006031
R-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//1.1e-95:479:96//AF004828
R-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds.//1.3e-100:527:93//AB018268
R-NT2RP3003491//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//4.0e-08:495:59//AE001398
R-NT2RP3003500//W.suaveolens mitochondrial ATP9 gene.//0.0074:514:59//X77238
R-NT2RP3003543//Human clone A9A2BRB7 (CAC)n/(GTG)n repeat-containing mRNA.//1.3e-31:217:88//U00952
R-NT2RP3003552
R-NT2RP3003555//Dictyostelium discoideum interaptin (abpD) gene, complete cds.//0.98:321:61//AF057019
R-NT2RP3003564
R-NT2RP3003572//Human DNA sequence from BAC 992D9 on chromosome 22q12.1 contains STS.//0.0015:507:59//AL008638
R-NT2RP3003576//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//1.2e-39:359:79//AC003007
R-NT2RP3003589//Plasmodium falciparum MAL3P8, complete sequence.//0.014:539:58//AL034560
R-NT2RP3003625//Human DNA sequence from clone 1042K10 on chromosome 22q13.1-13.2. Contains the ADSL gene for Adenylosuccinate lyase (EC 4.3.2.2, Adenylosuccinase, ASL) and 4 novel genes (one with probable rabGAP domains and Src homology domain 3). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//1.8e-44:448:77//AL022238
R-NT2RP3003656//Homo sapiens chromosome 17, clone hRPK.401_O_9, complete sequence.//0.34:257:62//AC005291
R-NT2RP3003659//O.fuscipennis 16S rRNA gene, partial.//0.021:145:65//Z93701
R-NT2RP3003665//HS_3078_B2_C09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=18 Row=F, genomic survey sequence.//1.3e-75:397:95//AQ140580
R-NT2RP3003672
R-NT2RP3003686
R-NT2RP3003701//Human BAC clone GS310A05 from 7q21-q22, complete sequence.//6.4e-17:464:62//AC002452
R-NT2RP3003716//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 774G10, WORKING DRAFT SEQUENCE.//0.00072:425:62//AL034410
R-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds.//1.7e-101:492:97//AB018300
R-NT2RP3003746//Homo sapiens Chromosome 16 BAC clone CIT987-SK502C10, complete sequence.//3.7e-07:217:66//AC003009
R-NT2RP3003795//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//8.1e-26:456:68//Z98052
R-NT2RP3003799//cSRL-138g10-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-138g10, genomic survey sequence.//4.9e-09:117:77//B01736
R-NT2RP3003800//Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds.//2.8e-106:551:95//AF077754
R-NT2RP3003805
R-NT2RP3003809//Homo sapiens full-length insert cDNA clone YZ95A01.//3.6e-106:533:97//AF086107
R-NT2RP3003819//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 34606, WORKING DRAFT SEQUENCE.//6.0e-44:288:81//Z84487
R-NT2RP3003825//Mus domesticus interleukin 1 receptor antagonist (IL-1RA) mRNA.//0.0014:410:58//M64404
R-NT2RP3003828
R-NT2RP3003831//****ALU WARNING: Human Alu-J subfamily consensus sequence.//2.3e-41:289:85//U14567
R-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence.//1.6e-108:541:97//AF070611
R-NT2RP3003842//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//1.5e-46:457:74//AC002980

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R-NT2RP3003846//Plasmodium falciparum MAL3P3, complete sequence.//3.5e-06:356:62//Z98547
R-NT2RP3003870//Homo sapiens full-length insert cDNA clone ZD75H11.//8.2e-09:68:98//AF086402
R-NT2RP3003876//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE.//0.0027:180:66//AL031650
R-NT2RP3003914//Dictyostelium discoideum DNA for transposable element Tdd-3 tandem array.//0.029:234:62//X53439
R-NT2RP3003918
R-NT2RP3003932//Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds.//0.00087:164:67//AF029215
R-NT2RP3003989
R-NT2RP3003992//Sequence 1 from patent US 5591825.//0.56:235:59//I33465
R-NT2RP3004013//HS_3018_A1_G09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=17 Row=M, genomic survey sequence.//0.00026:421:60//AQ119904
R-NT2RP3004016//Drosophila melanogaster DNA sequence (P1s DS03465 (D149) and DS08544 (D187)), complete sequence.//4.8e-12:308:62//AC004532
R-NT2RP3004041//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 598F2, WORKING DRAFT SEQUENCE.//0.42:190:64//AL021579
R-NT2RP3004051//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//3.6e-21:332:69//AC006130
R-NT2RP3004070//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.0e-05:476:57//AC005308
R-NT2RP3004078//Homo sapiens chromosome 19, cosmid R30335, complete sequence.//2.0e-86:486:93//AC005784
R-NT2RP3004093//Human PAC clone 257C22A from 13q12-q13, complete sequence.//5.3e-11:230:69//AC002525
R-NT2RP3004095//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//7.5e-93:551:92//AC005038
R-NT2RP3004110//Homo sapiens 12p13.3 PAC RPCI5-940J5 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.6e-104:317:100//AC006064
R-NT2RP3004125//Pongo pygmaeus CT microsatellite, clone #3, from the tandemly repeated genes encoding U2 small nuclear RNA (RNU2 locus).//0.73:168:60//U36532
R-NT2RP3004145//Homo sapiens full-length insert cDNA clone ZE09H03.//2.3e-89:427:99//AF086542
R-NT2RP3004148//Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence.//0.013:134:70//U78721
R-NT2RP3004155//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//3.8e-10:101:87//AC004081
R-NT2RP3004206//Homo sapiens clone DJ0794K21, complete sequence.//1.5e-06:442:57//AC005533
R-NT2RP3004207//Mouse mRNA for seizure-related gene product 6.//1.7e-07:220:69//D29763
R-NT2RP3004209//Human cosmid Q7A10 (D21S246) insert DNA, complete sequence.//7.3e-89:504:92//D42052
R-NT2RP3004215//Caenorhabditis elegans cosmid F11A6, complete sequence.//0.018:353:59//Z81498
R-NT2RP3004242//Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence.//4.5e-06:407:60//AE001415
R-NT2RP3004246//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence.//2.8e-105:534:97//AC005385
R-NT2RP3004253//RPCI11-78J12.TJ RPCI11 Homo sapiens genomic clone R-78J12, genomic survey sequence.//4.0e-64:382:90//AQ281324
R-NT2RP3004258//Rattus norvegicus Zis mRNA, complete cds.//7.0e-60:417:84//AF013967
R-NT2RP3004262//Mus musculus heat shock protein hsp40-3 gene, complete cds.//2.7e-43:528:73//AF092536
R-NT2RP3004334//Homo sapiens chromosome 17, clone hRPC.1110_E_20, complete sequence.//1.4e-06:435:62//AC004231
R-NT2RP3004341//CITBI-E1-2503F11.TR CITBI-E1 Homo sapiens genomic clone 2503F11, genomic survey sequence.//0.0018:210:65//AQ263365
R-NT2RP3004348//Homo sapiens chromosome 17, clone hRPK.85_B_7, complete sequence.//7.1 e-46:340:83//AC005695
R-NT2RP3004349//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 117O3, WORKING DRAFT SEQUENCE.//9.4e-29:263:79//AL020995
R-NT2RP3004378//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monoamine oxidase B (MAOB), ESTs and polymorphic CA repeats.//2.0e-67:422:90//Z95125

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R-NT2RP3004399//HS_3046_A1_E02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3046 Col=3 Row=I, genomic survey sequence.//0.00014:186:67//AQ137619
R-NT2RP3004424//RPCI11-59I14.TJ RPCI11 Homo sapiens genomic clone R-59I14, genomic survey sequence.//7.4e-71:370:95//AQ201461
R-NT2RP3004428//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y66A7, WORKING DRAFT SEQUENCE.//0.096:205:64//AL022282
R-NT2RP3004451//Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence.//0.0029:396:60//AC005824
R-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds.//2.9e-106:526:98//AB007917
R-NT2RP3004466
R-NT2RP3004470//Homo sapiens chromosome 5, Bac clone 5m9 (LBNL H220), complete sequence.//8.3e-06:229:64//AC005895
R-NT2RP3004472//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.87:442:59//AC005504
R-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds.//1.6e-105:521:97//AB007925
R-NT2RP3004480//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//3.9e-38:322:81//U47024
R-NT2RP3004490//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//4.2e-96:527:92//AC003982
R-NT2RP3004498//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//2.3e-43:342:82//AC006023
R-NT2RP3004503//Human cosmid g1572c101, complete sequence.//2.3e-25:392:68//AC000357
R-NT2RP3004504//M.musculus mRNA for CPEB protein.//1.8e-28:387:70//Y08260
R-NT2RP3004507
R-NT2RP3004527//Homo sapiens chromosome 14, BAC CITB-135H17 containing the RAD51L1 gene, complete sequence.//0.68:244:62//AC004518
R-nnnnnnnnnnnn//Mouse oncogene (ect2) mRNA, complete cds.//2.6e-79:525:84//L11316
R-NT2RP3004544
R-NT2RP3004566
R-NT2RP3004569//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.96:296:58//AC004709
R-NT2RP3004572//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//8.2e-12:457:63//AC005083
R-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//2.4e-97:488:96//AB007946
R-NT2RP3004594//Homo sapiens BAC clone NH0436H22 from 2, complete sequence.//1.7e-10:368:61//AC005234
R-NT2RP3004617
R-NT2RP3004618//F2H16TF IGF Arabidopsis thaliana genomic clone F2H16, genomic survey sequence.//0.96:212:64//B26414
R-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acetylglucosamine-6-O-sulfotransferas e (GlcNAc6ST), complete cds.//2.2e-55:291:95//AB014679
R-NT2RP4000008//H.sapiens polyA site DNA sequence.//2.5e-25:202:85//Z24749
R-NT2RP4000023//CIT-HSP-2372A9.TF CIT-HSP Homo sapiens genomic clone 2372A9, genomic survey sequence.//3.6e-51:313:89//AQ112388
R-NT2RP4000035//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.3e-69:536:81//AC005015
R-NT2RP4000049//Homo sapiens TRAIL receptor 2 mRNA, complete cds.//2.1e-58:289:82//AF016266
R-NT2RP4000051//Homo sapiens Chromosome 22q11.2 Cosmid Clone 20b In DGCR Region, complete sequence.//0.56:462:58//AC000074
R-NT2RP4000078//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00021:460:60//AC005506
R-NT2RP4000102//Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence.//1.6e-08:518:58//AC004648
R-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//3.5e-106:536:96//AB011538
R-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds.//1.1e-110:554:97//AB007952
R-NT2RP4000147
R-NT2RP4000150//Rat proto-oncogene (Ets-1) mRNA, complete cds.//3.5e-46:395:83//L20681
R-NT2RP4000151
R-NT2RP4000159//Caenorhabditis elegans cosmid R02F11.//0.00011:261:63//AF016439
R-NT2RP4000167//RPCI11-59L8.TK RPCI11 Homo sapiens genomic clone R-59L8, genomic survey sequence.//

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6.2e-26:163:93//AQ200049
R-NT2RP4000185
R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//4.6e-99:505 :96//AB014600
R-NT2RP4000212//, complete sequence.//1.0e-106:538:96//AC005300
R-NT2RP4000214//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.2e-39:272:88//AC005261
R-NT2RP4000218//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//1.6e-09:457:60//AC004081
R-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//9.0e-69:354:96//AJ006470
R-NT2RP4000246//Mus musculus mRNA for NDPP-1 protein, complete cds.//2.0e-27:344:73//D10727
R-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence.//9.7e-78:381:99//AF091092
R-NT2RP4000263//CIT-HSP-2336N24.TF CIT-HSP Homo sapiens genomic clone 2336N24, genomic survey sequence.//0.26:124:69//AQ043515
R-nnnnnnnnnnnn//ORF 5' of ECLF2...ECRF3=G protein-coupled receptor homolog [herpesvirus saimiri HVS, host-squirrel monkey, Genomic, 4 genes, 3720 nt].//0.12:326:61//S76368
R-NT2RP4000312//Human DNA sequence from clone 523E19 on chromosome 6p11.2-12.3 Contains ESTs STS and GSSs, complete sequence.//2.2e-111:538:98//AL033384
R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequence.//1.4e-108:515:99//AF070524
R-NT2RP4000323//S.cerevisiae telomeric sequence DNA, clone YLP108CA-2-i.//0.048:107:69//M34311
R-NT2RP4000355//Homo sapiens clone DJ1136A10, WORKING DRAFT SEQUENCE, 4 unordered pieces.//4.3e-39:350:79//AC004972
R-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//2.4e-109:520:99//AB018281
R-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//8.7e-109:527:98//AF044195
R-NT2RP4000370//Homo sapiens PAC clone DJ0777O23 from 7p14-p15, complete sequence.//9.9e-25 :348:72//AC005154
R-NT2RP4000376//Rattus norvegicus phospholipase A-2-activating protein (plap) mRNA, complete cds.//2.2e-69:391:89//U17901
R-NT2RP4000381//Homo sapiens chromosome 17, clone hRPK.394_K_10, complete sequence.//0.066:197:63//AC006080
R-NT2RP4000415//345F19.TV CIT978SKA1 Homo sapiens genomic clone A-345F19, genomic survey sequence.//0.10:79:75//B15527
R-NT2RP4000417//Homo sapiens full-length insert cDNA clone ZD52B10.//9.6e-96:468:97//AF086313
R-NT2RP4000424//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//1.8e-08:489:59//AL021026
R-NT2RP4000448//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.3e-07:510:60//AC005505
R-NT2RP4000449//HS_2037_B2_A09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037 Col=18 Row=B, genomic survey sequence.//1.3e-58:375:88//AQ243047
R-NT2RP4000455//Phocine herpesvirus type 1 glycoprotein D (gD) gene, partial cds.//0.62:133:63//U92271
R-nnnnnnnnnnnn
R-NT2RP4000480//cSRL-54b11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone CSRL-54b11, genomic survey sequence.//2.1e-19:145:88//B05082
R-nnnnnnnnnnnn
R-NT2RP4000500
R-NT2RP4000515//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.4e-05:411:59//AC005140
R-NT2RP4000517//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//2.7e-21:230:77//AC003007
R-NT2RP4000518//Homo sapiens DNA sequence from PAC 206D15 on chromosome 1q24. Contains a Reduced Folate Carrier protein (RFC) LIKE gene, a mitochondrial ATP Synthetase protein 8 (ATP8, MTATP8) LIKE pseudogene, an unknown gene and the last exon of the JEM1 gene coding for the Basic-Leucine Zipper nuclear factor JEM-1. Contains ESTs, an STS and a BAC end sequence (GSS), complete sequence.//0.0080:461:59//AL021068
R-NT2RP4000519
R-NT2RP4000524

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R-NT2RP4000528//Homo sapiens chromosome 17, clone hRPK.138_P_22, complete sequence.//0.99:158:66//AC005697

R-NT2RP4000541//Homo sapiens Chromosome 22q11.2 Cosmid Clone 33e In DGCR Region, complete sequence.//1.0:309:59//AC000078

R-NT2RP4000556//Rattus norvegicus cell cycle protein p55CDC gene, complete cds.//0.0031:126:72//AF052695

R-NT2RP4000588//Homo sapiens BAC clone RG208K23 from 7q31, complete sequence.//1.0:186:64//AC004161

R-NT2RP4000614//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-62, complete sequence.//1.4e-06:526:58//AL009013

R-NT2RP4000638//Homo sapiens chromosome 17, clone hCIT.468_F_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//6.9e-48:497:75//AC004666

R-NT2RP4000648//CIT-HSP-2300I7.TR CIT-HSP Homo sapiens genomic clone 2300I7, genomic survey sequence.//0.22:110:68//AQ012747

R-NT2RP4000657//Lycodichthys dearborni type III antifreeze peptide gene, clone 5'LD-1/NotI-EcoRI subclone SphI-XbaI, partial cds.//0.0065:189:63//U20443

R-NT2RP4000704//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 409J21, WORKING DRAFT SEQUENCE.//0.22:334:60//Z83824

R-NT2RP4000724//Homo sapiens Chromosome 22q11.2 Cosmid Clone 56c In DGCR Region, complete sequence.//2.2e-70:448:88//AC000080

R-NT2RP4000728//CIT-HSP-2310K14.TF CIT-HSP Homo sapiens genomic clone 2310K14, genomic survey sequence.//0.00013:289:61//AQ019669

R-NT2RP4000739//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces.//0.53:254:61//AC004765

R-NT2RP4000781//P.cepacia fusaric acid-resistance genes encoding 5 proteins, complete cds.//1.0:392:59//D12503

R-NT2RP4000817//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//0.59:378:58//AC003037

R-NT2RP4000833//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//3.4e-53:307:85//AL023808

R-NT2RP4000837//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//7.0e-50:367:77//AE000660

R-NT2RP4000855

R-NT2RP4000865//Homo sapiens chromosome 17, clone HRPC905N1, complete sequence.//1.5e-78:479:88//AC003098

R-NT2RP4000878//Mus musculus mRNA for myeloid associated differentiation protein.//4.5e-09:186:69//AJ001616

R-NT2RP4000879//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.8e-08:364:60//AC004153

R-nnnnnnnnnnnn//Human S-adenosylmethionine decarboxylase (AMD1) gene, exons 5-9.//3.5e-90:459:96//M88006

R-nnnnnnnnnnnn//H.sapiens ung gene for uracil DNA-glycosylase.//7.6e-09:392:61//X89398

R-NT2RP4000925//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//5.8e-45:264:92//U42975

R-nnnnnnnnnnnn//epstein-barr virus simple repeat array (ir3).//0.00012:367:61//J02079

R-NT2RP4000928//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence.//1.0:138:68//AB006698

R-NT2RP4000929//Human DNA sequence from PAC 293L6 on chromosome 22, complete sequence.//0.45:288:62//Z82197

R-NT2RP4000955//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 633O19, WORKING DRAFT SEQUENCE.//1.1e-09:322:62//AL022302

R-NT2RP4000973//Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions.//2.3e-06:326:62//AF003528

R-NT2RP4000975

R-NT2RP4000979//HS_3009_B1_F08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=15 Row=L, genomic survey sequence.//2.3e-14:117:89//AQ090957

R-NT2RP4000984//Human immunodeficiency virus type 1 envelope glycoprotein (env) gene, C2-V3 region, isolate HIV194UG011TIN.01_di1PD, partial cds.//0.11:219:62//U44882

R-NT2RP4000989//Sequence 30 from patent US 5552281.//3.5e-25:154:97//I25669

R-NT2RP4000996//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2),

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CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//3.8e-07:421:59//AF030694
R-NT2RP4000997//Homo sapiens chromosome 17, clone 104H12, complete sequence.//4.2e-37:499:72//AC000003
R-NT2RP4001004//HS_3163_A2_H02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=4 Row=O, genomic survey sequence.//2.8e-38:241:90//AQ168515
R-NT2RP4001006//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//7.1e-55:372:73//AC006023
R-NT2RP4001010//Homo sapiens full-length insert cDNA clone ZD38E12.//3.3e-09:153:74//AF086247
R-NT2RP4001029//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//2.1e-34:361:78//U20086
R-NT2RP4001041//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//9.9e-84:435:96//AC005216
R-NT2RP4001057//Homo sapiens KIAA0399 mRNA, partial cds.//6.2e-50:282:94//AB007859
R-NT2RP4001064//H.sapiens NOS2 gene, exon 15.//0.71:183:61//X85771
R-NT2RP4001078//Human D-site binding protein gene, exon 4 and complete cds.//1.9e-114:569:97//U48213
R-NT2RP4001079//Homo sapiens mRNA for putative Ca^{2+}-transporting ATPase, partial.//2.4e-118:574:98//AJ010953
R-NT2RP4001080//Plasmodium falciparum chromosome 2, section 66 of 73 of the complete sequence.//0.013:430:58//AE001429
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0592 protein, partial cds.//1.8e-119:548:95//AB011164
R-NT2RP4001095//Homo sapiens cosmids IM0525, LC1233, Qc3C1, LB1439, Qc12C11 and 220B3 from Xq28, complete sequence.//2.8e-39:312:81//AF003626
R-NT2RP4001100//Human DNA sequence from cosmid U85A3, between markers DXS366 and DXS87 on chromosome X contains rad21 and T-cell cyclophorin pseudogenes, STS.//8.7e-41:389:78//Z78021
R-NT2RP4001117//Canis familiaris sec61 homologue mRNA, complete cds.//2.8e-12:292:68//M96629
R-NT2RP4001122//Caenorhabditis elegans cosmid F44D12, complete sequence.//0.97:129:66//Z68298
R-NT2RP4001126//HS_3146_A1_805_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3146 Col=9 Row=C, genomic survey sequence.//0.013:268:63//AQ141093
R-NT2RP4001138
R-NT2RP4001143//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 64K7, WORKING DRAFT SEQUENCE.//1.8e-31:380:68//AL031668
R-NT2RP4001148//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.2e-83:325:92//AC005095
R-NT2RP4001149//Mouse mRNA for thymic epithelial cell surface antigen, complete cds.//8.1e-32:553:67//D67067
R-NT2RP4001150//AK011 Genomic DNA Hordeum vulgare genomic clone tel44a similar to barley TAS, genomic survey sequence.//0.91:132:63//AQ248412
R-NT2RP4001159//Cloning vector pAP3neo DNA, complete sequence.//4.0e-118:437:97//AB003468
R-NT2RP4001174//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//1.7e-33:289:82//AC002996
R-nnnnnnnnnnnn//P.falciparum mRNA for AARP2 protein.//0.93:187:64//Y08924
R-NT2RP4001207
R-NT2RP4001210//CIT-HSP-2042D13.TF CIT-HSP Homo sapiens genomic clone 2042D13, genomic survey sequence.//3.8e-06:268:63//B74772
R-NT2RP4001213//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//4.7e-16:371:66//M99593
R-NT2RP4001219//HS_2190_A1_A06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2190 Col=11 Row=A, genomic survey sequence.//2.4e-06:288:61//AQ216635
R-NT2RP4001228//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P2, WORKING DRAFT SEQUENCE.//0.024:357:58//AL031745
R-NT2RP4001235//HS_3047_A1_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=13 Row=L, genomic survey sequence.//0.0033:301:63//AQ126918
R-NT2RP4001256//HS_3007_A2_B06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=12 Row=C, genomic survey sequence.//1.5e-11:140:80//AQ118389
R-NT2RP4001260//Plasmodium falciparum chromosome 2, section 63 of 73 of the complete sequence.//0.0013:486:59//AE001426
R-NT2RP4001274//RPCI11-24O21.TKBF RPCI-11 Homo sapiens genomic clone RPCI-11-24O21, genomic survey sequence.//3.9e-25:142:99//AQ013887

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R-nnnnnnnnnnnn//Homo sapiens full-length insert cDNA clone ZD55D10.//1.2e-10:90:92//AF086334
R-NT2RP4001313//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence.//7.7e-23:466:66//AF009326
R-NT2RP4001315//CIT-HSP-2312C6.TR CIT-HSP Homo sapiens genomic clone 2312C6, genomic survey sequence.//0.98:305:62//AQ018036
R-NT2RP4001339
R-NT2RP4001345
R-NT2RP4001351//Fruitfly strain g20 mitochondrial DNA, A+T-rich region, partial sequence.//0.00082:260:59//AB003097
R-NT2RP4001353//RPCI11-55N17.TJ RPCI11 Homo sapiens genomic clone R-55N17, genomic survey sequence.//0.74:106:66//AQ081821
R-NT2RP4001372
R-NT2RP4001373//Homo sapiens chromosome 17, clone hRPK.394_K_10, complete sequence.//1.5e-09:473:60//AC006080
R-NT2RP4001375
R-NT2RP4001379//CIT-HSP-2335A10.TF CIT-HSP Homo sapiens genomic clone 2335A10, genomic survey sequence.//9.4e-41:441:75//AQ040083
R-NT2RP4001389//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//2.4e-22:276:73//AC004691
R-NT2RP4001407//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.49:254:61//AC005140
R-NT2RP4001414
R-NT2RP4001433//Human prohibitin (PHB) gene, exons 1-7.//6.6e-66:357:90//L14272
R-NT2RP4001442//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.11:307:59//AC005308
R-NT2RP4001447//cSRL-58d2-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-58d2, genomic survey sequence.//0.0039:112:71//B05220
R-NT2RP4001474
R-NT2RP4001483
R-NT2RP4001498//Plasmodium falciparum (clone Dd2) heat shock protein 86 gene, complete cds.//1.2e-07:339:61//L34027
R-NT2RP4001502//HS_2187_B1_C10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2187 Col=19 Row=F, genomic survey sequence.//1.3e-20:183:81//AQ214108
R-NT2RP4001507//Arabidopsis thaliana chromosome 1 BAC T17H3 sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.15:333:62//AC005916
R-NT2RP4001524//Genomic sequence from Human 13, complete sequence.//0.96:159:65//AC001226
R-NT2RP4001529//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//9.5e-34:337:80//U20086
R-NT2RP4001547//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00027:336:63//AC004710
R-nnnnnnnnnnnn//Arabidopsis thaliana BAC T12H20.//1.5e-11:517:60//AF080119
R-NT2RP4001555//Human DNA sequence from PAC 481A17 on chromosome X contains ESTs.//0.0069:305:62//Z82212
R-NT2RP4001567//RPCI11-61A2.TJ RPCI11 Homo sapiens genomic clone R-61A2, genomic survey sequence.//0.0072:180:60//AQ200771
R-NT2RP4001568
R-NT2RP4001571//Trypanoplasma borreli kinetoplast ribosomal protein S12 (RPS12), putative cryptogene (GRII), 12S ribosomal RNA, and apocytochrome b (CYb) genes, primary transcripts, and cytochrome c oxidase subunit III (COIII) gene, complete cds.//1.6e-09:555:58//U14181
R-NT2RP4001574//HS_2247_B1_B05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2247 Col=9 Row=D, genomic survey sequence.//1.1e-41:254:90//AQ182345
R-NT2RP4001575//Human DNA sequence from clone 1033B10 on chromosome 6p21.2-21.31. Contains the BING5 gene, exons 11 to 15 of the BING4 gene, the gene for GalT3 (beta3-Galactosyltransferase), the RPS18 (40S ribosomal protein S18) gene, the SACM2L (suppressor of actin mutation 2, yeast, homolog) gene, a pseudogene similar to TAT-SF1, a Pseudogene similar to zinc finger genes, the RING1 gene, the gene for HKE6 (RING2), the gene for HKE4 (RING5), the RXRB (Retinoid X receptor beta) gene, the COL11A2 (collagen, type XI, alpha 2) gene, the HLA-DPB2 pseudogene and part of the HLA-DPA3 pseudogene. Contains predicted CpG islands, ESTs, STSs, and GSSs, complete sequence.//1.1e-118:567:98//AL031228
R-NT2RP4001592//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING

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DRAFT SEQUENCE.//2.5e-09:370:61//AL031650
R-NT2RP4001610//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//0.99:73:75//AC002364
R-NT2RP4001614
R-NT2RP4001634//Homo sapiens full-length insert cDNA clone YU73B11.//5.8e-101:526:94//AF087969
R-NT2RP4001638//Homo sapiens clone 23967 unknown mRNA, partial cds.//5.4e-115:559:97//AF007151
R-NT2RP4001644//M.musculus mRNA for map kinase interacting kinase, Mnk2.//6.8e-33:286:79//Y11092
R-NT2RP4001656//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.2e-109:515:99//AC000384
R-NT2RP4001677//Genomic sequence from Human 9q34, complete sequence.//0.19:504:58//AC000397
R-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//4.5e-115:583:96//U96629
R-NT2RP4001725//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.98:301:60//AC000380
R-nnnnnnnnnnn//Caenorhabditis elegans cosmid F48E3.//2.2e-17:328:64//U28735
R-NT2RP4001739//RPCI11-74E7.TJ RPCI11 Homo sapiens genomic clone R-74E7, genomic survey sequence.//1.1e-08:141:65//AQ268408
R-NT2RP4001753//H.sapiens HZF3 mRNA for zinc finger protein.//1.7e-111:552:96//X78926
R-NT2RP4001760//Mouse oncogene (ect2) mRNA, complete cds.//9.3e-27:358:72//L11316
R-NT2RP4001790//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.7e-99:484:98//AC005020
R-NT2RP4001803//HS_3087_B2_B05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3087 Col=10 Row=D, genomic survey sequence.//2.7e-96:471:97//AQ121405
R-NT2RP4001822
R-NT2RP4001823
R-NT2RP4001828//Human DNA sequence from PAC 179115, BRCA2 gene region chromosome 13q12-q13 contains Klotho ESTs and CpG island.//4.1e-14:136:83//Z92540
R-NT2RP4001838//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.5e-06:418:60//AE001372
R-NT2RP4001849//P.falciparum serine rich protein (SERP I) gene.//0.64:135:67//J03983
R-NT2RP4001889//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//4.3e-26:212:82//AC004548
R-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.8e-111:570:96//AC005014
R-NT2RP4001896
R-NT2RP4001901
R-NT2RP4001927//Borrelia burgdorferi (section 32 of 70) of the complete genome.//1.0:242:60//AE001146
R-NT2RP4001938//Human aminopeptidase N gene, exon 1.//3.3e-42:195:85//M55523
R-NT2RP4001946//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.97:371:57//AC004157
R-NT2RP4001950//RPCI11-69C18.TJ RPCI11 Homo sapiens genomic clone R-69C18, genomic survey sequence.//4.7e-91:552:89//AQ236641
R-NT2RP4001953//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//6.6e-70:325:84//Z93023
R-NT2RP4001966//Rat mRNA for growth potentiating factor, complete cds.//5.5e-37:141:86//D42148
R-NT2RP4001975//Human Newcastle disease virus inducible protein mRNA, partial 3'UTR region.//1.0e-46:242:98//U25276
R-NT2RP4002018//RPCI11-76I23.TV RPCI11 Homo sapiens genomic clone R-76I23, genomic survey sequence.//7.9e-89:438:97//AQ268536
R-NT2RP4002047//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//4.1e-07:325:62//AL031297
R-NT2RP4002052//Human DNA sequence from clone 352E11 on chromosome 22q13.1-13.31. Contains GSSs, complete sequence.//0.31:452:57//AL022353
R-NT2RP4002058//RPCI11-69O1.TJ RPCI11 Homo sapiens genomic clone R-69O1, genomic survey sequence.//0.23:163:64//AQ268418
R-NT2RP4002071//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1172A22, WORKING DRAFT SEQUENCE.//1.1e-11:407:62//AL034386
R-NT2RP4002075//Human DNA sequence from clone 21F7 on chromosome 6q16.1-21. Contains part of an exon

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of a putative new gene and STSs and GSSs, complete sequence.//0.085:350:61//AL033375
R-NT2RP4002078//RPCI11-79I16.TV RPCI11 Homo sapiens genomic clone R-79I16, genomic survey sequence.// 3.3e-87:452:95//AQ283131
R-nnnnnnnnnnnn
R-NT2RP4002083//Homo sapiens mineralocorticoid receptor (MLR), exon 5.//0.50:256:61//AF068619
R-NT2RP4002408//CIT-HSP-2376023.TF CIT-HSP Homo sapiens genomic clone 2376O23, genomic survey sequence.//6.8e-62:320:96//AQ111163
R-NT2RP4002791//Human PAC clone DJ318C15 from Xq23, complete sequence.//0.022:435:61//AC002476
R-NT2RP4002888//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//6.0e-56:660:71// AC002383
R-NT2RP4002905//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-20, complete sequence.//0.0017:533:57//AL008972
R-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds.//8.7e-114:605:94//AB007934
R-OVARC1000004//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//2.1e-43:326: 74//AC005510
R-OVARC1000006//HS_2253_B1_F01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=1 Row=L, genomic survey sequence.//3.7e-35:191:98//AQ069124
R-OVARC1000013//HS_2212_A2_G06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2212 Col=12 Row=M, genomic survey sequence.//0.14:212:63//AQ210584
R-OVARC1000014//Human DNA sequence from PAC 463A9, on chromosome Xq25 contains STS.//0.0053:356: 62//Z80232
R-OVARC1000017
R-OVARC1000035//RPCI11-65E1.TJ RPCI11 Homo sapiens genomic clone R-65E1, genomic survey sequence.// 3.3e-05:236:63//AQ237194
R-OVARC1000058//Homo sapiens DNA sequence from BAC 390C10 on chromosome 22q11.21-12.1. Contains an Immunoglobulin LIKE gene and a pseudogene similar to Beta Crystallin. Contains ESTs, STSs, GSSs and taga and tat repeat polymorphisms, complete sequence.//2.7e-48:325:82//AL008721
R-OVARC1000060//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27K12, WORKING DRAFT SEQUENCE.//5.0e-21:297:70//AL033397
R-OVARC1000068//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.00038:553:58//X95276
R-OVARC1000071//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 596C15, WORKING DRAFT SEQUENCE.//5.1e-110:599:93//AL031387
R-OVARC1000085//DNA encoding component HC5 of human proteasome.//2.7e-65:366:92//E03413
R-nnnnnnnnnnnn//CIT-HSP-2172N17.TF CIT-HSP Homo sapiens genomic clone 2172N17, genomic survey sequence.//0.80:285:59//B94391
R-OVARC1000091
R-OVARC1000092//CIT-HSP-2373J20.TR CIT-HSP Homo sapiens genomic clone 2373J20, genomic survey sequence.//1.4e-17:141:85//AQ111520
R-OVARC 1000106
R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//2.6e-100:495:97//AF069250
R-OVARC1000114//Homo sapiens partial XPGC gene, exon 2.//9.5e-49:392:80//X71342
R-OVARC1000133//Human Chromosome 16 BAC clone CIT987SK-A-362G6, complete sequence.//0.00020:243: 65//U95740
R-OVARC1000145//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence.// 1.8e-16:370:67//AC005385
R-OVARC1000148//CIT-HSP-2386P14.TF.1 CIT-HSP Homo sapiens genomic clone 2386P14, genomic survey sequence.//1.1e-05:55:98//AQ240492
R-OVARC1000151//M.musculus GEG-154 mRNA.//9.8e-21:192:81//X71642
R-OVARC1000168//CIT-HSP-2336F6.TR CIT-HSP Homo sapiens genomic clone 2336F6, genomic survey sequence.//0.050:176:62//AQ042932
R-OVARC1000191//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.7e-08:534:58//AC005506
R-OVARC1000198//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//5.2e-111:556:96//AC004604
R-OVARC1000209//Blacus sp. 16S ribosomal RNA gene, partial sequence.//0.55:165:67//AF003501
R-OVARC1000212//Mouse DNA for beta-casein.//0.56:225:63//X13484
R-OVARC1000240//Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.//6.2e-38:193:82//

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AC005670
R-OVARC1000241//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//1.1e-25:312:73//AF060194
R-OVARC1000288//Human HepG2 3' region MboI cDNA, clone hmd1d01m3.//5.4e-07:128:70//D17131
R-OVARC1000302//Homo sapiens chromosome 17, clone hRPK.651_L_9, complete sequence.//1.7e-10:100:88//AC005971
R-OVARC1000304//Mouse mRNA from Mov10 locus.//7.9e-66:379:81//X52574
R-OVARC 1000309
R-OVARC1000321//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//6.5e-83:453:94//AC005236
R-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//5.0e-58:455:81//U19614
R-OVARC1000335//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0483I23; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.034:429:60//AC005690
R-OVARC1000347//Mus musculus HRS gene, complete cds.//4.6e-06:339:61//AF020308
R-OVARC1000384//D.discoideum glycoprotein 24 A and B (GP24A and GP24B) genes, complete cds.//0.48:296:62//M27588
R-OVARC1000408//Homo sapiens DNA from chromosome 19-cosmid R27740 containing MEF2B and RSRFR2 genes, genomic sequence.//9.4e-39:286:87//AD000812
R-OVARC1000411//CIT-HSP-2303H10.TF CIT-HSP Homo sapiens genomic clone 2303H10, genomic survey sequence.//1.5e-07:94:84//AQ016720
R-OVARC1000414//Homo sapiens genomic DNA, 21q region, clone: 149C3X10, genomic survey sequence.//1.8e-32:296:75//AG002388
R-OVARC1000420//Homo sapiens clone DJ1137M13, complete sequence.//2.0e-48:354:77//AC005378
R-OVARC1000427//D.discoideum vegetative specific gene V18 gene for ribosomal protein.//2.5e-09:370:59//X15382
R-OVARC1000431//HS_2199_A2_E02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2199 Col=4 Row=I, genomic survey sequence.//1.3e-34:186:98//AQ093722
R-OVARC1000437//Gallus gallus tensin mRNA, 3' end.//1.3e-15:160:80//L06662
R-OVARC1000440//Homo sapiens BAC clone NH0538D15 from 7q11.23-q21.1, complete sequence.//0.0054:337:61//AC006043
R-OVARC1000442//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.0e-45:322:86//AQ037381
R-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds.//1.1e-77:418:94//AB014583
R-OVARC1000461//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 215D11, WORKING DRAFT SEQUENCE.//0.62:333:59//AL034417
R-OVARC1000465//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//1.1e-81:489:91//AF023451
R-OVARC1000466//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//0.0088:98:72//AC004526
R-OVARC1000473//Homo sapiens full-length insert cDNA clone YI53C10.//3.2e-92:317:100//AF085851
R-OVARC1000479//Rattus norvegicus mRNA for TIP120, complete cds.//2.7e-70:502:84//D87671
R-OVARC1000486//Dictyostelium discoideum FusC (fusC) gene, partial cds.//0.52:411:58//AF019984
R-OVARC1000496
R-OVARC1000520//Homo sapiens PAC clone DJ412A9 from 22, complete sequence.//3.8e-17:294:71//AC005005
R-OVARC1000526//Homo sapiens clone GS438P06, WORKING DRAFT SEQUENCE, 17 unordered pieces.//4.5e-109:547:96//AC005024
R-OVARC1000533//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//3.0e-46:264:93//AC004510
R-OVARC1000543//Caenorhabditis elegans cosmid F10C1.//0.00063:417:59//U49831
R-OVARC1000556//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//1.5e-39:144:92//AL022069
R-OVARC1000557//Homo sapiens chromosome 19, cosmid R32469, complete sequence.//1.5e-81:429:96//AC005197
R-OVARC1000564//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//0.83:301:58//AC004223
R-OVARC1000573//Homo sapiens Xq28 genomic DNA in the region of the ALD locus containing the genes for creatine transporter (SLC6A8), CDM, adrenoleukodystrophy (ALD), Na^+-isocitrate dehydrogenase gamma subunit

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(IDH), and translocon-associated protein delta (TRAP) genes, complete cds, plexin related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq28lu1 gene and cytochrome C (CCp) pseudogene.//2.4e-44:300:88//U52111

R-OVARC1000578//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//6.4e-48:436:78//AF001549

R-OVARC1000588//Homo sapiens chromosome 19, cosmid F19847, complete sequence.//2.7e-32:313:78//AC005952

R-OVARC 1000605

R-OVARC1000622//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//6.2e-43:328:83//AC006012

R-OVARC1000640//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.9e-47:514:73//AC005840

R-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds.//1.6e-29:162:100//AB011162.

R-OVARC1000678//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.50:270:60//AC005140

R-nnnnnnnnnnnn//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//1.4e-83:549:86//AJ001713

R-OVARC1000681//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 257E24, WORKING DRAFT SEQUENCE.//3.2e-13:160:76//AL034424

R-OVARC1000689//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds.//0.90:230:61//U32943

R-OVARC1000700//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//5.1e-15:133:85//AC005754

R-OVARC1000703//Homo sapiens chromosome 22, clone hRPC.130_H_16, complete sequence.//6.9e-48:525:73//AC005585

R-OVARC1000730//HS_3018_B1_H10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00019:198:63//AQ093513

R-OVARC1000746//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.98:154:65//X95276

R-OVARC1000769//Human coagulation factor XI gene, intron 2, partial, clone pTZ18R.//2.0e-30:187:78//M21185

R-OVARC1000771

R-OVARC1000781//Sequence 5 from Patent WO9722695.//8.4e-47:401:77//A63552

R-OVARC1000787//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//7.8e-111:567:96//AC004542

R-OVARC1000800//Homo sapiens mitochondrial HSP75 mRNA, complete cds.//1.3e-17:119:95//L15189

R-OVARC1000802//Homo sapiens chromosome 5, BAC clone 120c13 (LBNL H171), complete sequence.//2.3e-51:482:78//AC005574

R-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//3.6e-105:536:95//Y1771

R-OVARC1000846//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence.//2.7e-107:538:96//AC004494

R-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//3.6e-114:579:96//AF045584

R-OVARC1000862//M.musculus Fif mRNA.//2.3e-20:346:73//X71978

R-OVARC1000876//Plasmodium falciparum chromosome 2, section 53 of 73 of the complete sequence.//9.1e-08:427:58//AE001416

R-OVARC1000883//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//5.6e-34:357:78//U20086

R-OVARC1000885//Lycopersicon esculentum alcohol dehydrogenase homolog (GAD3) mRNA, partial cds.//0.47:305:60//U21801

R-OVARC 1000886

R-OVARC1000891//HS_3082_A2_F04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3082 Col=8 Row=K, genomic survey sequence.//1.1e-16:187:79//AQ122500

R-OVARC1000897//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//7.2e-07:476:60//AL020989

R-OVARC1000912

R-OVARC1000915//Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000924//Homo sapiens Chromosome 22q11.2 Cosmid Clone cosk In NF1 Region, complete sequence.//1.6e-77:465:90//AC002471

R-OVARC1000936//HS_2195_A2_C12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=24 Row=E, genomic survey sequence.//2.4e-76:463:90//AQ191108

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R-OVARC1000937//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 250D10, WORKING DRAFT SEQUENCE.//0.0028:161:65//Z99716
R-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//3.5e-62:526:78//AB005549
R-OVARC1000948//Hypera postica NADH dehydrogenase subunit 1 (ND1) gene, partial cds, tRNA-Leu gene, complete sequence, and 16S ribosomal gene, partial sequence, mitochondrial genes encoding mitochondrial products.//0.018:212:61//U61169
R-OVARC1000959//CIT-HSP-2371K16.TR CIT-HSP Homo sapiens genomic clone 2371K16, genomic survey sequence.//1.1e-45:303:87//AQ111323
R-OVARC1000960//Homo sapiens BAC clone GS293C05 from 7q21-q22, complete sequence.//7.5e-44:353:81//AC005021
R-OVARC1000971//H.sapiens DNA for repeat unit locus D18S51(285 bp).//2.2e-07:223:70//X91255
R-OVARC1000984
R-OVARC1000996//Human DNA sequence from clone 272L16 on chromosome 1q32.1-32.3. Contains the 3' end of the LAMB3 gene for Laminin, Beta 3 (Nicein, Kalinin, BM600) and a novel Rat Ca^{2+}/Calmodulin dependent Protein Kinase LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D1S491 and a ca repeat polymorphism, complete sequence.//1.3e-06:179:70//AL023754
R-OVARC1000999//Homo sapiens chromosome 17, clone hCIT.457_L_16, complete sequence.//5.8e-71:332:87//AC003957
R-OVARC1001000//HS_3032_B1_G11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=21 Row=N, genomic survey sequence.//5.1e-51:257:99//AQ096695
R-OVARC1001004//Homo sapiens from UWGC:y18c282 from 6p21, complete sequence.//5.6e-92:473:96//AC004190
R-OVARC1001010//RPCI11-10P1.TV RPCI-11 Homo sapiens genomic clone RPCI-11-10P1, genomic survey sequence.//4.1e-05:201:65//B71813
R-OVARC1001011//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.9e-18:219:69//AC005520
R-OVARC1001032//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//2.7e-89:464:86//AL022345
R-OVARC1001034//Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence.//1.4e-18:451:64//AC005220
R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds.//1.3e-99:501:96//AF099149
R-OVARC1001040//Homo sapiens chromosome 17, clone hRPK.1096_G_20, complete sequence.//9.7e-17:180:78//AC005410
R-OVARC1001044
R-OVARC1001051//H.sapiens mRNA for homologue to yeast ribosomal protein L41.//3.7e-15:124:88//Z12962
R-OVARC1001055//Homo sapiens, clone hRPK.15_A_1, complete sequence.//2.0e-30:292:76//AC006213
R-OVARC1001062//Sequence 65 from patent US 5691147.//2.6e-54:312:92//I76237
R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//2.3e-95:463:98//AF082657
R-OVARC1001072//Gallus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds.//0.92:272:59//U47276
R-OVARC1001074//HS_2205_A1_D07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2205 Col=13 Row=G, genomic survey sequence.//1.3e-35:205:94//AQ184530
R-OVARC1001085
R-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//4.5e-95:325:98//AJ005897
R-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//1.0e-73:386:95//AF051782
R-OVARC1001117//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence.//6.1e-37:314:81//AC005272
R-OVARC1001118//Homo sapiens chromosome 5, P1 clone 1195e2 (LBNL H73), complete sequence.//1.5e-44:390:77//AC005372
R-OVARC1001129//Rickettsia prowazekii strain Madrid E, complete genome; segment 1/4.//0.81:461:57//AJ235270
R-OVARC1001161//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 850H21, WORKING DRAFT SEQUENCE.//4.6e-08:342:64//AL031680
R-OVARC1001162//CIT-HSP-2171J2.TR CIT-HSP Homo sapiens genomic clone 2171J2, genomic survey sequence.//5.9e-48:347:85//B89781
R-OVARC1001167//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces.//

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1.3e-28:427:70//AC004963
R-OVARC1001169//RPCI11-36P6.TV RPCI-11 Homo sapiens genomic clone RPCI-11-36P6, genomic survey sequence.//0.56:113:72//AQ045859
R-OVARC1001170//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence.//8.8e-39:301:85//AC002549
R-OVARC1001173//Human clone HS2.30 Alu-Ya5 sequence.//2.4e-35:183:83//U67213
R-OVARC1001180//Homo sapiens 12q24.1 NOVECTOR P443K8 () complete sequence.//9.1e-41:516:72//AC005907
R-OVARC1001188//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//1.2e-14:134:85//AC004796
R-OVARC1001200//ALS=85 kda insulin-like growth factor binding protein-3 complex acid-labile subunit [baboons, liver, mRNA Partial, 1818 nt].//0.12:345:60//S83462
R-OVARC1001232//Bovine tyrosine hydroxylase mRNA, complete cds.//0.66:257:59//M36794
R-OVARC1001240//Homo sapiens chromosome 17, clone hCIT.124_H_2, complete sequence.//1.4e-41:284:87//AC006071
R-OVARC1001243//HS_2055_B2_C01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=2 Row=F, genomic survey sequence.//0.59:83:75//AQ243142
R-OVARC1001261//Crocodylus porosus mRNA for transthyretin.//0.93:121:66//AJ223148
R-OVARC1001268
R-OVARC1001270//Plasmodium falciparum MAL3P6, complete sequence.//0.0031:295:62//Z98551
R-OVARC1001271//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence.//1.6e-107:544:97//AC004494
R-OVARC1001282//Homo sapiens Xp22-39-47 PAC RPCI1-199J3 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.025:402:59//AC006062
R-OVARC1001296//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//1.1e-05:319:62//U97018
R-nnnnnnnnnnnn//Sequence 13 from patent US 5624818.//5.4e-85:577:84//I41142
R-OVARC1001329//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30G7, WORKING DRAFT SEQUENCE.//4.2e-71:282:88//AL034402
R-OVARC1001330//Homo sapiens PAC clone DJ0697H17 from 7q11.23-q21.1, complete sequence.//0.19:256:59//AC004862
R-OVARC1001339//Homo sapiens 12q13 PAC RPCI1-316M24 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.5e-49:366:83//AC004242
R-OVARC1001341//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 695O20, WORKING DRAFT SEQUENCE.//4.8e-26:447:69//AL032818
R-OVARC1001342//Homo sapiens chromosome 10 clone CIT987SK-1175G20 map 10q25.2-10q25.3, complete sequence.//5.5e-86:569:86//AC005874
R-OVARC1001344//Homo sapiens chromosome 5, BAC clone 261j17 (LBNL H190), complete sequence.//2.8e-46:424:78//AC005350
R-OVARC1001357//Sequence 1 from patent US 5597707.//3.0e-42:250:93//I34297
R-OVARC1001360//Homo sapiens chromosome 17, clone hRPK.786_O_4, complete sequence.//0.20:335:60//AC005863
R-OVARC 1001369
R-OVARC1001372//S.scrofa DNA for myogenin 3'flanking region (285 bp).//6.9e-29:249:83//X89210
R-OVARC1001376//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//2.1e-50:491:73//AC004491
R-OVARC1001381//Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence.//9.3e-20:422:60//AC005821
R-OVARC1001391
R-nnnnnnnnnnnn
R-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds.//9.9e-110:561:95//AB00665
R-OVARC1001419//CIT-HSP-2362F16.TR CIT-HSP Homo sapiens genomic clone 2362F16, genomic survey sequence.//7.6e-47:242:98//AQ074668
R-OVARC1001425//Homo sapiens PAC clone DJ1108A12 from 14q24.3, complete sequence.//2.3e-20:211:66//AC005157
R-OVARC1001436//Human DNA flanking 3' end of transposon L1.1.//0.18:148:66//M80341
R-OVARC1001442
R-OVARC1001453//Human PAC clone DJ525N14 from Xq23, complete sequence.//2.3e-19:181:81//AC002086

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R-OVARC1001476//CITBI-E1-2517B6.TR CITBI-E1 Homo sapiens genomic clone 2517B6, genomic survey sequence.//0.24:308:59//AQ278655
R-OVARC1001480//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 753D4, WORKING DRAFT SEQUENCE.//0.99:294:62//AL031676
R-OVARC1001489//E.caballus microsatellite DNA marker (clone ASB32).//0.87:81:71//X93546
R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//9.3e-116:585:96//AF016507
R-OVARC1001506//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13F4 ~complete genomic sequence, complete sequence.//2.6e-40:285:86//AC002039
R-OVARC1001525//Homo sapiens clone NH0215P16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:320:59//AC006036
R-OVARC1001542//Homo sapiens hJTB mRNA, complete cds.//5.0e-110:566:95//AB016488
R-OVARC1001547
R-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//5.9e-33:216:92//AF031165
R-OVARC1001600//Human Chromosome X, complete sequence.//3.0e-22:157:89//AC002418
R-OVARC1001610//HS_3070_A2_A06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3070 Col=12 Row=A, genomic survey sequence.//0.47:107:66//AQ103523
R-OVARC1001611//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQENCE.//0.17:236:63//AL034423
R-OVARC1001615//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 310O13, WORKING DRAFT SEQUENCE.//1.3e-19:248:70//AL031658
R-OVARC1001668//HS_3228_A2_E12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3228 Col=24 Row=I, genomic survey sequence.//4.6e-13:156:76//AQ188379
R-OVARC1001702//CITBI-E1-2501P16.TR.1 CITBI-E1 Homo sapiens genomic clone 2501P16, genomic survey sequence.//1.6e-41:217:99//AQ241965
R-OVARC1001703
R-OVARC1001711//CITBI-E1-2502N10.TF CITBI-E1 Homo sapiens genomic clone 2502N10, genomic survey sequence.//2.0e-14:220:72//AQ266194
R-OVARC1001726//CIT-HSP-2320O1.TF CIT-HSP Homo sapiens genomic clone 2320O1, genomic survey sequence.//0.021:170:62//AQ038145
R-OVARC1001731//Human mRNA for fibroblast tropomyosin TM30 (pl).//2.5e-72:422:90//X05276
R-OVARC1001745//Human DNA sequence from clone 796I11 on chromosome 20q12. Contains ESTs, an STS and GSSs, complete sequence.//7.6e-44:314:84//AL031257
R-nnnnnnnnnnnn//S.cerevisiae N-acetyltransferase (AAA1) mRNA, complete cds.//1.6e-08:396:60//M23166
R-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//3.5e-108:567:94//U97670
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0675 protein, complete cds.//6.3e-108:529:97//AB014575
R-OVARC1001768//Caenorhabditis elegans cosmid Y57G11A, complete sequence.//0.24:205:64//Z99279
R-OVARC1001791//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//4.6e-58:558:76//AC005066
R-OVARC1001795
R-OVARC1001802//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//1.1e-37:346:78//U89337
R-OVARC1001805//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//3.0e-112:581:95//AL023694
R-OVARC1001812//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin, Type 1 Cytoskeletal 18 (KRT18, CYK18, K18, CK18) pseudogene and an STS, complete sequence.//6.6e-41:345:81//AL031585
R-OVARC1001813//CITBI-E1-2508J18.TR CITBI-E1 Homo sapiens genomic clone 2508J18, genomic survey sequence.//1.6e-72:386:95//AQ263046
R-OVARC1001820//Human PAC clone DJ525N14 from Xq23, complete sequence.//4.8e-41:320:83//AC002086
R-OVARC1001828//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//3.4e-08:527:58//AC004688
R-OVARC1001846//CIT-HSP-2014F15.TR CIT-HSP Homo sapiens genomic clone 2014F15, genomic survey sequence.//0.0045:165:67//B58905

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R-OVARC1001861//M.musculus mRNA for pMEM2 protein.//9.5e-28:405:68//X95350
R-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence.//5.9e-104:571:91//AF070611
R-OVARC1001879//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//9.1e-20:206:80//AL031864
R-OVARC1001880//RPCI11-42I15.TJ RPCI11 Homo sapiens genomic clone R-42I15, genomic survey sequence.//3.9e-50:287:88//AQ052700
R-OVARC1001883//Homo sapiens chromosome 17, clone hCIT.123_J_14, complete sequence.//6.1e-13:457:63//AC003950
R-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//2.5e-86:346:90//AF061749
R-OVARC1001901//Homo sapiens testis specific methyl-CpG binding protein MBD2 (MBD2) mRNA, partial cds.//7.2e-89:421:100//AF072246
R-OVARC1001911//Homo sapiens full-length insert cDNA clone ZD52F10.//8.2e-106:510:98//AF086315
R-OVARC1001916
R-OVARC1001928
R-OVARC1001942//S.cerevisiae N-acetyltransferase (AAA1) mRNA, complete cds.//0.0013:231:63//M23166
R-OVARC1001943//Human immunodeficiency virus type 1, strain FRMP329, envelope glycoprotein V3 region (env) gene, partial cds.//0.14:173:64//U58826
R-OVARC1001949//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//1.3e-09:306:63//M99593
R-OVARC1001950//Homo sapiens chromosome 17, clone hRPK.112_H_10, complete sequence.//8.2e-38:385:75//AC005666
R-OVARC1001987
R-OVARC1001989//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y57G11, WORKING DRAFT SEQUENCE.//6.3e-08:355:60//Z92841
R-OVARC1002044//Human DNA sequence from clone 681J21 on chromosome 1q23.2-24.3 Contains CpG island, complete sequence.//5.0e-42:298:86//AL031286
R-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds.//1.4e-107:542:96//AB007934
R-OVARC1002066//Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence.//0.23:210:61//AC004411
R-OVARC1002082//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.4e-99:546:92//AC006015
R-OVARC1002107//Human DNA sequence from PAC 417G15 on chromosome Xq25-Xq26. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), pseudogene, ESTs.//4.4e-34:375:74//AL009174
R-OVARC1002127
R-OVARC1002138//CIT-HSP-2290O18.TF CIT-HSP Homo sapiens genomic clone 2290O18, genomic survey sequence.//2.4e-07:316:62//AQ003988
R-OVARC1002143//RPCI11-54M8.TJ RPCI11 Homo sapiens genomic clone R-54M8, genomic survey sequence.//2.3e-35:220:90//AQ083241
R-OVARC1002156
R-OVARC1002158//CITBI-E1-2514D4.TF CITBI-E1 Homo sapiens genomic clone 2514D4, genomic survey sequence.//1.6e-12:140:79//AQ265720
R-OVARC1002165//CIT-HSP-2307C9.TF CIT-HSP Homo sapiens genomic clone 2307C9, genomic survey sequence.//5.0e-59:291:99//AQ020420
R-OVARC1002182//P. falciparum SD17 gene for knob-associated histidine-rich protein.//0.74:161:65//Y00060
R-PLACE1000004//D.discoideum gene for protein kinase.//0.00081:263:59//Z37981
R-PLACE1000005//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0082:477:58//AC005507
R-PLACE1000007//Homo sapiens clone 24422 mRNA sequence.//1.2e-14:100:97//AF070557
R-PLACE1000014//Homo sapiens genomic DNA, chromosome 21q22.2, p1 clone: T1212 and T1601, WORKING DRAFT SEQUENCE.//2.8e-44:405:77//D83253
R-PLACE1000031//Homo sapiens clone UWGC:y23c049 from 6p21, complete sequence.//1.8e-24:291:73//AC006162
R-PLACE1000040//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y105C5, WORKING DRAFT SEQUENCE.//0.00039:289:61//Z98855
R-PLACE1000048//Human BAC clone RG210I04, complete sequence.//4.7e-83:518:89//AC002462
R-PLACE1000050//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING

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DRAFT SEQUENCE, 8 unordered pieces.//0.98:73:76//AC005505
R-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//5.9e-21:125:98//L22154
R-PLACE1000066
R-PLACE1000078//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.2e-87:456:95//AC005848
R-PLACE1000081
R-PLACE1000094//RPCI11-91K6.TV RPCI11 Homo sapiens genomic clone R-91K6, genomic survey sequence.//2.3e-83:409:98//AQ282619
R-PLACE1000133//Homo sapiens chromosome 17, clone hRPK.746_E_8, complete sequence.//1.8e-06:420:57//AC005358
R-PLACE1000142
R-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//1.3e-112:594:94//AF058291
R-PLACE1000185
R-PLACE1000213//CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence.//8.2e-80:410:97//AQ022149
R-PLACE1000214//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-09, complete sequence.//1.6e-05:548:59//AL008989
R-PLACE1000236//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 695O20, WORKING DRAFT SEQUENCE.//2.2e-16:118:91//AL032818
R-PLACE1000246//X.laevis mRNA for XLCL2 protein.//6.5e-13:66:95//Z14122
R-PLACE1000292//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 111B22, WORKING DRAFT SEQUENCE.//6.6e-41:322:84//Z98200
R-PLACE1000332//Homo sapiens chromosome 17, clone hCIT.281_F_24, complete sequence.//1.8e-16:598:62//AC004706
R-PLACE1000347//Homo sapiens PAC clone DJ1090P18 from 7q21-q22, complete sequence.//2.3e-11:237:69//AC005326
R-PLACE1000374//Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence.//8.7e-09:492:58//AC005278
R-PLACE1000380//Plasmodium falciparum chromosome 2, section 1 of 73 of the complete sequence.//0.59:354:59//AE001364
R-PLACE1000383//Mus musculus myotubularin related protein 1 (Mtmr1) mRNA, complete cds.//0.55:65:84//AF073997
R-PLACE1000401//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.6e-17:152:83//AC005015
R-PLACE1000406//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence.//0.51:346:58//AB020742
R-PLACE1000420//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 2/15, WORKING DRAFT SEQUENCE.//1.5e-25:243:79//AP000009
R-PLACE1000421//HS_2251_B2_G12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2251 Col=24 Row=N, genomic survey sequence.//1.4e-82:430:95//AQ192807
R-PLACE1000424//Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.//1.8e-36:483:71//AC002073
R-PLACE1000435//Homo sapiens chromosome 21q22.2 cosmid clone Q71A3, complete sequence.//2.6e-37:371:76//AF015724
R-PLACE1000444//Homo sapiens chromosome 17, clone hRPK.227_G_15, complete sequence.//1.0e-54:429:81//AC005899
R-PLACE1000453//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//0.66:103:72//AF059580
R-PLACE1000481//Human DNA sequence from clone 960O17 on chromosome Xp11.21-11.22 Contains EST, CA repeat(DXS991), STS, GSS, complete sequence.//0.019:171:66//AL022166
R-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//3.2e-17:221:72//U35245
R-PLACE1000540//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00045:480:60//AC005308
R-PLACE1000547//Homo sapiens chromosome 19, cosmid F17987, complete sequence.//9.6e-32:231:85//AC004790
R-PLACE1000562//, complete sequence.//1.8e-45:280:92//AC005409

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R-PLACE1000564//Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds.//0.0079:180:65//U41302
R-PLACE1000583//Homo sapiens chromosome 17, clone hRPK.799_N_11, complete sequence.//1.5e-37:414:74//AC005323
R-nnnnnnnnnnnn//Human guanylate binding protein isoform I (GBP-2) mRNA, complete cds.//1.9e-77:542:82//M55542
R-PLACE1000596//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00019:482:59//AC005506
R-PLACE1000599//Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S2A1T, TCRBV6S5A1N1, TCRBV30S1P, TCRBV31S1, TCRBV13S5, TCRBV6S1A1N1, TCRBV32S1P, TCRBV5S5P, TCRBV1S1A1N1, TCRBV12S2A1T, TCRBV21S1, TCRBV8S4P, TCRBV12S3, TCRBV21S3A2N2T, TCRBV8S5P, TCRBV13S1 genes from bases 1 to 267156 (section 1 of 3).//5.6e-51:369:85//U66059
R-PLACE1000610//HS_3071_A1_C05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=9 Row=E, genomic survey sequence.//0.051:147:65//AQ103341
R-PLACE1000636//HS_3220_B2_E09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220 Col=18 Row=J, genomic survey sequence.//0.010:253 :64//AQ181157
R-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//1.6e-99:506:96//AF102265
R-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin)).//4.5e-101:559:92//AJ005896
R-PLACE1000706//nuclear protein TIF1 [mice, mRNA, 3951 nt].//9.1e-10:331:63//S78219
R-PLACE1000712//Homo sapiens full-length insert cDNA clone ZD76G10.//1.0e-69:345:98//AF086408
R-PLACE1000716//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//1.0:174:62//AC002300
R-PLACE1000748//Plasmodium falciparum MAL3P3, complete sequence.//1.0e-06:337:60//Z98547
R-PLACE1000749//cSRL-15g9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-15g9, genomic survey sequence.//8.8e-26:236:80//B02791
R-PLACE1000755//HS_2183_B1_H11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=21 Row=P, genomic survey sequence.//0.47:151:65//AQ064202
R-PLACE1000769//Homo sapiens clone DJ0647J21, WORKING DRAFT SEQUENCE, 10 unordered pieces.//7.0e-38:492:74//AC004847
R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//2.6e-101:513:96//AB014548
R-PLACE1000786//Human putative outer mitochondrial membrane 34 kDa translocase hTOM34 mRNA, complete cds.//0.078:180:68//U58970
R-nnnnnnnnnnnn
R-PLACE1000798//Homo sapiens cosmid D66B10, chromosome 21 5' of IFNAR1.//5.1e-26:348:72//AF039904
R-PLACE1000841//Human guanine nucleotide regulatory protein (NET1) mRNA, complete cds.//1.4e-26:110:95//U02081
R-nnnnnnnnnnnn//Homo sapiens full-length insert cDNA clone ZD55D10.//1.4e-13:93:96//AF086334
R-PLACE1000856//Anopheles quadrimaculatus NADH dehydrogenase subunits (1-4, 4L, 5-6); cytochrome oxidase subunits (1-3); adenosine triphosphatase subunits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large and small subunits).//2.7e-09:484:59//L04272
R-PLACE1000863
R-PLACE1000909//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.0e-05:274:60//AC005505
R-PLACE1000931//RPCI11-66P7.TK RPCI11 Homo sapiens genomic clone R-66P7, genomic survey sequence.//3.4e-73:369:97//AQ237489
R-PLACE1000948//RPCI11-64K15.TK RPCI11 Homo sapiens genomic clone R-64K15, genomic survey sequence.//6.6e-06:258:62//AQ239337
R-PLACE1000972//Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence.//8.3e-20:223:76//AC005553
R-PLACE1000977//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00030:448:59//AC005506
R-PLACE1000979
R-PLACE1001000//CIT-HSP-229718.TF CIT-HSP Homo sapiens genomic clone 229718, genomic survey se-

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quence.//7.0e-07:64:95//AQ004997
R-PLACE1001007//Human endothelial nitric oxide synthase gene, complete cds.//0.0078:215:64//D26607
R-PLACE1001010
R-PLACE1001015//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 150C2, WORKING DRAFT SEQUENCE.//1.5e-16:452:63//AL022318
R-PLACE1001024//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 417M14, WORKING DRAFT SEQUENCE.//0.99:186:63//AL024498
R-PLACE1001036//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.5e-15:313:68//AC005377
R-PLACE1001062//Homo sapiens chromosome 17, clone hCIT54K19, complete sequence.//7.3e-16:119:84//AC003664
R-PLACE1001076
R-PLACE1001088//Human DNA sequence from cosmid 203C2, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//0.97:332:59//Z74696
R-PLACE1001092//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.2e-07 :302:62//AC005139
R-PLACE1001104//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//0.057:280:60//AE001372
R-PLACE1001118//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//4.9e-06:334:60//Z84480
R-PLACE1001136//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.1e-31:331:75//AC005412
R-PLACE1001168//HS_2036_A1_H04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2036 Col=7 Row=O, genomic survey sequence.//0.40:144:63//AQ230662
R-PLACE1001171
R-PLACE1001185
R-PLACE1001238//Human coxVIb gene, last exon and flanking sequence.//3.4e-36:349:76//X58139
R-PLACE1001241//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-20, complete sequence.//0.11:258:61//AL008972
R-PLACE1001257//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B4P3; HTGS phase 1, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.9e-46:484:73//AC000016
R-PLACE1001272//Homo sapiens chromosome 21q22.3 PAC 191P10, complete sequence.//0.89:119:65//AF045448
R-PLACE1001279//Caenorhabditis elegans cosmid Y39A1C, complete sequence.//0.99:95:69//AL023839
R-PLACE1001280//CIT-HSP-2328B24.TF CIT-HSP Homo sapiens genomic clone 2328B24, genomic survey sequence.//5.4e-24:147:76//AQ042129
R-PLACE1001294//M.musculus GEG-154 mRNA.//1.3e-22:472:65//X71642
R-PLACE1001304//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//2.2e-22:139:77//AC003682
R-PLACE1001311//Loligo pealei repeat region.//0.84:232:64//Z18286
R-PLACE1001323//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//7.2e-39:308:83//Z84480
R-PLACE1001351//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y39B6, WORKING DRAFT SEQUENCE.//0.0018:408:59//Z95399
R-PLACE1001366//Human Na+/phosphate co-transporter gene, exon 1, partial sequence.//2.2e-46:369:82//D89927
R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds.//7.1e-80:431:93//AF009615
R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence.//3.6e-35:192:97//AF055030
R-PLACE1001384//Homo sapiens mRNA for multi PDZ domain protein.//2.6e-86:456:94//AJ001319
R-PLACE1001387
R-PLACE1001395//Nyctalus leisleri mitochondrial D-loop, partial sequence.//0.054:148:68//U95355
R-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//6.7e-70:352:98//AC005412
R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence.//8.0e-44:242:95//AF091087
R-PLACE1001414//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence.//0.12:53:84//AC006241

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R-PLACE1001440//Homo sapiens Xq28 genomic DNA in the region of the ALD locus containing the genes for creatine transporter (SLC6A8), CDM, adrenoleukodystrophy (ALD), Na^+-isocitrate dehydrogenase gamma subunit (IDH), and translocon-associated protein delta (TRAP) genes, complete cds, plexin related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq281u1 gene and cytochrome C (CCp) pseudogene.//1.0:250:61//U52111
R-PLACE1001456//Borrelia burgdorferi (section 16 of 70) of the complete genome.//0.0077:173:62//AE001130
R-PLACE1001468//HS_3050_A2_D07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=14 Row=G, genomic survey sequence.//0.00023:202:65//AQ133920
R-PLACE1001484//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//7.2e-17:180:80//AC002368
R-PLACE1001502//RPCI11-24F2.TP RPCI-11 Homo sapiens genomic clone RPCI-11-24F2, genomic survey sequence.//0.15:203:66//B84401
R-PLACE1001503//HS_2183_A1_B10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=19 Row=C, genomic survey sequence.//1.3e-38:181:82//AQ022613
R-PLACE1001517//Homo sapiens hGAA1 mRNA, complete cds.//6.4e-56:339:90//AB006969
R-PLACE1001534//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 620E11, WORKING DRAFT SEQUENCE.//8.6e-59:304:97//AL031667
R-PLACE1001545//Homo sapiens chromosome 3, clone hRPK.165_I_16, complete sequence.//2.6e-18:171:82//AC 005669
R-PLACE1001551
R-PLACE1001570//M.capricolum DNA for CONTIG MC188.//0.0043:305:57//Z33135
R-PLACE1001602//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//2.5e-82:408:98//AB020860
R-PLACE1001603//Homo sapiens KE05 protein mRNA, complete cds.//1.5e-40:295:84//AF064605
R-PLACE1001610//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.5e-39:307:82//AC005037
R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//4.9e-41:217:97//AF054174
R-PLACE1001632//Human DNA binding protein (HPF2) mRNA, complete cds.//1.4e-08:178:65//M27878
R-PLACE1001634//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone H06C16, WORKING DRAFT SEQUENCE.//0.00026:221:62//Z92791
R-PLACE1001640//Homo sapiens chromosome 17, clone hRPK.651_L_9, complete sequence.//2.6e-83:441:95//AC005971
R-PLACE1001672//H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA26H8.//0.91:115:69//Z79253
R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//1.5e-111:545:97//AF069250
R-PLACE1001692//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.0e-46:478:75//AC005077
R-PLACE1001705//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 250D10, WORKING DRAFT SEQUENCE.//0.79:91:73//Z99716
R-PLACE1001716//Homo sapiens Xp22 PAC RPCI1-167A22 (from Roswell Park Cancer Center) complete sequence.//0.96:172:66//AC002349
R-PLACE1001720
R-PLACE1001729//Human interleukin-13 (IL-13) precursor gene, complete cds.//0.79:280:60//U31120
R-PLACE1001739//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.0:109:65//AC005261
R-PLACE1001740//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//5.3e-11:249:67//AC006027
R-PLACE1001745
R-PLACE1001746//Homo sapiens chromosome 4 clone B200N5 map 4q25, complete sequence.//6.0e-05:337:61//AC005509
R-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//1.3e-91:540:89//AF061243
R-PLACE1001756//Human BAC clone RG302F04 from 7q31, complete sequence.//0.074:344:62//AC002463
R-PLACE1001761
R-PLACE1001771//Homo sapiens full-length insert cDNA clone ZD79C11.//4.4e-57:298:96//AF086426
R-PLACE1001781//T.thermophila micronuclear DNA containing to chromosomal breakage sequence Cbs-1, clone Tt819.//4.6e-05:282:61//M15711
R-PLACE1001799//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.015:331:58//AC004710
R-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//

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4.1e-92:463:95//AF058953
R-PLACE1001821//***ALU WARNING: Human Alu-J subfamily consensus sequence.//3.6e-36:281:82//U14567
R-PLACE1001845//Mus musculus Paneth cell enhanced expression PCEE mRNA, complete cds.//9.1e-26:313:73//U37351
R-PLACE1001869
R-PLACE1001897//Mus musculus homeobox protein (D1x5) mRNA, complete cds.//0.0043:207:64//AF033011
R-PLACE1001912//RPCI11-25F23.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-25F23, genomic survey sequence.//6.3e-33:248:67//AQ013567
R-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds.//5.0e-73:363:98//AF070671
R-PLACE1001928//Homo sapiens chromosome 17, clone hRPK.642_C_21, complete sequence.//0.98:248:60//AC005245
R-PLACE1001983//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y40H7, WORKING DRAFT SEQUENCE.//0.12:157:61//AL021389
R-PLACE1001989//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//1.4e-44:376:80//AL023755
R-PLACE1002046//CITBI-E1-2520J24.TF CITBI-E1 Homo sapiens genomic clone 2520J24, genomic survey sequence.//4.5e-20:144:89//AQ280117
R-PLACE1002052//Human DNA sequence from cosmid U160A4, between markers DXS366 and DXS87 on chromosome X contains STS.//0.025:362:57//Z80900
R-PLACE1002066//Leishmania tarentolae maxicircle DNA fragment.//0.0034:197:62//X02438
R-PLACE1002072//Homo sapiens chromosome 5, P1 clone 854b11 (LBNL H44), complete sequence.//9.7e-06:414:60//AC004763
R-PLACE1002073
R-PLACE1002090//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 ~complete genomic sequence, complete sequence.//1.8e-06:278:63//AC002302
R-PLACE1002115//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y214H10, WORKING DRAFT SEQUENCE.//6.0e-12:327:64//AL022344
R-PLACE1002119//Mus musculus IERS (Ier5) mRNA, complete cds.//5.1e-67:442:86//AF079527
R-PLACE1002140//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1.
Contains ESTs, STSs and GSSs, complete sequence.//2.2e-80:403:97//AL022162 R-PLACE1002150//Human DNA sequence from PAC 145B12 on chromosome Xq27-Xq28. Contains EST, CA repeat and STS.//0.043:455:59//AL008706
R-PLACE1002157//Human DNA sequence from Fosmid 65B7 on chromosome 22q11.2-qter. Contains exons 6-12 of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter), complete sequence.//9.8e-58:384:79//Z83849
R-PLACE1002163//Canis familiaris MHC class IIA DLA-DQA (DQA 1 allele) gene, exon 2, partial cds.//0.82:96:70//U44785
R-PLACE1002171//Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence.//0.83:196:65//AC004456
R-PLACE1002205//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.//0.0017:193:61//Z94056
R-PLACE1002213//Homo sapiens chromosome 19, fosmid 37308, complete sequence.//8.0e-42:330:81//AC004152
R-PLACE1002227//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//2.1e-10:126:80//AC003071
R-PLACE1002256//Homo sapiens clone DJ0853H20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.7e-06:478:57//AC004907
R-PLACE1002259//Human DNA sequence from cosmid U75A4 on chromosome X.//6.5e-81:501:88//Z82255
R-PLACE1002319//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00023:549:58//AC005505
R-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds.//4.9e-94:501:93//AB018271
R-PLACE1002395//Homo sapiens chromosome 19, cosmid R34382, complete sequence.//1.4e-69:385:93//AC005329
R-PLACE1002399//Human HepG2 3' region cDNA, clone hmd5d06.//2.4e-71:411:92//D16939
R-PLACE1002433//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 173D1, WORKING DRAFT SEQUENCE.//0.85:176:63//AL031984

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R-PLACE1002437//Human BAC clone RG114A06 from 7q31, complete sequence.//0.0040:213:63//AC002542
R-PLACE1002438//CITBI-E1-2501M20.TF.1 CITBI-E1 Homo sapiens genomic clone 2501M20, genomic survey sequence.//0.70:247:61//AQ242104
R-PLACE1002450//Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3.// 0.00060:471:59//AJ229041
R-PLACE1002465//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.// 2.5e-10:98:81//AC004854
R-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//1.7e-25:199:71//U69262
R-PLACE1002477//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//1.2e-11:382:63//Z92545
R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds.//1.1e-53:307:91//AF042273
R-PLACE1002499//Plasmodium falciparum MAL3P6, complete sequence.//0.56:270:60//Z98551
R-PLACE1002500//CIT-HSP-2337C20.TR CIT-HSP Homo sapiens genomic clone 2337C20, genomic survey sequence.//3.2e-42:297:85//AQ037614
R-PLACE1002514//Human DNA Sequence *** SEQUENCING IN PROGRESS *** from clone 212A2, WORKING DRAFT SEQUENCE.//7.8e-16:221:73//Z95114
R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//1.6e-86:582:85//AB018256
R-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1, complete sequence.//9.0e-91:453:97// AC004774
R-PLACE1002537//Hansenula wingei mitochondrial gene for NADH dehydrogenase subunit 5, complete cds.// 0.0042:489:60//D16253
R-PLACE1002571//Apis mellifera ligustica complete mitochondrial genome.//0.034:493:55//L06178
R-PLACE1002578//Homo sapiens chromosome 5, Pac clone 9c13 (LBNL H127), complete sequence.//2.5e-44: 292:84//AC006084
R-PLACE1002583//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//3.1e-17:517:61//AF045555
R-PLACE1002591
R-PLACE1002598//Caenorhabditis elegans cosmid Y37D8A, complete sequence.//0.080:308:60//AL032626
R-PLACE1002604//Human cosmid LL12NC01-88A9. ETV6 gene, exons 6, 7 and 8 and partial cds.//0.0013:176: 65//U63313
R-PLACE1002625//HS_2233_B2_H04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2233 Col=8 Row=P, genomic survey sequence.//5.2e-13:137:79//AQ146663
R-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//5.8e-46:272:94// AF079765
R-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//1.2e-77:390:97//AF068180
R-PLACE1002714//Mus musculus clone OST2473, genomic survey sequence.//1.3e-35:328:78//AF046656
R-PLACE1002722//Sequence 1 from patent US 5686597.//1.7e-42:276:89//I73723
R-PLACE1002768//Homo sapiens Xp22 bins 169-171 BAC GSHB-383H3 (Genome Systems Human BAC Library) complete sequence.//0.0098:197:64//AC005185
R-PLACE1002772//Homo sapiens PAC clone DJ0560O14 from 7q21.1-q21.2, complete sequence.//6.7e-49:378: 82//AC006145
R-PLACE1002782
R-PLACE1002794
R-PLACE1002811//CIT-HSP-2316H11.TF CIT-HSP Homo sapiens genomic clone 2316H11, genomic survey sequence.//6.0e-50:250:100//AQ034981
R-PLACE1002815//Sequence 2 from patent US 5747660.//2.7e-59:312:84//AR005279
R-PLACE1002816//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.3e-59:339:93//AC004466
R-PLACE1002834//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and-9.//1.4e-78:413:95// M27877
R-PLACE1002839//Homo sapiens PAC clone DJ0015I23 from 22, complete sequence.//6.5e-25:301:74// AC004819
R-PLACE1002851//CIT-HSP-2317M9.TR CIT-HSP Homo sapiens genomic clone 2317M9, genomic survey sequence.//0.0011:210:61//AQ040519
R-PLACE1002853//Human interleukin 6 (IL6) gene, 3' flank.//5.8e-06:327:61//J03049

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R-PLACE1002881
R-PLACE1002908//HS_3064_A1_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=7 Row=G, genomic survey sequence.//1.9e-09:156:72//AQ142985
R-PLACE1002941
R-PLACE1002962
R-PLACE1002968//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUCI, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete sequence.//1.9e-32:314:77//AL022721
R-PLACE1002991//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//1.6e-42:343:81//AL023755
R-PLACE1002993//Homo sapiens PAC clone DJ0899E09 from 7q11.23-q21.1, complete sequence.//0.56:88:72//AC004921
R-PLACE1002996//HS_2064_A1_A05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2064 Col=9 Row=A, genomic survey sequence.//4.9e-18:117:95//AQ243211
R-PLACE1003025//Homo sapiens PAC clone DJ0560O14 from 7q21.1-q21.2, complete sequence.//0.26:428:58//AC006145
R-PLACE1003027//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence.//1.3e-95:465:98//AC005920
R-PLACE1003044
R-PLACE1003092//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-89, complete sequence.//3.6e-05:358:60//AL010266
R-PLACE1003100//HS_2244_A2_H12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2244 Col=24 Row=O, genomic survey sequence.//2.3e-42:288:86//AQ084224
R-PLACE1003108//Homo sapiens clone DJ0781A18, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00066:233:61//AC004885
R-PLACE1003136//Plasmodium falciparum MAL3P2, complete sequence.//0.019:429:57//AL034558
R-PLACE1003145
R-PLACE1003153//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//3.2e-05:390:58//AC004616
R-PLACE1003174//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence.//2.4e-06:390:60//AB015479
R-PLACE1003176
R-PLACE1003190//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//4.0e-78:406:81//AC005095
R-PLACE1003200//Plasmodium falciparum MAL3P6, complete sequence.//0.016:411:57//Z98551
R-PLACE1003205//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00084:288:61//AC005139
R-PLACE1003238//Homo sapiens full-length insert cDNA clone ZD79H11.//7.6e-114:567:96//AF086432
R-PLACE1003249//Human Chromosome X, complete sequence.//1.3e-45:317:85//AC002416
R-PLACE1003256//Homo sapiens chromosome 17, clone HCIT421K24, complete sequence.//1.0e-45:328:85//AC004099
R-PLACE1003258
R-PLACE1003296//Diphoropria sp. 16S ribosomal RNA gene, mitochondrial gene encoding mitochondrial rRNA, partial sequence.//0.050:228:59//U39952
R-PLACE1003302//Figure 2. Nucleotide and translated protein sequences of HPF1, 2, and-9.//1.7e-91:458:96//M27877
R-PLACE1003334//Homo sapiens DNA sequence from BAC 217C2 on chromosome 22q13-ql3.33. Contains a gene for the presumtive isolog of Rat RTP60 (nuclear pore complex protein Npap60). Contains ESTs, complete sequence.//4.3e-34:370:71//Z82243
R-PLACE1003342//CIT-HSP-2311D21.TF CIT-HSP Homo sapiens genomic clone 2311D21, genomic survey sequence.//1.0:159:68//AQ020460
R-PLACE1003343//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.1e-05:330:61//AC004153
R-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//3.4e-98:469:98//U92715
R-PLACE1003361

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R-PLACE1003366//Homo sapiens CAG repeated sequence.//0.018:319:61//AJ006805
R-PLACE1003369//T18H17-T7 TAMU Arabidopsis thaliana genomic clone T18H17, genomic survey sequence.//0.050:155:63//B20174
R-PLACE1003373//Homo sapiens chromosome 17, clone hRPC.1050_D_4, complete sequence.//1.2e-62:434:83//AC004771
R-PLACE1003375//Dictyostelium discoideum golvesin (gol) gene, complete cds.//0.042:263:57//U89350
R-PLACE1003383//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epitherium cancer, segment 10/10.//1.7e-83:429:96//AB020878
R-PLACE1003401//Homo sapiens chromosome 17, clone hRPK.85_B_7, complete sequence.//2.4e-13:175:76//AC005695
R-PLACE1003420//Homo sapiens PAC clone DJ0988G15 from 7q33-q35, complete sequence.//2.1e-05:340:61//AC005587
R-PLACE1003454//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-64, complete sequence.//0.47:411:58//AL009014
R-PLACE1003478//M.capricolum DNA for CONTIG MC175.//0.51:253:59//Z33125
R-PLACE1003493//Homo sapiens chromosome 17, clone hRPK.394_K_10, complete sequence.//4.6e-37:319:81//AC006080
R-PLACE1003516//CIT-HSP-2295M19.TF CIT-HSP Homo sapiens genomic clone 2295M19, genomic survey sequence.//1.0e-40:251:90//AQ007480
R-PLACE1003519//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.//2.7e-29:163:89//AF064859
R-PLACE1003521//HS_3252_A2_G05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=10 Row=M, genomic survey sequence.//0.00017:274:60//AQ221562
R-PLACE1003528//HS_2041_B1_B07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2041 Col=13 Row=D, genomic survey sequence.//6.6e-40:219:83//AQ230483
R-PLACE1003537//Drosophila melanogaster mitochondrial cytochrome c oxidase subunits, ATPase6, 7 tRNAs (Trp, Cys, Tyr, Leu(UUR), Lys, Asp, Gly) genes, and unidentified reading frames A61, 2 and 3.//8.3e-05:300:61//J01404
R-PLACE1003553//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//2.7e-87:450:96//AL031297
R-PLACE1003566
R-PLACE1003575//Homo sapiens chromosome 16, cosmid clone 325D7, complete sequence.//4.7e-20:148:78//AC003965
R-PLACE1003583//Human DNA sequence from PAC 388N15 on chromosome Xq21.1.//3.5e-18:287:68//Z99571
R-PLACE1003584
R-PLACE1003592//Homo sapiens cosmid 223D9 from Xq28, complete sequence.//2.5e-10:153:73//AF061032
R-PLACE1003593//Human BAC clone RG030H15 from 7q31, complete sequence.//6.9e-07:240:65//AC002066
R-PLACE1003596//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y87G2, WORKING DRAFT SEQUENCE.//0.13:393:60//AL022597
R-PLACE1003602//Homo sapiens mRNA expressed in placenta.//2.4e-95:576:88//D83200
R-PLACE1003605//Homo sapiens BAC clone RG331C24 from 7q21, complete sequence.//2.9e-19:302:71//AC002081
R-nnnnnnnnnnnn
R-PLACE1003618//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191E19, WORKING DRAFT SEQUENCE.//8.3e-57:469:80//AL034451
R-PLACE1003625//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.1e-05:339:62//AC004688
R-PLACE1003638//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1104E15, WORKING DRAFT SEQUENCE.//2.5e-38:279:84//AL022312
R-PLACE1003669//HS_3054_A2_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=14 Row=I, genomic survey sequence.//0.014:265:61//AQ132713
R-PLACE1003704//HS_3213_A1_D12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=23 Row=G, genomic survey sequence.//0.80:195:61//AQ176784
R-PLACE1003709//Human BAC clone RG126M09 from 7q21-q22, complete sequence.//0.018:152:61//AC002067
R-PLACE1003711//Human endothelial nitric oxide synthase gene, complete cds.//1.7e-61:366:89//D26607
R-PLACE1003723//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//2.7e-

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44:505:73//AL022336
R-PLACE1003738//H.sapiens DNA sequence.//0.93:185:60//Z22357
R-PLACE1003760//Human globin gene.//5.9e-97:538:91//M69023
R-PLACE1003762//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence.//4.6e-13:134:79//AC003070
R-PLACE1003768//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence.//5.4e-12:189:71//AC005919
R-PLACE1003771//Homo sapiens BAC clone GS164B05 from 7p21-p22, complete sequence.//1.7e-119:619:95//AC004160
R-PLACE1003783
R-PLACE1003784//Homo sapiens chromosome 19, CIT-HSP-87m17 BAC clone, complete sequence.//5.6e-15:204:74//AC004659
R-PLACE1003795//CIT-HSP-2374C8.TR CIT-HSP Homo sapiens genomic clone 2374C8, genomic survey sequence.//7.0e-37:234:89//AQ114933
R-PLACE1003833//Homo sapiens full-length insert cDNA clone ZE15C06.//4.4e-59:313:95//AF086558
R-PLACE1003850
R-PLACE1003858
R-nnnnnnnnnnn
R-PLACE1003870//Homo sapiens Chromosome 22q11.2 Cosmid Clone 15a10 In DGCR Region, complete sequence.//8.7e-33:285:81//AC000072
R-nnnnnnnnnnn
R-PLACE1003886
R-PLACE1003888//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//0.73:127:65//AC004069
R-PLACE1003900//Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.//1.9e-05:239:59//L78810
R-PLACE1003903//Homo sapiens full=length insert cDNA clone ZD78D11.//8.1e-74:369:97//AF086422
R-PLACE1003915//Mus musculus bone morphogenetic protein-6 (BMP-6) gene, exons 6 and 7 and complete cds.//0.56:247:61//U73520
R-PLACE1003923//Caenorhabditis elegans cosmid Y57G11C, complete sequence.//0.67:213:63//Z99281
R-PLACE1003932//Human DNA sequence from cosmid U90B3, on chromosome Xp11, contains ESTs.//8.7e-49:342:85//Z74022
R-PLACE1003936//H.sapiens gene for ventricular myosin light chain 2.//2.6e-09:394:61//Z15030
R-PLACE1003968//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-62, complete sequence.//1.3e-07:245:65//AL010247
R-PLACE1004104
R-PLACE1004114//Human PAC clone RG212D03, complete sequence.//5.0e-07:336:61//AC002485
R-PLACE1004118//HS_3092_B1_B01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=1 Row=D, genomic survey sequence.//0.80:207:60//AQ128151
R-PLACE1004128//Rattus norvegicus guanine nucleotide binding protein beta 4 subunit mRNA, partial cds.//1.8e-06:193:66//AF022085
R-PLACE1004149//HS_2253_A2_F11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=22 Row=K, genomic survey sequence.//2.4e-59:315:95//AQ129711
R-PLACE1004156//Homo sapiens Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//8.3e-53:299:76//AC005295
R-PLACE1004161
R-PLACE1004183//Homo sapiens for TOM1-like protein.//1.3e-80:434:93//AJ010071
R-PLACE1004197//RPCI11-69N15.TK RPCI11 Homo sapiens genomic clone R-69N15, genomic survey sequence.//0.0078:170:65//AQ265515
R-PLACE1004203//Homo sapiens semaphorin L (SEMAL) mRNA, complete cds.//3.4e-105:501:98//AF030698
R-PLACE1004242//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//6.1e-65:373:86//AL021326
R-PLACE1004256//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence.//0.011:383:61//AC006031
R-PLACE1004257//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence.//3.4e-09:576:59//AC004470
R-PLACE1004258//HS_3034_A1_B12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3034 Col=23 Row=C, genomic survey sequence.//1.4e-35:359:77//AQ128936

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R-PLACE1004270//CITBI-E1-2504K14.TR CITBI-E1 Homo sapiens genomic clone 2504K14, genomic survey sequence.//2.7e-06:150:74//AQ261108
R-PLACE1004274//Homo sapiens BAC clone NH0436H22 from 2, complete sequence.//0.025:116:72//AC005234
R-PLACE1004277//Homo sapiens two pore domain K^+ channel (TASK-2) mRNA, complete cds.//4.4e-106:581:91//AF084830
R-PLACE1004284//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.59:231:60//AC005308
R-PLACE1004289//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence.//5.8e-31:340:75//AC005920
R-PLACE1004302//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.4e-90:572:86//AC005095
R-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//1.9e-113:590:94//Y11588
R-PLACE1004336//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1013A10, WORKING DRAFT SEQUENCE.//2.3e-65:292:82//AL033383
R-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//2.4e-70:379:93//AF100153
R-PLACE1004376//CIT-HSP-2287M8.TF CIT-HSP Homo sapiens genomic clone 2287M8, genomic survey sequence.//0.47:173:61//AQ000837
R-PLACE1004384//CIT-HSP-2316J11.TF CIT-HSP Homo sapiens genomic clone 2316J11, genomic survey sequence.//0.035:109:69//AQ037817
R-PLACE1004388//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-82, complete sequence.//4.2e-06:381:60//AL010149
R-PLACE1004405//Homo sapiens clone GS512I21, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.20:270:60//AC005027
R-PLACE1004425//Homo sapiens PAC clone DJ0733B09 from 7p14-p13, complete sequence.//1.3e-96:516:94//AC005532
R-PLACE1004428//Human DNA sequence from clone 888M10 on chromosome 1p36.11-36.31 Contains part of gene KIAA0453, EST, STS, GSS, complete sequence.//5.8e-10:279:65//AL031296
R-PLACE1004437//Human NAD^+-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//2.9e-88:516:88//U49283
R-PLACE1004451//HS_2258_B2_F01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2258 Col=2 Row=L, genomic survey sequence.//0.82:172:61//AQ221189
R-PLACE1004460
R-PLACE1004467//Syrian hamster carbamoylphosphate synthetase-aspartate transcarbamylasedihydroorotase (CAD) gene, exons 1 and 2.//1.2e-24:311:62//M31621
R-PLACE1004471//Homo Sapiens Chromosome X clone bWXD75, complete sequence.//2.1e-34:333:70//AC004389
R-PLACE1004473
R-PLACE1004491//Drosophila melanogaster Oregon-R mitochondrial A+T region.//1.0e-08:485:60//U11584
R-PLACE1004506
R-PLACE1004510//Plasmodium falciparum chromosome 2, section 64 of 73 of the complete sequence.//0.0094:543:56//AE001427
R-PLACE1004516//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//0.00011:343:59//AC003071
R-PLACE1004518
R-PLACE1004548//Homo sapiens Xp22 BAC GS-551O19 (Genome Systems Human BAC library) and cosmids U199A7 and U209F2 (Lawrence Livermore X chromosome cosmid library) containing part of human chloride channel 4 gene, complete sequence.//4.9e-40:245:80//AC003666
R-PLACE1004550
R-PLACE1004564//B.taurus mRNA for cleavage and polyadenylation specificity factor.//2.7e-82:532:86//X75931
R-PLACE1004629//Homo sapiens chromosome 7 clone UWGC:g3586a230 from 7p14-15, complete sequence.//0.015:437:59//AC004800
R-PLACE1004645//CIT-HSP-2370D6.TR CIT-HSP Homo sapiens genomic clone 2370D6, genomic survey sequence.//0.033:76:75//AQ110136
R-PLACE1004646//Homo sapiens cosmid 120C12 from Xq28, complete sequence.//2.0e-23:237:79//AF036876
R-PLACE1004658//Homo sapiens Chromosome 12p13.3 BAC RPCI11-21K20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//7.1e-09:94:87//AC005343
R-nnnnnnnnnnnn//RPCI11-79G23.TV RPCI11 Homo sapiens genomic clone R-79G23, genomic survey se-

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quence.//2.2e-81:433:94//AQ283692
R-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//2.7e-24:263:74//U07561
R-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds.//1.1e-89:513:91// AF035606
R-PLACE1004681//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 3/11.//1.3e-96:498:95//AB020860
R-PLACE1004686
R-PLACE1004691//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 2/11.//2.1e-33:290:80//AB020859
R-PLACE1004693//Caenorhabditis elegans cosmid Y2H9A, complete sequence.//1.0:195:60//AL021448
R-PLACE1004716//CITBI-E1-2519C14.TR CITBI-E1 Homo sapiens genomic clone 2519C14, genomic survey sequence.//5.0e-43:245:93//AQ276965
R-PLACE1004722//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0022:360:60//AC005507
R-PLACE1004736
R-PLACE1004740
R-nnnnnnnnnnnn//Homo sapiens ubiquitin-protein ligase E3-alpha (UBR1) mRNA, partial cds.//5.4e-105:575:92// AF061556
R-PLACE1004751//Homo sapiens Xq28 BACs 360 F12, GSHB-555C13, complete sequence.//9.0e-26:317:76// AC002523
R-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds.//8.5e-88:437:96//AF084367
R-PLACE1004777//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//0.050:138:65//AP000010
R-PLACE1004793//Human endogenous retrovirus HERV-K(HML6) proviral clone HML6.17 putative polymerase and envelope genes, partial cds, and 3'LTR.//5.1e-58:313:80//U60269
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0606 protein, partial cds.//5.8e-98:580:88//AB011178
R-PLACE1004813//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//5.3e-09:256:64//AC005140
R-PLACE1004814//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//3.5e-107:358:99//AF069250
R-PLACE1004815//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence.//3.8e-61:353:89// AC004126
R-PLACE1004824//Homo sapiens chromosome 17, clone hCIT.468_F_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.7e-42:364:79//AC004666
R-PLACE1004827//Homo sapiens Xp22 BAC GS-594A7 (Genome Systems Human BAC library) contains Bmx gene, complete sequence.//2.7e-14:156:79//AC003669
R-PLACE1004836//HS_2270_A2_H10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=20 Row=O, genomic survey sequence.//8.6e-51:267:96//AQ164110
R-PLACE1004838//CIT-HSP-2343E10.TR CIT-HSP Homo sapiens genomic clone 2343E10, genomic survey sequence.//0.071:168:63//AQ058544
R-PLACE1004840//Sequence 4 from patent US 5728819.//1.6e-26:150:98//I92820
R-PLACE1004868//Human Chromosome X clone bWXD342, complete sequence.//0.57:344:59//AC004072
R-PLACE1004885//HS_3235_B2_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=14 Row=J, genomic survey sequence.//1.1e-38:175:78//AQ210193
R-PLACE1004900//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.0e-44:334:84//AL022577
R-PLACE1004902
R-nnnnnnnnnnnn//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//7.7e-58:377:87//Z82209
R-PLACE1004918//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.// 0.00084:373:60//AC004605
R-PLACE1004930//Homo sapiens MDC-3.13 isoform 1 mRNA, complete cds.//2.0e-100:532:93//AF099936
R-PLACE1004934//Homo sapiens clone RG062N11, WORKING DRAFT SEQUENCE, 2 unordered pieces.// 0.00030:198:66//AC005683
R-PLACE1004937//Caenorhabditis elegans SEL-10 (sel-10) mRNA, complete cds.//1.3e-13:367:61//AF020788

BNSDOCID: <EP___1074617A2_I_>

R-PLACE1004969//Human DNA sequence from clone LUCA7 on chromosome 3, complete sequence.//0.97:116:71//Z84494
R-PLACE1004972
R-PLACE1004979//Plasmodium falciparum MAL3P4, complete sequence.//0.74:304:60//AL008970
R-PLACE1004982//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-05:495:57//AC005308
R-PLACE1004985//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 451B21, WORKING DRAFT SEQUENCE.//2.5e-10:410:60//AL033522
R-PLACE1005026//Homo sapiens PAC clone DJ0907C10 from 7q31-3q32, complete sequence.//2.7e-56:158:99//AC004925
R-PLACE1005027
R-PLACE1005046//Homo sapiens chromosome 19, cosmid F20237, complete sequence.//3.1e-63:438:86//AC005775
R-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SEQUENCE, 35 unordered pieces.//6.1e-87:301:98//AC005867
R-PLACE1005066//Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVEP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs and an AAAT repeat polymorphism, complete sequence.//1.1e-09:453:61//AL023584
R-PLACE1005077//H.sapiens genes for semenogelin I and semenogelin II.//2.6e-05:199:66//Z47556
R-PLACE1005085//Homo sapiens chromosome 17, clone hRPK.293_K_20, complete sequence.//2.1e-42:384:69//AC005495
R-PLACE1005086//RPCI11-30H10.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30H10, genomic survey sequence.//0.13:112:67//B87788
R-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds.//2.5e-97:531:92//L40401
R-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//1.3e-91:504:92//AC004476
R-PLACE1005108//Homo sapiens BAC129, complete sequence.//4.0e-28:232:84//U85195
R-PLACE1005111//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 566H6, WORKING DRAFT SEQUENCE.//3.0e-18:174:74//AL031845
R-PLACE1005128
R-PLACE1005146
R-PLACE1005162//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//2.4e-07:273:61//AC005140
R-nnnnnnnnnnnn//Rat alternatively spliced mRNA.//8.1e-20:185:82//M93018
R-PLACE1005181//HS_2182_B2_B05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=10 Row=D, genomic survey sequence.//4.9e-05:193:65//AQ030787
R-PLACE1005187//Arabidopsis thaliana chromosome II BAC T14A4 genomic sequence, complete sequence.//0.00073:264:60//AC006161
R-PLACE1005206//Homo sapiens full-length insert cDNA YN66A06.//6.3e-64:343:93//AF075043
R-PLACE1005232//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 25J6, WORKING DRAFT SEQUENCE.//1.3e-34:286:81//Z84476
R-PLACE1005243
R-PLACE1005261//Caenorhabditis elegans cosmid ZK666, complete sequence.//0.66:180:60//Z49132
R-PLACE1005266//Homo sapiens clone RG122E10, complete sequence.//1.3e-15:166:78//AC005067
R-PLACE1005277//CITBI-E1-2514D4.TF CITBI-E1 Homo sapiens genomic clone 2514D4, genomic survey sequence.//2.5e-34:358:74//AQ265720
R-PLACE1005287//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//4.1e-07:495:60//AL031744
R-PLACE1005305//HS_3180_B2_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3180 Col=4 Row=H, genomic survey sequence.//1.1e-42:308:85//AQ169443
R-PLACE1005308
R-PLACE1005313//Human Chromosome 11 pac pDJ227b23, WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.00048:320:60//AC000383
R-PLACE1005327//chromosome 1 specific transcript KIAA0491.//5.4e-103:537:94//AB007960
R-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569, complete sequence.//2.2e-94:536:91//AC004794
R-PLACE1005335//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.3e-32:313:79//AC000380

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R-PLACE1005373//Homo sapiens BAC129, complete sequence.//8.8e-10:229:68//U85195
R-PLACE1005374//Homo sapiens chromosome 17, clone hRPK.401_O_9, complete sequence.//3.0e-44:434:77//AC005291
R-PLACE1005409//Human BAC clone RG167B05 from 7q21, complete sequence.//8.8e-105:529:96//AC003991
R-PLACE1005453//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//4.7e-39:302:82//AC002477
R-PLACE1005467//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167P19, WORKING DRAFT SEQUENCE.//1.1e-40:328:81//Z93014
R-PLACE1005471//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Aminotransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//6.4e-68:409:90//AL022310
R-PLACE1005477//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32B1, WORKING DRAFT SEQUENCE.//0.020:216:66//AL023693
R-PLACE1005480//Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence.//2.8e-44:327:70//AC005392
R-PLACE1005481//Homo sapiens-chromosome 17, clone hRPC.1164_O_3, complete sequence.//4.2e-23:284:74//AC004703
R-PLACE1005494//Danio rerio homeobox protein LIM-3 (lim3) gene, exon 4.//0.19:468:60//AF031631
R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cds.//1.6e-55:277:98//AF071185
R-PLACE1005526//Human mRNA for alpha-1 type II collagen.//0.10:227:63//X16468
R-PLACE1005528//Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.//2.3e-76:395:96//AP000038
R-PLACE1005530//C.familiaris CA repeat sequence (isolate).//0.023:90:75//X86184
R-PLACE1005550//Fugu rubripes GSS sequence, clone 048A08bH1, genomic survey sequence.//2.0e-09:235:64//AL025928
R-PLACE1005554//Homo sapiens chromosome 17, clone hRPK.215_P_18, complete sequence.//0.069:305:60//AC005969
R-PLACE1005557//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence.//4.3e-105:587:91//AC004707
R-PLACE1005574//Human BAC 367D17 from chromosome 18, complete sequence.//1.5e-17:274:67//AC003971
R-PLACE1005584//Homo sapiens PAC clone DJ1186C01 from 7q21.2-q31.1, complete sequence.//2.7e-15:191:77//AC004991
R-PLACE1005595//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence.//6.4e-90:453:96//AC004126
R-PLACE1005603//Homo sapiens cosmid clone U169D2 from Xp22.1-22.2, complete sequence.//0.69:322:61//U72788
R-PLACE1005611//Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds.//0.059:473:56//U42599
R-PLACE1005623//Homo sapiens full-length insert cDNA clone ZD76B03.//1.6e-113:575:95//AF086405
R-PLACE1005630//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.6e-79:270:94//AC005840
R-PLACE1005639//Human BAC clone RG022J17 from 7q21, complete sequence.//8.2e-56:441:83//AC002382
R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//3.2e-110:585:93//AF083255
R-PLACE1005656//Homo sapiens chromosome 17, clone hRPK.628_E_12, complete sequence.//8.6e-08:505:58//AC005701
R-PLACE1005666//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat.//3.2e-27:307:72//Z82203
R-PLACE1005698//344B22.TV CIT978SKA1 Homo sapiens genomic clone A-344B22, genomic survey sequence.//0.030:91:70//B15144
R-PLACE1005727//Human variable number tandem repeat (VNTR) region, allele 17R1 3' to collagen type II (COL2A1) gene.//5.2e-10:587:59//L10171
R-PLACE1005730//Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.//0.0039:239:58//L78810
R-PLACE1005739//Mus musculus IFN-gamma induced (Mg11) mRNA, complete cds.//2.2e-21:270:72//U15635
R-PLACE1005755//Caenorhabditis elegans cosmid M03F4.//6.9e-08:219:64//U64601
R-PLACE1005763//Human mRNA for KIAA0118 gene, partial cds.//1.0e-45:268:87//D42087
R-PLACE1005799//Human X chromsome mRNA for CCG1 protein inv. in cell proliferation.//0.030:91:78//X07024
R-PLACE1005802//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.4e-69:391:92//

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AC004827
R-PLACE1005803
R-PLACE1005804//Human BAC clone RG341D10 from 7p15-p21, complete sequence.//1.8e-21:175:75// AC002530
R-PLACE1005828//Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.9e-56:333:91//AC004150
R-PLACE1005834//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P2, WORKING DRAFT SEQUENCE.//0.020:513:55//AL031745
R-PLACE1005845//Rabbit mRNA for protein phosphatase 2A-beta.//1.8e-10:182:69//Y00763 R-PLACE1005850
R-PLACE1005851//Homo sapiens clone DJ0789I05, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.5e-06:318:63//AC004887
R-PLACE1005876//B.taurus mRNA for cleavage and polyadenylation specificity factor.//6.7e-28:366:72//X75931
R-PLACE1005884//Human DNA sequence from cosmid V526F1, between markers DXS366 and DXS87 on chromosome X contains STS.//1.0e-06:306:64//Z70281
R-PLACE1005898//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0094:449:59//AC005139
R-PLACE1005921//CITBI-E1-2509N21.TF CITBI-E1 Homo sapiens genomic clone 2509N21,-genomic survey sequence.//4.8e-84:494:89//AQ261347
R-PLACE1005923//RPCI11-65N9.TJ RPCI11 Homo sapiens genomic clone R-65N9, genomic survey sequence.// 8.3e-97:520:93//AQ237243
R-PLACE1005925//Human DNA sequence from clone 231L4 on chromosome Xq27.1-27.3 Contains GSS, STS, complete sequence.//5.2e-67:578:78//AL022719
R-PLACE1005932//Caenorhabditis elegans cosmid Y52B11A, complete sequence.//0.0035:176:62//AL032654
R-PLACE1005934
R-PLACE1005936//Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence.// 0.00021:272:62//AF069716
R-PLACE1005951
R-PLACE1005953//Caenorhabditis elegans cosmid F09E5.//1.3e-07:349:60//U37429
R-PLACE1005955//Human HepG2 3' region MboI cDNA, clone hmd1d01m3.//8.3e-08:128:70//D17131
R-PLACE1005966//Pontia protodice large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//7.0e-09:549:59//AF044863
R-PLACE1005968//Rattus norvegicus mRNA for p47, complete cds.//1.1e-51:394:81//AB002086
R-PLACE1005990//Homo sapiens chromosome 12p13.3 clone RPCI11-407G6, WORKING DRAFT SEQUENCE, 51 ordered pieces.//4.4e-63:369:91//AC005866
R-PLACE1006002//Human cosmid CRI-JC2015 at D10S289 in 10sp13.//5.9e-27:299:74//U15177
R-PLACE1006003//Mus musculus clone OST18050, genomic survey sequence.//3.5e-07:164:67//AF046375
R-PLACE1006011//Mus musculus poly-(ADPribosyl)-transferase homolog PARP mRNA, complete cds.//1.1e-32:266:83//AF072521
R-PLACE1006017//Homo sapiens Chromosome 22q11.2 Cosmid Clone 31e In DGCR Region, complete sequence.//1.8e-17:164:82//AC000077
R-PLACE1006037//Mus musculus B6D2F1 clone 2C11B mRNA.//2.0e-49:557:72//U01139
R-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.3e-13:128:81//X99906
R-PLACE1006076//Homo sapiens clone DJ0781A18, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.3e-18:220:74//AC004885
R-PLACE1006119//Plasmodium berghei (STRAIN ANKA) gamma-GCS gene, complete CDS.//0.0050:271:63// AJ005122
R-PLACE1006129//Drosophila melanogaster, chromosome 2R, region 31C1-31D6, P1 clone DS08879, complete sequence.//0.43:178:65//AC005454
R-PLACE1006139//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence.//7.5e-13:222:68// AC004849
R-PLACE1006143//Plasmodium falciparum MAL3P6, complete sequence.//0.00019:455:59//Z98551
R-PLACE1006157//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.00018:351:60//AL034557
R-PLACE1006159//Homo sapiens chromosome 10 clone LA10NC01_124_D_3 map 10q25.1, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.0e-113:586:96//AC006103
R-PLACE1006164//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//1.0e-

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28:342:75//U91328
R-PLACE1006167//Homo sapiens full-length insert cDNA clone ZE14E04.//4.6e-77:426:93//AF086555
R-nnnnnnnnnnnn//Mouse mRNA for alpha-adaptin (C).//3.0e-46:188:82//X14972
R-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds.//1.6e-116:597:95//AF091433
R-PLACE1006195//Homo sapiens chromosome 19, fosmid 39554, complete sequence.//8.8e-11:148:74//AC004410
R-PLACE1006196
R-PLACE1006205//Genomic sequence from Mouse 11, complete sequence.//8.4e-44:332:85//AC000398
R-PLACE1006223//Human DNA sequence from cosmid U74C11, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//0.041:215:61//Z73362
R-PLACE1006225//Caenorhabditis elegans cosmid Y69H2, complete sequence.//9.7e-13:358:63//Z98877
R-PLACE1006236//Plasmodium falciparum MAL3P4, complete sequence.//0.00019:538:58//AL008970
R-nnnnnnnnnnnn//Homo sapiens BAC clone RG118D07 from 7q31, complete sequence.//3.1e-96:497:95//AC004142
R-PLACE1006246//Homo sapiens clone NH0144M13, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.029:499:56//AC006034
R-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//9.2e-96:499:95//AB014548
R-PLACE1006262//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//0.00043:160:66//AC004087
R-PLACE1006288//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20N2, WORKING DRAFT SEQUENCE.//3.5e-120:611:96//AL031320
R-PLACE1006318
R-PLACE1006325//Plasmodium falciparum MAL3P8, complete sequence.//1.0:426:57//AL034560
R-PLACE1006335//Human DNA sequence from PAC 849L7 on chromosome Xq21.//0.96:173:66//AL008987
R-PLACE1006357//P.falciparum complete gene map of plastid-like DNA (IR-B).//1.9e-07:491:58//X95276
R-PLACE1006360//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//0.25:484:56//AE001398
R-PLACE1006368//Caenorhabditis elegans cosmid Y38H6C, complete sequence.//1.0:240:59//AL031630
R-PLACE1006371//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence.//3.7e-101:574:91//AC004232
R-PLACE1006382
R-PLACE1006385//Mus musculus intersectin-EH binding protein Ibp2 mRNA, partial cds.//1.4e-50:350:86//AF057286
R-PLACE1006412//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//5.1e-51:339:82//AC004854
R-PLACE1006414//Homo sapiens 12p13.3 PAC RPCI5-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-38:297:84//AC004804
R-PLACE1006438//Homo sapiens full-length insert cDNA YH73H06.//7.6e-73:422:90//AF074985
R-PLACE1006445//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018K9, WORKING DRAFT SEQUENCE.//3.0e-07:376:61//AL031726
R-PLACE1006469
R-PLACE1006470//Mouse B1 repetitive sequence DNA.//1.0:96:66//M24152
R-PLACE1006482//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 447C4, WORKING DRAFT SEQUENCE.//3.0e-101:535:94//AL021977
R-PLACE1006492//Homo sapiens chromosome 17, clone hRPK.180_P_8, complete sequence.//0.78:44:95//AC005972
R-PLACE1006506//R.norvegicus BSP gene.//1.0:206:60//X86100
R-PLACE1006521//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13L8, genomic survey sequence.//9.0e-17:414:61//B75158
R-PLACE1006531//Plasmodium falciparum coronin gene, isolate 3D7.//0.98:186:63//AJ002197
R-PLACE1006534//Anopheles gambiae complete mitochondrial genome.//0.051:412:61//L20934
R-PLACE1006540//Homo sapiens clone UWGC:y55c025 from 6p21, complete sequence.//7.5e-41:470:70//AC004209
R-PLACE1006552//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y47D3, WORKING DRAFT SEQUENCE.//0.57:355:57//Z98865
R-PLACE1006598//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.016:291:58//AC004710
R-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//

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2.9e-116:590:95//U97670
R-PLACE1006617//Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.//2.2e-45:209:88//AC004050
R-PLACE1006626//C. elegans cosmid K12H4.//1.2e-16:344:64//L14331
R-PLACE1006629//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//2.8e-25:343:70//AC006128
R-PLACE1006640//CIT-HSP-2169L1.TF CIT-HSP Homo sapiens genomic clone 2169L1, genomic survey sequence.//0.00020:201:62//B90038
R-PLACE1006673//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.4e-42:309:84//AC004882
R-PLACE1006678//Homo sapiens PAC clone DJ1166G19 from 7p12-p11.2, complete sequence.//6.4e-09:454:59//AC006024
R-PLACE1006704//Human DNA sequence from clone 249C1 on chromosome Xq21.1-22.2 Contains GSS, complete sequence.//0.56:226:63//AL022154
R-PLACE1006731//Homo sapiens clone 23923 mRNA sequence.//6.0e-101:486:98//AF038172
R-PLACE1006754//Homo sapiens chromosome 19, cosmid R29124, complete sequence.//1.4e-68:381:93//AC005626
R-PLACE1006760//Homo sapiens clone 24800 mRNA sequence.//6.2e-72:397:92//AF070622
R-PLACE1006779//Rattus norvegicus intestinal trefoil factor gene, promoter and partial cds.//1.6e-11:420:61//U20984
R-PLACE1006782//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y47D3, WORKING DRAFT SEQUENCE.//0.60:321:58//Z98865
R-PLACE1006792//Homo sapiens chromosome 4 clone C0026P05 map 4P16, complete sequence.//2.9e-40:379:77//AC005599
R-PLACE1006795//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//6.2e-07:291:63//AC005083
R-PLACE1006800//HS_2270_B1_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=3 Row=H, genomic survey sequence.//4.1e-76:367:99//AQ085793
R-PLACE1006805//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.00058:354:59//AC005507
R-PLACE1006815//HS_3028_B1_B04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3028 Col=7 Row=D, genomic survey sequence.//1.5e-33:251:77//AQ120174
R-PLACE1006819//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//1.4e-76:544:84//Z86062
R-PLACE1006829
R-PLACE1006860
R-PLACE1006867//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 323M4, WORKING DRAFT SEQUENCE.//3.2e-107:549:95//AL033378
R-PLACE1006878//Homo sapiens full-length insert cDNA clone ZB55G05.//1.4e-46:241:97//AF086155
R-PLACE1006883//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence.//1.3e-38:283:85//AC004232
R-nnnnnnnnnnnn
R-PLACE1006904//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat.//4.1e-15:477:62//Z82203
R-PLACE1006917//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//1.3e-42:305:87//AC005184
R-PLACE1006932
R-PLACE1006935//Human DNA sequence from PAC 117P19 on chromosome X.//0.0014:114:74//Z86061
R-nnnnnnnnnnnn//Mouse mRNA for germ cell specific protein APG-1, complete cds.//9.5e-85:590:83//D49482
R-PLACE1006961//Homo sapiens chromosome 17, clone hRPK.349_A_8, complete sequence.//6.7e-42:295:86//AC005544
R-PLACE1006962//Homo sapiens Xp22 PAC RPCI1-167A22 (from Roswell Park Cancer Center) complete sequence.//1.1e-19:302:71//AC002349
R-PLACE1006966//HS_2219_B2_C02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=4 Row=F, genomic survey sequencer.//0.019:180:63//AQ145873
R-PLACE1006989
R-PLACE1007014

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R-PLACE1007021//Homo sapiens chromosome 12p13.3 clone RPCI3-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces.//1.6e-23:362:70//AC005845
R-PLACE1007045//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32B1, WORKING DRAFT SEQUENCE.//2.3e-90:584:86//AL023693
R-PLACE1007053//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.4e-108:550:96//AC004895
R-PLACE1007097//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucoronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//1.8e-103:552:93//AL021368
R-PLACE1007105//Mus musculus muskelin mRNA, complete cds.//2.7e-32:379:73//U72194
R-PLACE1007111//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.14:422:57//AC004688
R-PLACE1007112//Cynips cornifex cytb gene.//0.020:427:58//AJ228479
R-PLACE1007132//Homo sapiens full-length insert cDNA YH77E09.//5.7e-107:535:96//AF074987
R-PLACE1007140//Homo sapiens clone RG030L05, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.36:408:58//AC005050
R-PLACE1007178//Homo sapiens clone HEA4 Cri-du-chat region mRNA.//0.99:63:73//AF009283
R-PLACE1007226
R-PLACE1007238
R-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//2.0e-91:534:89//D50495
R-PLACE1007242//CITBI-E1-2512M9.TF CITBI-E1 Homo sapiens genomic clone 2512M9, genomic survey sequence.//1.3e-05:117:76//AQ279454
R-PLACE1007243//Prototheca wickerhamii 263-11 complete mitochondrial DNA.//0.21:284:58//U02970
R-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//6.9e-113:607:93//Y15908
R-PLACE1007274//Homo sapiens chromosome 17, clone hRPK.394_K_10, complete sequence.//4.4e-10:135:74//AC006080
R-PLACE1007276//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence.//1.7e-36:435:72//AF069291
R-PLACE1007282//B.garinii (strain Tls1) p83/100 gene (partial).//0.95:183:60//X81533
R-PLACE1007286//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13L8, genomic survey sequence.//6.1e-55:519:76//B75158
R-PLACE1007301//Human DNA sequence from PAC 106H8 on chromosome 1q24. Contains PHOSPHATIDYLINISITOL-GLYCAN class C (PIG-C) and DYNAMIN-3 genes. Contains ESTs and STSs and a CpG island.//0.75:180:62//Z97195
R-PLACE1007317//Drosophila dasycnemia 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence.//0.59:236:59//U94253
R-PLACE1007342
R-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//3.7e-65:367:91//AF096870
R-PLACE1007367//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.0e-06:385:62//AC005507
R-PLACE1007375//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.10:309:59//AC004709
R-PLACE1007386//Reclinomonas americana mitochondrial DNA, complete genome.//0.0012:403:58//AF007261
R-PLACE1007402//HS_2055_A2_D03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=6 Row=G, genomic survey sequence.//0.0046:88:79//AQ234824
R-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence.//7.6e-112:590:94//AF093771
R-PLACE1007416//Homo sapiens chromosome 19, cosmid R26894, complete sequence.//0.96:98:70//AC005594
R-PLACE1007450//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE.//1.7e-39:308:82//Z98304
R-PLACE1007452//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//2.6e-59:389:82//AC004081
R-PLACE1007460
R-PLACE1007478//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC li-

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brary) complete sequence.//7.0e-08:335:60//AC004241
R-PLACE1007484
R-PLACE1007488//Glossina morsitans morsitans 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence.//2.5e-05:421:61//AF072373
R-PLACE1007507//Plasmodium falciparum MAL3P7, complete sequence.//2.3e-09:577:57//AL034559
R-PLACE1007511//Homo sapiens chromosome 17, clone hRPC.1110_E_20, complete sequence.//1.2e-79:387:96//AC004231
R-PLACE1007524//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//3.4e-09:148:73//AC003682
R-PLACE1007525//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//4.7e-38:297:82//AC004381
R-PLACE1007544
R-PLACE1007547//Human laminin alpha 4 chain (LAMA4*-1) mRNA, complete cds.//4.0e-17:108:97//U77706
R-PLACE1007557//Human BAC clone RG343P13 from 7q31, complete sequence.//2.2e-45:390:77//AC002465
R-PLACE1007583//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 545L17, WORKING DRAFT SEQUENCE.//1.0e-56:302:95//AL031665
R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence.//1.5e-102:554:93//AF038179
R-PLACE1007618
R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence.//1.4e-103:537:94//AF038176
R-PLACE1007632//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.3e-76:289:94//AC005840
R-PLACE1007645//Homo sapiens full-length insert cDNA clone ZD76G10.//0.0080:96:77//AF086408
R-PLACE1007649//CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence.//1.1e-82:412:97//AQ022149
R-PLACE1007677//Plasmodium falciparum chromosome 2, section 4 of 73 of the complete sequence.//0.0041:470:57//AE001367
R-PLACE1007688
R-PLACE1007690//Human Chromosome 16 BAC clone CIT987SK-A-418G10, complete sequence.//1.3e-22:162:91//AC002044
R-PLACE1007697
R-PLACE1007705//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE.//4.4e-121:624:95//AL031662
R-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//1.8e-73:374:96//AF061243
R-PLACE1007725//Caenorhabditis elegans cosmid F38A5.//0.070:186:60//U70854
R-PLACE1007729//Human endogenous retrovirus HERV-K(HML6) proviral clone HML6.17 putative polymerase and envelope genes, partial cds, and 3'LTR.//3.8e-53:415:81//U60269
R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//2.1e-92:556:89//AB014585
R-PLACE1007737//Homo sapiens clone Sb19.12 Alu-Yb8 sequence.//4.0e-43:302:77//AF015169
R-PLACE1007743//Plasmodium falciparum MAL3P8, complete sequence.//1.0e-06:533:59//AL034560
R-PLACE1007746//T.brucei mitochondrial maxicircle DNA encoding cytochrome c oxidase subunit I (COI), and NADH dehydrogenase subunits 4 and 5, complete cds.//0.28:386:58//M14820
R-PLACE1007791//D.discoideum gene for protein kinase.//0.17:263:60//Z37981
R-PLACE1007807//Human DNA sequence from clone 878O8 on chromosome Xq21.1-21.33. Contains an EST, STSs, a GSS and genomic marker DXS472, complete sequence.//1.1e-72:324:88//AL031116
R-PLACE1007810//Homo sapiens chromosome 7 common fragile site, complete sequence.//2.2e-14:325:67//AF017104
R-PLACE1007829//Human BAC clone GS165I04 from 7q21, complete sequence.//0.00052:455:61//AC002379
R-PLACE1007843//P.falciparum complete gene map of plastid-like DNA (IR-A).//0.0050:447:57//X95275
R-PLACE1007846//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//2.2e-111:570:95//AP000010
R-PLACE1007852//HS_3028_B2_F04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3028 Col=8 Row=L, genomic survey sequence.//1.3e-12:209:71//AQ131021
R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//6.6e-110:574:94//AB018309
R-PLACE1007866//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//1.6e-43:551:70//AL022162
R-PLACE1007877//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//1.6e-22:222:78//AC005754

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R-PLACE1007897//HS_3113_B2_E04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3113 Col=8 Row=J, genomic survey sequencer.//2.9e-72:381:95//AQ186905
R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487.//8.8e-88:460:95//AB007956
R-PLACE1007946//Human chromosome Y cosmid 54E8 genomic sequence, WORKING DRAFT SEQUENCE.//4.9e-23:172:78//AC003095
R-PLACE1007954//Homo sapiens BAC clone NH0414C23 from Y, complete sequence.//1.7e-27:303:75//AC006157
R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//3.9e-102:513:95//AF084530
R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//2.2e-87:465:93//AF079529
R-PLACE1007969//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//4.8e-72:556:81//U13262
R-PLACE1007990//E.tenella antigen LPMC61 mRNA, partial cds.//0.043:273:63//M30933
R-PLACE1008000//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 668J24, WORKING DRAFT SEQUENCE.//8.8e-10:453:62//AL034346
R-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//9.0e-114:563:96//AC005628
R-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP107 mRNA, complete cds.//2.6e-44:509:72//L31840
R-PLACE1008045//Homo sapiens chromosome 5, BAC clone 79a6 (LBNL H172), complete sequence.//0.32:137:66//AC005592
R-PLACE1008080//Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence.//0.082:292:59//AC006232
R-PLACE1008095//Homo sapiens BAC clone NH0364H22 from 2, complete sequence.//5.4e-27:260:76//AC005036
R-PLACE1008111//Human variable number tandem repeat (VNTR) region, allele 12R1 3' to collagen type II (COL2A1) gene.//2.2e-07:444:59//L10157
R-PLACE1008122//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence.//1.9e-11:384:63//AC005919
R-PLACE1008129//Homo sapiens clone DJ1087M19, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.0e-10:189:66//AC004955
R-PLACE1008132//Human HepG2 3' region cDNA, clone hmd5d06.//7.4e-47:320:86//D16939
R-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds.//2.6e-32:410:70//D14849
R-PLACE1008181//Caenorhabditis elegans cosmid C31H2.//0.055:358:60//U41748
R-PLACE1008198
R-nnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds.//4.8e-103:551:93//AB011102
R-PLACE1008209//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1125A11, WORKING DRAFT SEQUENCE.//4.6e-16:250:71//AL034549
R-PLACE1008231//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.13:341:60//AC004688
R-PLACE1008244//P.falciparum P.195 gene.//0.11:212:66//A04562
R-PLACE1008273//Human MEST mRNA, complete cds.//0.00013:52:100//D78611
R-nnnnnnnnnnn
R-PLACE1008280//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence.//1.5e-05:104:76//AC005272
R-PLACE1008309//Human 'at'-rich region adjacent to alpha satellite DNA.//0.70:138:63//M80308
R-PLACE1008329//Homo sapiens chromosome 10 clone CIT-HSP-1240G16 map 10q25.1, complete sequence.//0.00061:150:68//AC005886
R-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//4.8e-74:252:98//AC005176
R-PLACE100833//Genomic sequence from Human 13, complete sequence.//1.0:176:65//AC001226
R-PLACE1008356//Homo sapiens meningioma-expressed antigen 5 (MEA5) mRNA, 3' UTR.//2.5e-98:556:90//AF036145
R-PLACE1008368//HS-1039-A1-C10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 821 Col=19 Row=E, genomic survey sequence.//1.2e-05:375:62//B36336

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R-PLACE1008369//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE.//2.8e-10:466:61//AP000011
R-PLACE1008392//Homo sapiens chromosome 17, clone hRPK.471_L_13, complete sequence.//1.0e-46:282:82//AC005244
R-PLACE1008398//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 215D11, WORKING DRAFT SEQUENCE.//4.1e-101:529:94//AL034417
R-PLACE1008401//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//0.18:379:58//AC004604
R-nnnnnnnnnnn//Homo sapiens mRNA for p115, complete cds.//1.6e-101:521:95//D86326
R-PLACE1008405//Human cosmidCRI-JC2015 at D10S289 in 10sp13.//6.8e-22:328:71//U15177
R-PLACE1008424
R-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 7/11.//7.5e-101:505:96//AB020864
R-PLACE1008429//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence.//1.2e-11:118:78//AL022576
R-PLACE1008437//H.sapiens genomic DNA (PAC 838L14) from chromosome 11, WORKING DRAFT SEQUENCE.//2.2e-06:159:69//Y12335
R-PLACE1008455
R-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//1.2e-109:588:93//AC004526
R-PLACE1008465//CIT978SK-A-28A11.TVE CIT978SK Homo sapiens genomic clone A-28A11, genomic survey sequence.//1.1e-10:133:77//B78696
R-PLACE1008488
R-PLACE1008524//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 34B21, WORKING DRAFT SEQUENCE.//7.3e-120:612:95//AL031778
R-PLACE1008531//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//8.5e-96:510:93//AF045555
R-PLACE1008532
R-PLACE1008533
R-PLACE1008568//HS_3218_B2_D08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=16 Row=H, genomic survey sequence.//0.0042:295:62//AQ214623
R-PLACE1008584//Human PAC clone DJ0596009 from 7p15, complete sequence.//5.0e-26:254:66//AC003074
R-PLACE1008621//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//4.0e-78:498:86//AC006120
R-nnnnnnnnnnnn
R-PLACE1008626//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//5.5e-06:228:67//AL031297
R-PLACE1008627//Cricetulus griseus mRNA for Zn finger factor.//3.4e-20:335:71//Y12836
R-PLACE1008629//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.55:326:58//AC004826
R-PLACE1008630//Homo sapiens genomic DNA, 21q region, clone: B175P11X96, genomic survey sequence.//0.13:440:55//AG011096
R-PLACE1008643//Human BAC clone RG083J23 from 7q31, complete sequence.//1.3e-58:356:82//AC004001
R-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//2.4e-88:434:97//AF044333
R-PLACE1008693//CIT-HSP-2025M9.TR CIT-HSP Homo sapiens genomic clone 2025M9, genomic survey sequence.//1.2e-41:300:82//B64742
R-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//4.8e-31:320:75//AF038406
R-PLACE1008715//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 799N4, WORKING DRAFT SEQUENCE.//0.074:478:58//AL022147
R-PLACE1008748//CIT-HSP-2170P12.TR CIT-HSP.Homo sapiens genomic clone 2170P12, genomic survey sequence.//8.5e-42:160:86//B90841
R-PLACE1008757//Homo sapiens 12q24.2 PAC RPCI4-765H13 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.99:211:61//AC005864
R-PLACE1008790//Rattus norvegicus clone1 polymeric immunoglobulin receptor mRNA 3' untranslated region, GA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats.//0.052:108:68//U00762

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R-PLACE1008798//Homo sapiens full-length insert cDNA clone YZ86C05.//7.7e-58:285:100//AF086088
R-PLACE1008807//CIT-HSP-2366014.TR CIT-HSP Homo sapiens genomic clone 2366O14, genomic survey sequence.//3.5e-35:223:89//AQ079210
R-PLACE1008808//Homo sapiens exonuclease homolog RAD1 (RAD1) mRNA, complete cds.//2.3e-97:499:95//AF030933
R-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//9.7e-45:394:78//AF032668
R-PLACE1008851//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.9e-28:207:87//AC004581
R-nnnnnnnnnnnn//CIT-HSP-2172B3.TF CIT-HSP Homo sapiens genomic clone 2172B3, genomic survey sequence.//8.9e-30:166:97//B93289
R-PLACE1008867//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//3.5e-76:404:95//AC005058
R-PLACE1008887//Homo sapiens clone DJ0943F02, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.7e-37:585:67//AC004932
R-PLACE1008902//Homo sapiens chromosome Y, clone hCIT.494_G_17, complete sequence.//0.0022:409:60//AC005820
R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds.//8.2e-55:344:89//AB018308
R-PLACE1008925//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y53F4, WORKING DRAFT SEQUENCE.//0.0014:398:58//Z92860
R-PLACE1008934
R-PLACE1008941//Homo sapiens chromosome 17, clone hRPK.293_K_20, complete sequence.//9.8e-84:429:92//AC005495
R-PLACE1008947
R-PLACE1009020
R-PLACE1009027//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//1.3e-82:434:95//AL031117
R-PLACE1009039//Human DNA sequence from clone 276K20 on chromosome 6p22.1-22.3. Contains STSs, GSSs and a putative CpG island, complete sequence.//0.00010:297:58//AL031391
R-PLACE1009045//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence.//2.9e-06:160:70//AC004707
R-PLACE1009048//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//1.3e-16:339:66//AL023694
R-PLACE1009050//Aedes aegypti gene sequence, primary transcript.//0.40:393:59//L17023
R-PLACE1009060//Mus musculus mRNA for Alix-SF (ALG-2-interacting protein X, short form, complete CDS.//0.00075:79:83//AJ005074
R-PLACE1009090//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//6.7e-13:212:73//AC004783
R-PLACE1009094//Caenorhabditis elegans cosmid C49F8, complete sequence.//0.49:221:61//Z70206
R-PLACE1009099
R-PLACE1009110//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//5.1e-17:301:66//AC004025
R-PLACE1009111//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.2e-06:234:61//AC005140
R-PLACE1009130//Plasmodium falciparum MAL3P6, complete sequence.//7.5e-06:426:58//Z98551
R-PLACE1009150//Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRAFT SEQUENCE.//2.3e-118:614:95//AJ011929
R-PLACE1009155//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE.//1.4e-107:584:93//AP000031
R-PLACE1009158//Homo sapiens full-length insert cDNA clone YP10D03.//1.9e-105:539:95//AF085876
R-PLACE1009166//Homo sapiens chromosome 17, clone hRPK.180_P_8, complete sequence.//2.8e-44:360:71//AC005972
R-PLACE1009172//Human cosmid QLL2C9 from Xq28.//4.1e-37:401:74//Z47046
R-PLACE1009174//Homo sapiens PAC clone DJ0907C10 from 7q31-3q32, complete sequence.//2.1e-17:140:81//AC004925
R-PLACE1009183//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and

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STSs, complete sequence.//1.9e-46:572:69//Z84480
R-PLACE1009186//Human Chromosome X, complete sequence.//0.016:322:61//AC004070
R-PLACE1009190//Plasmodium falciparum MAL3P8, complete sequence.//0.050:487:58//AL034560
R-PLACE1009200//H.sapiens mRNA for sortilin.//1.0e-31:195:92//X98248
R-PLACE1009230//Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence.// 1.8e-75:364:85//AC005392
R-PLACE1009246//Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mRNA, complete cds.//6.6e-44:525:71//U22818
R-PLACE1009308
R-PLACE1009319//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.00010:132:75//AC004801
R-PLACE1009328//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//3.3e-87:576: 85//AC006120
R-PLACE1009335//Borrelia burgdorferi (section 62 of 70) of the complete genome.//0.32:315:60//AE001176
R-PLACE1009338//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//6.8e-05:411:59//AC005140
R-PLACE1009368//Homo sapiens PAC clone DJ1179J19 from 7q11.23-q21, complete sequence.//0.00040:280: 61//AC004989
R-PLACE1009375//D. yakuba mitochondrial DNA for origin of replication, small ribosomal RNA , transfer RNAs tRNA-fMet, tRNA-Gln, tRNA-Ile and tRNA-Val.//1.1e-08:444:60//X05915
R-PLACE1009388
R-PLACE1009398//Homo sapiens BAC clone GS011E15 from 5q31, complete sequencer.//0.065:279:61// AC002427
R-nnnnnnnnnnnn//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.0e-06:253:64//AC005038
R-PLACE1009410//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence.//9.8e-112:561: 96//AC005919
R-PLACE1009434//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//2.2e-21:126:79//AL031120 R-PLACE1009443//Homo sapiens nucleolar protein Nop30 and cytoplasmic protein Myp (NOP) gene, alternatively spliced products, complete cds.//4.5e-14:117:91// AF064598
R-PLACE1009444//Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds.//9.6e-85:479:90//L36151
R-PLACE1009459
R-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence.//5.6e-101:540:94//AC004531
R-PLACE1009477//Homo sapiens, clone hRPK.15_A_1, complete sequence.//3.4e-46:284:91//AC006213
R-PLACE1009493//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//5.5e-107:581: 92//U91321
R-PLACE1009524//Homo sapiens DNA sequence from PAC 63G5 on chromosome-22q12.3-13.1. Contains part of a gene for a human SEC7 homolog B2-1 (cytohesin-2, Arno, ARF exchange factor) LIKE protein, an unknown gene and a gene coding for a Leucine rich protein. Contains ESTs, STSs and GSSs, complete sequence.//0.74: 301:61//Z94160
R-PLACE1009539//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SEQUENCE.//5.7e-29:357:74//AL031427
R-PLACE1009542//CIT-HSP-2166P10.TRB CIT-HSP Homo sapiens genomic clone 2166P10, genomic survey sequence.//2.6e-10:145:75//B89614
R-PLACE1009571//RPCI11-61J16.TK RPCI11 Homo sapiens genomic clone R-61J16, genomic survey sequence.//0.016:68:80//AQ202146
R-PLACE1009581
R-PLACE1009595//Homo sapiens clone DJ56J10, complete sequence.//1.8e-38:365:79//AC005006
R-PLACE1009596//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 501A4, WORKING DRAFT SEQUENCE.//1.2e-29:314:76//Z98051
R-PLACE1009607//cSRL-77g9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-77g9, genomic survey sequence.//2.1e-05:142:69//B06230
R-PLACE1009613//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-89, complete sequence.//3.6e-08:434:59//AL010266
R-PLACE1009621//Sequence 50 from patent US 5691147.//1.5e-20:235:73//I76222
R-PLACE1009622//CIT-HSP-2023D13.TFB CIT-HSP Homo sapiens genomic clone 2023D13, genomic survey

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sequence.//0.72:176:62//B81271
R-PLACE1009637//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.0068:396:59//X95276
R-PLACE1009639//Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project).//0.013:521:58//AL021811
R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds.//1.0e-107:589:92//AB011159
R-PLACE1009665//Human PAC clone DJ0658N05 from 7p21, complete sequence.//8.4e-72:487:85//AC003075
R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//2.0e-61:310:97//AF062534
R-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence.//2.8e-103:542:94//AC006011
R-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete sequence.//4.6e-85:518:88//AC000109
R-PLACE1009731//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//0.0033:215:65//AL022398
R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds.//6.2e-116:598:95//AF046024
R-PLACE1009794
R-nnnnnnnnnnnn//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//7.5e-88:191:96//AL030996
R-PLACE1009845//Homo sapiens DNA sequence from PAC 234H5 on chromosome 6q21. Contains an unknown gene, ESTs and STSs, complete sequence.//8.7e-19:226:69//Z98172
R-PLACE1009879//Homo sapiens genomic DNA, 21q region, clone: 149C3A68, genomic survey sequence.//2.1e-29:230:76//AG002672
R-PLACE1009886//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//0.99:203:61//AC004945
R-PLACE1009888//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//5.3e-91:577:88//AC006116
R-nnnnnnnnnnnn
R-PLACE1009921//Homo sapiens cosmid clone HDAB (1S149) insert DNA, complete cosmid.//4.7e-81:385:84//M63005
R-PLACE1009924//HS_3151_B1_B10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3151 Col=19 Row=D, genomic survey sequence.//5.5e-47:240:99//AQ167412
R-PLACE1009925//CIT978SK-A-931F6.TV CIT978SK Homo sapiens genomic clone A-931F6, genomic survey sequence.//0.00010:159:68//B51673
R-PLACE1009935//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.081:238:65//AC005308
R-PLACE1009947//Homo sapiens PAC clone 248015 from 13q12-q13, complete sequence.//1.0:353:58//AC002483
R-PLACE1009971//Homo sapiens full-length insert cDNA clone ZD38E12.//3.7e-11:152:75//AF086247
R-PLACE1009992
R-PLACE1009995//Plasmodium falciparum chromosome 2, section 4 of 73 of the complete sequence.//0.0019:305:61//AE001367
R-PLACE1009997//Homo sapiens chromosome 10 clone CIT987SK-1175G20 map 10q25.2-10q25.3, complete sequence.//1.8e-43:462:76//AC005874
R-PLACE1010023//HS_3018_B1_H10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00013:198:63//AQ093513
R-PLACE1010031//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//7.4e-115:581:96//AL031775
R-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//1.9e-05:136:74//X84692
R-PLACE1010069//CIT-HSP-2328B12.TF CIT-HSP Homo sapiens genomic clone 2328B12, genomic survey sequence.//2.6e-60:324:94//AQ042094
R-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//4.6e-87:543:88//AF065482
R-PLACE1010076//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0473M13; HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//6.3e-08:489:58//AC005699
R-PLACE1010083

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R-PLACE1010089//F19F22-Sp6 IGF Arabidopsis thaliana genomic clone F19F22, genomic survey sequence.// 0.14:400:59/B10583
R-PLACE1010096//R.norvegicus mRNA for 100 kDa protein.//4.3e-91:562:87//X64411
R-PLACE1010102//Apis mellifera tRNA-Leu cytochrome oxidase II intergenic spacer region, mitochondrial sequence.//1.5e-08:357:60//AF039556
R-PLACE1010105//Plasmodium falciparum chromosome 2, section 11 of 73 of the complete sequence.//4.0e-09: 510:59//AE001374
R-PLACE1010106//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE.//1.4e-12:194:73//Z98304
R-PLACE1010134
R-PLACE1010148//HS_3128_A1_D09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3128 Col=17 Row=G, genomic survey sequence.//0.17:281:61//AQ140790
R-PLACE1010152//Mouse mRNA for arylhydrocarbon receptor, complete cds.//3.1e-45:351:81//D38417
R-PLACE1010181//Homo sapiens clone DJ0914M06, WORKING DRAFT SEQUENCE, 1 unordered pieces.// 3.6e-06:207:66//AC004928
R-PLACE1010194 11HS_2232_B1_H10_MR CIT Approved Human Genomic Sperm Library D. Homo sapiens genomic clone Plate=2232 Col=19 Row=P, genomic survey sequence.//2.4e-08:134:74//AQ185425
R-PLACE1010202//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin, Type 1 Cytoskeletal 18 (KRT18, CYK18, K18, CK18) pseudogene and an STS, complete sequence.//0.00035:383: 61//AL031585
R-PLACE1010231//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 287G14, WORKING DRAFT SEQUENCE.//1.2e-95:519:94//AL033377
R-PLACE1010261
R-PLACE1010270//H.sapiens CpG island DNA genomic Msc1 fragment, clone 85a6, reverse read cpg85a61rt1a.// 0.068:171:63//Z63482
R-PLACE1010274//S.douglasii gene for cytochrome b.//4.5e-07:276:63//X59280
R-PLACE1010293//Homo sapiens chromosome 2 PAC RPCI3-417E16 (Roswell Park Cancer Institute Human PAC library) complete sequence.//4.7e-91:522:90//AC004464
R-PLACE1010321
R-PLACE1010324//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y38E10, WORKING DRAFT SEQUENCE.//5.7e-08:484:57//AL021149
R-PLACE1010329//Homo sapiens Chromosome 22q11.2 Cosmid Clone 50d10 In IGLC Region, complete sequence.//7.9e-35:328:79//AC000024
R-PLACE1010341//Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces.// 1.3e-31:418:66//AC004971
R-PLACE1010362
R-PLACE1010364//Mus cookii mitochondrion DNA fragment.//0.23:162:64//M77098
R-PLACE1010383//Homo sapiens chromosome 17, clone hCIT.186_H_2, complete sequence.//1.4e-105:543:95// AC004675
R-PLACE1010401//Human Chromosome 15q11-q13 PAC clone pDJ223c9 from the Prader-Willi/Angelman Syndrome region, complete sequence.//0.00017:268:62//AC004137
R-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds.//8.6e-79:556:83//AF003927
R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds.//7.3e-88:438:96//AF039081
R-PLACE1010492//HS_3169_B2_B04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3169 Col=8 Row=D, genomic survey sequence.//0.98:171:63//AQ169892
R-PLACE1010522//WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.34:407:62//AC006082
R-nnnnnnnnnnn
R-PLACE1010562//CITBI-E1-2503B16.TF CITBI-E1 Homo sapiens genomic clone 2503B16, genomic survey sequence.//6.4e-17:152:84//AQ265929
R-PLACE1010579//Torulopsis glabrata mitochondrial gene for ribosomal protein varl.//1.7e-05:271:65//X02893
R-PLACE1010580
R-PLACE1010599
R-PLACE1010616//Human BAC clone RG343P13 from 7q31, complete sequence.//3.0e-13:151:75//AC002465
R-PLACE1010622//Arabidopsis thaliana BAC F1104.//0.00031:366:60//AF096370
R-PLACE1010624//Homo sapiens chromosome 7q22 sequence, complete sequence.//8.2e-34:322:79// AF053356
R-PLACE1010628//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.// 2.3e-97:515:94//AC004846

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R-PLACE1010629//HS_3003_A2_C08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=16 Row=E, genomic survey sequence.//5.6e-60:321:95//AQ130493
R-PLACE1010630//Plasmodium falciparum chromosome 2, section 19 of 73 of the complete sequence.//0.051:372:59//AE001382
R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds.//2.6e-92:497:93//AB011102
R-PLACE1010661//CIT-HSP-2008K15.TR CIT-HSP Homo sapiens genomic clone 2008K15, genomic survey sequence.//5.7e-27:160:95//B57089
R-PLACE1010662//Caenorhabditis elegans cosmid C12C8, complete sequence.//9.4e-09:151:73//Z81467
R-PLACE1010702//CIT-HSP-2314C3.TR CIT-HSP Homo sapiens genomic clone 2314C3, genomic survey sequence.//1.3e-90:459:96//AQ028536
R-PLACE1010714//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//5.3e-08:478:58//U49822
R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds.//3.8e-55:300:95//AF092564
R-PLACE1010739//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs, complete sequence.//3.4e-89:507:90//Z95400
R-PLACE1010743
R-PLACE1010761//Homo sapiens chromosome 17, clone hRPK.294_J_22, complete sequence.//3.0e-103:511:97//AC005921
R-PLACE1010771
R-PLACE1010786
R-PLACE1010800//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces.//1.8e-43:545:71//AC005682
R-PLACE1010802//Phoebis agarithe large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//1.9e-09:492:59//AF044862
R-PLACE1010811//Homo sapiens Xp22 BAC GSHB-257G1 (Genome Systems BAC Library) complete sequence.//0.041:415:59//AC002524
R-PLACE1010833
R-PLACE1010856//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0022:512:55//AC004153
R-PLACE1010857//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 11/11//4.9e-85:507:90//AB020868
R-PLACE1010870//RPCI11-59K21:TK RPCI11 Homo sapiens genomic clone R-59K21, genomic survey sequence.//8.2e-85:422:97//AQ195697
R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//7.0e-100:501:96//AB011182
R-PLACE1010891//Homo sapiens chromosome X, clone 592, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.10:162:61//AC002489
R-PLACE1010896//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00032:409:59//AC005505
R-PLACE1010900//Homo sapiens DNA, trinucleotide repeats region.//3.2e-07:180:71//AB018488
R-PLACE1010916//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.041:205:60//AL034557
R-PLACE1010917
R-PLACE1010925//HS_2027_B2_B09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=18 Row=D, genomic survey sequence.//1.6e-46:404:77//AQ247031
R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds.//4.2e-65:402:89//AB011126
R-nnnnnnnnnnn//Homo sapiens intersectin short form mRNA, complete cds.//1.9e-80:441:93//AF064243
R-PLACE1010944
R-PLACE1010947//D.discoideum rasG gene.//0.00044:181:65//Z11533
R-PLACE1010954//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//3.0e-51:518:74//AC005077
R-PLACE1010960//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 451B21, WORKING DRAFT SEQUENCE.//0.022:292:63//AL033522
R-PLACE1010965//Human mariner1 transposase gene, complete consensus sequence.//1.0e-64:444:84//U52077
R-PLACE1011026//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.59:345:61//

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AJ235272
R-PLACE1011032//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//0.62:82:75//Z93242
R-PLACE1011041//H.sapiens DNA sequence.//0.051:162:66//Z22248
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0581 protein, partial cds.//2.9e-100:563:91//AB011153
R-PLACE1011054//Human DNA sequence from PAC 46H23, BRCA2 gene region chromosome 13q12-13 contains Klotho, ESTs.//4.7e-29:280:73//Z84483
R-PLACE1011056//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 341D10, WORKING DRAFT SEQUENCE.//1.7e-39:288:84//Z97985
R-PLACE1011057//CIT-HSP-2014F10.TF CIT-HSP Homo sapiens genomic clone 2014F10, genomic survey sequence.//2.4e-60:370:90//B58896
R-PLACE1011090//Homo sapiens chromosome 4 clone B200N5 map 4q25, complete sequence.//0.12:489:59//AC005509
R-PLACE1011109//Homo sapiens chromosome Y, clone 486, O, 2, complete sequence.//8.4e-43:427:76//AC002531
R-PLACE1011114//Homo sapiens mRNA from HIV associated non-Hodgkin's lymphoma (clone hl1-14).//1.7e-29:179:94//Y16709
R-PLACE1011133//HS-1058-B1-H02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 780 Col=3 Row=P, genomic survey sequence.//1.0:133:63//44006
R-PLACE1011143//H.sapiens CpG island DNA genomic Mse1 fragment, clone 127a4, forward read cpg127a4.ft1a.//1.0:127:67//Z56550
R-PLACE1011160//Homo sapiens HRIHFB2038 mRNA, partial cds.//2.4e-95:534:91//AB015333
R-PLACE1011165//Human Cosmid g5129s232 from 7q31.3, complete sequence.//0.47:355:58//AC003968
R-PLACE1011185//Homo sapiens clone DJ0038I10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.3e-26:403:70//AC004820
R-PLACE1011203//paramecium species 4.51er mt dna dimer: replication init. region, clone 1.//1.0e-10:379:60//K00908
R-PLACE1011219//HS_3036_B1_F08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=15 Row=L, genomic survey sequence.//2.6e-39:253:88//AQ104587
R-PLACE1011221//Homo sapiens T-cell receptor alpha delta locus from bases 250472 to 501670 (section 2 of 5) of the Complete Nucleotide Sequence.//0.32:279:60//AE000659
R-PLACE1011229//HS_3002_B1_E10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=19 Row=J, genomic survey sequence.//9.3e-31:317:74//AQ303626
R-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.2e-109:571:94//AC005014
R-PLACE1011273//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//0.00027:337:61//M97514
R-PLACE1011291
R-PLACE1011296//H.sapiens steroid reductase pseudogene.//4.2e-37:326:80//M68887
R-PLACE1011310//H.sapiens 5' flanking sequence of gene for corticotropin.//0.0017:416:60//X67661
R-PLACE1011325//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.3.0e-10:511:59//AE001398
R-PLACE1011332//Homo sapiens chromosome 17, clone HCIT3L16, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.3e-06:250:64//AC002344
R-PLACE1011340//Human BAC clone RG341D10 from 7p15-p21, complete sequence.//0.67:290:58//AC002530
R-PLACE1011375//Mus musculus Kv3.4 gene, exon 4.//6.8e-23:190:86//AJ010310
R-PLACE1011399//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.22:359:60//AC005140
R-PLACE1011419//Human DNA sequence from cosmid U90B3, on chromosome Xp11, contains ESTs.//5.1e-32:282:81//Z74022
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds.//1.5e-112:600:94//AB011102
R-PLACE1011452//Homo sapiens clone DJ0945F02, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.9e-77:303:85//AC006013
R-PLACE1011465
R-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds.//7.9e-103:515:96//AB018255
R-PLACE1011492//A-837A4.TP CIT978SK Homo sapiens genomic clone A-837A4, genomic survey sequence.//6.5e-37:234:82//B14085
R-PLACE1011503//Homo sapiens chromosome 17, clone hRPC.1171_I_10, complete sequence./0.99:267:60//

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AC004687
R-PLACE1011520//Homo sapiens clone DJ1119N05, complete sequence.//2.0e-116:591:96//AC004968
R-PLACE1011563//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-13:566:59//AC004688
R-PLACE1011567//Plasmodium-falciparum MAL3P6, complete sequence.//0.62:358:61//Z98551
R-PLACE1011576//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//8.7e-45:400:78//AC003973
R-PLACE1011586//Homo sapiens chromosome 17, clone HRPC890E16, complete sequence.//2.2e-59:338:93//AC004477
R-PLACE1011635//C.pasteurianum pfl gene and act gene.//0.71:288:60//X93463
R-PLACE1011641//Mycoplasma genitalium random genomic clone sg11, partial cds.//0.023:232:60//U02205
R-PLACE1011643//Homo sapiens chromosome 19, cosmid R33590, complete sequence.//1.4e-21:432:67//AC005620
R-PLACE1011649//Homo sapiens clone 24432 mRNA sequence.//7.8e-72:414:91//AF070535
R-PLACE1011650//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//5.1e-27:174:79//AC002477
R-PLACE1011664//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone. 460D19, WORKING DRAFT SEQUENCE.//7.4e-05:238:65//AL031905
R-PLACE1011675//CIT-HSP-2370M16.TR CIT-HSP Homo sapiens genomic clone 2370M16, genomic survey sequence.//1.3e-27:233:81//AQ108283
R-PLACE1011682//H.sapiens HLA-DMB gene.//2.3e-22:390:67//X76776
R-PLACE1011719//Homo sapiens 12q24.2 BAC RPCI11-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//3.1e-24:409:66//AC004806
R-PLACE1011725//Homo sapiens unknown mRNA downregulated by induced differentiation with 13-cis retinoic acid.//0.13:143:65//AF026526
R-PLACE1011729//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//1.1e-15:157:82//AL022345
R-PLACE1011749//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.5e-38:314:81//AC005089
R-PLACE1011762//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//1.9e-35:538:68//AC002383
R-PLACE1011778//CIT-HSP-2326C17.TV CIT-HSP Homo sapiens genomic clone 2326C17, genomic survey sequence.//2.8e-58:346:91//AQ028782
R-PLACE1011783//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 229A8, WORKING DRAFT SEQUENCE.//4.6e-38:288:84//Z86090
R-PLACE1011858//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence./4.1e-104:524:97//AL031321
R-PLACE1011874//Homo Sapiens Chromosome X clone bWXD312, complete sequence.//2.1e-100:511:95//AC004478
R-PLACE1011875
R-PLACE1011891//Human lens membrane protein (mp19) gene, exon 11.//0.0011:195:64//L04193
R-PLACE1011896//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//0.010:110:74//AL022398
R-PLACE1011922//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence.//3.5e-10:152:74//AF042090
R-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//7.0e-98:546:92//AF059617
R-PLACE1011962//CIT-HSP-2294L24.TF CIT-HSP Homo sapiens genomic clone 2294L24, genomic survey sequence.//0.31:131:63//AQ006352
R-PLACE1011964//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence.//2.5e-08:393:63//AC002994
R-PLACE1011982//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence.//9.6e-09:463:62//AB016889
R-PLACE1011995//Human Down Syndrome region of chromosome 21, clone A12H1-2H4.//2.7e-39:294:82//U44738
R-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//2.5e-104:540:95//AB018256
R-PLACE2000003//Human PAC clone DJ404F18 from Xq23, complete sequence.//4.9e-10:439:63//AC004000

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R-PLACE2000007//Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 3.//1.0:151:66//L78722
R-PLACE2000011//Homo sapiens clone 614 unknown mRNA, complete sequence.//1.5e-103:524:95//AF091080
R-PLACE2000015//Homo sapiens PAC clone DJ269005 from Xq23, complete sequence.//0.94:372:57//AC005191
R-PLACE2000017//Homo sapiens chromosome 17, clone hCIT.162_E_12, complete sequence.//3.0e-55:299:86//AC006236
R-PLACE2000021//CIT-HSP-2343C18.TR CIT-HSP Homo sapiens genomic clone 2343C18, genomic survey sequence.//4.5e-54:295:94//AQ058140
R-PLACE2000033//H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form).//6.5e-38:298:82//X69907
R-PLACE2000034//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.3e-34:200:79//AC005628
R-PLACE2000039//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.//1.8e-49:274:89//AC003083
R-PLACE2000047//CIT-HSP-2373C2.TR CIT-HSP Homo sapiens genomic clone 2373C2, genomic survey sequence.//1.8e-48:389:79//AQ112243
R-PLACE2000050//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 11771 5, WORKING DRAFT SEQUENCE.//0.0027:95:76//AL022315
R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds.//2.9e-39:429:72//AB011147
R-PLACE2000062//Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.//5.9e-40:310:84//AC004832
R-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//1.9e-109:550:95//AF027219
R-PLACE2000097//Homo sapiens chromosome 12p13.3 clone RPCI11-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//1.6e-106:553:95//AC005910
R-PLACE2000100//Human DNA sequence from clone 301K23 on chromosome 1p35.1-36.21. Contains the 5' part of a novel gene similar to predicted yeast and worm genes. Contains ESTs and GSSs, complete sequence.//1.8e-38:285:84//AL031730
R-PLACE2000103//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20208, WORKING DRAFT SEQUENCE.//4.3e-113:559:97//AL031848
R-PLACE2000111//Rat MLC1V gene encoding alkali myosin ventricel light chain, exon 1.//0.00041:347:61//X16325
R-PLACE2000115//Cervus elaphus MHC class II DRB pseudogene, intron 2 microsatellite.//0.50:165:63//U63067
R-PLACE2000132
R-PLACE2000136//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-30, complete sequence.//0.0032:310:61//AL008974
R-PLACE2000140//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 11703, WORKING DRAFT SEQUENCE.//1.1e-111:566:96//AL020995
R-PLACE2000164
R-PLACE2000170//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0024K08; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.9e-40:390:76//AC005598
R-PLACE2000172
R-PLACE2000176
R-PLACE2000187//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 268H5, WORKING DRAFT SEQUENCE.//8.7e-45:298:87//AL008718
R-PLACE2000216//Dog nonerythroid beta-spectrin mRNA, 3' end.//5.6e-88:495:92//L02897
R-PLACE2000223
R-PLACE2000235//HS_3159_B1_B06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3159 Col=11 Row=D, genomic survey sequence.//1.8e-88:454:96//AQ179271
R-PLACE2000246//Homo sapiens chromosome 3p clone RPCI4-544D10, WORKING DRAFT SEQUENCE, 58 unordered pieces.//9.1e-41:282:86//AC005902
R-PLACE2000264//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//8.3e-35:305:80//Z97181
R-PLACE2000274//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//3.5e-18:325:67//AC002394
R-PLACE2000302//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.5e-39:287:85//AC003043
R-PLACE2000305//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 16915, WORKING DRAFT SEQUENCE.//1.2e-43:295:85//Z93015
R-PLACE2000317//Human DNA sequence from clone 245G19 on chromosome Xp22.11-22.2 Contains serine-threonine kinase (Txp3) gene, a pseudogene similar to ALPHA-1 PROTEIN ((CONNEXIN 43, CX43, GAP JUNC-

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TION 43 KD HEART PROTEIN)), and the 3' end of the RS1 (X-linked juvenile retinoschisis precursor protein) gene. Contains ESTs, STSs and GSSs, complete sequence.//4.0e-05:284:65//Z92542
R-PLACE2000335//Homo sapiens clone DJ0755D09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.5e-26:334:70//AC006147
R-PLACE2000342//Fugu rubripes cosmid 258N02 containing IGFII, TH, NAP2 genes.//4.0e-05:254:64//AL021880
R-PLACE2000347//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 799N4, WORKING DRAFT SEQUENCE.//1.6e-82:504:88//AL022147
R-PLACE2000359//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 40E16, WORKING DRAFT SEQUENCE.//2.0e-36:314:80//AL031963
R-PLACE2000366//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796F18, WORKING DRAFT SEQUENCE.//2.0e-48:389:80//AL031291
R-PLACE2000371
R-PLACE2000373//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 324M8, WORKING DRAFT SEQUENCE.//0.61:231:61//AL008734
R-PLACE2000379//Homo sapiens clone DJ0892G19, complete sequence.//3.5e-11:287:67//AC004917
R-PLACE2000394//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence.//6.8e-108:553:96//AL031432
R-PLACE2000398//Homo sapiens clone RG074A24, WORKING DRAFT SEQUENCE, 25 unordered pieces.//2.9e-26:326:73//AC005059
R-PLACE2000399
R-PLACE2000404//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//6.5e-84:434:96//AC005216
R-PLACE2000411//P.clarkii mRNA; repeat region (ID 2R).//0.47:104:70//Z54273
R-PLACE2000419
R-PLACE2000425//Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions.//1.9e-40:447:74//AF003528
R-PLACE2000427
R-PLACE2000433//Human Chromosome 15 pac pDJ24m8, complete sequence.//3.5e-40:286:85//AC000379
R-PLACE2000435
R-PLACE2000438//Homo sapiens full-length insert cDNA clone ZE04D01.//2.2e-107:523:98//AF086521
R-PLACE2000450 4.1e-42:328:79//AG006257
R-PLACE2000455
R-PLACE2000458//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete-sequence.//5.1e-116:570:97//AC005740
R-PLACE2000465//Human BAC clone RG191D16, complete sequence.//6.3e-37:408:75//AC002460
R-PLACE2000477//M.musculus tex264 mRNA (3'region).//7.5e-06:117:76//X80427
R-PLACE3000004
R-PLACE3000029//Human DNA sequence from PAC 506G2 contains STSs and a CpG island.//5.8e-34:308:78//Z82976
R-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//1.1e-36:273:87//Y17267
R-PLACE3000070//Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence.//2.3e-10:181:71//AC004648
R-PLACE3000103//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30A23, WORKING DRAFT SEQUENCE.//1.2e-48:495:74//AL022156
R-PLACE3000119//Homo sapiens Chromosome 22q12 BAC Clone 58b8 In Meningioma Deletion Region, complete sequence.//3.4e-39:283:85//AC000026
R-PLACE3000124//Homo sapiens chromosome 5, P1 clone 793c5 (LBNL H57), complete sequence.//9.2e-23:171:76//AC005200
R-PLACE3000136//U.arctos microsatellite DNA, clone UarMU23.//0.00052:171:65//Y09645
R-PLACE3000142//HS_3037_82_B02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=4 Row=D, genomic survey sequence.//0.88:121:66//AQ097023
R-PLACE3000147//Mus musculus DNA for ADAMTS-1, complete cds.//3.3e-23:472:66//AB001735
R-PLACE3000148//Human DNA from cosmid L27h9, Huntington's Disease Region, chromosome 4p16.3 contains CpG island.//3.5e-11:176:73//Z49237
R-PLACE3000155//Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence.//6.9e-106:549:94//AC005277
R-PLACE3000156//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//7.0e-38:545:70//AC002383

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R-PLACE3000157
R-PLACE3000158//, complete sequence.//1.4e-33:283:81//AC005500
R-PLACE3000160
R-PLACE3000169//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//5.2e-43:229:85//AC006130
R-PLACE3000194
R-PLACE3000197//Homo sapiens chromosome 17, clone hRPK.401_O_9, complete sequence.//7.2e-61:394:89//AC005291
R-PLACE3000199//Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD)1 N-acetyltransferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq281u2 gene.//0.23:309:57//U52112 R-PLACE3000207//CIT-HSP-384B14.TR CIT-HSP Homo sapiens genomic clone 384B14, genomic survey sequence.//1.1e-15:156:81//B54637
R-PLACE3000208//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 591N18, WORKING DRAFT SEQUENCE.//1.3e-16:139:87//AL031594
R-PLACE3000218//HS_3185_B1_B01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=1 Row=D, genomic survey sequence.//3.5e-07:120:75//AQ155720
R-PLACE3000220//Homo sapiens chromosome 17, clone HRPC1096F1, complete sequence.//2.4e-44:363:80//AC004167
R-PLACE3000226//Caenorhabditis elegans cosmid M01G5.//0.88:95:77//AF078786
R-PLACE3000230//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//5.3e-69:536:81//U95626
R-PLACE3000242//Sequence 1 from patent US 5599918.//3.2e-62:546:78//I35489
R-PLACE3000244//M.musculus mRNA for 200 kD protein.//1.7e-45:404:75//X80169
R-PLACE3000254//Human mRNA for KIAA0309 gene, partial cds.//7.5e-28:174:94//AB002307
R-PLACE3000271//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//3.9e-54:492:77//AL034379
R-PLACE3000276//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//5.4e-12:176:69//AC004081
R-PLACE3000304//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//5.7e-114:555:97//AC005328
R-PLACE3000310//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 467L1, WORKING DRAFT SEQUENCE.//6.2e-51:314:84//Z98884
R-PLACE3000320//Homo sapiens elastin gene, exons 5-27 and alternatively spliced products, partial cds.//2.5e-44:289:90//U93037
R-PLACE3000322//Human argininosuccinate lyase (ASL) gene, exon 3.//5.9e-20:153:88//M21006
R-PLACE3000331//Homo sapiens clone DJ0592G07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-43:230:84//AC005480
R-PLACE3000339
R-PLACE3000341//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.5e-111:550:97//AC006055
R-PLACE3000350//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//1.5e-44:314:78//AL022323
R-PLACE3000352//HS_3095_B1_E09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3095 Col=17 Row=J, genomic survey sequence.//8.5e-73:356:99//AQ123142
R-PLACE3000353//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y22F5, WORKING DRAFT SEQUENCE.//0.21:194:63//Z99712
R-PLACE3000362//Plasmodium falciparum coronin gene, isolate 3D7.//0.26:360:60//AJ002197
R-PLACE3000363
R-PLACE3000365//Human BAC clone RG343P13 from 7q31, complete sequence.//4.6e-52:487:76//AC002465
R-PLACE3000373//HS_3202_B1_G05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3202 Col=9 Row=N, genomic survey sequence.//2.4e-75:437:90//AQ252699
R-PLACE3000388//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 732E4, WORKING DRAFT SEQUENCE.//6.4e-61:515:81//AL008722
R-PLACE3000399//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.00098:444:60//AC005231
R-PLACE3000400//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING

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DRAFT SEQUENCE, 7 unordered pieces.//0.78:155:66//AC005506
R-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.// 8.0e-47:223:81//AC006023
R-PLACE3000402//Homo sapiens chromosome 17, clone 104H12, complete sequence.//1.0:179:63//AC000003
R-PLACE3000405//Homo sapiens chromosome 7qtelo BAC F6, complete sequence.//2.4e-44:466:74//AF104455
R-PLACE3000406//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 268H5, WORKING DRAFT SEQUENCE.//7.7e-49:471:75//AL008718
R-PLACE3000413
R-PLACE3000416//Homo sapiens *** SEQUENCING IN PROGRESS *** from PAC 1577, WORKING DRAFT SEQUENCE.//5.4e-42:416:77//AJ009612
R-PLACE3000425//Human DNA sequence from PAC 130G2 on chromosome 6p22.2-22.3. Contains ribosomal protein L29 pseudogene, ESTs and STSs.//1.1e-41:366:78//AL008627
R-PLACE3000455//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469D22, WORKING DRAFT SEQUENCE.//3.8e-98:549:92//AL031284
R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA, complete cds.//1.9e-82:440:92// U43899
R-PLACE3000477
R-PLACE4000009//R.norvegicus mRNA encoding 45kDa protein which binds to heymann nephritis antigen gp330.//6.6e-17:344:68//Z11995
R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds.//2.7e-83:433:95//AB018352
R-PLACE4000034//cSRL-51C5-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-51C5, genomic survey sequence.//0.54:116:66//B04984
R-PLACE4000049//Human BAC clone GS165I04 from 7q21, complete sequence.//0.29:313:59//AC002379
R-PLACE4000052//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.0058:466:57//AL034557
R-PLACE4000063//Homo sapiens chromosome 7q22 sequence, complete sequence.//0.98:246:61//AF053356
R-PLACE4000089//RPCI11-15I1.TUB RPCI-11 Homo sapiens genomic clone RPCI-11-15I1, genomic survey sequence.//3.2e-07:284:60//B82414
R-PLACE4000093//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.4e-07:429:60//AC005506
R-PLACE4000100
R-PLACE4000106//Homo sapiens clone 24561 unknown mRNA, partial cds.//9.3e-100:419:91//AF055010
R-PLACE4000128//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//9.6e-45:284: 90//AC003007
R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//1.6e-19:118:100// AB007969
R-PLACE4000147//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//8.9e-17:208:73// AC005034
R-PLACE4000156//Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family protein. Contains ESTs, STSs and GSSs, complete sequence.//3.7e-43:281:90//AL021939
R-PLACE4000192
R-PLACE4000222//Homo sapiens clone DJ1129J21, WORKING DRAFT SEQUENCE, 25 unordered pieces.// 5.4e-44:280:82//AC005631
R-PLACE4000233//Homo sapiens full-length insert cDNA YH59G06.//1.8e-79:414:97//AF074981
R-PLACE4000247//Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence.//5.7e-59:558: 76//AC005821
R-PLACE4000250//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.7e-44:313:84//AQ037381
R-PLACE4000252//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence.//1.5e-39:311:83// AC005920
R-PLACE4000261//H.sapiens BF1P-g1H03np gene for immunoglobulin heavy chain variable region.//0.33:197: 61//Z80410
R-PLACE4000269//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//1.4e-31:327: 68//AC005510
R-PLACE4000270//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.3e-32:345:74//D87675
R-PLACE4000300//Sequence 61 from patent US 5744300.//0.0017:51:98//AR003339
R-PLACE4000320//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete

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sequence.//8.2e-41:295:85//Z99495
R-PLACE4000323//Human chromosome 11 187a8 cosmid. complete sequence.//1.3e-32:404:75//U73640
R-PLACE4000326
R-PLACE4000344//Homo sapiens PAC clone DJ0988G15 from 7q33-q35, complete sequence.//0.32:135:68//AC005587
R-PLACE4000367//H.sapiens gene encoding RING finger protein.//0.61:146:67//Y07829
R-PLACE4000369//HS_3181_A1_B02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3181 Col=3 Row=C, genomic survey sequence.//7.1e-80:424:94//AQ173222
R-PLACE4000379//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1104E15, WORKING DRAFT SEQUENCE.//1.7e-05:160:65//AL022312
R-PLACE4000387//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.4e-47:351:81//AC004913
R-PLACE4000392//Human DNA sequence from clone 751H9 on chromosome 6q13. Contains part of an unknown gene, ESTs, STSs and GSSs, complete sequence.//8.5e-88:541:88//AL034377
R-PLACE4000401//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//2.7e-17:143:83//AC000406
R-PLACE4000411
R-PLACE4000445//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.028:91:78//AC005628
R-PLACE4000465//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30A23, WORKING DRAFT SEQUENCE.//1.6e-43:532:71//AL022156
R-PLACE4000489//Plasmodium falciparum chromosome 2, section 64 of 73 of the complete sequence.//4.1e-06:357:61//AE001427
R-PLACE4000494//Homo sapiens 12p13.3 PAC RPCI5-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.7e-37:416:74//AC005865
R-PLACE4000522
R-PLACE4000548//Homo sapiens 12p13.3 PAC RPCI5-1096D14 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.0020:383:60//AC005342
R-PLACE4000558//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//2.9e-44:465:75//AC002996
R-THYRO1000026//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 37E16, WORKING DRAFT SEQUENCE.//2.2e-43:354:82//Z83844
R-THYRO1000034//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.022:327:60//AE001422
R-THYRO1000035//HS_3018_B2_F10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=20 Row=L, genomic survey sequence.//2.3e-36:228:91//AQ092318
R-THYRO1000040//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.0:367:56//AC004157
R-THYRO1000070//***ALU WARNING: Human Alu-Sq subfamily consensus sequence.1/1e-44:284:89//U14573
R-THYRO1000072//***ALU WARNING: Human Alu-J subfamily consensus sequence.//6.6e-33:150:83//U14567
R-THYRO1000085
R-THYRO1000092//Homo sapiens chromosome 7qtelo BAC F6, complete sequence.//3.3e-36:301:78//AF104455
R-THYRO1000107//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 125I3, WORKING DRAFT SEQUENCE.//1.4e-35:282:82//AL033528
R-THYRO1000111//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//4.0e-32:351:65//AC002300
R-THYRO1000121//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//6.6e-77:507:85//U91318
R-THYRO1000124//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.66:334:59//AC005840
R-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds.//2.3e-88:449:96//AF087142
R-THYRO1000132//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 212A2, WORKING DRAFT SEQUENCE.//1.1e-40:298:84//Z95114
R-THYRO1000156//Homo sapiens chromosome 17, clone hRPK.849_N_15, complete sequence.//3.4e-37:425:73//AC005703
R-THYRO1000163//RPCI11-1B20.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-1B20, genomic survey sequence.//8.4e-38:276:84//B63536
R-THYRO1000173//Human DNA sequence from PAC 323B6 on chromosome X contains ESTs CpG island.//1.1e-

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70:553:81//Z83841
R-THYRO1000186//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 410I8, WORKING DRAFT SEQUENCE.//6.7e-41:345:81//AL031732
R-THYRO1000187//Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial cds for thymopoietin beta.//1.3e-43:356:80//U18271
R-THYRO1000190//Homo sapiens chromosome 17, clone HRPC843B9, complete sequence.//2.6e-40:386:77//AC004139
R-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//1.1e-108:535:97//AJ005698
R-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//1.4e-113:559:97//AB014552
R-THYRO1000206//Rat PMSG-induced ovarian mRNA, 3'sequence, N4.//4.0e-43:318:86//D84482
R-THYRO1000221//Human DNA from overlapping chromosome 19 cosmids R31396, F25451, and R31076 containing COX6B and UPKA, genomic sequence, complete sequence.//2.7e-44:452:76//AC002115
R-THYRO1000241//Homo sapiens Cosmid Clone p129d11 unknown chromosomal location, complete sequence.//4.8e-58:447:81//AC000039
R-THYRO 1000242
R-THYRO1000253//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//3.4e-56:300:84//Z95152
R-THYRO1000270
R-THYRO1000279//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 531H16, WORKING DRAFT SEQUENCE.//4.8e-113:584:96//AL031664
R-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//1.1e-98:566:91//AB016068
R-THYRO1000320//HS_2033_B1_A07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=13 Row=B, genomic survey sequence.//0.97:211:63//AQ233366
R-THYRO1000327//Sequence 1 from patent US 5541298.//2.8e-52:289:93//I24058
R-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//1.1e-111:559:96//AB018333
R-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds.//4.6e-47:317:87//U29091
R-THYRO1000368//HS_3049_A1_E12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3049 Col=23 Row=I, genomic survey sequence.//7.0e-11:111:83//AQ126777
R-nnnnnnnnnnnn
R-THYRO1000387//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//2.4e-101:545:93//AC006019
R-THYRO1000394//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.6e-46:233:88//AC006078
R-THYRO1000395//Mouse MIPP mRNA for a placenta-expressed gene.//2.3e-57:395:85//X58523
R-THYRO 1000401
3.3e-111:546:97//AF051907
R-THYRO1000438//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.7e-44:289:89//AC005231
R-THYRO1000452//Homo sapiens chromosome 17, clone hRPK.243_K_12, complete sequence.//6.7e-27:222:82//AC005668
R-THYRO1000471//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 102D24, WORKING DRAFT SEQUENCE.//2.4e-36:369:76//AL021391
R-THYRO1000484//Homo sapiens clone DJ1099N07, complete sequence.//1.6e-43:288:81//AC004962
R-THYRO1000488//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//1.6e-95:512:94//AC005740
R-THYRO1000501//HS _2208_A1_G11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=21 Row=M, genomic survey sequence.//0.0063:189:63//AQ091586
R-THYRO1000502//Homo sapiens eIF-1A, Y isoform (EIF1AY) mRNA, complete cds.//0.19:468:60//AF000987
R-THYRO1000505//Homo sapiens chromosome 19, cosmid R31546, complete sequence.//0.20:214:58//AC004798
R-THYRO1000558
R-THYRO 1000569
R-THYRO1000570//Homo sapiens full-length insert cDNA clone ZD76G10.//4.3e-41:209:100//AF086408
R-nmmmnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds.//8.2e-107:533:97//AF075587
R-THYRO 000596//Mus musculus mitochondrial DNA polymerase accessory subunit (MtPolB) mRNA, nuclear gene encoding mitochondrial protein, partial cds.//0.36:170:67//AF006072

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R-THYRO1000602//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.2e-53:289:92//D87675
R-THYRO 1000605
R-THYRO1000625//Homo sapiens chromosome 19, cosmid R29425, complete sequence.//1.3e-31:261:82//AC005546
R-THYRO1000637//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//4.0e-06:249:63//AL022323
R-THYRO1000641//P.falciparum glutamic acid-rich protein gnen, complete cds.//3.1e-08:244:68//J03998
R-THYRO1000658//***ALU WARNING: Human Alu-Sp subfamily consensus sequence.//3.9e-49:282:93//U14572
R-nnnnnnnnnnn
R-THYRO1000666//Homo sapiens DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence.//1.9e-20:215:77//AL031005
R-THYRO1000676//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//1.2e-06:227:64//AC004069
R-THYRO1000684
R-THYRO1000699
R-THYRO1000712
R-THYRO1000734//Human BAC clone RG191D16, complete sequence.//3.7e-14:468:64//AC002460
R-THYRO1000748//Homo sapiens cosmid 123E15, complete sequence.//2.6e-11:182:73//AF024533
R-THYRO1000756//Sequence 21 from patent US 5552281.//1.4e-15:106:98//I25660
R-THYRO1000777//Plasmodium falciparum MAL3P2, complete sequence.//1.0:175:66//AL034558
R-THYRO1000783//CIT-HSP-2335P6.TF CIT-HSP Homo sapiens genomic clone 2335P6, genomic survey sequence.//1.2e-81:391:99//AQ038226
R-THYRO1000787//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//9.4e-07:494:58//AC004617
R-THYRO1000793
R-THYRO1000796//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167P19, WORKING DRAFT SEQUENCE.//1.7e-42:379:79//Z93014
R-THYRO1000805//Human Chromosome 11 pac pDJ610i20, WORKING DRAFT SEQUENCE, 18 unordered pieces.//4.7e-40:362:76//AC002555
R-THYRO1000815//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 316D5, WORKING DRAFT SEQUENCE.//4.0e-58:295:92//Z82199
R-THYRO1000829//Sequence 7 from patent US 5716622.//0.97:362:61//I87788
R-THYRO1000843//Homo sapiens Chromosome 15q11-q13 PAC clone pDJ351h23 from the Prader-Willi/Angelman Syndrome region, complete sequence.//3.3e-57:522:76//AC004738
R-THYRO1000852//Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE, 9 unordered pieces.//4.2e-17:291:69//AC005849
R-THYRO1000855//Human DNA sequence from clone 366B10 on chromosome 22q12.2-12.3. Contains GSSs, complete sequence.//1.1e-41:419:75//AL031592
R-THYRO1000865//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1125A11, WORKING DRAFT SEQUENCE.//9.0e-47:294:84//AL034549
R-THYRO1000895//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 380F5, WORKING DRAFT SEQUENCE.//3.7e-111:569:96//AL031719
R-THYRO1000916//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.0e-97:554:92//AC006015
R-THYRO1000926//Homo sapiens CAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//9.6e-109:566:94//AF079529
R-THYRO1000934//Homo sapiens full-length insert cDNA clone ZD69A10.//1.6e-104:539:95//AF086378
R-THYRO1000951//Homo sapiens Chromosome 11q12 pac pDJ57I14, WORKING DRAFT SEQUENCE, 29 unordered pieces.//8.9e-61:479:81//AC004229
R-THYRO1000952//Human autoimmune thyroid disease-related antigen mRNA.//5.3e-16:116:93//M28639
R-THYRO1000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds.//3.2e-59:321:95//AF047440
R-THYRO1000975//Homo sapiens chromosome 19, cosmid F18718, complete sequence.//1.9e-44:396:79//AC006126
R-THYRO1000983//Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.//0.99:71:78//AC005562
R-THYRO1000984//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//6.7e-42:320:84//AC006078

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R-THYRO1000988//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//6.7e-39:292:78//Z84466
R-THYRO1001003//HS_3051_B1_H01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, genomic survey sequence.//2.5e-39:310:83//AQ253727
R-THYRO1001031//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//2.5e-50:300:88//Z84466
R-THYRO1001033//CIT-HSP-2007J14.TF CIT-HSP Homo sapiens genomic clone 2007J14, genomic survey sequence.//5.1e-26:143:100//B56677
R-THYRO1001062//CIT-HSP-2386P3.TF.1 CIT-HSP Homo sapiens genomic clone 2386P3, genomic survey sequence.//1.4e-48:316:87//AQ239882
R-THYRO1001093
R-THYRO1001100//Homo sapiens BAC clone RG152G17 from 7q22-q31.1, complete sequence.//0.47:102:73//AC005070
R-THYRO1001120
R-THYRO1001121//Homo sapiens mRNA for beta-tubulin folding cofactor D.//8.9e-81:429:94//AJ006417
R-THYRO1001133//CIT-HSP-2381I10.TR CIT-HSP Homo sapiens genomic clone 2381I10, genomic survey sequence.//4.7e-12:237:67//AQ111077
R-THYRO1001134
R-THYRO1001142//H.sapiens CpG island DNA genomic Mse1 fragment, clone 81d1, reverse read cpg81d1.rt1a.//0.95:214:60//Z56037
R-THYRO1001173//cSRL-27c11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-27c11, genomic survey sequence.//4.6e-26:262:77//B04145
R-THYRO1001177
R-THYRO1001189//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.0e-41:281:87//AC003973
R-THYRO 1001204
R-THYRO1001213//Human Alu repeat sequence A6.//3.8e-38:236:88//U12581
R-THYRO1001262//Homo sapiens, clone hRPK.16_A_1, complete sequence.//8.7e-53:442:79//AC006227
R-THYRO1001271//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0224P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 13 unordered pieces.//0.53:330:61//AC004630
R-THYRO 1001290
R-THYRO1001313//H.sapiens CpG island DNA genomic Mse1 fragment, clone 195h3, forward read cpg195h3.ft1b.//0.046:126:66//Z57783
R-THYRO1001320//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//3.0e-58:476:80//Z82207
R-THYRO100132//Plasmodium falciparum MAL3P2, complete sequence.//1.0e-08:408:62//AL034558
R-nnnnnnnnnnn
R-THYRO1001347//Homo sapiens mRNA for KIAA0745 protein, partial cds.//3.2e-08:266:64//AB018288
R-THYRO1001363//cSRL-72f5-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-72f5, genomic survey sequence.//1.7e-85:471:92/B05884
R-THYRO1001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map 10q25, complete sequence.//1.8e-109:584:94//AC005660
R-THYRO1001374
R-THYRO1001401//Human pigment epithelium-derived factor gene, complete cds.//4.2e-51:333:88//U29953
R-THYRO1001403//Human PAC clone DJ222H05 from Xq25-q26, complete sequence.//8.7e-38:307:82//AC002377
R-THYRO1001405
R-THYRO1001406//RPCI11-69F22.TK RPCI1 Homo sapiens genomic clone R-69F22, genomic survey sequence.//1.9e-67:400:90//AQ238297
R-THYRO1001411//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 80N2, WORKING DRAFT SEQUENCE.//2.2e-06:349:63//AL031123
R-THYRO1001426//*** SEQUENCING IN PROGRESS *** Homo sapiens genomic DNA (PAC 1118i22) from chromosome 11; HTGS phase 1, WORKING DRAFT SEQUENCE.//2.2e-89:506:86//AJ002553
R-THYRO1001434//Microcentus caryae 12S mitochondrial ribosomal RNA, small subunit, mitochondrial gene, partial sequence.//1.0:176:61//U77877
R-THYRO1001458//Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.//3.3e-07:196:67//AL021578

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R-THYRO1001480//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered piece.//1.2e-99:517:95//AC006001
R-THYRO1001487//Homo sapiens, WORKING DRAFT SEQUENCE, 97 unordered pieces.//8.5e-14:221:70//AC004085
R-THYRO10001534//HS_2242_B2_H04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=8 Row=P, genomic survey sequence.//0.00012:141:68//AQ182326
R-THYRO1001537//Human DNA sequence from clone 111F4 on chromosome Xq23 Contains GSSs, complete sequence.//0.42:323:60//AL023876
R-THYRO1001541//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.7e-42:370:78//AC005077
R-THYRO1001559//Homo sapiens 12q24.2 PAC RPCI5-944M2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0:144:67//AC005868
R-THYRO1001570//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.43:268:61//AC005308
R-THYRO1001573//M.avium rpsL gene.//0.98:131:66//X80120
R-THYRO1001584//A.longa plastid genes for ribosomal proteins and tRNAs.//0.29:502:58//X75653
R-THYRO1001595//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//1.5e-33:319:78//AL023808
R-THYRO1001602//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence.//4.4e-13:320:67//AC005919
R-THYRO1001605//Human DNA sequence from PAC 358H7 on chromosome X.//1.9e-32:391:76//Z77249
R-THYRO1001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//1.9e-81:448:92//AJ002190
R-THYRO1001637//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 688G8, WORKING DRAFT SEQUENCE.//5.4e-41:381:78//AL031671
R-THYRO1001656//HS_2201_B2_A08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2201 Col=16 Row=B, genomic survey sequence.//0.096:162:63//AQ293168
R-THYRO1001661//Human immunoglobulin-associated (B29) gene, promoter and exon 1, partial cds.//1.0:229:62//U22954
R-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//4.8e-110:562:95//AJ225089
R-THYRO1001673//CIT-HSP-2327D12.TR CIT-HSP Homo sapiens genomic clone 2327D12, genomic survey sequence.//1.5e-17:224:68//AQ042426
R-THYRO1001703//Homo sapiens clone 198 unknown mRNA, partial sequence.//1.6e-44:251:93//AF091072
R-THYRO1001706//Homo sapiens clone DJ0935K16, complete sequence.//1.8e-26:378:68//AC006011
R-THYRO1001721//, complete sequence.//1.3e-101:571:92//AC005500
R-nnnnnnnnnnn
R-THYRO1001745//Homo sapiens chromosome 5, PAC clone 247f3 (LBNL H85), complete sequence.//1.1e-15:193:70//AC004777
R-THYRO1001746//Human inter-alpha-trypsin inhibitor light chain (ITI) gene, exon 3.//0.54:260:61//M88244
R-THYRO1001772//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30A23, WORKING DRAFT SEQUENCE.//1.6e-12:285:64//AL022156
R-THYRO1001793
R-THYRO1001809//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1071N3, WORKING DRAFT SEQUENCE.//2.5e-43:486:74//AL031728
R-THYRO1001854//Homo sapiens chromosome 17, clone hRPK.74_E_22, complete sequence.//5.0e-41:245:87//AC005696
R-THYRO1001895//Human Chromosome 11p14.3 PAC clone 6-106f23, complete sequence.//4.4e-12:419:61//AC005137
R-THYRO1001907//Homo sapiens Chromosome 22q11.2 Cosmid Clone 24b In DGCR Region, complete sequence.//8.1e-35:340:78//AC000075
R-VESEN1000122//Homo sapiens Luman mRNA, complete cds.//1.3e-23:138:98//AF009368
R-Y79AA1000013
R-Y79AA1000033//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//9.9e-112:551:97//AC006027
R-Y79AA1000037//CIT-HSP-2334F3.TR CIT-HSP Homo sapiens genomic clone 2334F3, genomic survey sequence.//0.16:308:60//AQ036673
R-Y79AA1000059//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//6.1e-

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56:314:88//AC002300
R-Y79AA1000065//Human carboxylesterase gene, exon 5.//0.64:203:63//D21079
R-Y79AA1000131//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0548N01; HTGS phase 1, WORKING DRAFT SEQUENCE, 31 unordered pieces.//7.0e-18:169:79//AC004795
R-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome Iq24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.1e-106:474:98//AL031864
R-Y79AA1000202//CIT978SK-A-518G2.TP CIT978SK Homo sapiens genomic clone A-518G2, genomic survey sequence.//1.0e-10:78:97//B68074
R-Y79AA1000214//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.// 6.5e-59:386:90//AC004854
R-Y79AA1000230//Cytauxzoon felis 18S ribosomal RNA.//1.0:167:62//L19080
R-Y79AA1000231//HS_3009_A1_H03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=5 Row=O, genomic survey sequence.//6.4e-52:348:88//AQ090225
R-Y79AA1000258//Hepatitis C virus HCV-B9 gene for NS5, partial cds.//0.65:127:65//D10558
R-Y79AA1000268//Human DNA sequence from PAC 162H14 on chromosome 22. Contains 3' part of a FIBULIN 1 like gene and ESTs, complete sequence.//4.7e-40:300:84//Z98047
R-Y79AA10003131//Human DNA sequence from PAC 179I15, BRCA2 gene region chromosome 13q12-q13 contains Klotho ESTs and CpG island.//5.0e-14:136:83//Z92540
R-Y79AA1000328
R-Y79AA1000342//S.clavuligerus linear plasmid pSCL (complete sequence).//0.55:189:65//X54107
R-Y79AA1000346//Human MEST mRNA, complete cds.//0.00013:52:100//D78611
R-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//8.8e-36:300:81//X84692
R-Y79AA1000355//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//5.7e-45:403: 80//AL022163
R-Y79AA1000368
R-Y79AA1000405//RPCI11-16B12.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16B12, genomic survey sequence.//0.10:171:65//B88000
R-Y79AA1000410//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 92N15, WORKING DRAFT SEQUENCE.//4.1e-50:361:83//Z93097
R-Y79AA1000420//Plasmodium falciparum merozoite surface protein 4, merozoite surface protein 5, merozoite surface protein 2, and adenylosuccinate lyase genes, complete cds.//0.071:474:57//AF033037
R-Y79AA1000469//Homo sapiens clone NH0140K04, complete sequence.//1.8e-86:221:90//AC005033
R-Y79AA1000480//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//2.1e-14:179: 72//AC004057
R-Y79AA1000538//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//4.5e-43:321:83//AC005282
R-Y79AA1000539//Homo sapiens PAC clone DJ0074M20 from X, complete sequence.//0.0012:275:59// AC006143
R-Y79AA1000540//Z.diploperemnis repetitive DNA (clone ZEAR 260).//0.0017:258:62//X53609
R-Y79AA1000560//Mouse mRNA for alpha-adaptin (C).//6.1e-32:390:70//X14972
R-Y79AA1000574//Homo sapiens chromosome 9q34, clone 23B4, complete sequence.//0.96:224:61//AC002325
R-Y79AA1000627//Homo sapiens full-length insert cDNA ZA77G02.//6.3e-100:533:94//AF075117
R-Y79AA1000705//RPCI11-76G7.TV RPCI11 Homo sapiens genomic clone R-76G7, genomic survey sequence.// 4.6e-88:429:98//AQ268433
R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds.//2.7e-112:586: 95//AF093670
R-Y79AA1000748
R-Y79AA1000752
R-Y79AA1000774//CIT-HSP-2288K24.TF CIT-HSP Homo sapiens genomic clone 2288K24, genomic survey sequence.//5.3e-45:316:86//AQ005014
R-Y79AA1000782//Human mRNA for KIAA0246 gene, partial cds.//5.0e-17:107:100//D87433
R-Y79AA1000784//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00034:520:55//AC005505
R-Y79AA1000794//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 989H11, WORKING DRAFT SEQUENCE.//0.015:322:60//Z83851
R-Y79AA1000800//M.musculus tex264 mRNA (3'region).//1.1e-06:104:78//X80427

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R-nnnnnnnnnnnn//CIT-HSP-2295G6.TF CIT-HSP Homo sapiens genomic clone 2295G6, genomic survey sequence.//0.67:152:62//AQ007605
R-Y79AA1000805//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//3.1e-26:423:68//U73642
R-Y79AA1000824//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 329A5, WORKING DRAFT SEQUENCE.//1.1e-08:449:61//Z97832
R-Y79AA1000827//Triticum aestivum heat shock protein 101 kDa (HSP101) mRNA, complete cds.//1.0:101:69//AF083344
R-Y79AA1000850//Homo sapiens small optic lobes homolog (SOLH) mRNA, complete cds.//0.40:386:59//U85647
R-Y79AA1000962//CIT-HSP-2298N11.TR CIT-HSP Homo sapiens genomic clone 2298N11, genomic survey sequence.//0.00019:253:65//AQ013111
R-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//1.7e-58:446:80//U38253
R-Y79AA1000969
R-Y79AA1000976//CIT-HSP-2350C4.TF CIT-HSP Homo sapiens genomic clone 2350C4, genomic survey sequence.//3.3e-60:295:100//AQ061422
R-Y79AA1000985//Mus musculus pericentrin mRNA, complete cds.//5.9e-38:348:76//U05823
R-Y79AA1001023
R-Y79AA1001041
R-Y79AA1001048
R-Y79AA1001061//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-427H10, complete sequence.//1.2e-60:537:78//AC004626
R-Y79AA1001068//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.3e-41:405:77//AC005031
R-Y79AA1001077
R-Y79AA1001078//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.0e-09:534:59//AC004801
R-Y79AA1001105//Staphyloccous epidermidis trimethoprim resistance plasmid pSK639//0.0072:309:63//U40259
R-Y79AA1001145//RPCI11-59N12.TK RPCI11 Homo sapiens genomic clone R-59N12, genomic survey sequence.//3.7e-07:256:64//AQ200068
R-Y79AA1001167//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 5/15, WORKING DRAFT SEQUENCE.//0.55:223:61//AP000012
R-Y79AA1001177//Human gene for Gi3 alpha protein, intron 7 through exon 9, variant U6 gene, and snRNP E protein pseudogene LH87.//7.0e-09:203:69//X54048
R-Y79AA1001185
R-Y79AA1001211//Homo sapiens 12p13.3 BAC RPCI11-543P15 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//2.1e-32:277:81//AC005912
R-Y79AA1001216//Human chromosome 12p13 sequence, complete sequence.//0.98:325:59//U47924
R-Y79AA1001228//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAB16, complete sequence.//0.0034:378:59//AB018112
R-Y79AA1001233//Homo sapiens clone DJ1178G13, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.19:106:72//AC004988
R-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin)).//3.4e-109:549:95//AJ005892
R-Y79AA1001281
R-Y79AA1001299//Homo sapiens SNF5/INI1 gene, exon 9.//6.3e-24:133:100//Y17126
R-Y79AA1001312//Human immunodeficiency virus type 1 variant 43 polymerase pseudogene, partial cds.//0.0070:284:58//U45372
R-Y79AA1001323//Fugu rubripes GSS sequence, clone 027L23aG3, genomic survey sequence.//0.11:125:70//AL025355
R-Y79AA1001384//W.makrii mitochondrial CYTB and tRNA genes.//0.070:209:65//X66594
R-Y79AA1001391//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P2, WORKING DRAFT SEQUENCE.//0.80:163:62//AL031745
R-Y79AA1001394//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//0.99:241:63//AC004221
R-Y79AA1001402//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.25:81:80//AC005924
R-Y79AA1001493
R-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs,

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complete sequence.//1.3e-35:207:95//AL034430
R-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//2.7e-44:285:81//D14336
R-nnnnnnnnnnnn//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//0.70:365:60//AL023574
R-Y79AA1001548//Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds.//5.9e-95:517:91//L36151
R-Y79AA1001555
R-Y79AA1001585
R-Y79AA1001594//Human DNA sequence from PAC 60G11 on chromosome X; contains STS.//6.6e-19:241:76//Z94722
R-Y79AA1001603//H.sapiens CpG island DNA genomic Mse1 fragment, clone 72f8, forward read cpg72f8.ft1a.//3.3e-21:131:96//Z62766
R-Y79AA1001613
R-Y79AA1001647//Human DNA sequence from PAC 36J3, between markers DXS1192 and DXS102 on chromosome X.//6.3e-08:338:63//Z82975
R-Y79AA1001665//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 1/15, WORKING DRAFT SEQUENCE.//3.2e-11:114:84//AP000008
R-Y79AA1001679//O.cuniculus lambda-crystallin mRNA, complete cds.//3.9e-15:270:68//M22743
R-nnnnnnnnnnnn//RPCI11-42M5.TJ RPCI11 Homo sapiens genomic clone R-42M5, genomic survey sequence.//0.013:64:89//AQ052792
R-Y79AA1001696//Apis mellifera ligustica complete mitochondrial genome.//9.3e-09:428:58//L06178
R-Y79AA1001705
R-Y79AA1001711//Mus musculus 60 kDa ribonucleoprotein Ro gene, partial cds.//2.2e-45:554:75//AF042139
R-Y79AA1001781//Plasmodium falciparum chromosome 2, section 39 of 73 of the complete sequence.//1.0:414:57//AE001402
R-nnnnnnnnnnnn//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 510D11, WORKING DRAFT SEQUENCE.//2.8e-05:329:61//Z98044
R-Y79AA1001827//Oryctolagus cuniculus PiUS mRNA, complete cds.//2.3e-90:557:89//U74297
R-Y79AA1001846//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//2.1e-34:306:78//Z95152
R-Y79AA1001848//Sequence 11 from patent US 5449616.//1.0:221:59//I14369
R-Y79AA1001866//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence.//0.0089:527:58//AB016874
R-Y79AA1001874
R-Y79AA1001875//M.musculus mRNA for Rab7 protein.//5.8e-45:170:92//X89650
R-Y79AA1001923//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.0:138:68//AL022577
R-Y79AA1002027//Liverwort Marchantia polymorpha chloroplast genome DNA.//0.71:153:67//X04465
R-Y79AA1002083//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 172B20, WORKING DRAFT SEQUENCE.//1.0:178:64//AL022319
R-Y79AA1002089//Homo sapiens clone GS111G14, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.3e-49:377:81//AC005011
R-Y79AA1002093//Homo sapiens (clone SEL366) 17q YAC (368C7) RNA.//4.0e-32:174:99//L77612
R-Y79AA1002103//CIT-HSP-2328I21.TR CIT-HSP Homo sapiens genomic clone 2328I21, genomic survey sequence.//1.9e-44:245:96//AQ044502
R-Y79AA1002115//CITBI-E1-2514F10.TF CITBI-E1 Homo sapiens genomic clone 2514F10, genomic survey sequence.//1.8e-24:249:78//AQ265752
R-Y79AA1002125//RPCI11-15J6.TV RPCI-11 Homo sapiens genomic clone RPCI-11-15J6, genomic survey sequence.//8.5e-21:147:91//B75354
R-Y79AA1002139
R-Y79AA1002204
R-nnnnnnnnnnnn//Human ankyrin G (ANK-3) mRNA, complete cds.//0.040:319:59//U13616
R-Y79AA1002209//Psilotum nudum RT gene for reverse transcriptase (PT4).//0.99:106:65//X65415
R-Y79AA1002210

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R-Y79AA1002211//H.sapiens NGAL gene.//1.0:311:59//X99133
R-Y79AA1002220//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//5.9e-07:535:57//AL034557
R-Y79AA1002229
R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//6.1e-117:564:98//AB014592
R-Y79AA1002246
R-Y79AAI002258//Homo sapiens mRNA for HIP3, complete cds.//1.3e-92:453:97//AB013384
R-Y79AA1002298//HS_3071_B2_E08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=16 Row=J, genomic survey sequence.//1.9e-56:384:87//AQ171331
R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//2.5e-108:403:99//AB014534
R-Y79AA1002311//Homo sapiens chromosome 10 clone CIT987SK-1173I12 map 10q25, complete sequence.//1.1e-07:368:61//AC005887
R-Y79AA1002351
R-Y79AA1002361//H.sapiens CpG island DNA genomic Mse1 fragment, clone 65b9, reverse read cpg65b9.rt1a.//0.57:59:79//Z62206
R-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence.//2.0e-98:385:99//AC005920
R-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//5.4e-59:490:76//AC004662
R-Y79AA1002416//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//6.3e-08:103:80//AC004087
R-Y79AA1002431
R-nnnnnnnnnnnn//Mouse transcriptional control element.//0.064:84:71//M17284
R-Y79AA1002472//Homo sapiens chromosome 19, BAC CTY-B-393i15 (BC301323), complete sequence.//1.6e-103:525:96//AC006116
R-Y79AA1002482//Homo sapiens chromosome 18, clone hRPK.474_N_24, complete sequence.//9.7e-38:302:83//AC006238
R-Y79AA1002487//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.23:266:61//X95276

Homology Search Result Data 4.

[0307] The result of the homology search of the Human Unigene using the clone sequence of 5'-end.
[0308] Data include

the name of clone,
title of the top hit data,
the P-value: the length of the compared sequence: identity (%), and
the Accession No. of the top hit data, as in the order separated by //.

[0309] Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000005//EST//4.3e-87:422:97//Hs.147830:AI222069
F-HEMBA1000012//Human endosome-associated protein (EEA1) mRNA, complete cds//0.82:170:64//Hs.2864:L40157
F-HEMBA1000020//Homo sapiens beta 2 gene//4.0e-74:529:83//Hs.150244:U83668
F-HEMBA1000030//ESTs//1.1e-91:494:93//Hs.7958:W22078
F-HEMBA1000042//ESTs//3.5e-22:228:77//Hs.145406:AI253247
F-HEMBA1000046//ESTs, Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharomyces cerevisiae]//0.00019:192:65//Hs.7900:W22411
F-HEMBA1000050//EST//0.81:74:72//Hs.156298:AI336759
F-HEMBA1000076//ESTs//0.11:252:62//Hs.131939:AI417910
F-HEMBA1000111//ESTs//8.5e-89:449:96//Hs.41105:N66734
F-HEMBA1000129//Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds//0.27:342:61//Hs.14207:U86453
F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//6.8e-169:791:98//Hs.27197:AB018340
F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.4e-37:243:88//Hs.2397:Z70200
F-HEMBA1000156//ESTs, Weakly similar to The KIAA0138 gene product is novel. [H.sapiens]//5.3e-80:383:98//

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Hs.135552:AI215187
F-HEMBA1000158//Homo sapiens OPA-containing protein mRNA, complete cds//2.1e-07:265:63//Hs.85313:AF071309
F-HEMBA1000168//ESTs//6.1e-35:257:85//Hs.13533:H23079
F-HEMBA1000180//ESTs, Moderately similar to RETROVIRUS-RELATED POL POLYPROTEIN [H.sapiens]//1.3e-18:111:96//Hs.163863:W28729
F-HEMBA1000185//H.sapiens ERF-2 mRNA//1.0:125:68//Hs.78909:U07802
F-HEMBA1000193//EST//1.5e-48:266:95//Hs.160642:AI240133
F-HEMBA1000201//Human Ini1 mRNA, complete cds//6.5e-75:440:92//Hs.155626:U04847
F-HEMBA1000213//ESTs//0.21:239:62//Hs.26838:AA527529
F-HEMBA1000216//Homo sapiens clone 23698 mRNA sequence//1.1e-57:529:68//Hs.8136:U81984
F-HEMBA1000227//Human RNA-binding protein CUG-BP/hNab50 (NAB50) mRNA, complete cds//1.3e-05:311:64//Hs.81248:U63289
F-HEMBA1000231
F-HEMBA1000243//EST//5.9e-52:359:85//Hs.141433:N23377
F-HEMBA1000244//H.sapiens mRNA for cytokine inducible nuclear protein//0.0022:350:60//Hs.74019:X83703
F-HEMBA1000251//ESTs//3.2e-84:443:95//Hs.21068:N47460
F-HEMBA1000264//ESTs//0.76:227:61//Hs.5159:AA588562
F-HEMBA1000280//EST//1.7e-12:149:75//Hs.103418:AA035568
F-HEMBA1000282//ESTs//1.7e-16:164:79//Hs.123111:AA813186
F-HEMBA1000288//ESTs//5.4e-06:154:68//Hs.54174:N64406
F-HEMBA1000290//Human novel homeobox mRNA for a DNA binding protein//3.8e-07:412:61//Hs.37035:U07664
F-HEMBA1000302//EST/1.2e-41:238:94//Hs.147245:AI206095
F-HEMBA1000303
F-HEMBA1000304//ESTs//3.5e-11:96:87//Hs.163057:AA728946
F-HEMBA1000307//EST//7.7e-05:280:62//Hs.146462:AI124898
F-HEMBA1000327//ESTs//5.3e-92:435:99//Hs.100605:AA305965
F-HEMBA1000333//Human mRNA for KIAA0206 gene, partial cds//0.84:395:56//Hs.79299:D86961
F-HEMBA1000338//ESTs, Moderately similar to novel stromal cell protein [M.musculus]//2.4e-38:317:80//Hs.99189:X84712
F-HEMBA1000351//Human Line-1 repeat mRNA with 2 open reading frames//0.020:334:59//Hs.23094:M19503
F-HEMBA1000355//Myosin, heavy polypeptide 11, smooth muscle//0.11:336:61//Hs.78344:AF001548
F-HEMBA1000356//H.sapiens ERF-2 mRNA//0.031:317:59//Hs.78909:U07802
F-HEMBA1000357//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:441:78//Hs.154326:D42087
F-HEMBA1000366//ESTs//0.025 :56:87//Hs.141629:H74010
F-HEMBA1000369//Homo sapiens PAC clone DJ0669B10 from 7q33-q35//0.99:433:58//Hs.159899:AC004853
F-HEMBA1000376//Oxytocin receptor//3.4e-43:569:70//Hs.2820:X64878
F-HEMBA1000387//ESTs//8.2e-104:535:94//Hs.78110:AA741320
F-HEMBA1000390//Homo sapiens BAC clone RG119C02 from 7p15//2.3e-141:712:95//Hs.22900:AC004520
F-HEMBA1000392//Homo sapiens clone 24619 mRNA sequence//1.7e-47:461:74//Hs.139088:AF070533
F-HEMBA1000396//ESTs, Weakly similar to hypothetical protein [H.sapiens]//1.2e-26:351:70//Hs.138992:C14008
F-HEMBA1000411//EST//2.8e-27:401:71//Hs.138719:N52915
F-HEMBA1000418//ESTs//0.0094:375:61//Hs.40140:AI079253
F-HEMBA1000422//EST//6.2e-23:225:78//Hs.132635:A1032875
F-HEMBA1000428//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//7.6e-31:616:66//Hs.159897:AB007970
F-HEMBA1000434//EST//0.0031:157:64//Hs.162328:AA559034
F-HEMBA1000442//EST//1.0:201:61//Hs.162434:AA577398
F-HEMBA1000456//Fanconi anemia complementation group C//0.58:362:59//Hs.37953:X66893
F-HEMBA1000459//EST//9.2e-21:157:86//Hs.132635:AI032875
F-HEMBA1000460//ESTs//2.9e-77:409:95//Hs.27135:W49590
F-HEMBA1000464//ESTs//6.6e-17:365:65//Hs.150675:AA127853
F-HEMBA1000469
F-HEMBA1000488//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//0.15:253:58//Hs.104640:AF000561
F-HEMBA1000490//Homo sapiens kinectin mRNA, complete cds//0.71:539:56//Hs.82709:Z22551
F-HEMBA1000491//ESTs//2.0e-21:361:65//Hs.152453:AA864970
F-HEMBA1000501//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.5e-39:312:77//Hs.5247:AF029750

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F-HEMBA1000504//Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os)//1.3e-08:57:100//Hs.155095:D13666
F-HEMBA1000505//Homo sapiens KE04p mRNA, complete cds//1.0:197:62//Hs.131962:AF064093
F-HEMBA1000508//EST//0.67:156:60//Hs.162898:AA659646
F-HEMBA1000518
F-HEMBA1000519//EST//6.8e-52:300:91//Hs.149580:AI281881
F-HEMBA1000520//ESTs, Weakly similar to coded for by C. elegans cDNA CEESB82F [C.elegans]//2.9e-16:132:84//Hs.155871:AA533783
F-HEMBA1000523//ESTs, Highly similar to TESTIS-SPECIFIC PROTEIN PBS13 [Mus musculus]//2.1e-25:192:87//Hs.22383:R51067
F-HEMBA1000531//ESTs, Weakly similar to heat shock protein [H.sapiens]//2.4e-57:288:97//Hs.116022:AA455706
F-HEMBA1000534//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.8e-47:153:88//Hs.113283:AF018080
F-HEMBA1000540//ESTs//8.6e-07:60:100//Hs.109755:AA180809
F-HEMBA1000542//Human lysyl oxidase-like protein mRNA, complete cds//0.088:581:57//Hs.65436:U24389
F-HEMBA1000545//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//7.8e-106:731:83//Hs.139107:K00629
F-HEMBA1000555//Human mRNA for KIAA0242 gene, partial cds//0.75:283:58//Hs.77495:D87684
F-HEMBA1000557//ESTs//3.9e-27:389:71//Hs.125087:AA495729
F-HEMBA1000561//Homo sapiens mRNA for KIAA0760 protein, partial cds//3.8e-64:665:72//Hs.137168:AB018303
F-HEMBA1000563//ESTs//3.8e-51:257:98//Hs.47122:AI338977
F-HEMBA1000568//EST//0.12:270:61//Hs.134833 :AI091046
F-HEMBA1000569//H.sapiens mRNA encoding GPI-anchored protein p137//3.8e-19:409:62//Hs.119283:Z48042
F-HEMBA1000575//EST//0.060:156:64//Hs.126277:AA826681
F-HEMBA1000588//ESTs, Weakly similar to weakly similar to myosin heavy chain [C.elegans]//7.7e-41:217:96//Hs.55084:AA479162
F-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e-44:228:97//Hs.155218:AJ007509
F-HEMBA1000592//ESTs, Weakly similar to sorting nexin 1 [H.sapiens]//1.7e-27:463:65//Hs.13794:AA203241
F-HEMBA1000594//Human clone 230971 defective mariner transposon Hsmar2 mRNA sequence//4.0e-68:574:79//Hs.159176:U92019
F-HEMBA1000604//ESTs//3.3e-21:158:74//Hs.142924:AI092535
F-HEMBA1000608//Homo sapiens mRNA for KIAA0456 protein, partial cds//3.7e-120:561:99//Hs.5003:AB007925
F-HEMBA1000622//Homo sapiens DEC-205 mRNA, complete cds//5.2e-34:592:68//Hs.153563:AF011333
F-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//7.4e-22:166:84//Hs.26252:AA643235
F-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//2.1e-138:639:99//Hs.60103:AB014590
F-HEMBA1000655//ESTs//1.2e-54:503:77//Hs.140864:AA176174
F-HEMBA1000657//Mucin 1, transmembrane//0.99:219:61//Hs.89603:J05582
F-HEMBA1000662//ESTs//2.2e-52:257:99//Hs.63243:AI123912
F-HEMBA1000673//H.sapiens mRNA for translin associated protein X//1.7e-47:366:79//Hs.96247:X95073
F-HEMBA1000682//Oxytocin receptor//4.7e-59:673:72//Hs.2820:X64878
F-HEMBA1000686
F-HEMBA1000702
F-HEMBA1000705//EST//0.047:363:60//Hs.136379:AA521309
F-HEMBA1000719//ESTs//2.7e-68:333:98//Hs.146195:AI039850
F-HEMBA1000722//ESTs//0.49:283:60//Hs.21108:N92630
F-HEMBA1000726//EST//1.1e-45:183:87//Hs.149580:AI281881
F-HEMBA1000727//ESTs//4.8e-95:442:100//Hs.22119:AA885491
F-HEMBA1000747
F-HEMBA1000749//ESTs//8.0e-14:108:77//Hs.154892:AI091568
F-HEMBA1000752//EST//1.3e-25:344:69//Hs.160992:H52716
F-HEMBA1000769//ESTs//0.0018:206:63//Hs.153268:AA887239
F-HEMBA1000773//ESTs//0.56:336:58//Hs.105964:N35803
F-HEMBA1000774//EST//4.0e-38:312:79//Hs.162197:AA535216
F-HEMBA1000791//ESTs//2.8e-87:413:99//Hs.112050:AA431300

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F-HEMBA1000817//ESTs//5.6e-124:617:96//Hs.101366:AA167536
F-HEMBA1000822//ESTs//0.94:347:58//Hs.23905:AA928542
F-HEMBA1000827//EST//0.064:133:60//Hs.138738:N58367
F-HEMBA1000843
F-HEMBA1000851//Fragile X mental retardation 1//0.014:219:62//Hs.89764:X69962
F-HEMBA1000852//Arylsulfatase D//6.7e-38:244:75//Hs.43887:X83572
F-HEMBA1000867
F-HEMBA1000869//ESTs//5.1 e-33:166:77//Hs.141186:R99609
F-HEMBA1000870//EST//0.032:130:66//Hs.157351:AI367237
F-HEMBA1000872//ESTs//2.4e-20:134:92//Hs.155982:AA406047
F-HEMBA1000876//EST//5.3e-20:233:72//Hs.124339:AA829660
F-HEMBA1000908//ESTs//5.4e-28:219:84//Hs.12247:AI203154
F-HEMBA1000910//Human DNA sequence from clone 14O9 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//2.8e-11:309:65//Hs.4943:Z98046
F-HEMBA1000918//ESTs//0.11:234:59//Hs.96499:AA252537
F-HEMBA1000919//Human mRNA for histone H1x, complete cds//0.18:221:64//Hs.109804:D64142
F-HEMBA1000934//Homo sapiens mRNA for KIAA0547 protein, complete cds//3.8e-09:360:62//Hs.36850:AB011119
F-HEMBA1000942//ESTs, Highly similar to PMS4 homolog mismatch repair protein [H.sapiens]//9.4e-10:77:93//Hs.111445:H00596
F-HEMBA1000943//ESTs, Highly similar to ZINC FINGER PROTEIN 10 [Homo sapiens]//0.0039:54:92//Hs.58338:AA609476
F-HEMBA1000946//Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide-synthetase, phosphoribosylaminoimidazole synthetase//0.93:132:66//Hs.82285:X54199
F-HEMBA1000960//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//0.080:128:71//Hs.118972:AA761369
F-HEMBA1000968//Human transposon-like element mRNA//2.8e-95:352:87//Hs.84775:M23161
F-HEMBA1000971//ESTs//8.4e-88:417:98//Hs.128631:AI127903
F-HEMBA1000972//EST//0.75:134:64//Hs.117228:AA682775
F-HEMBA1000974//ESTs//1.3e-103:497:98//Hs.126786:U74314
F-HEMBA1000975//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds//1.3e-05:424:59//Hs.159564:AF061936
F-HEMBA1000985//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.0036:389:60//Hs.127338:AB007961
F-HEMBA1000986//ESTs//0.00025:272:64//Hs.12364:H09132
F-HEMBA1000991//Homo sapiens mRNA for Hrs, complete cds//3.9e-24:193:84//Hs.24756:U43895
F-HEMBA1001007//EST//0.96:70:71//Hs.163258:AA828835
F-HEMBA1001008//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.9e-43:472:74//Hs.46468:U45984
F-HEMBA1001009//Immunoglobulin mu//0.18:367:59//Hs.75758:X58529
F-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//1.4e-140:661:98//Hs.158287:AB007937
F-HEMBA1001019//EST//4.1e-14:251:68//Hs.148769:AI239572
F-HEMBA1001020//Von Hippel-Lindau syndrome//2.2e-28:253:69//Hs.78160:AF010238
F-HEMBA1001022
F-HEMBA1001024//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.8e-28:376:72//Hs.159897:AB007970
F-HEMBA1001026//Homo sapiens klotho mRNA, complete cds//1.3e-05:745:57//Hs.94592:AB005142
F-HEMBA1001043//ESTs//2.1e-28:448:67//Hs.112469:AA598515
F-HEMBA1001051//EST//3.1e-48:310:87//Hs.149580:AI281881
F-HEMBA1001052//EST//0.94:149:67//Hs.31216:AI017971
F-HEMBA1001059//N-ACETYLGALACTOSAMINE-6-SULFATASE PRECURSOR//4.6e-165:777:98//Hs.159479:U06088
F-HEMBA1001060//ESTs//6.8e-14:150:78//Hs.24821:AA044813
F-HEMBA1001071//Alpha-1 type 3 collagen//3.5e-32:181:96//Hs.119571:X14420
F-HEMBA1001077//ESTs, Moderately similar to transcription intermediary factor 1 [H.sapiens]//1.1e-98:487:97//

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Hs.147802:R71297
F-HEMBA1001080//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//0.013:385:58//Hs.69949:M94172
F-HEMBA1001085//Human hSIAH2 mRNA, complete cds//0.55:338:59//Hs.20191:U76248
F-HEMBA1001088//Human PINCH protein mRNA, complete cds//7.3e-73:303:78//Hs.83987:U09284
F-HEMBA1001094//Interleukin 8//0.092:530:58//Hs.624:M17017
F-HEMBA1001099
F-HEMBA1001109//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.4-61:341:85//Hs.5247:AF029750
F-HEMBA1001121//EST//7.3e-13:265:64//Hs.142423:AA412497
F-HEMBA1001122//Homo sapiens mRNA for KIAA0471 protein, complete cds//0.066:649:56//Hs.5347:AB007940
F-HEMBA1001123//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.5e-10:231:68//Hs.27349:AB007917
F-HEMBA1001133//EST//0.50:222:63//Hs.131018:AI015747
F-HEMBA1001137//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.2e-73:527:77//Hs.159277:AB018341
F-HEMBA1001140//Homo sapiens mRNA for KIAA0682 protein, complete cds//0.020:141:65//Hs.7482:AB014582
F-HEMBA1001172//EST//0.77:158:60//Hs.158894:AI378457
F-HEMBA1041174//ESTs//1.4e-63:363:92//Hs.132798:AA922226
F-HEMBA1001197//ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]//5.0e-54:555:71//Hs.55165:AA573499
F-HEMBA1001208//EST//6.2e-26:213:77//Hs.146964:AI183463
P-HEMBA1001213//Human mRNA for KIAA0013 gene, complete cds//0.026:569:57//Hs.48824:D87717
F-HEMBA1001226//ESTs/1.9e-11:407:65//Hs.157977:AI369694
F-HEMBA1001235//ESTs//0.0042:161:63//Hs.155170:AA167748
F-HEMBA1001247//ESTs//1.2e-91:429:99//Hs.143304:AI084058
F-HEMBA1001257//Human zinc finger protein (MAZ) mRNA//0.017:330:62//Hs.7647:M94046
F-HEMBA1001265
F-HEMBA1001281
F-HEMBA1001286//Natriuretic peptide precursor B//0.76:163:63//Hs.937:AL021155
F-HEMBA1001289//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5.1e-30:530:64//Hs.154050:AC004131
F-HEMBA1001294//Homo sapiens mRNA for matrilin-3//0.00023:657:56//Hs.119534:AJ224741
F-HEMBA1001299//Small inducible cytokine A5 (RANTES)//2.2e-27:271:77//Hs.155464:AF088219
F-HEMBA1001302//ESTs, Moderately similar to Cab45a [M.musculus]//3.3e-53:272:97//Hs.154563:AI129590
F-HEMBA1001303//ESTs, Weakly similar to RNA splicing-related protein [R.norvegicus]//2.6e-66:241:99//Hs.120847:AA731201
F-HEMBA1001310//ESTs//2.0e-21:133:93//Hs.159116:W55873
F-HEMBA1001319//Homo sapiens mRNA for KIAA0758 protein, partial cds//0.23:562:58//Hs.22039:AB018301
F-HEMBA1001323//Wingless-type MMTV integration site 5A, human homolog//2.5e-31:165:99//Hs.152213:L20861
F-HEMBA1001326//ESTs, Highly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION [Saccharomyces cerevisiae]//8.9e-08:185:68//Hs.108734:AI073427
F-HEMBA1001327//ESTs//0.085:337:60//Hs.114157:AA703013
F-HEMBA1001330//EST//0.0018:225:63//Hs.127987:AA970569
F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds//3.6e-105:516:97//Hs.9006:AF057358
F-HEMBA1001361//ESTs//1.2e-62:317:97//Hs.6639:R39794
F-HEMBA1001375//ESTs//0.93:180:60//Hs.148425 :AI198074
F-HEMBA1001377//ESTs//9.2e-87:414:99//Hs.48469:N62156
F-HEMBA1001383//ESTs//0.0023:336:60//Hs.140622:AA844353
F-HEMBA1001387//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]//1.0e-132:643:97//Hs.124217:AA020848
F-HEMBA1001388
F-HEMBA1001391//ESTs//5.6e-32:191:93//Hs.71628:N41660
F-HEMBA1001398
F-HEMBA1001405//EST//1.0:135:63//Hs.146833:AI151117
F-HEMBA1001407//ESTs/10.53:390:57//Hs.150447:AI017798
F-HEMBA1001411//EST//8.8e-06:270:62//Hs.145386:AI253108

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F-HEMBA1001413
F-HEMBA1001415//EST//1.3e-12:176:75//Hs.133172:AI051605
F-HEMBA1001432//RING3 PROTEIN//0.57:345:59//Hs.75243:D42040
F-HEMBA1001433//ESTs//1.3e-21:333:69//Hs.131648:AI025726
F-HEMBA1001435//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.2e-74:469:80//Hs.1361:M55053
F-HEMBA1001442//EST//0.29:181:64//Hs.116883:AA663031
F-HEMBA1001446//ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]//6.8e-47:550:71//Hs.55165:AA573499
F-HEMBA1001450//Homo sapiens GTPase-activating protein (SIPA1) mRNA, complete cds//0.82:312:58//Hs.7019:AB005666
F-HEMBA1001454//ESTs//1.2e-46:297:80//Hs.152395:AA533107
F-HEMBA1001455//ESTs//7.3e-103:502:97//Hs.112860:AA442412
F-HEMBA1001463//Human mRNA for KIAA0392 gene, partial cds//8.7e-51:323:88//Hs.40100:AB002390
F-HEMBA1001476//Homo sapiens mRNA for KIAA0572 protein, partial cds//6.2e-104:489:99//Hs.14409:AB011144
F-HEMBA1001478//EST//0.013:205:61//Hs.157309:AI365451
F-HEMBA1001497//Small inducible cytokine A5 (RANTES)//5.9e-45:307:84//Hs.155464:AF088219
F-HEMBA1001510//H.sapiens mRNA for G13 protein//2.1e-71:405:92//Hs.42853:X98054
F-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//4.5e-105:773:82//Hs.23094:M19503
F-HEMBA1001517//EST//3.6e-09:271:65//Hs.162347:AA564902
F-HEMBA1001522//ESTs//4.3e-13:85:95//Hs.126707:AI376869
F-HEMBA1001526
F-HEMBA1001533//EST//1.0:75:73//Hs.145360:AI252476
F-HEMBA1001557//EST//3.5e-13:261:64//Hs.161496:N66580
F-HEMBA1001566//EST//3.7e-07:354:64//Hs.43830:N26652
F-HEMBA1001569//Homo sapiens mRNA for vesicle associated membrane protein 2 (VAMP2)//8.0e-68:338:97//Hs.91589:M36205
F-HEMBA1001570//ESTs//1.5e-47:369:82//Hs.107657:AA126814
F-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//7.0e-175:678:99//Hs.159597:AJ012449
F-HEMBA1001581//ESTs//4.4e-07:237:67//Hs.152304:AA605184
F-HEMBA1001585//ESTs//1.1e-11:81:100//Hs.16364:AI357228
F-HEMBA1001589//Human mRNA for KIAA0166 gene, complete cds//0.82:210:64//Hs.115778:D79988
F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds//2.6e-110:855:78//Hs.90998:D50918
F-HEMBA1001608//EST//1.0:201:60//Hs.136747:AA749210
F-HEMBA1001620//ESTs//1.5e-39:211:98//Hs.131063:AI016400
F-HEMBA1001635//ESTs//4.0e-33:168:100//Hs.122655:AI361870
F-HEMBA1001636//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//0.038:198:64//Hs.34579:AI338536
F-HEMBA1001640//ESTs//1.1e-24:315:71//Hs.34114:AA776899
F-HEMBA1001647//Human plectin (PLEC1) mRNA, complete cds//0.00049:629:61//Hs.79706:U53204
F-HEMBA1001651//EST//3.6e-07:285:63//Hs.132558:AA948560
F-HEMBA1001655//ESTs//1.4e-95:497:96//Hs.59563:AA203283
F-HEMBA1001658//EST//0.18:251:59//Hs.117724:H47121
F-HEMBA1001661
F-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//7.9e-146:669:99//Hs.107254:AC005943
F-HEMBA1001675//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//2.0e-57:447:79//Hs.158095:AB007953
F-HEMBA1001678//ESTs//4.0e-50:360:83//Hs.146811:AA410788
F-HEMBA1001681//EST//1.0:165:58//Hs.136790:AA776060
F-HEMBA1001702//EST//0.015:312:61//Hs.162839:AA648760
F-HEMBA1001709//EST//0.85:131:65//Hs.131451:AI023995
F-HEMBA1001711//ESTs//0.084:425:56//Hs.125346:AI302836
F-HEMBA1001712//EST//0.26:214:59//Hs.159088:AI383114
F-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus nor-

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vegicus]//3.0e-30:195:92//Hs.132948:AA194452
F-HEMBA1001718//EST//0.0044:275:60//Hs.125969:AA889554
F-HEMBA1001723//INTERLEUKIN ENHANCER-BINDING FACTOR//0.24:501:57//Hs.101524:U58197
F-HEMBA1001731//EST//1.2e-06:261:63//Hs.132331:AI028363
F-HEMBA1001734//ESTs//0.018:177:63//Hs.129631:AI000415
F-HEMBA1001744//EST//8.7e-77 :420:92//Hs.133226:AI052250
F-HEMBA1001745//Homo sapiens mRNA for TSC403 protein, complete cds//0.37:300:62//Hs.10887:AB013924
F-HEMBA1001746//ESTs//0.31:168:66//Hs.27237:N68328
F-HEMBA1001761//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//0.76:218:60//Hs.135553:N41598
F-HEMBA1001781//Homo sapiens chromosome 19, cosmid R30953//0.98:219:60//Hs.98776:AC005622
F-HEMBA1001784//Homo sapiens mRNA for KJAA0474 protein, complete cds//6.4e-09:265:67//Hs.158232:AB007943
F-HEMBA1001791
F-HEMBA1001800//EST//3.1e-41:331:81//Hs.127142:AA937570
F-HEMBA1001803//EST//0.0062:269:59//Hs.49075:N64817
F-HEMBA1001804//Human POU domain protein (Brn-3b) mRNA, complete cds//1.8e-07:439:59//Hs.266:U06233
F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//2.-5e-175:809:98//Hs.118164:AB007969
F-HEMBA1001809//ESTs//6.0e-101:497:97//Hs.155127:AA625305
F-HEMBA1001815
F-HEMBA1001819//Human kruppel-related zinc finger protein (ZNF184) mRNA, partial cds//4.9e-80:842:70//Hs.158174:U66561
F-HEMBA1001820//EST//0.057:214:62//Hs.148715:A1223845
F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds//6.7e-42:510:65//Hs.66392:AF064244
F-HEMBA1001824//Homo sapiens OPA-containing protein mRNA, complete cds//5.2e-13:253:68//Hs.85313:AF071309
F-HEMBA1001835//Human mRNA for KIAA0235 gene, partial cds//0.96:288:60//Hs.6151:D87078
F-HEMBA1001844//ESTs//1.1e-29:197:80//Hs.l55243:N70293
F-HEMBA1001847//Human mRNA for KIAA0326 gene, partial cds//2.0e-23:379:68//Hs.6833:AB002324
F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//2.8e-185:865:98//Hs.78946:AB014517
F-HEMBA1001864//EST//0.27:145:63//Hs.162585:AA593121
F-HEMBA1001866//ESTs. Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]//3.2e-39:293:84//Hs.152332:AI141922
F-HEMBA1001869//ESTs, Weakly similar to ASH1 [D.melanogaster]//8.1e-70:367:95//Hs.15423:T84036
F-HEMBA1001888//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//5.4e-86:835:76//Hs.158095:AB007953
F-HEMBA1001896
F-HEMBA1001910//Human calpain-like protease (htra-3) mRNA, complete cds//0.43:114:71//Hs.6133:U94346
F-HEMBA1001912//ESTs//4.1e-79:398:97//Hs.26660:AI312633
F-HEMBA1001913//Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds//0.00031:200:62//Hs.9573:AF027302
F-HEMBA1001915//EST//0.082:128:64//Hs.126542:AA916511
F-HEMBA1001918//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.46:374:59//Hs.31575:AF100141
F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//6.7e-186:855:99//Hs.154934:AF000145
F-HEMBA1001939//ESTs//4.9e-34:342:77//Hs.132711:AI377295
F-HEMBA1001940//ESTs//8.6e-15:149:81//Hs.141129:R86221
F-HEMBA1001942//ESTs//0.0014:271:62//Hs.124514:AI219882
F-HEMBA1001945//EST//0.98:142:64//Hs.161540:N85943
F-HEMBA1001950//ESTs//0.99:188:64//Hs.28639:R78360
F-HEMBA1001960//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//0.30:85:69//Hs.25674:AF072242
F-HEMBA1001962//ESTs//0.0012:289:59//Hs.125492:AA938930
F-HEMBA1001964//EST//0.73:153:64//Hs.112161:AA477708
F-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/

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Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs//4.6e-156:720:99//Hs.11050:AL031178
F-HEMBA1001979//ESTs//0.86:184:67//Hs.77208:AA044732
F-HEMBA1001987//ESTs, Moderately similar to hTAFII68 [H.sapiens]//2.8e-29:151:100//Hs.124106:AA948100
F-HEMBA1001991//Homo sapiens clone 24540 mRNA sequence//0.049:121:70//Hs.153529:AF070581
F-HEMBA1002003//Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)//9.8e-09:294:63//Hs.99936:X14487
F-HEMBA1002008//ESTs//0.12:299:59//Hs.132803 :W63582
F-HEMBA1002018//PROTEIN-TYROSINE PHOSPHATASE ZETA PRECURSOR//0.98:212:64//Hs.78867:M93426
F-HEMBA1002022//Human p37NB mRNA, complete cds//0.00044:58:96//Hs.155545:U32907
F-HEMBA1002035//EST//6.4e-07:145:68//Hs.135336:AI049827
F-HEMBA1002039//EST//0.99:79:67//Hs.98451:AA426057
F-HEMBA1002049//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-26:223:81//Hs.105292:AA504776
F-HEMBA1002084
F-HEMBA1002092
F-HEMBA1002100//Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds//5.6e-21:124:96//Hs.101842:L32832
F-HEMBA1002102//ESTs, Highly similar to ANKYRIN [Mus musculus]//5.9e-09:434:62//Hs.135102:AI190276
F-HEMBA1002113//ESTs//0.049:255:63//Hs.106137:AI129973
F-HEMBA1002119
F-HEMBA1002125//H.sapiens ERF-2 mRNA//0.026:341:59//Hs.78909:U07802
F-HEMBA1002139//ESTs//0.082:309:60//Hs.36383:W52393
F-HEMBA1002144//Human mRNA for KIAA0227 gene, partial cds//5.6e-06:601:60//Hs.79170:D86980
F-HEMBA1002150//Homo sapiens mRNA for KIAA0720 protein, partial cds//5.6e-06:353:62//Hs.23741:AB018263
F-HEMBA1002151
F-HEMBA1002153//EST//0.014:328:60//Hs.149115:AI244695
F-HEMBA1002160//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//5.6e-49:303:79//Hs.158241:AB007976
F-HEMBA1002161//Myosin, heavy polypeptide 7, cardiac muscle, beta//1.2e-40:616:67//Hs.929:M57965
F-HEMBA1002162//Homo sapiens mRNA for XPR2 protein//3.4e-48:749:67//Hs.44766:AJ007590
F-HEMBA1002166//Small inducible cytokine A5 (RANTES)//2.1e-60:485:79//Hs.155464:AF088219
F-HEMBA1002177//Homo sapiens yotiao mRNA, complete cds//2.4e-19:151:86//Hs.114808:AF026245
F-HEMBA1002185//EST//0.00011:233:65//Hs.125552:AA884141
F-HEMBA1002189//EST//5.1 e-24:193:81//Hs.163161:AA778363
F-HEMBA1002191//Homo sapiens mRNA for KIAA0689 protein, partial cds//0.27:382:59//Hs.21992:AB014589
F-HEMBA1002199//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.2e-14:199:72//Hs.159897:AB007970
F-HEMBA1002204//ESTs//0.46:312:59//Hs.61210:AA024696
F-HEMBA1002212//ESTs//1.0:191:63//Hs.149752:AI285767
F-HEMBA1002215//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculus]//1.6e-47:251:96//Hs.59906:AA001281
F-HEMBA1002226//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//2.4e-57:375:71//Hs.67619:AB007957
F-HEMBA1002229//Homo sapiens KIAA0395 mRNA, partial cds//7.9e-47:377:80//Hs.43681:AL022394
F-HEMBA1002237//EST//0.044:1 37:66//Hs.144448:AA812455
F-HEMBA1002241
F-HEMBA1002253//EST//2.2e-41:219:96//Hs.137065:AA888887
F-HEMBA1002257//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds//1.1e-152:731:97//Hs.159564:AF061936
F-HEMBA1002265//ESTs//5.4e-11:337:65//Hs.112639:AI125420
F-HEMBA1002267//Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA, complete cds//1.0:395:60//Hs.150926:AF017445
F-HEMBA1002270//ESTs//2.5e-87:504:89//Hs.124440:H95404
F-HEMBA1002321//Homo sapiens oxidized low-density lipoprotein receptor mRNA, complete cds//0.17:338:60//Hs.77729:AB010710
F-HEMBA1002328//ESTs//7.9e-103:480:99//Hs.123318:AI201982

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F-HEMBA1002337//Human mRNA for KIAA0118 gene, partial cds//0.93:220:61//Hs.154326:D42087
F-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8e-187:872:98//Hs.6162:AB018314
F-HEMBA10023481/EST//1.0e-19:285:70/Ms.121860:AA776692
F-HEMBA1002349//EST//0.011:385:59//Hs.148533:AI200996
F-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//2.4e-189:872:99//Hs.119023:AF092563
F-HEMBA1002381//EST//7.9e-34:236:77//Hs.162197:AA535216
F-HEMBA1002389//ESTs//4.3e-59:342:92//Hs.133391:AA535144
F-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//2.2e-159:775:97//Hs.25527:AC005954
F-HEMBA1002419//EST, Moderately similar to ROD CGMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE BETA-SUBUNIT [H.sapiens]//1.0:144:65//Hs.136096:W27141
F-HEMBA1002430//Human clone 23695 mRNA sequence//2.7e-06:563:59//Hs.90798:U79289
F-HEMBA1002439//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//0.11:111:67//Hs.162154:AA528561
F-HEMBA1002458//ESTs, Weakly similar to hypothetical protein B, 6.8K [H.sapiens]//1.3e-71:346:98//Hs.136121:W26490
F-HEMBA1002460//ESTs//2.1e-94:484:96//Hs.106441:R53160
F-HEMBA1002462//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//0.00024:240:64//Hs.113286:U77783
F-HEMBA1002469//Human mRNA for KIAA0122 gene, partial cds//1.3e-109:603:92//Hs.154583:D50912
F-HEMBA1002475//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.025:261:63//Hs.89631:U48508
F-HEMBA1002477//Homo sapiens mRNA for KIAA0561 protein, partial cds//2.8e-45:331:83//Hs.6189:AB011133
F-HEMBA1002486//EST//0.00039:174:67//Hs.96680:AA303235
F-HEMBA1002495
F-HEMBA1002498//ESTs//1.2e-91:460:97//Hs.118327:W79161
F-HEMBA1002503//H.sapiens mRNA for MACH-alpha-2 protein//4.8e-13:164:74//Hs.19949:X98173
F-HEMBA1002508//Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.1e-79:460:83//Hs.113283:AF018080
F-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//9.0e-159:738:98//Hs.6764:AJ011972
F-HEMBA1002515//ESTs//3.6e-08:185:69//Hs.118701:AA420795
F-HEMBA1002538//ESTs//0.97:68:73//Hs.134672:AI087951
F-HEMBA1002542//Homo sapiens mRNA for chemokine LEC precursor, complete cds//6.1e-46:238:87//Hs.10458:AF088219
F-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds//1.1e-138:655:98//Hs.68900:AF016903
F-HEMBA1002552//Human Hep27 protein mRNA, complete cds//2.8e-08:173:68//Hs.102137:U31875
F-HEMBA1002555//Homo sapiens mRNA for APC 2 protein, complete cds//0.00020:603:57//Hs.20912:AB012162
F-HEMBA1002558//ESTs//6.0e-25:262:77//Hs.136304:AA431205
F-HEMBA1002561//Humanclone 23574 mRNA sequence//4.7e-17:268:72//Hs.79385:U90905
F-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds//4.3e-142:457:99//Hs.151411:AF075587
F-HEMBA1002583//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//2.8e-30:156:100//Hs.32170:AB015132
F-HEMBA1002590//ESTs//1.0e-30:277:77//Hs.139158:AA226159
F-HEMBA1002592//ESTs//2.4e-20:233:75//Hs.159329:AI378363
F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds//1.4e-176:820:99//Hs.20141:AB011169
F-HEMBA1002621//EST//0.99:208:60//Hs.159127:AI384013
F-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//9.2e-189:632:97//Hs.91338:AB018351
F-HEMBA1002628//Human mRNA for KIAA0336 gene, complete cds//0.079:231:65//Hs.125129:AB002334
F-HEMBA1002629//Human density enhanced phosphatase 1 mRNA, complete cds//1.3e-07:473:61//Hs.1177:U10886
F-HEMBA1002645//ESTs//2.6e-32:209:88//Hs.141323:N80390
F-HEMBA1002651
F-HEMBA1002659//Human vascular endothelial growth factor related protein VRP mRNA, complete cds//0.74:223:60//Hs.79141:U43142
F-HEMBA1002661//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-122:781:85//Hs.23094:M19503

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F-HEMBA1002666//ESTs//0.39:117:65//Hs.3794:T08497
F-HEMBA1002678//EST//0.0081:148:64//Hs.156768:AI351368
F-HEMBA1002679//Cyclic nucleotide gated channel (photoreceptor). cGMP gated 1 (alpha)//0.00096:418:61//Hs.1323:S42457
F-HEMBA1002688//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.8e-11:541:601/Hs.124161:AF065164
F-HEMBA10026961/Homo sapiens DNA from chromosome 19, cosmid R29144//1.9e-06:345:61//Hs.155647:AC004221
F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete cds//6.0e-12:327:62//Hs.13245:AB007924
F-HEMBA1002712
F-HEMBA1002716//EST//1.2e-56:284:97//Hs.131329:AA922800
F-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.7e-127:614:97//Hs.132942:AB014521
F-HEMBA1002730//Homo sapiens microsomal glutathione S-transferase 3 (MGST3) mRNA, complete cds//0.21:157:66//Hs.111811 :AB007867
F-HEMBA1002742//EST//0.97:138:60//Hs.160545:71596
F-HEMBA1002746//Human HOX4C mRNA for a homeobox protein//0.72:347:58//Hs.74061:X59372
F-HEMBA1002748//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.24:83:74//Hs.40806:AA018786
F-HEMBA1002750//ESTs//5.8e-37:185:76//Hs.140577:AA827817
F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//2.9e-178:834:98//Hs.74750:AB011126
F-HEMBA1002770//ESTs, Highly similar to TIP120 [R.norvegicus]//8.0e-98:492:96//Hs.11833:AI299947
F-HEMBA1002777//Homo sapiens prostate apoptosis response protein par-4 mRNA, complete cds//3.9e-05:528:59//Hs.128208:U63809
F-HEMBA1002779//ESTs//8.1e-134:662:96//Hs.107295:W80392
F-HEMBA1002780//ESTs//3.8e-41:421:74//Hs.141576:N90326
F-HEMBA1002794//Protein kinase C, mu//4.8e-06:244:67//Hs.2891:X75756
F-HEMBA1002801//ESTs//2.1e-24:182:87//Hs.124633:AA856938
F-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//3.4e-169:820:97//Hs.28307:AF071185
F-HEMBA1002816//ESTs//2.5e-91:387:94//Hs.8008:R52744
F-HEMBA1002818//Homo sapiens UPH1 (UPH1) mRNA, complete cds//7.0e-122:733:89//Hs.6059:AF093119
F-HEMBA1002826//ESTs//0.00015:235:62//Hs.119383:M279904
F-HEMBA1002833
F-HEMBA1002850//EST//0.0014:201:65//Hs.156235:AA770550
F-HEMBA1002863//ESTs//1.2e-50:295:91//Hs.57980:W68823
F-HEMBA1002876//ESTs, Weakly similar to HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II [C.elegans]//4.9e-18:110:94//Hs.13322:AA151730
F-HEMBA1002886//EST//0.99:184:65//Hs.160684:AE79429
F-HEMBA1002896//ESTs//2.1e-11:72:100//Hs.149215:AI051679
F-HEMBA1002921
F-HEMBA1002924//EST//3.7e-05:291:64//Hs.134677:AI088001
F-HEMBA1002934//ESTs//2.3e-42:324:80//Hs.141658:N77915
F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds//1.6e-174:803:99//Hs.14687:AB011148
F-HEMBA1002937//ESTs, Weakly similar to homologous to mouse gene PC326:GenBank Accession Number M95564 [H.sapiens]//8.1e-36:256:85//Hs.36899:AA130053
F-HEMBA1002939//H.sapiens mRNA for cytokine inducible nuclear protein//1.1e-05:479:59//Hs.74019:X83703
F-HEMBA1002944//Human putative endothelin receptor type B-like protein mRNA, complete cds//0.83:326:58//Hs.27747:U87460
F-HEMBA1002951//ESTs//6.1e-08:137:70//Hs.26762:AA913925
F-HEMBA1002954//ESTs//9.3e-39:249:89//Hs.146185:R19099
F-HEMBA1002968//ESTs//0.73:142:64//Hs.136371:AA506092
F-HEMBA1002970//EST//2.9e-10:103:82//Hs.162580:AA593828
F-HEMBA1002971//ESTs//3.5e-21:190:81//Hs.61170:AA454219
F-HEMBA1002973//Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)//1.5e-37:247:89//Hs.188:L20971

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F-HEMBA1002997//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//1.7e-05:797:58//Hs.50758:AF092564
F-HEMBA1002999//EST//9.9e-38:453:70//Hs.161635:W22525
F-HEMBA1003021//Small inducible cytokine A5 (RANTES)//4.6e-49:373:81//Hs.155464:AF088219
F-HEMBA1003033//ESTs//5.0e-64:340:95//Hs.154270:N26486
F-HEMBA1003034//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.4e-70:330:78//Hs.113283:AF018080
F-HEMBA1003035//Homo sapiens mRNA for testican-3//0.041:623:57//Hs.159425:AJ001454
F-HEMBA1003037//EST//0.53:59:74//Hs.148011:M268003
F-HEMBA1003041//ESTs, Weakly similar to F58G11.6 [C.elegans]//1.7e-64:337:95//Hs.l05907:AA186514
F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds//3.2e-166:777:98//Hs.44097:AF054182
F-HEMBA1003064//ESTs//3.2e-07:320:65//Hs.23466:AI223438
F-HEMBA1003067
F-HEMBA1003071//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.5e-15:611:59//Hs.124161:AF065164
F-HEMBA1003077//Homo sapiens KIAA0405 mRNA, complete cds//2.2e-29:542:62//Hs.48998:AB007865
F-HEMBA1003078//CYTOCHROME P450 IVF3//2.0e-29:452:67//Hs.106242:AB002454
F-HEMBA1003079//EST//2.0e-20:273:73//Hs.138001:AI034461
F-HEMBA1003083//EST//2.0e-48:314:86//Hs.149580:AI281881
F-HEMBA1003086//ESTs//2.6e-20:237:73//Hs.129331:AI090721
F-HEMBA1003096//ESTs, Weakly similar to HMG-box transcription factor [M.musculus]//0.98:216:61//Hs.97865:AA405872
F-HEMBA1003098//EST//2.9e-19:239:73//Hs.152366:AA486721
F-HEMBA1003117//H.sapiens ERF-2 mRNA//0.0048:447:59//Hs.78909:U07802
F-HEMBA1003129//Homo sapiens clone 24407 mRNA sequence//1.9e-06:507:58//Hs.12432:AF070575
F-HEMBA1003133//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.038:288:63//Hs.6162:AB018314
F-HEMBA1003136
F-HEMBA1003142//ESTs//3.6e-112:526:99//Hs.55982:AA284279
F-HEMBA1003148//Homo sapiens mRNA for dachshund protein//2.2e-184:850:99//Hs.63931:AJ005670
F-HEMBA1003166//Homo sapiens mRNA for KIAA0688 protein, complete cds//1.1e-24:171:83//Hs.l41874:AB014588
F-HEMBA1003175//EST//0.91:168:60//Hs.123335:AA810740
F-HEMBA1003179//EST, Weakly similar to hypothetical protein in purB 5' region [E.coli]//4.7e-20:118:97//Hs.ll8831:AA211895
F-HEMBA1003197//ESTs//0.049:265:58//Hs.153718:AI215523
F-HEMBA1003199//SOX-3 PROTEIN//0.00034:383:60//Hs.157429:X71135
F-HEMBA1003202//ESTs//7.1e-84:408:98//Hs.130134:AA905412
F-HEMBA1003204//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.6e-33:154:85//Hs.113283:AF018080
F-HEMBA1003212//ESTs//1.0e-31:159:84//Hs.134067:AI076765
F-HEMBA1003220//EST//8.6e-29:317:73//Hs.150552:AI053784
F-HEMBA1003222//ESTs//0.77:208:62//Hs.85451:AA181310
F-HEMBA1003229//EST//0.084:233:60//Hs.98176:AA417012
F-HEMBA1003235//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.00054:432:58//Hs.l32206:AF039694
F-HEMBA1003250
F-HEMBA1003257//Homo sapiens fibroblast growth factor 18 (FGF18) mRNA, complete cds//4.3e-08:426:64//Hs.49585:AF075292
F-HEMBA1003273//EST//0.00078:195:65//Hs.158019:AA867991
F-HEMBA1003276//EST//6.6e-09:159:74//Hs.162664:AA605020
F-HEMBA1003278//ESTs//0.89:257:63//Hs.23207:R42864
F-HEMBA1003281//ESTs//2.6e-33:175:98//Hs.122278:AA781867
F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1,4-galactosyltransferase mRNA, complete cds//2.9e-146:539:97//Hs.13225:AF038662
F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//1.6e-167:799:98//Hs.12836:AB011109
F-HEMBA1003296//EST//0.0013:49:97//Hs.137157:R44912
F-HEMBA1003304//ESTs//0.047:164:64//Hs.94448:AA770160
F-HEMBA1003309//ESTs//7.8e-123:589:98//Hs.l05486:AA521012

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F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//1.5e-189:865:99//Hs.124224:AB001872
F-HEMBA1003322//H.sapiens mRNA for sigma 3B protein//4.5e-49:399:80//Hs.154782:X99459
F-HEMBA1003327//EST//7.7e-10:165:72//Hs.114826:AA056254
F-HEMBA1003328//EST//0.00023:128:67//Hs.126467:AA913328
F-HEMBA1003330
F-HEMBA1003348//Human mRNA for KIAA0331 gene, complete cds//4.8e-26:256:78//Hs.146395:AB002329
F-HEMBA1003369//Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTC, and RAD23A genes, genomic sequence//0.37:187:65//Hs.80265:AD000092
F-HEMBA1003370//ESTs//8.2e-36:196:79//Hs.139158:AA226159
F-HEMBA1003373//ESTs//1.0:195:61//Hs.127307:AI263819
F-HEMBA1003376//Clathrin, light polypeptide (Lcb)//2.3e-29:606:64//Hs.73919:X81637
F-HEMBA1003380//ESTs//2.5e-21:303:70//Hs.37528:H58017
F-HEMBA1003384//ESTs//0.14:281:61//Hs.159650:N95552
F-HEMBA1003395//ESTs//0.53:121:70//Hs.144873:AI202488
F-HEMBA1003402//EST//0.029:148:66//Hs.116798:AA633813
F-HEMBA1003403//Adducin 2 (beta) {alternative products }//5.0e-05:445:61//Hs.90951:U43959
F-HEMBA1003408//ESTs//9.0e-12:87:98//Hs.70266:Z78309
F-HEMBA1003417//Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)//9.5e-05:541:58//Hs.89709:L35546
F-HEMBA1003418//ESTs//3.5e-85:399:100//Hs.154489:AA564962
F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//2.0e-149:686:99//Hs.25812:AF058696
F-HEMBA1003447//Human mRNA for KIAA0380 gene, complete cds//0.43:271:60//Hs.47822:AB002378
F-HEMBA1003461//Glycoprotein Ib (platelet), beta polypeptide//4.8e-08:775:58//Hs.3847:U59632
F-HEMBA1003463//ESTs//3.3e-22:121:99l/Hs.130847:AA058578
F-HEMBA1003480//Homo sapiens mRNA for KIAA0700 protein, partial cds//0.16:321:60//Hs.13999:AB014600
F-HEMBA1003528//ESTs//3.8e-53:315:91//Hs.129688:AA057443
F-HEMBA1003531//Human mRNA for KIAA0033 gene, partial cds//4.9e-51:451:78//Hs.22271:D26067
F-HEMBA1003538//ESTs//1.2e-82:415:96//Hs.162075:AI392811
F-HEMBA1003545//ISL1 transcription factor, LIM/homeodomain, (islet-1)//5.0e-75:736:73//Hs.505:U07559
F-HEMBA1003548//ESTs//8.7e-77:411:95//Hs.163443:R23311
F-HEMBA1003555//Human nucleotide-binding protein mRNA, complete cds//3.6e-33:562:64//Hs.81469:U01833
F-HEMBA1003556
F-HEMBA1003560//EST//3.7e-29:202:86//Hs.136858:AA767122
F-HEMBA1003568//ESTs//2.4e-06:214:65//Hs.143371:AI342327
F-HEMBA1003569//Human metastasis-associated mtal mRNA, complete cds//2.0e-58:455:66//Hs.101448:U35113
F-HEMBA1003571//ESTs//0.0025:198:63//Hs.116448:AA648972
F-HEMBA1003579//ESTs//6.0e-110:513:99//Hs.97372:AA398546
F-HEMBA1003581//ESTs, Highly similar to TALIN [Mus musculus]//3.6e-19:108:99//Hs.18420:AA599232
F-HEMBA1003591//ESTs, Weakly similar to R74.5 [C.elegans]//5.2e-85:487:92//Hs.57937:W68285
F-HEMBA1003595//Membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)//2.8e-06:439:62//Hs.83532:X59405
F-HEMBA1003597//ESTs//0.0025:200:64//Hs.8473:T40827
F-HEMBA1003598//ESTs//0.18:187:63//Hs.98641:AA429916
F-HEMBA1003615//ESTs, Highly similar to phosphorylation regulatory protein HP-10 [H.sapiens]//2.4e-133:644:97//Hs.3566:AA314782
F-HEMBA1003617//Homa sapiens mRNA for HRIHFB2157, partial cds//7.9e-171:501:97//Hs.124956:AB015344
F-HEMBA1003621//Homo sapiens protein inhibitor of activated STAT protein PIASx-alpha mRNA, complete cds//4.4e-16:161:78/IHs.111323:AF077954
F-HEMBA1003622//EST//0.0085:251:62//Hs.97343:AA401750
F-HEMBA1003630//ESTs//7.5e-05:304:61//Hs.87131:AA233159
F-HEMBA1003637//Homo sapiens homolog of the Aspergillus nidulans sudD gene product mRNA, complete cds//7.9e-26:546:63//Hs.109901:AF013591
F-HEMBA1003640//ESTs//1.1e-11:267:661/Hs.34359:AI122791
F-HEMBA1003645
F-HEMBA1003646
F-HEMBA1003656

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F-HEMBA1003662
F-HEMBA1003667//ESTs//1.5e-27:235:81//Hs.55855:AA621381
F-HEMBA1003679//ESTs//4.3e-49:251:97//Hs.152811:AA630906
F-HEMBA1003680//Human plectin (PLEC1) mRNA, complete cds//3.4e-06:464:61//Hs.79706:U53204
F-HEMBA1003684//ESTs, Weakly similar to zinc finger protein C2H2-171 [H.sapiens]//1.6e-100:478:98//Hs.118866:AI017072
F-HEMBA1003690//Homo sapiens mRNA for KIAA0600 protein, partial cds//9.5e-74:606:77//Hs.9028:AF039691
F-HEMBA1003692//ESTs//4.2e-43:252:92//Hs.39748:AA487187
F-HEMBA1003711//Homo sapiens mRNA for KIAA0544 protein, partial cds//0.81:254:62//Hs.32316:AB011116
F-HEMBA1003714//ESTs//6.4e-98:495:95//Hs.43846:N49995
F-HEMBA1003715//ESTs//1.3e-11:228:69//Hs.101237:AA708760
F-HEMBA1003720//Homo sapiens clone 23892 mRNA sequence//5.5e-45:692:68//Hs.91916:AF035317
F-HEMBA1003725//EST//2.5e-46:228:100//Hs.160069:AA926921
F-HEMBA1003729//ESTs//4.1e-48:253:96//Hs.26270:AA258839
F-HEMBA1003733//Human Line-1 repeat mRNA with 2 open reading frames//8.6e-102:753:81//Hs.23094:M19503
F-HEMBA1003742//Homo sapiens chromosome 19, cosmid R31180//0.16:242:62//Hs.153325:AC005390
F-HEMBA1003758//ESTs//9.3e-12:408:61//Hs.148459:AI198946
F-HEMBA1003760//Homo sapiens clone 23698 mRNA sequence//9.7e-35:430:69//Hs.8136:U81984
F-HEMBA1003773//EST//0.76:191:61//Hs.127020:AA934920
F-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]//1.7e-24:224:81//Hs.18171:AA524327
F-HEMBA1003784//ESTs//0.13:120:67//Hs.161993:AA503172
F-HEMBA1003799//Interleukin 9 receptor//2.0e-17:263:70//Hs.1702:L39064
F-HEMBA1003803//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.13:222:61//Hs.89230:AF031815
F-HEMBA1003804//ESTs//1.4e-112:275:98//Hs.72132:AF039239
F-HEMBA1003805//Human p62 mRNA, complete cds//1.1e-11:523:60//Hs.119537:M88108
F-HEMBA1003807//ESTs//4.1e-08:279:68//Hs.115679:AI379721
F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cds//3.3e-85:586:87//Hs.6051:AB014516
F-HEMBA1003836//EST//6.8e-06:98:74//Hs.145447:AI204220
F-HEMBA1003838//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3.8e-40:151:88//Hs.139007:H74314
F-HEMBA1003856//ESTs//8.6e-53286:95//Hs.116645:AI005167
F-HEMBA1003864//Human mRNA for KIAA0369 gene, complete cds//0.11:144:66//Hs.21355:AB002367
F-HEMBA1003866//Homo sapiens semaphorin F homolog mRNA, complete cds//4.3e-30:580:63//Hs.27621 : U52840
F-HEMBA1003879//Nuclear cap binding protein, 80kD//6.7e-10:87:95//Hs.89563:D32002
F-HEMBA1003880
F-HEMBA1003885//Homo sapiens mRNA for KIAA0752 protein, partial cds//4.2e-18:302:67//Hs.23711:AB018295
F-HEMBA1003893//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.2e-49:295:92//Hs.114673:W72675
F-HEMBA1003902//ESTs//1.1e-11:165:74//Hs.54632:AA976236
F-HEMBA1003908//Homo sapiens mRNA for KIAA0525 protein, partial cds//0.081:345:58//Hs.78494:AB011097
F-HEMBA1003926/IEST//2.5e-32:253 :83//Hs.132635:AI032875
F-HEMBA1003937//Human mRNA for KIAA0391 gene, complete cds//2.9e-38:313:69//Hs.154668:AB002389
F-HEMBA1003939//ESTs//3.4e-07:150:71//Hs.148926:R59562
F-HEMBA1003942//EST, Weakly similar to 24 KD PROTEIN [Xenopus laevis]//0.0029:222:61//Hs.l44236:W52380
F-HEMBA1003950//ESTs//0.98:200:62//Hs.163912:W20055
F-HEMBA1003953//Zinc finger protein 7 (KOX 4, clone HF.16)//0.00014:271:66//Hs.2076:M29580
F-HEMBA1003958//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.1e-44:243:76//Hs.91146:N73230
F-HEMBA1003959//ESTs//0.067:251:59//Hs.39915:H78567
F-HEMBA1003976//EST//6.7e-09:109:81//Hs.154635:AI138965
F-HEMBA1003978
F-HEMBA1003985//EST//0.32:115:69//Hs.102617:N47009
F-HEMBA1003987//ESTs//7.8e-07:60:100//Hs.66058:AA424456
F-HEMBA1003989//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//

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0.022:349:58//Hs.104640:AF000561
F-HEMBA1004000//EST//7.2e-07:200:66//Hs.119082:AA358468
F-HEMBA1004011//EST//0.019:241:62//Hs.116989:AA676493
F-HEMBA1004012//ESTs//3.6e-09:177:68//Hs.106132:AA812573
F-HEMBA1004015//ESTs//3.0e-86:407:99//Hs.115679:AI379721
F-HEMBA1004024//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.2e-51:359:84//Hs.l5519:AB018315
F-HEMBA1004038//ESTs//1.2e-58:324:94//Hs.61658:AI239930
F-HEMBA1004042//EST//0.00088:272:6l//Hs.155763:AI312281
F-HEMBA1004045//EST//2.7e-20:408:66//Hs.l62529:AA584160
F-HEMBA1004048//Transforming growth factor beta//0.026:462:57//Hs.6101:M60315
F-HEMBA1004049//ESTs//8.1e-68:430:86/JHs.146307:AA584638
F-HEMBA1004055//Human chromosome 3p21.1 gene sequence//1.5e-10:457:58//Hs.82837:L13435
F-HEMBA1004056//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//1.5e-46:199:80//Hs.46328:D87942
F-HEMBA1004074//ESTs//3.0e-23:219:74//Hs.70279:AA757426
F-HEMBA1004086//EST//0.36:189:62//Hs.156218:AA770107
F-HEMBA1004097//NADH-CYTOCHROME B5 REDUCTASE//1.0:302:57//Hs.75666:M28713
F-HEMBA1004111//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.3e-39:335:79//Hs.46468:U45984
F-HEMBA1004131//Human mRNA for KIAA0202 gene, partial cds//1.9e-24:610:61//Hs.80712:D86957
F-HEMBA1004132//EST//3.5e-06:143:70//Hs.136799:AA780064
F-HEMBA1004133//ESTs//1.0:157:68//Hs.161226:AI419759
F-HEMBA1004138//H.sapiens mRNA for RanGTPase activating protein 1//0.00055:343:62//Hs.5923:X82260
F-HEMBA1004143
F-HEMBA1004146
F-HEMBA1004150//EST//0.0046:402:57//Hs.147027:AI186056
F-HEMBA1004164//Homo sapiens mRNA for KIAA0798 protein, complete cds//1.8e-15:591:60//Hs.159277:AB018341
F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//1.5e-134:649:97//Hs.59988:AF067855
F-HEMBA1004199
F-HEMBA1004200//ESTs//0.0083:150:66//Hs.116424:AI375427
F-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays]//1.2e-35:205:94//Hs.10092:AI189282
F-HEMBA1004203//ESTs//3.9e-14:237:70//Hs.118273:AA626040
F-HEMBA1004207//Leptin receptor//1.1e-167:791:98//Hs.54515:U50748
F-HEMBA1004225//ESTs//0.00087:231:64//Hs.13109:AA192514
F-HEMBA1004227//ESTs, Weakly similar to F55A11.4 [C.elegans]//0.012:156:67//Hs.l63588:AI073878
F-HEMBA1004238
F-HEMBA1004241//ESTs//8.7e-05:51:96//Hs.162826:AA679571
F-HEMBA1004246//EST//1.2e-36:198:96//Hs.121343:AA758522
F-HEMBA1004248//Homo sapiens insulin induced protein 1 (INSIG1) gene, complete cds//1.1e-28:295:72//Hs.56205:U96876
F-HEMBA1004264//Human HCF1 gene related mRNA sequence//3.1e-07:553:60//Hs.83634:U52112
F-HEMBA1004267//Homo sapiens mRNA for KIAA0688 protein, complete cds//4.9e-73:490:77//Hs.141874:AB014588
F-HEMBA1004272
F-HEMBA1004274//EST//0.43:154:61//Hs.125347:AA876444
F-HEMBA1004275//Human mRNA for KIAA0333 gene, partial cds//0.71:118:65//Hs.155313:AB002331
F-HEMBA1004276//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.0:364:56//Hs.118738:AB018343
F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds//6.9e-187:868:99//Hs.101766:AF022795
F-HEMBA1004289
F-HEMBA1004295//EST//0.20:149:62//Hs.162415:AA573484
F-HEMBA1004306//ESTs//0.041:177:64//Hs.158234:AI270047
F-HEMBA1004312//ESTs//0.83:253:59//Hs.121898:AI336314
F-HEMBA1004321//Zinc finger protein 136 (clone pHZ-20)//2.3e-40:452:65//Hs.69740:U09367
F-HEMBA1004323//EST//0.44:134:64//Hs.145464:AI204532

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F-HEMBA1004327//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//0.017:209:64//Hs.43627:U35612
F-HEMBA1004330//ESTs//4.5e-27:171:91//Hs.112838:AA614062
F-HEMBA1004334//EST//2.4e-53:556:75//Hs.139093:AA166888
F-HEMBA1004335//Homo sapiens mRNA for KIAA0706 protein, complete cds//0.49:80:73//Hs.139648:AB014606
F-HEMBA1004341
F-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds//2.7e-39:270:86//Hs.80686:D89667
F-HEMBA1004354//Human CHL1 potential helicase (CHLR1), complete cds//1.3e-46:190:92//Hs.27424:U75968
F-HEMBA1004356//Thyrotropin-releasing hormone receptor//0.15:296:62//Hs.3022:D85376
F-HEMBA1004366//ESTs, Weakly similar to transposon LRE2 reverse transcriptase homolog [H.sapiens]//7.8e-10:396:61//Hs.33688:AA020928
F-HEMBA1004372//ESTs//0.90:172:62//Hs.145611:R68800
F-HEMBA1004389//Zinc finger protein 148 (pHZ-52)//8.0e-28:359:67//Hs.112180:AF039019
F-HEMBA1004394//ESTs//0.023:357:58//Hs.47212:N51250
F-HEMBA1004396//EST//3.4e-22:244:74//Hs.162554:AA584818
F-HEMBA1004405//EST//4.0e-43:214:100//Hs.33100:H42199
F-HEMBA1004408//ESTs, Weakly similar to The ha1539 protein is related to cyclophilin. [H.sapiens]/1.4e-20:144:88//HS.121076:AI246426
F-HEMBA1004429//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//4.8e-18:248:72//Hs.69747:M35531
F-HEMBA1004433//Small inducible cytokine A5 (RANTES)//8.2e-39:248:81//Hs.155464:AF088219
F-HEMBA1004460//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-87:650:81//Hs.113283:AF018080
F-HEMBA1004461//ESTs//0.057:217:61//Hs.26989:Z41606
F-HEMBA1004479//Homo sapiens clone 23698 mRNA sequence//4.9e-17:223:71//Hs.8136:U81984
F-HEMBA1004482//EST//0.0056:261:59//Hs.45012:N39450
F-HEMBA1004499//ESTs//4.1e-68:340:97//Hs.134266:AA992600
F-HEMBA1004502//ESTs//7.7e-32:195:91//Hs.134906:H93431
F-HEMBA1004506//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-89:758:76//Hs.23094:M19503
F-HEMBA1004507//ESTs, Weakly similar to T19B10.6 [C.elegans]//1.4e-61:296:99//Hs.114622:AA693492
F-HEMBA1004509//Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds//0.014:265:61//Hs.43543:AF042800
F-HEMBA1004534//Filamin 1 (actin-binding protein-280)//5.0e-74:678:74//Hs.76279:X53416
F-HEMBA1004538//EST//0.00047:268:58//Hs.136870:AA805381
F-HEMBA1004542//Human butyrophilin protein (BT3.3) mRNA, partial cds//0.74:74:75//Hs.87497:U90552
F-HEMBA1004554
F-HEMBA1004560//ESTs//3.1e-19:240:73//Hs.112637:AA805331
F-HEMBA1004573//EST//2.4e-59:290:99//Hs.112908:AA620802
F-HEMBA1004577//ESTs, Weakly similar to UTR1 PROTEIN [S.cerevisiae]//1.2e-17:334:67//Hs.24536:AA479825
F-HEMBA1004586//Von Hippel-Lindau syndrome//5.1 e-35:337:78//Hs.78160:AF010238
F-HEMBA1004596//ESTs//3.3e-32:189:94//Hs.42530:N41661
F-HEMBA1004604//Human hindlimb expressed homeobox protein backfoot (Bft) mRNA, complete cds//0.42:186:66//Hs.84136:1170370
F-HEMBA1004610//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.3e-16:297:68//Hs.106008:AA147606
F-HEMBA1004617//EST//0.027:188:61//Hs.l59094:AI383198
F-HEMBA1004629//ESTs//7.8e-09:348:63//Hs.138358:T66178
F-HEMBA1004631//EST//0.0012:268:60//Hs.150685:AA923416
F-HEMBA1004632//ESTs//0.82:125:67//Hs.143619:AI360891
F-HEMBA1004637//ESTs//0.0034:229:64//Hs.157178:AI346780
F-HEMBA1004638//ESTs//2.0e-11:166:71//Hs.128657:AI017522
F-HEMBA1004666//EST//0.44:294:58//Hs.44780:N36083
F-HEMBA1004669//ESTs//1.7e-28:200:86//Hs.8084:W22796
F-HEMBA1004670//Mucin 1, transmembrane//0.060:416:57//Hs.89603:J05582
F-HEMBA1004672//ESTs//0.27:44:95//Hs.86237:AA206141
F-HEMBA1004693//ESTs//5.3e-55:301:95//Hs.159066:AI093252
F-HEMBA1004697//H.sapiens mRNA for ribosomal protein L18a homologue//0.64:313:61//Hs.118578:X80821

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F-HEMBA1004705//Homo sapiens KIAA0432 mRNA, complete cds//4.5e-19:230:73//Hs.155174:AB007892
F-HEMBA1004709//ESTs//3.1e-31:176:88//Hs.152413:AA780515
F-HEMBA1004711//Cholinergic receptor, nicotinic, delta polypeptide//1.0:244:57//Hs.99975:X55019
F-HEMBA1004725//Homo sapiens agrin precursor mRNA, partial cds//0.24:328:60//Hs.68900:AF016903
F-HEMBA1004730//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5.9e-32:476:70//Hs.116874:AA524909
F-HEMBA1004733//ESTs//3.8e-16:96:79//Hs.152413:AA780515
F-HEMBA1004734//Human epidermoid carcinoma mRNA for ubiquitin-conjugating enzyme E2 similar to Drosophila bendless gene product, complete cds//0.16:329:58//Hs.75355:D83004
F-HEMBA1004736//Human Line-1 repeat mRNA with 2 open reading frames//2.0e-61:663:71//Hs.23094:M19503
F-HEMBA1004748//ESTs//1.5e-05:343:63//Hs.42241:H96813
F-HEMBA1004751//ESTs//3.7e-32:147:80//Hs.138788:N54504
F-HEMBA1004752//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.00020:521:59//Hs.91400:AB006626
F-HEMBA1004753//Homo sapiens DEC-205 mRNA, complete cds//5.1e-46:337:84//Hs.153563:AF011333
F-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds//3.1e-24:416:65//Hs.76460:U49082
F-HEMBA1004758//Homosapiens transcription factor SL1 mRNA, complete cds//1.2e-136:769:91//Hs.153088:L39060
F-HEMBA1004763//Loricrin//0.0018:227:62//Hs.155657:M61120
F-HEMBA1004768//Human Line-1 repeat mRNA with.2 open reading frames//4.5e-115:909:78//Hs.23094:M19503
F-HEMBA1004770//Human Rad50 (Rad50) mRNA, complete cds//0.020:728:57//Hs.41587:U63139
F-HEMBA1004771
F-HEMBA1004776//ESTs, Weakly similar to progesterone receptor-related protein p23 [H.sapiens]//1.0:158:63//Hs.62004:AF039235
F-HEMBA1004778//ESTs//1.2e-70:336:99//Hs.113052:AI222106
F-HEMBA1004795
F-HEMBA1004803//ESTs//5.0e-75:454:88//Hs.138632:H97952
F-HEMBA1004806//EST//0.080:142:65//Hs.160268:AI148971
F-HEMBA1004807//Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3//4.5e-48:171:92//Hs.134510:L01042
F-HEMBA1004816//EST//1.0e-17:175:71//Hs.140680:AA873646
F-HEMBA1004820//ESTs//1.3e-136:629:99//Hs.160726:AI300481
F-HEMBA1004847//ESTs//2.1 e-09:66:98//Hs.158161:AA312511
F-HEMBA1004850//EST//0.033:253:64//Hs.158782:A376601
F-HEMBA1004863//Homo sapiens mRNA for KIAA0578 protein, partial cds//0.83:179:62//Hs.22998:AB011150
F-HEMBA1004864//ESTs, Weakly similar to ANON-66Db [D.melanogaster]//1.7e-13:81:100//Hs.75884:AA446987
F-HEMBA1004865//ESTs//0.92:148:65//Hs.126980:AA934077
F-HEMBA1004880//H.sapiens mRNA for retrotransposon//1.2e-30:264:79//Hs.6940:Z48633
F-HEMBA1004889//Growth arrest-specific l//0.20:146:68/Hs.65029:L13698
F-HEMBA1004900//ESTs//1.6e-32:196:93//Hs.132032:R85304
F-HEMBA1004909//ESTs//3.4e-13:154:75//Hs.151467:N51106
F-HEMBA1004918//EST//0.78:122:61//Hs.145491:AI254348
F-HEMBA1004923//ELK1, member of ETS oncogene family//1.6e-40:340:79//Hs.116549:AL009172
F-HEMBA1004929//Cardiac gap junction protein//0.0048:588:57//Hs.74471:X52947
F-HEMBA1004930//ESTs//1.5e-17:227:74//Hs.148739:AI224959
F-HEMBA1004933//Human pseudoautosomal homeodomain-containing protein (PHOG) mRNA, complete cds//0.11:182:65//Hs.105932:U89331
F-HEMBA1004934
F-HEMBA1004944//EST//1.2e-67:349:96//Hs.162281:AA553981
F-HEMBA1004954//ESTs//0.0i4:404:60//Hs.11177:AA417813
F-HEMBA1004956//EST//2.3e-05:208:64//Hs.146958:AI174478
F-HEMBA1004960//ESTs//0.79:169:62//Hs.11637:W03274
F-HEMBA1004972
F-HEMBA1004973//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.073:574:58//Hs.154139:AB007914
F-HEMBA1004977//EST//4.4e-12:86:94//Hs.157819:AI361946

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F-HEMBA1004978//ESTs//0.097:337:60//Hs.114157:AA703013
F-HEMBA1004980//EST//3.2e-10:169:65//Hs.149123:AI244750
F-HEMBA1004983//EST//0.93:85:71//Hs.162267:AA553589
F-HEMBA1004995//ESTs//0.46:296:61//Hs.135168:AI394026
F-HEMBA1005008//ESTs//1.5e-20:156:85//Hs.114140:U35429
F-HEMBA1005009//Homo sapiens chromosome 7q22 sequence//1.5e-52:379:72//Hs.151887:AF053356
F-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//4.5e-148:693:98//Hs.31921:AB014548
F-HEMBA1005029//Homo sapiens mRNA for KIAA0660 protein, complete cds//1.0:215:65//Hs.6727:AB014560
F-HEMBA1005035//ESTs, Weakly similar to HYPOTHETICAL 82.8 KD PROTEIN B0303.4 IN CHROMOSOME III [C.elegans]//9.4e-106:503:98//Hs.21362:AF039237
F-HEMBA1005039//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//5.8e-60:272:89//Hs.103948:K00627
F-HEMBA1005047//Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA, complete cds//0.078:442:59//Hs.100602:AF010193
F-HEMBA1005050//H.sapiens ERF-2 mRNA//0.0025:251:63//Hs.78909:U07802
F-HEMBA1005062//ESTs//0.020:268:59//Hs.146181:AI264462
F-HEMBA1005066//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//1.5e-59:411:85//Hs.129727:AF035587
F-HEMBA1005075//Human mRNA for KIAA0383 gene, partial cds//0.00010:395:57//Hs.27590:AB002381
F-HEMBA1005079//Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex)//3.5e-26:344:72//Hs.89479:X66785
F-HEMBA1005083//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.59:631:59//Hs.27910:AF049105
F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//4.1e-163:762:98//Hs.11170:AF080561
F-HEMBA1005113//ESTs//0.52:109:68//Hs.106330:AI031916
F-HEMBA1005123//Homo sapiens mRNA for KIAA0761 protein, partial cds//1.3e-52:468:78//Hs.93121:AB018304
F-HEMBA1005133//ESTs//1.6e-27:366:73//Hs.151467:N51106
F-HEMBA1005149//EST//3.3e-37:304:80//Hs.132635:AI032875
F-HEMBA1005152//ESTs//3.9e-09:285:62//Hs.155876:AA593021
F-HEMBA1005159//EST//8.4e-05:289:64//Hs.125563:AA884216
F-HEMBA1005185//ESTs//1.4e-22:129:96//Hs.14920:AA910914
F-HEMBA1005201//EST//4.0e-16:96:98//Hs.89002:AA282197
F-HEMBA1005202
F-HEMBA1005206//Homo sapiens sox1 gene//0.0079:431:58//Hs.144029:Y13436
F-HEMBA1005219//ESTs//4.3e-47:299:88//Hs.5019:W26547
F-HEMBA1005223//ESTs//0.00030:168:66//Hs.76487:N37081
F-HEMBA1005232//EST//0.0078:209:61//Hs.46852:N48302
F-HEMBA1005241//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//6.0e-54:399:79//Hs.129735:AF010144
F-HEMBA1005244//ESTs//2.5e-14:85:10011Hs,128744:AI191922
F-HEMBA1005251//ESTs//0.012:49:95//Hs.161554:AA393896
F-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//4.7e-151:705:98//Hs.72660:AB011157
F-HEMBA1005274//ESTs//7.1e-09:298:64//Hs.145522:AI261380
F-HEMBA1005275//ESTs//7.9e-13:375:63//Hs.148974:AA001777
F-HEMBA1005293//Homo sapiens clone 23662 mRNA sequence//7.7e-22:338:65//Hs.12451:U97018
F-HEMBA1005296//ESTs//0.055:299:60//Hs.86320:AI149232
F-HEMBA1005304//Small inducible cytokine A5 (RANTES)//1.7e-45:322:85//Hs.155464:AF088219
F-HEMBA1005311
F-HEMBA1005314//ESTs//8.1e-39:199:98//Hs.119974:AI279516
F-HEMBA1005315//ESTs//1.9e-07:266:64//Hs.141440:N21615
F-HEMBA1005318//ESTs//5.3e-06:161:72//Hs.119411:AA937117
F-HEMBA1005331//Human checkpoint suppressor 1 mRNA, complete cds//0.00075:310:63//Hs.111597:U68723
F-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial//4.4e-153:740:97//Hs.29361:AJ007581
F-HEMBA1005353//EST//5.4e-09:2-22:68//Hs.119508:AA485732
F-HEMBA1005359//Zinc finger protein 137 (clone pHZ-30)//5.7e-100:500:88//Hs.151689:U09414
F-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds//2.5e-70:572:73//Hs.43265:

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AF071787
F-HEMBA1005372//ESTs//0.00045:163:66//Hs.164058:AI417905
F-HEMBA1005374//Human melanoma antigen recognized by T-cells (MART-1) mRNA//6.1e-43:341:81//Hs.154069:U06452
F-HEMBA1005382//EST//2.4e-32:167:99//Hs.147186:AI93053
F-HEMBA1005389//ESTs//0.0021:245:59//Hs.104463:AA804448
F-HEMBA1005394//ESTs, Weakly similar to No definition line found [C.elegans]//1.0e-130:620:98//Hs.108990:N25951
F-HEMBA1005403//ESTs, Weakly similar to No definition line found [C.elegans]//7.7e-151:727:97//Hs.17118:AI033807
F-HEMBA1005408//ESTs//3.2e-70:426:89//Hs.158078:H24513
F-HEMBA1005410//EST//2.5e-25:460:67//Hs.138765:N70347
F-HEMBA1005411
F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//3.3e-171:537:99//Hs.4854:AF041248
F-HEMBA1005426//EST//1.0:148:64//Hs.44469:N33323
F-HEMBA1005443//Zinc finger protein 157 (HZF22)//9.0e-34:259:72//Hs.89897:U28687
F-HEMBA1005447//EST//3.9e-10:211:70//Hs.145960:AI276783
F-HEMBA1005468//ESTs//8.4e-53:390:81//Hs.152395:AA533107
F-HEMBA1005469//Human (clone E5.1) RNA-binding protein mRNA, complete cds//3.1e-29:155:99//Hs.75104:L37368
F-HEMBA1005472//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-88:481:92//Hs.23094:M19503
F-HEMBA1005474//Small inducible cytokine A5 (RANTES)//4.2e-29:257:78//Hs.155464:AF088219
F-HEMBA1005475//Homo sapiens antigen NY-CO-16 mRNA, complete cds//5.3e-09:414:60//Hs.132206:AF039694
F-HEMBA1005497//Glucocorticoid receptor alpha { alternative products}//8.7e-41:588:69//Hs.102761:U25029
F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21//1.1e-28:318:73//Hs.159530:AC004957
F-HEMBA1005506//Human mRNA for KIAA0010 gene, complete cds//0.67:351:58//Hs.155287:D13635
F-HEMBA1005508//ESTs//0.45:326:59//Hs.102756:AA526911
F-HEMBA1005511//Human mRNA for KIAA0355 gene, complete cds//4.2e-49:400:79//Hs.153014:AB002353
F-HEMBA1005513//ESTs, Weakly similar to males-absent on the first [D.melanogaster]//5.3e-76:378:97//Hs.22767:N99220
F-HEMBA1005517//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds//0.54:623:56//Hs.143551:AF048693
F-HEMBA1005518//ESTs//0.10:207:60//Hs.72447:AA160575
F-HEMBA1005520//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.1e-55:288:85//Hs.144563:AF057280
F-HEMBA1005526//Small inducible cytokine A5 (RANTES)//5.4e-48:176:76//Hs.155464:AF088219
F-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//1.2e-30:166:96//Hs.17035:AI080471
F-HEMBA1005530
F-HEMBA1005548//Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds//4.6e-18:391:64//Hs.30250:AF055376
F-HEMBA1005552//ESTs//1.8e-46:238:88//Hs.138856:H47461
F-HEMBA1005558//Human involucrin mRNA//3.0e-07:501:60//Hs.157091:M13903
F-HEMBA1005568//ESTs//0.013:259:63//Hs.13669:H47257
F-HEMBA1005570//ESTs//0.0084:442:59//Hs.125384:AI346507
F-HEMBA1005576//Homo sapiens mRNA for KIAA0463 protein, partial cds//1.9e-128:610:98//Hs.77738:AB007932
F-HEMBA1005577//ESTs//0.98:199:61//Hs.146226:AI312873
F-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//9.1e-53:830:64//Hs.57929:AB011538
F-HEMBA1005582
F-HEMBA1005583
F-HEMBA1005588//ESTs//1.3e-35:386:70//Hs.55855:AA621381
F-HEMBA1005593//S-ADENOSYLMETHIONINE SYNTHETASE ALPHA AND BETA FORMS//0.54:439:591/Hs.2137:D49357
F-HEMBA1005595//Human mRNA for KIAA0325 gene, partial cds//5.5e-06:378:57//Hs.7720:AB002323

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F-HEMBA1005606//EST//2.0e-60:324:94//Hs.5062:D19609
F-HEMBA1005609//ESTs//6.0e-39:378:76//Hs.142242:H06982
F-HEMBA1005616//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//8.2e-22:721:61//Hs.144563:AF057280
F-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]//1.8e-89:454:96//Hs.19400:AA662845
F-HEMBA1005627//EST//1.0:161:60//Hs.162765:AA622535
F-HEMBA1005631//EST//0.74:124:62//Hs.156185:AA723734
F-HEMBA1005632//ESTs//1.0:96:70//Hs.141321:N70199
F-HEMBA1005634//EST//6.6e-10:105:73//Hs.159692:AI416956
F-HEMBA1005666
F-HEMBA1005670//Homo sapiens mRNA for KIAA0570 protein, complete cds//2.7e-45:255:79//Hs.114293:AB011142
F-HEMBA1005679//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//1.2e-37:356:77//Hs.139107:K00629
F-HEMBA1005680
F-HEMBA1005685
F-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//3.3e-71:497:85//Hs.26988:U66406
F-HEMBA1005705//ESTs//0.00093:149:65//Hs.163564:R43678
F-HEMBA1005717//EST//0.018:115:66//Hs.160541:AI270143
F-HEMBA1005732//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)//2.6e-20:151:88//Hs.77393:D14697
F-HEMBA1005737//ESTs//9.5e-34:235:88//Hs.160197:AA393754
F-HEMBA1005746//ESTs//0.20:260:59//Hs.112451:AI264024
F-HEMBA1005755//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//1.8e-48:425:78//Hs.103948:K00627
F-HEMBA1005765//Small inducible cytokine A5 (RANTES)//1.3e-36:280:81//Hs.155464:AF088219
F-HEMBA1005780//ESTs//1.0:139:67//Hs.88684:AA885141
F-HEMBAI0058131/ESTs//0.012:209:63//Hs.113365:R77747
F-HEMBA1005815//Human calpain-like protease (htra-3) mRNA, complete cds//2.0e-07:439:62//Hs.6133:U94346
F-HEMBA1005822//ESTs//9.3e-06:444:59//Hs.124344:T10577
F-HEMBA1005829//ESTs//1.1e-47:394:80//Hs.146811:AA410788
F-HEMBA1005834//Human Line-1 repeat mRNA with 2 open reading frames//7.9e-42:690:66//Hs.23094:M19503
F-HEMBA1005852//Human plectin (PLEC1) mRNA, complete cds//0.17:470:56//Hs.79706:U53204
F-HEMBA1005853//EST//0.013:211:60//Hs.162604:AA595150
F-HEMBA1005884//Homosapiens mRNA, chromosome 1 specific transcript KIAA0484//1.4e-53:332:83//Hs.158095:AB007953
F-HEMBA1005891//ESTs//1.1e-77:393:97//Hs.28545:AI268097
F-HEMBA1005894//Human G protein-coupled receptor (STRL22) mRNA, complete cds//7.2e-45:411:77//Hs.46468:U45984
F-HEMBA1005909//Human neuropeptide y2 receptor mRNA, complete cds//0.00054:477:59//Hs.37125:U42766
F-HEMBA1005911//Thromboxane A2 receptor//4.1e-45:419:75//Hs.89887:D38081
F-HEMBA1005921//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//2.0e-46:434:78//Hs.125231:AF068006
F-HEMBA1005931//ESTs, Weakly similar to kruppel-related zinc finger protein [H.sapiens]//1.2e-46:228:100//Hs.152178:AI224880
F-HEMBA1005934//EST//3.1e-14:121:85//Hs.150003:AI291588
F-HEMBA1005962//EST//0.0010:212:62//Hs.163197:AA767883
F-HEMBA1005963
F-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//4.2e-151:697:99//Hs.26285:AF082516
F-HEMBA1005991//EST//3.0e-07:361:59//Hs.146442:AI127530
F-HEMBA1005999//EST//1.2e-14:350:66//Hs.122326:AA782526
F-HEMBA1006002
F-HEMBA1006005//ESTs, Weakly similar to TH1 protein [D.melanogaster]//0.98:197:61//Hs.5184:AA709151
F-HEMBA1006031
F-HEMBA1006035
F-HEMBA1006036//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.4e-92:617:84//Hs.113283:AF018080
F-HEMBA1006042//ESTs//6.3e-41:161:81//Hs.41186:R99609

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F-HEMBA1006067//ESTs//2.0e-74:354:99//Hs.43321:AI139422
F-HEMBA1006081
F-HEMBA1006090//EST//1.2e-12:340:62//Hs.61195:AI418788
F-HEMBA1006091//ESTs//4.7e-98:473:98//Hs.9658:AA506313
F-HEMBA1006100//ESTs//7.1 e-22:273:73//Hs.144407:AA737799
F-HEMBA1006108//ESTs, Weakly similar to ZK792.1 [C.elegans]//2.1e-26:273:66//Hs.8763:W30741
F-HEMBA1006121//EST//0.00012:232:59//Hs.117096:AA677968
F-HEMBA1006124//EST//0.047:251:62//Hs.132257:AI027222
F-HEMBA1006130//Human HOX4C mRNA for a homeobox protein//1.0:150:62//Hs.74061:X59372
F-HEMBA1006138//ESTs//1.8e-27:132:84//Hs.141575:AA211734
F-HEMBA1006142//EST//2.5e-47:310:87//Hs.149580:AI281881
F-HEMBA1006155
F-HEMBA1006158//ESTs//5.1e-105:506:98//Hs.93468:N40575
F-HEMBA1006173//ESTs//2.5e-24:195:84//Hs.79092:H29627
F-HEMBA1006182//ESTs//2.5e-19:237:72//Hs.141840:AA028117
F-HEMBA1006198//ESTs//0.017:133 :67//Hs.142168:AA292540
F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//8.6e-177:836:98//Hs.109268:AF070557
F-HEMBA1006248//Human zinc finger protein (MAZ) mRNA//0.0014:221:67//Hs.7647:M94046
F-HEMBA1006252
F-HEMBA1006253//EST//1.3e-100:467:100//Hs.146619:AI140706
F-HEMBA1006259//Homo sapiens mRNA for KIAA0798 protein, complete cds//0.00037:158:69//Hs.159277:AB018341
F-HEMBA1006268//ESTs//1.1e-20:376:67//Hs.72814:AA706631
F-HEMBA1006272//EST//4.8e-20:252:69//Hs.162992:AA688140
F-HEMBA1006278//H.sapiens PAP mRNA//6.5e-57:610:71//Hs.49007:X76770
F-HEMBA1006283
F-HEMBA1006284//ESTs//0.00017:248:63//Hs.143840:AI189964
F-HEMBA1006291
F-HEMBA1006293
F-HEMBA1006309//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA, complete cds//0.76:416:58//Hs.46465:U45285
F-HEMBA1006310//Homo sapiens mRNA for KIAA0602 protein, partial cds//9.3e-49:637:68//Hs.37656:AB011174
F-HEMBA1006328//ESTs//1.8e-71:429:88//Hs.139922:AA281350
F-HEMBA1006334//EST//0.082:267:57//Hs.136449:AA572789
F-HEMBA1006344//ESTs//6.2e-08:67:94//Hs.42302:AI032142
F-HEMBA1006347//ESTs, Weakly similar to males-absent on the first [D.melanogaster]//5.3e-76:378:97//Hs.22767:N99220
F-HEMBA1006349//ESTs//0.87:276:60//Hs.23628:H03287
F-HEMBA1006359//Zinc finger protein 43 (HTF6)//4.4e-117:823:81//Hs.74107:X59244
F-HEMBA1006364//EST//0.0012:168:66//Hs.156756:AI351026
F-HEMBA1006377//Homo sapiens RalBP1-interacting protein (POB1) mRNA, complete cds//0.0028:422:59//Hs.80667:AF010233
F-HEMBA1006380//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds//0.41:265:61//Hs.8813:AF032922
F-HEMBA1006381//ESTs//3.8e-78:382:98//Hs.132171:AI042531
F-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//2.1e-49:395:80//Hs.23094:M19503
F-HEMBA1006416//EST//7.3e-12:154:77//Hs.134086:AI077477
F-HEMBA1006419//EST//4.6e-51:179:86//Hs.149580:AI281881
F-HEMBA1006421//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.9e-46:517:72//Hs.51048:X68830
F-HEMBA1006424//ESTs//2.7e-08:380:60//Hs.44369:AI206835
F-HEMBA1006426//ESTs//3.0e-98:465:99//Hs.129251:AA993264
F-HEMBA1006438//EST//1.3e-29:183:93//Hs.147412:AI209194
F-HEMBA1006445
F-HEMBA1006446//EST//0.14:200:59//Hs.160695:AI282889
F-HEMBA1006461//Thiopurine S-methyltransferase//1.4e-29:210:72//Hs.51124:AF019369
F-HEMBA1006467
F-HEMBA1006471//ESTs//1.4e-05:391:60//Hs.121282:AI091453
F-HEMBA1006474//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]//1.1e-13:346:63//Hs.31257:

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AA875998
F-HEMBA1006483//Thromboxane A2 receptor//2.2e-51:386:82//Hs.89887:D38081
F-HEMBA1006485//EST//5.4e-111:516:99//Hs.61925:AA039532
F-HEMBA1006486//EST//4.7e-23:286:72//Hs.137800:AA886897
F-HEMBA1006489//ESTs//2.5e-06:137:71//Hs.28621:AA910431
F-HEMBA1006492
F-HEMBA1006494//ESTs//8.5e -24:299:72//Hs.153413:AI248625
F-HEMBA1006497//EST//0.00034:431:61//Hs.130057:AA903389
F-HEMBA1006502//ESTs//2.6e-11:131:80//Hs.141267:H22072
F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//7.3e-141:470:98//Hs.153858:AB014566
F-HEMBA1006521//ESTs, Weakly similar to 3-oxoacyl-[acyl-carrier protein] reductase [E.coli]//3.9e-98:483:97//Hs.94811:AA011185
F-HEMBA1006530//EST//1.7e-42:530:71//Hs.163207:AA808002
F-HEMBA1006535//ESTs//2.9e-84:404:98//Hs.128679:AI160081
F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//4.4e-173:654:98//Hs21301:AF093419
F-HEMBA1006546//ESTs//2.8e-45:391:78//Hs.146307:AA584638
F-HEMBA1006559//Homo sapiens KIAA0438 mRNA, complete cds//2.1e-47:363:79//Hs.21490:AB007898
F-HEMBA1006562//ESTs//4.5e-09:116:75//Hs.142368:AI198425
F-HEMBA1006566//EST//0.85:100:68//Hs.13052:T67136
F-HEMBA1006569//ESTs//2.7e-06:213:64//Hs.44372:AI346522
F-HEMBA1006579//EST//0.064:160:62//Hs.126244:AA873479
F-HEMBA1006583//Homo sapiens Jagged 2 mRNA, complete cds//1.7e-07:533:60//Hs.106387:AF029778
F-HEMBA1006595//Small inducible cytokine A5 (RANTES)//6.8e-69:328:81//Hs.155464:AF088219
F-HEMBA1006597//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.6e-38:441:69//Hs.23711:AB018295
F-HEMBA1006612//ESTs//8.8e-135:668:97//Hs.7942:AA205862
F-HEMBA1006617//EST//4.6e-31:254:81//Hs.132635:AI032875
F-HEMBA1006624//ESTs, Weakly similar to HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION [S.cerevisiae]//2.5e-75:379:97//Hs.40911:AI391502
F-HEMBA1006631//ESTs//1.4e-126:612:98//Hs.131737:AI343331
F-HEMBA1006635//EST//0.65:145:63//Hs.104560:AA340589
F-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]//9.1e-27:170:92//Hs.109818:AA411185
F-HEMBA1006643//ESTs, Moderately similar to putative p150 [H.sapiens]//9.7e-05:259:65//Hs.105747:AA505003
F-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//3.9e-28:108:93//Hs.6196:U40282
F-HEMBA1006652//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L7 [Drosophila melanogaster]//3.0e-87:452:96//Hs.159574:AA190615
F-HEMBA1006653
F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//2.9e-92:438:98//Hs.8173:AC005189
F-HEMBA1006665//Homo sapiens clone 23892 mRNA sequence//2.8e-18:180:80//Hs.91916:AF035317
F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56//1.6e-16:122:90//Hs.5092:Y12065
F-HEMBA1006676
F-HEMBA1006682//EST//0.12:193:61//Hs.128367:AA974575
F-HEMBA1006695//ESTs//5.6e-27:110:80//Hs.159510:AA297145
F-HEMBA1006696//EST//3.2e-12:160:75//Hs.146472:AI128198
F-HEMBA1006708
F-HEMBA1006709//ESTs//0.69:60:80//Hs.152752:AA643545
F-HEMBA1006717//ESTs/12.6e-31:286:78//Hs.55573:W37226
F-HEMBA1006737//ESTs//1.6e-37:189:99//Hs.97490:AA394105
F-HEMBA1006744//Human mRNA for KIAA0118 gene, partial cds//1.9e-52:360:84//Hs.154326:D42087
F-HEMBA1006754//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//2.0e-92:817:78//Hs.129727:AF035587
F-HEMBA1006758//Human mRNA for KIAA0327 protein, complete cds//4.0e-10:576:56//Hs.149323:AB002325
F-HEMBA1006767//ESTs//1.7e-18:252:72//Hs141073:W72720
F-HEMBA1006779//EST//9.1e-26:395:69//Hs.145366:AI252657

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F-HEMBA1006780//EST//1.0:93:69//Hs.116946:AA680250
F-HEMBA1006789//ESTs//0.0060:276:59//Hs.144121:AI369798
F-HEMBA1006795//Human Line-1 repeat mRNA with 2 open reading frames//4.1e-37:781:64//Hs.23094:M19503
F-HEMBA1006796//Human clone 23803 mRNA, partial cds//1.4e-07:202:68//Hs.34054:U79298
F-HEMBA1006807//ESTs, Moderately similar to HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMOSOME III [C.elegans]//4.8e-110:523:98/IHs.125790:AA287723
F-HEMBA1006821//EST//5.1e-II:246:66//Hs.150542:AI051551
F-HEMBA1006824//ESTs//1.4e-29:158:98//Hs.127712:AA961624
F-HEMBA1006832//EST//3.1e-24:277:74//Hs.139357:AA420970
F-HEMBA1006849//ESTs//0.99:332:57//Hs.128993:AA985327
F-HEMBA1006865
F-HEMBA1006877//ESTs, Highly similar to HYPOTHETICAL 113.8 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION [Saccharomyces cerevisiae]//2.4e-61:311:97//Hs.127793:W25938
F-HEMBA1006885//ESTs, Highly similar to HYPOTHETICAL 29.1 KD PROTEIN IN URA7-POL12 INTERGENIC REGION [Saccharomyces cerevisiae]//9.1e-128:805:87//Hs.32376:AA758214
F-HEMBA1006900//EST//6.8e-05:255:63//Hs.163173:AA781592
F-HEMBA1006914//EST//0.065 :366:6211Hs.162914:AA666199
F-HEMBA1006921//ESTs//2.9e-42:347:82//Hs.159266:AI376989
F-HEMBA1006926//Human I kappa BR mRNA, complete cds//0.90:545:59//Hs.154764:U16258
F-HEMBA1006929//EST//0.00013:403:61//Hs.162642:AA602539
F-HEMBA1006936//ESTs//0.00014:60:93//Hs.8737:W22712
F-HEMBA1006938//ESTs//4.7e-51:256:98//Hs.143651:AI150382
F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//4.4e-92:437:98//Hs.42644:AJ010841
F-HEMBA1006949//H.sapiens mRNA for retrotransposon//6.9e-43:385:76//Hs.6940:Z48633
F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.8e-144:740:94//Hs.14934:AF004828
F-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2.3-sialyltransferase//1.9e-79:447:89//Hs.75268:X74570
F-HEMBA1006993//ESTs//5.4e-19:380:66//Hs.152635:AA600968
F-HEMBA1006996//ESTs//0.17:242:59//Hs.106879:AA054723
F-HEMBA1007002
F-HEMBA1007017//EST//1.0:59:72//Hs.113400:R39282
F-HEMBA1007018//Homo sapiens dynein light intermediate chain 2 (LIC2) mRNA, complete cds//2.5e-78:827:70//Hs.43003:AF035812
F-HEMBA1007045
F-HEMBA1007051//EST//0.85:65:73//Hs.158641:AI370659
F-HEMBA1007052
F-HEMBA1007062
F-HEMBA1007066//ESTs//0.94:160:63//Hs.56071:W52212
F-HEMBA1007073//ESTs//3.6e-50:246:80//Hs.142678:H37845
F-HEMBA1007078//Human arginine-rich nuclear protein mRNA, complete cds//6.7e-75:417:91//Hs.80510:M74002
F-HEMBA1007080
F-HEMBA1007085//Guanylate cyclase 2D, membrane (retina-specific)//1.3e-06:568:61//Hs.1974:M92432
F-HEMBA1007087//Human mevalonate pyrophosphate decarboxylase (MPD) mRNA, complete cds//0.95:541:57//Hs.3828:U49260
F-HEMBA1007112//ESTs//3.4e-104:494:98//Hs.19207:AA039595
F-HEMBA1007113//ESTs//0.71:246:62//Hs.96235:AA196354
F-HEMBA1007121//ESTs/I3.Se-69:335:98//Hs.140519:AA643182
F-HEMBA1007129
F-HEMBA1007147//ESTs//3.2e-07:235:641/Hs.124813:W46172
F-HEMBA1007149//ESTs//7.2e-08:161:68//Hs.121179:AA757136
F-HEMBA1007151
F-HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds//6.6e-64:318:97//Hs.22396:AF062085
F-HEMBA1007178//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.2e-39:248:90//Hs.157148:AA311921
F-HEMBA1007194//ESTs//2.3e-107:503:99//Hs.100605:AA305965

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F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//5.6e-158:478:98//Hs.3363:D86987
F-HEMBA1007206//EST//0.23:119:66//Hs.144402:AA609252
F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//1.6e-177:839:98//Hs.27197:AB018340
F-HEMBA1007243//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)//2.7e-56:647:69//Hs.82314:M31642
F-HEMBA1007251//Human plectin (PLEC1) mRNA, complete cds//0.19:210:67//Hs.79706:U53204
F-HEMBA1007256//Homo sapiens clone 24407 mRNA sequence//1.0:144:6411Hs.12432:AF070575
F-HEMBA1007267//Human homolog of yeast mutL (hPMS1) gene, complete cds//0.99:239:60//Hs.111749:U13695
F-HEMBA1007273//ESTs//5.6e-24:271:73//Hs.144951:N34836
F-HEMBA1007279//ESTs//6. 1e-36:185:78//Hs.141022:H06475
F-HEMBA1007281//ESTs//0.74:94:65//Hs.162533:AA584529
F-HEMBA1007288//EST//0.83:99:67//Hs.127878:AA968637
F-HEMBA1007300//EST//3.6e-62:355:91//Hs.150139:AI300062
F-HEMBA1007301//Collagen, type I, alpha 1//1.5e-09:406:61//Hs.111913:Z74615
F-HEMBA1007319//EST//0.0068:50:96//Hs.163362:AA890506
F-HEMBA1007320//ESTs//1.0:133:66//Hs.38032:N63634
F-HEMBA1007322//ESTs//0.0077:187:66//Hs.4852:R84241
F-HEMBA1007327//ESTs, Weakly similar to HOST CELL FACTOR C1 [H.sapiens]//3.5e-09:144:76//Hs.20597:W58370
F-HEMBA1007341//ESTs//7.5e-61:302:98//Hs.154944:AA494130
F-HEMBA1007342//ESTs//2.9e-12:289:64//Hs.135555:AA911006
F-HEMBA1007347//EST//0.44:89:70//Hs.65949:Z40561
F-HEMBB1000005//ESTs//1.6e-07:337:60//Hs.126718:AA916568
F-HEMBB1000008//H.sapiens mRNA for translin associated protein X//1.1e-43:370:78//Hs.96247:X95073
F-HEMBB1000018//Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)//1.0:108:70//Hs.83428:M58603
F-HEMBB1000024//EST//5.4e-07:137:70//Hs.125389:AA878307
F-HEMBB1000025//EST//0.99:362:58//Hs.121221:AA757392
F-HEMBB1000030//H.sapiens mRNA for cylicin II//1.3e-10:525:62//Hs.3232:Z46788
F-HEMBB1000036
F-HEMBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//6.2e-102:450:98//Hs.20815:AF084928
F-HEMBB1000039//EST//0.0034:97:73//Hs.141684:W35358
F-HEMBB1000044//ESTs//0.0048:218:63//Hs.123161:AA807319
F-HEMBB1000048//EST//0.00025:222:62//Hs.122474:AA765131
F-HEMBB1000050//ESTs//5.6e-28:293:75//Hs.136839:H93717
F-HEMBB1000054//Human Line-1 repeat mRNA with 2 open reading frames//3.3e-54:259:88//Hs.23094:M19503
F-HEMBB1000055//ESTs//0.0017:289:62//Hs.125755:AA286923
F-HEMBB1000059//Homo sapiens mRNA for KIAA0761 protein, partial cds//5.9e-59:286:84//Hs.93121:AB018304
F-HEMBB1000083
F-HEMBB1000089//EST//0.0016:192:661/Hs.137093:AA917621
F-HEMBB1000099//ESTs//5.7e-20:213:76//Hs.57883:AA218645
F-HEMBB1000103//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//4.9e-43:418:74//Hs.103948:K00627
F-HEMBB1000113//EST//4.6e-23:221:76//Hs.142065:AA173763
F-HEMBB1000119//Homo sapiens ASMTL gene//2.5e-132:621:98//Hs.6315:Y15521
F-HEMBB1000136//ESTs112.3e-101:507:96//Hs.12659:AA195207
F-HEMBB1000141//ESTs//2.1e-15:283:69//Hs.126257:AI279044
F-HEMBB1000144//EST//4.5e-52:298:91//Hs.149580:AI281881
F-HEMBB1000173//Zinc finger protein 74 (Cos52)//2.4e-63:285:82//Hs.3057:X92715
F-HEMBB1000175//EST//1.0:101:65//Hs.162898:AA659646
F-HEMBB1000198//EST//0.99:179:56//Hs.116880:AA662457
F-HEMBB1000215//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.4e-15:139:82//Hs.101414:AB011129
F-HEMBB1000217//ESTs//3.4e-06:81:88//Hs.121151:T66277
F-HEMBB1000218//EST//0.11:136:63//Hs.134683:AI092013

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F-HEMBB1000226//Fragile X mental retardation 1//0.99:126:65//Hs.89764:X69962
F-HEMBB1000240//H.sapiens mRNA for Nup88 protein//1.0:334:57//Hs.90734:Y08612
F-HEMBB1000244//ESTs//3.2e-15:139:81//HS.134549:AI078483
F-HEMBB1000250//Homo sapiens protein associated with Myc mRNA, complete cds//2.1e-156:735:981/Hs.151411:AF075587
F-HEMBB1000258//EST//0.0091:325:60//Hs.97533:AA435884
F-HEMBB1000264//Human CHL1 potential helicase (CHLR1), complete cds//1.4e-33:100:100//Hs.27424:U75968
F-HEMBB1000266//Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)//0.0019:373:60//Hs.16533:D87930
F-HEMBB1000272//ESTs//1.3e-93:440:99//Hs.l09224:N46684
F-HEMBB1000274//ESTs//0.41:221:65//Hs.71990:AA151796
F-HEMBB1000284//EST//0.00024:108:73//Hs.100725:F13689
F-HEMBB1000307//EST//3.6e-10:149:73//Hs.140415:AA778574
F-HEMBB1000312//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.00092:252:65//Hs.41153:AB018326
F-HEMBB1000317//Thrombospondin 1//7.1e-05:342:59//Hs.87409:X14787
F-HEMBB1000318//EST//0.014:184:61//Hs.155758:AI311870
F-HEMBB1000335//EST//0.99:187:63//Hs.137424:AA243729
F-HEMBB1000336//EST//1.0:209:63//Hs.150410:AI003611
F-HEMBB1000337//EST//0.086:133:66//Hs.128207:AA972330
F-HEMBB1000338//EST//7.1e-07:129:72//Hs.140488:AA767127
F-HEMBB1000339//Small inducible cytokine A5 (RANTES)//1.2e-36:336:7611Hs.155464:AF088219
F-HEMBB1000341
F-HEMBB1000343//EST//0.66:163:63//Hs.150822:AI302729
F-HEMBB1000354//ESTs//7.e-61:292:100//Hs.152266:AA926874
F-HEMBB1000369//ESTs, Highly similar to t-BOP [M.musculus]/10.013:157:64//Hs.129982:AI420970
F-HEMBB1000374//ESTs//8.7e-53:454:79//Hs.133518:R69934
F-HEMBB1000376//ESTs//5.9e-14:87:97//Hs.163973:AA744348
F-HEMBB1000391//ESTs//0.033:237:64//Hs.135289:AI092963
F-HEMBB1000399//Homo sapiens mRNA for cell cycle checkpoint protein//9.4e-165:762:98//Hs.16184:AJ001642
F-HEMBB1000402//EST//0.013:291:59//Hs.149191:AI246155
F-HEMBB1000404//ESTs//3.0e-69:353:96//Hs.135857:AA947194
F-HEMBB1000420//EST//6.3e-52:258:98//Hs.136434:AA557925
F-HEMBB1000434//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//9.4e-73:364:83//Hs.129735AF010144
F-HEMBB1000438//ESTs//0.073:446:58//Hs.134632:AI223429
F-HEMBB1000441//Interleukin 10//1.7e-38:336:77//Hs.2180:M57627
F-HEMBB1000449//EST//5.5e-21:356:671/Hs.157848:AI362501
F-HEMBB1000455//ESTs//0.092:147:65//Hs.106446:N93227
F-HEMBB1000472
F-HEMBB1000480//EST//0.98:83:71//Hs.146462:AI124898
F-HEMBB1000487//ESTs//1.4e-59:341:92//Hs.48561:N79206
F-HEMBB1000490//ESTs//2.5e-27:200:79//Hs.56825:AI057560
F-HEMBB1000491
F-HEMBB1000493//ESTs//0.019:103:69//Hs.138358:T66178
F-HEMBB1000510//Glucocorticoid receptor alpha {alternative products}//1.6e-46:409:77//Hs.102761:U25029
F-HEMBB1000518//ESTs//3.7e-06:187:64//Hs.140989:R68413
F-HEMBB1000523//ESTs//0.69:332:59//Hg.106845:W19543
F-HEMBB1000530//H.sapiens mRNA for extracellular matrix protein collagen type XIV, C-terminus//2.1e-38:138:96//Hs.36131:Y11710
F-HEMBB1000550//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//7.7e-31:554:67//Hs.157142:U85996
F-HEMBB1000554//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.0e-27:282:75//Hs.158095:AB007953
F-HEMBB1000556//Homo sapiens mRNA for KIAA0750 protein, complete cds//2.0e-33:537:65//Hs.5444:AB018293
F-HEMBB1000564
F-HEMBB1000573//H.sapiens HCG II mRNA//7.5e-27:197:76//Hs.146333:X81001

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F-HEMBB1000575//Von Hippel-Lindau syndrome//2.7e-72:255:79//Hs.78160:AF010238
F-HEMBB1000586//Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272//0.011:338:59//Hs.79012:M18533
F-HEMBB10005891/PLATELET GLYCOPROTEIN V PRECURSOR//2.4e-22:228:79//Hs.73734:Z23091
F-HEMBB1000591//ESTs//1.0e-17:370:64//Hs.58156:W71990
F-HEMBB1000592//EST//0.0038:51:88//Hs.148022:AI269323
F-HEMBB1000593//Homo sapiens chromosome 7q22 sequence//4.7e-109:503:99//Hs.3386:AF053356
F-HEMBB1000598//Ribosomal protein L5//3.5e-29:537:66//Hs.118781:U66589
F-HEMBB1000623//H.sapiens mRNA for GAIP protein//0.89:376:59//Hs.22698:X91809
F-HEMBB1000630//Homo sapiens KIAA0404 mRNA, partial cds//0.074:168:61//Hs.105850:AB007864
F-HEMBB1000631//ESTs//1.7e-06:247:64//Hs.156864:AI346481
F-HEMBB1000632//Human mRNA for KIAA0351 gene, complete cds//5.1e-50:811:65//Hs.29963:AB002349
F-HEMBB1000637//Sialophorin (gpL115, leukosialin, CD43)//2.4e-79:304:85//Hs.80738:X52075
F-HEMBB1000638//EST//0.0076:92:75//Hs.125496:AA883735
F-HEMBB1000643//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.5e-45:477:74//Hs.51048:X68830
F-HEMBB1000649//Homo sapiens histone H2A.1b mRNA, complete cds//7.4e-52:533:75//Hs.51011:L19778
F-HEMBB1000652//ESTs//1.6e-49:345:84//Hs.132722:AA618531
F-HEMBB1000665//EST//0.44:152:63//Hs.149534:AI280924
F-HEMBB1000671//Human Line-1 repeat mRNA with 2 open reading frames//2.2e-79:280:85//Hs.23094:M19503
F-HEMBB1000673//ESTs//0.99:177:59//Hs.149864:N80474
F-HEMBB1000684//Protein kinase, interferon-inducible double stranded RNA dependent//2.6e-31:220:87//Hs.73821:M35663
F-HEMBB1000693//Homo sapiens neuroanl mRNA, complete cds//5.3e-120:575:97//Hs.158300:AF040723
F-HEMBB1000705//ESTs//4.7e-65:350:94//Hs.24610:R33125
F-HEMBB1000706//EST//8.6e-14:373:61//Hs.138281:RS5703
F-HEMBB1000709//EST//0.99:110:651/Hs.162437:AA577510
F-HEMBB1000725//RAS-RELATED PROTEIN RAB-8//1.7e-77:635:77//Hs.123109:X56741
F-HEMBB1000726//EST//1.3e-43:257:84//Hs.162197:AA535216
F-HEMBB1000738//EST//5.9e-13:259:64//Hs.159699:AI417328
F-HEMBB1000749//EST//3.1e-42:271:871/Hs.162197:AA535216
F-HEMBB1000763
F-HEMBB1000770//ESTs, Weakly similar to MOESIN/EZRIN/RADIXIN HOMOLOG [D.melanogaster]//0.021:111:72//Hs.38178:AA921830
F-HEMBB1000774//ESTs, Weakly similar to mTERF [H.sapiens]//2.5 e-116:580:97//Hs.5009:AA081390
F-HEMBB1000781//Human MEK kinase 3 mRNA, complete cds//5.3e-47:426:74//Hs.86201:U78876
F-HEMBB1000789//Homosapiens mRNA for KIAA0677 protein, complete cds//3.0e-65:672:71//Hs.155983:AB014577
F-HEMBB1000790//ESTs//1.2e-52:344:86//Hs.35254:AI133727
F-HEMBB1000794//ESTs//0.00098:289:59//Hs.138782:N73572
F-HEMBB1000807//ESTs//2.1e-91:434:99//Hs.61334:AI298375
F-HEMBB1000810//ESTs//0.038:92:71//Hs.148763:AA66887
F-HEMBB1000821//EST//0.94:129:62//Hs.162299:AA555154
F-HEMBB1000822//ESTs//7.5e-05:199:63//Hs.117018:AA832421
F-HEMBB1000826//ESTs//4.8e-13:343:65//Hs.153429:AI283069
F-HEMBB1000827
F-HEMBB1000831
F-HEMBB1000835//EST//4.3e-27:201:851/Hs.141451:N29915
F-HEMBB1000840//EST//6.3e-75:380:96//Hs.142557:AA464948
F-HEMBB1000848//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-135:875:85//Hs.23094:M19503
F-HEMBB1000852//Phosphoribosyl pyrophosphate amidotransferase//0.12:292:61//Hs.311:U00238
F-HEMBB1000870//EST//0.00091:246:62//Hs.126502:AA913831
F-HEMBB1000876//Homo sapiens ELISC-1 mRNA, partial cds//4.9e-34:200:94//Hs.128434:AF085351
F-HEMBB1000883//ESTs//0.42:107:67//Hs.154173:AI379823
F-HEMBB1000887
F-HEMBB1000888//ESTs//1.0:137:67//Hs.8121:AA521290
F-HEMBB1000890//ESTs//1.0:116:65//Hs.7105:T23433
F-HEMBB1000893//EST//0.0079:408:58//Hs.146504:AI129834

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F-HEMBB1000908//EST//9.2e-21:205:79//Hs.132635:AI032875
F-HEMBB1000910//Human mRNA for KIAA0231 gene, partial cds//0.16:327:60//Hs.7938:D86984
F-HEMBB1000913//ESTs//1.0e-12:233:68//Hs.137545:AA487049
F-HEMBB1000915//ESTs//2.5e-90:423:99//Hs.135254:AI095468
F-HEMBB1000917//EST//2.8e-49:241:100//Hs.162216:AA548089
F-HEMBB1000927//Hippocalcin//1.2e-31:528:65//Hs.89692:D16593
F-HEMBB1000947
F-HEMBB1000959//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//9.3e-48:572:72//Hs.2379:U23942
F-HEMBB1000973//ESTs//4.5e-26:286:76//Hs.137393:AA142938
F-HEMBB1000975//ESTs//0.78:180:66//Hs.104789:AA417124
F-HEMBB1000981
F-HEMBB1000985//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//6.7e-07:308:62//Hs.122967:AF059569
F-HEMBB1000991//EST//0.12:125:66//Hs.22945:R43713
F-HEMBB1000996//ESTs//6.9e-05:273:63//Hs.133116:AI054055
F-HEMBB1001004//Homo sapiens mRNA for KIAA0665 protein, complete cds//0.62:193:62//Hs.119004:AB014565
F-HEMBB1001008//EST//4.7e-09:203:65//Hs.105221:AA489025
F-HEMBB1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12//2.4e-17:384:67//Hs.108604:AC002310
F-HEMBB1001014//EST, Weakly similar to putative p150 [H.sapiens]//0.21:284:60//Hs.161547:W04991
F-HEMBB1001020//ESTs//9.7e-37:186:76//Hs.138852:AA284247
F-HEMBB1001024//ESTs, Highly similar to t-BOP [M.musculus]//0.11:242:61//Hs.129982:AI420970
F-HEMBB1001037//EST//0.0057:192:66//Hs.149987:AI291177
F-HEMBB1001047//ESTs//1.6e-22:360:70//Hs.120734:W58721
F-HEMBB1001051//H.sapiens mRNA for FAN protein//3.8e-29:160:98//Hs.78687:X96586
F-HEMBB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.0e-42:149:96//Hs.15832:AB014518
F-HEMBB1001058//Small inducible cytokine A5 (RANTES)//1.1e-45:349:82//Hs.155464:AF088219
F-HEMBB1001060//ESTs//1.6e-62:464:81//Hs.138663:N24942
F-HEMBB1001063
F-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.9e-148:736:95//Hs.12953:AF034803
F-HEMBB1001096//EST//0.017:154:66//Hs.130403:AA909272
F-HEMBB1001102//ESTs//2.1e-18:120:95//Hs.163767:R06293
F-HEMBB1001105//Human BRCA2 region, mRNA sequence CG016//0.30:84:75//Hs.112434:U50529
F-HEMBB1001112//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//9.3e-38:341:77//Hs.14038:R06800
F-HEMBB1001114//EST//6.4e-07:296:62//Hs.128420:AA975062
F-HEMBB1001117//EST//1.6e-99:464:99//Hs.130493:AA928139
F-HEMBB1001119
F-HEMBB1001126
F-HEMBB1001133//H.sapiens mRNA for translin associated protein X//1.2e-28:739:61//Hs.96247:X95073
F-HEMBB1001137
F-HEMBB1001142//Human mRNA for KIAA0331 gene, complete cds//2.1e-23:340:69//Hs.146395:AB002329
F-HEMBB1001151//ESTs//2.6e-30:252:79//Hs.6880:W26854
F-HEMBB1001153//ESTs//7.6e-16:97:96//Hs.113307:H16716
F-HEMBB1001169//ESTs//1.4e-32:374:71//Hs.161682:AA206863
F-HEMBB1001175//Human mRNA for ankyrin motif, complete cds//7.1e-36:509:66//Hs.73073:D78334
F-HEMBB1001177//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN HXT14-PHA2 INTERGENIC REGION [S.cerevisiae]//1.5e-65:312:100//Hs.86878:AA599183
F-HEMBB1001182//Electron-transfer-flavoprotein, beta polypeptide//0.94:199:64//Hs.74047:X71129
F-HEMBB1001199
F-HEMBB1001208//ESTs//0.12:120:69//Hs.130093:AA928802
F-HEMBB1001209//EST//0.00028:215:65//Hs.118276:W15258
F-HEMBB1001210//EST//2.9e-05:297:60//Hs.88840:AA281452
F-HEMBB1001218//Homo sapiens mRNA for KIAA0585 protein, partial cds//8.5e-37:260:76//Hs.72660:AB011157
F-HEMBB1001221//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//0.00046:650:58//Hs.

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158241:AB007976
F-HEMBB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Mus musculus]//6.7e-103:477:100//Hs.127835:AI378790
F-HEMBB1001242//Homo sapiens mRNA for LAK-1, complete cds//1.2e-31:458:67//Hs.129918:AB005754
F-HEMBB1001249//EST//0.26:203:63//Hs.140791:AA935909
F-HEMBB1001253//ESTs//4.0e-91:433:98//Hs.120636:AA325219
F-HEMBB1001254//ESTs//2.0e-24:180:85//Hs.136391:H04977
F-HEMBB1001267//Ataxia telangiectasia mutated (includes complementation groups A, C and D)//6.1e-24:146:78//Hs.51187:U82828
F-HEMBB1001271//ESTs//2.5e-05:686:58//Hs.115423:AI359248
F-HEMBB1001282//GA-binding protein transcription factor, beta subunit 2 (47kD)//0.39:531:57//Hs.78915:U13045
F-HEMBB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III [Caenorhabditis elegans]//4.9e-10:91:89//Hs.16606:W81021
F-HEMBB1001289//ESTs//6.4e-100:467:99//Hs.151720:AI287890
F-HEMBB1001294//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]//1.3e-135:654:98//Hs.124217:AA020848
F-HEMBB1001302
F-HEMBB1001304//ESTs//0.98:109:68//Hs.138972:AA047725
F-HEMBB1001314//ESTs//7.4e-39:285:77//Hs.144749:AI217339
F-HEMBB1001315//Small inducible cytokine A5 (RANTES)//1.9e-40:355:78//Hs.155464:AF088219
F-HEMBB1001317//Human Line-1 repeat mRNA with 2 open reading frames//4.7e-98:625:85//Hs.23094:M19503
F-HEMBB1001326//ESTs//0.00030:257:63//Hs.62208:H12380
F-HEMBB1001331//ESTs, Weakly similar to DFS70 [H.sapiens]//1.0e-48:332:87//Hs.43071:AA206222
F-HEMBB1001335
F-HEMBB1001337//Homo sapiens mRNA for KIAA0563 protein, complete cds//8.5e-56:282:87//Hs.15731:AB011135
F-HEMBB1001339//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.039:161:65//Hs.132206:AF039694
F-HEMBB1001346//Oxytocin receptor//4.2e-42:456:73//Hs.2820:X64878
F-HEMBB1001348//Homo sapiens mRNA for KIAA0570 protein, complete cds//1.2e-45:176:77//Hs.114293:AB011142
F-HEMBB1001356//EST//0.32:292:59//Hs.135771:AI005648
F-HEMBB1001364
F-HEMBB1001366//EST//7.8e-24:367:69//Hs.138765:N70347
F-HEMBB1001367//Small inducible cytokine A5 (RANTES)//8.7e-50:326:86//Hs.155464:AF088219
F-HEMBB1001369//EST//0.17:211:63//Hs.120066:AA707973
F-HEMBB1001380//Homo sapiens mRNA for KIAA0527 protein, partial cds//8.2e-36:225:79//Hs.129748:AB011099
F-HEMBB1001384
F-HEMBB1001387//ESTs//0.61:215:60//Hs.145915:AI342230
F-HEMBB1001394//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-94:568:83//Hs.23094:M19503
F-HEMBB1001410//Homo sapiens keratan sulfate proteoglycan mRNA, complete cds//0.021:373:58//Hs.125750:AF065988
F-HEMBB1001424//EST//0.20:307:58//Hs.135336:AI049827
F-HEMBB1001426//Homo sapiens clone 23579 mRNA sequence//8.3e-17:205:72//Hs.83466:AF038174
F-HEMBB1001429//ESTs, Highly similar to CYTOSOL AMINOPEPTIDASE [Bos taurus]//5.5e-153:729:96//Hs.21679:AF034175
F-HEMBB1001436//Human mRNA for KIAA0347 gene, complete cds//1.2e-44:316:85//Hs.101996:AB002345
F-HEMBB1001443
F-HEMBB1001449//Homo sapiens sodium bicarbonate cotransporter (HNBC1) mRNA, complete cds//0.033:478:58//Hs.5462:AF007216
F-HEMBB1001454//ESTs//1.4e-46:279:93//HS.104866:AA426038
F-HEMBB1001458//EST//1.7e-09:106:83//Hs.141422:N20920
F-HEMBB1001463//Homo sapiens mRNA for semaphorin E, complete cds//0.18:387:59//Hs.62705:AB000220
F-HEMBB1001464//Homo sapiens Coch-5B2 mRNA, complete cds//0.26:189:67//Hs.21016:AF006740
F-HEMBB1001482//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2e-27:292:74//Hs.137168:AB018303
F-HEMBB1001500//ESTs//8.1e-28:312:74//Hs.18498:N52088

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F-HEMBB1001521//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//8.8e-54:359:74//Hs.46328:D87942
F-HEMBB1001527//Protein tyrosine phosphatase, receptor type, f polypeptide//1.0:198:63//Hs.75216:Y00815
F-HEMBB1001531//ESTs//4.3e-33:403:75//Hs.44862:N38735
F-HEMBB1001535//ESTs//0.0029:47:93//Hs.124864:AA663093
F-HEMBB1001536//ESTs//0.0047:120:68//Hs.144858:R67748
F-HEMBB1001537//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D.melanogaster]//3.7e-20:297:73//Hs.42457:AA523306
F-HEMBB1001555//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//1.1e-35:188:77//Hs.102877:U41315
F-HEMBB1001562//ESTs//0.95:161:61//Hs.145075:AI208240
F-HEMBB1001564//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.4e-49:526:73//Hs.158095:AB007953
F-HEMBB1001565//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.9e-44:324:84//Hs.113283:AF018080
F-HEMBB1001585
F-HEMBB1001586//EST//0.84:132:64//Hs.145264:AI218708
F-HEMBB1001588//Human clone 23695 mRNA sequence//6.6e-20:327:67//Hs.90798:U79289
F-HEMBB1001603//ESTs//1.3e-12:84:96//Hs.13380:R60414
F-HEMBB1001618//ESTs//4.4e-11:349:63//Hs.132046:AA693680
F-HEMBB1001619//ESTs//2.1e-06:246:63//Hs.63428:AA058314
F-HEMBB1001630//EST//1.4e-07:334:62//Hs.145698:AI266713
F-HEMBB1001635//ESTs//0.92:282:60//Hs.126980:AA934077
F-HEMBB1001637//ELK1, member of ETS oncogene family//1.1e-27:395:64//Hs.116549:AL009172
F-HEMBB1001641//EST//0.11:53:81//Hs.112445:AA594279
F-HEMBB1001653//EST//0.91:124:64//Hs.144213:T40480
F-HEMBB1001665//Human mRNA for apolipoprotein E receptor 2, complete cds//7.0e-13:473:63//Hs.54481:D86407
F-HEMBB1001668//ESTs//0.94:83:69//Hs.146202:AI252519
F-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//2.3e-172:803:98//Hs.24439:AB014546
F-HEMBB1001684//ESTs, Highly similar to Tbc1 [M.musculus]//5.4e-20:110:100//Hs.106104:AA599496
F-HEMBB1001685//EST//2.2e-05:112:73//Hs.130984:AI015430
F-HEMBB1001695//Human novel homeobox mRNA for a DNA binding protein//1.6e-08:425:62//Hs.37035:U07664
F-HEMBB1001704//EST//5.8e-20:295:69//Hs.140231:AI054398
F-HEMBB1001706
F-HEMBB1001707//EST//0.091:241:60//Hs.136830:AA769219
F-HEMBB1001717//ESTs//2.9e-06:325:60//Hs.150063:AI298064
F-HEMBB1001735//Small inducible cytokine A5 (RANTES)//3.2e-46:326:83//Hs.155464:AF088219
F-HEMBB1001736//ESTs, Weakly similar to E04D5.1 [C.elegans]//5.4e-99:485:97//Hs.120581:W25578
F-HEMBB1001747//ESTs//8.3e-87:421:98//Hs.137051:AA884244
F-HEMBB1001749//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//3.5e-75:315:83//Hs.129735:AF010144
F-HEMBB1001753//ESTs//0.00013:35:100//Hs.139643:H06263
F-HEMBB1001756//ESTs//2.3e-89:433:98//Hs.128868:AA931077
F-HEMBB1001760//ESTs//6.5e-06:503:58//Hs.21766:AI357639
F-HEMBB1001762//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//2.9e-13:498:60//Hs.158241:AB007976
F-HEMBB1001785//EST//0.16:262:60//Hs.162526:AA584102
F-HEMBB1001797//ESTs//0.37:201:63//Hs.91559:AA806370
F-HEMBB1001802//ESTs//1.6e-06:447:58//Hs.134672:AI087951
F-HEMBB1001812//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.3e-54:311:81//Hs.92381:AB007956
F-HEMBB1001816//ESTs//2.2e-39:302:84//Hs.35985:AA783017
F-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds//7.6e-164:763:98//Hs.159396:AF056209
F-HEMBB1001834//TRICHOHYALIN//7.1e-05:548:60//Hs.82276:L09190
F-HEMBB1001836//Human mRNA for KIAA0033 gene, partial cds//4.0e-34:272:86//Hs.22271:D26067
F-HEMBB1001839//Pyruvate carboxylase//0.050:686:59//Hs.89890:S72370

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F-HEMBB1001850//EST//0.0035:204:61//Hs.7311:T23858
F-HEMBB1001863//Small inducible cytokine A5 (RANTES)//3.0e-48:357:82//Hs.155464:AF088219
F-HEMBB1001867//ESTs//2.2e-40:265:88//Hs.146323:AI251752
F-HEMBB1001868//ESTs//5.2e-06:131:73//Hs.123362:AA811371
F-HEMBB1001869//ESTs//1.0e-86:429:96//Hs.141208:AA825503
F-HEMBB1001872
F-HEMBB1001874//H.sapiens mRNA for CHD5 protein//0.0033:388:60//Hs.19923:Y12478
F-HEMBB1001875//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//0.32:346:60//Hs.100555:X98743
F-HEMBB1001880//EST//4.0e-28:171:92//Hs.151194:AI125868
F-HEMBB1001899//ESTs//0.17:242:62//Hs.136969:AA830918
F-HEMBB1001905
F-HEMBB1001906//ESTs//5.6e-49:290:92//Hs.127298:H09155
F-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds//1.2e-83:672:81//Hs.82210:U47742
F-HEMBB1001910//EST, Weakly similar to albumin [H.sapiens]//0.047:206:62//Hs.159777:Z19955
F-HEMBB1001911
F-HEMBB1001915//ESTs//0.92:136:71//Hs.144465:R68882
F-HEMBB1001921//EST//2.0e-19:398:67//Hs.44789:N36113
F-HEMBB1001922//ESTs//4.3e-05:370:59//Hs.123669:AA805245
F-HEMBB1001925//ESTs//5.7e-27:329:71//Hs.141071:H16398
F-HEMBB1001930//EST//0.043:157:63//Hs.161927:AA483904
F-HEMBB1001944//Human mRNA for KIAA0118 gene, partial cds//5.7e-55:444:80//Hs.154326:D42087
F-HEMBB1001945//ESTs//1.1e-19:142:88//Hs.7341:N57875
F-HEMBB1001947//Human mRNA for KIAA0392 gene, partial cds//1.8e-21:333:66//Hs.40100:AB002390
F-HEMBB1001950//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.020:384:60//Hs.8546:U97669
F-HEMBB1001952//EST//7.0e-13:302:63//Hs.120089:AA708101
F-HEMBB1001953//ATL-derived PMA-responsive (APR) peptide//0.97:252:60//Hs.96:D90070
F-HEMBB1001957//ESTs//6.1e-32:446:67//Hs.51305:T47418
F-HEMBB1001962//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//2.3e-31:390:70//Hs.1361:M55053
F-HEMBB1001967//H.sapiens mRNA for urea transporter//9.7e-52:322:88//Hs.66710:X96969
F-HEMBB1001973//Myelin oligodendrocyte glycoprotein {alternative products}//2.1e-48:426:78//Hs.53217:Z48051
F-HEMBB1001983
F-HEMBB1001988//ESTs//6.5e-05:237:63//Hs.49760:AA741051
F-HEMBB1001990//ESTs//0.25:171:64//Hs.7961:AA401205
F-HEMBB1001996//ESTs//1.8e-19:436:65//Hs.125539:AI339103
F-HEMBB1001997//EST//5.3e-33:294:76//Hs.161041:H82636
F-HEMBB1002002//ESTs//1.9e-06:224:67//Hs.110915:AA132964
F-HEMBB1002005//ESTs//5.8e-17:170:78//Hs.141825:AA017093
F-HEMBB1002009//ESTs//0.066:441:58//Hs.125313:AI201685
F-HEMBB1002015//EST//2.3e-18:310:68//Hs.145899:AI274951
F-HEMBB1002042//CYTOCHROME P450 IVB1//2.9e-11:446:62//Hs.687:X16699
F-HEMBB1002043//ESTs, Weakly similar to T06E6.d [C.elegans]//1.0:217:60//Hs.3487:AA425553
F-HEMBB1002044
F-HEMBB1002045
F-HEMBB1002049//Homo sapiens mRNA for KIAA0713 protein, partial cds//0.082:201:61//Hs.88756:AB018256
F-HEMBB1002050//Breakpoint cluster region protein BCR//0.84:267:59//Hs.2557:Y00661
F-HEMBB1002068//Homo sapiens mRNA for KIAA0612 protein, partial cds//8.1e-07:402:61//Hs.112499:AB014512
F-HEMBB1002069
F-HEMBB1002092//EST//5.1e-15:180:75//Hs.127928:AA969239
F-HEMBB1002094//EST//2.0e-52:264:98//Hs.71763:AA146625
F-HEMBB1002115//EST//0.0083:244:64//Hs.125353:AA877080
F-HEMBB1002134//ESTs//1.7e-69:398:91//Hs.157492:AI361027
F-HEMBB1002139//ESTs//0.64:145:71//Hs.157821:AI362013
F-HEMBB1002142//ESTs//0.013:311:59//Hs.150037:AI292214

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F-HEMBB1002152//ESTs//8.4e-12:121:82//Hs.119540:T95254
F-HEMBB1002189//EST//0.26:81:70//Hs.147726:AI220208
F-HEMBB1002190//Alcohol dehydrogenase 2 (class I), beta polypeptide//0.16:608:58//Hs.4:X03350
F-HEMBB1002193//Human sky mRNA for Sky, complete cds//6.6e-35:179:100//Hs.301:U18934
F-HEMBB1002217//Homo sapiens mRNA for zinc finger protein 10//3.7e-25:405:67//Hs.104115:X52332
F-HEMBB1002218//EST//0.015:241:61//Hs.105298:AA489813
F-HEMBB1002232//Small inducible cytokine A5 (RANTES)//9.0e-31:365:71//Hs.155464:AF088219
F-HEMBB1002247
F-HEMBB1002249//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//6.8e-47:418:77//Hs.125231:AF068006
F-HEMBB1002254//Homo sapiens mRNA for KIAA0594 protein, partial cds//5.0e-47:437:77//Hs.154872:AB011166
F-HEMBB1002255//ESTs//0.017:255:61//Hs.126786:U74314
F-HEMBB1002266//Homo sapiens retinoblastoma-associated protein HEC mRNA, complete cds//0.17:511:57//Hs.58169:AF017790
F-HEMBB1002280//EST//4.0e-35:182:98//Hs.127701:AA864998
F-HEMBB1002300
F-HEMBB1002306//Human G protein-coupled receptor (STRL22) mRNA, complete cds//6.3e-14:228:72//Hs.46468:U45984
F-HEMBB1002327//EST//4.3e-21:242:75//Hs.72377:AA161083
F-HEMBB1002329//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.7e-77:399:96//Hs.105837:AA536054
F-HEMBB1002340//INSULIN-DEGRADING ENZYME//1.0:319:60//Hs.1508:M21188
F-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein//1.4e-155:724:98//Hs.42644:AJ010841
F-HEMBB1002358//Deoxythymidylate kinase//1.1e-37:192:98//Hs.79006:L16991
F-HEMBB1002359//Human Rev interacting protein Rip-1 mRNA, complete cds//1.7e-06:66:96//Hs.154762:U00943
F-HEMBB1002364//EST//4.7e-16:201:73//Hs.149925:AI288838
F-HEMBB1002371//EST//2.4e-07:319:61//Hs.136459:AA577796
F-HEMBB1002381
F-HEMBB1002383//vasoactive intestinal peptide receptor 2//0.98:190:63//Hs.2126:L36566
F-HEMBB1002387//EST//2.1e-07:253:61//Hs.145993:AI277784
F-HEMBB1002409//ESTs//1.4e-11:94:91//Hs.125958:AI206456
F-HEMBB1002415//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.0e-32:371:73//Hs.159897:AB007970
F-HEMBB1002425//Fc fragment of IgA, receptor for//2.7e-32:156:82//Hs.54486:X54150
F-HEMBB1002442
F-HEMBB1002453//Human mRNA for KIAA0118 gene, partial cds//5.6e-53:461:77//Hs.154326:D42087
F-HEMBB1002457//ESTs//3.4e-25:184:70//Hs.140225:AA704101
F-HEMBB1002458//ESTs//7.0e-10:343:62//Hs.163816:N76274
F-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds//6.0e-89:493:92//Hs.159605:U43885
F-HEMBB1002489//Homo sapiens 195 kDa cornified envelope precursor mRNA, complete cds//0.019:228:63//Hs.74304:AF001691
F-HEMBB1002492//EST//0.24:149:62//Hs.146790:AI149051
F-HEMBB1002495//Fc fragment of IgE, high affinity I, receptor for; beta polypeptide//1.3e-22:331:71//Hs.30:M89796
F-HEMBB1002502//ESTs//1.3e-41:380:78//Hs.61199:AA024494
F-HEMBB1002509//ESTs//0.017:220:63//Hs.155263:AI273725
F-HEMBB1002510//ESTs//6.4e-102:476:99//Hs.152289:AI247354
F-HEMBB1002520//Human Line-1 repeat mRNA with 2 open reading frames//2.4e-50:580:72//Hs.23094:M19503
F-HEMBB1002522//EST//0.010:172:62//Hs.147224:AI205719
F-HEMBB1002531
F-HEMBB1002534//Small inducible cytokine A5 (RANTES)//3.7e-59:258:88//Hs.155464:AF088219
F-HEMBB1002545//ESTs//3.9e-24:181:86//Hs.13753:AI088102
F-HEMBB1002550//Syntaxin 5A//0.27:354:59//Hs.154546:U26648
F-HEMBB1002556//ESTs//1.7e-33:286:79//Hs.146173:AA906191
F-HEMBB1002579//EST//1.0:77:68//Hs.147935:AI250286
F-HEMBB1002582//ESTs//0.00032:178:68//Hs.139163:AA226095

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F-HEMBB1002590//ESTs//0.64:132:63//Hs.155688:AI003657
F-HEMBB1002596//ESTs//3.4e-19:462:64//Hs.124399:AA832336
F-HEMBB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds//3.0e-152:710:98//Hs.129826:AF089749
F-HEMBB1002601//EST//9.6e-13:368:62//Hs.137080:AA894817
F-HEMBB1002603//EST//0.10:144:63//Hs.158180:AI367945
F-HEMBB1002607//ESTs//0.024:345:62//Hs.143304:AI084058
F-HEMBB1002610//EST//2.1e-14:291:64//Hs.140573:AA826323
F-HEMBB1002613//ESTs//1.9e-17:192:75//Hs.141161:AA210711
F-HEMBB1002614//ESTs//0.0048:136:71//Hs.106280:R13901
F-HEMBB1002617//EST//0.034:320:59//Hs.41223:H89127
F-HEMBB1002623//ESTs//0.88:222:60//Hs.129920:AA167217
F-HEMBB1002635//Human MAP kinase mRNA, complete cds//3.1e-23:127:100//Hs.151051:U07620
F-HEMBB1002664//EST//0.00013:203:61//Hs.117141:AA678811
F-HEMBB1002677//ESTs//2.4e-22:439:66//Hs.132046:AA693680
F-HEMBB1002683//ESTs//0.23:224:61//Hs.128883:AI026679
F-HEMBB1002684//ESTs//7.2e-09:82:87//Hs.140457:H05124
F-HEMBB1002686//EST//0.25:189:62//Hs.132431:AA909674
F-HEMBB1002692//ESTs//0.00020:162:66//Hs.118180:N68504
F-HEMBB1002697//EST//7.2e-17:219:74//Hs.100459:T61992
F-HEMBB1002699//Homo sapiens transmembrane activator and CAML interactor (TACI) mRNA, complete cds//0.059:297:62//Hs.158341:AF023614
F-HEMBB1002702//ESTs//0.26:284:61//Hs.41250:H89588
F-HEMBB1002705//ESTs, Weakly similar to HYPOTHETICAL 38.5 KD PROTEIN IN SUI2-TDH2 INTERGENIC REGION [Saccharomyces cerevisiae]//0.0048:84:83//Hs.20814:AI242922
F-HEMBB1002712//ESTs//0.0025:317:58//Hs.7344:AA972729
F-MAMMA1000009//Human c-yes-1mRNA//1.0e-48:447:77//Hs.75680:M15990
F-MAMMA1000019
F-MAMMA1000020//EST//2.6e-84:431:95//Hs.143333:H51750
F-MAMMA1000025//EST//1.0:169:59//Hs.130165:AA906945
F-MAMMA1000043//Human NSCL-1 mRNA sequence//0.94:262:60//Hs.30956:M96739
F-MAMMA1000045//ESTs//1.7e-48:499:75//Hs.158469:AA897461
F-MAMMA1000055//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculus]//2.7e-18:330:63//Hs.59906:AA001281
F-MAMMA1000057//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//1.2e-50:367:75//Hs.133089:AF064019
F-MAMMA1000069//ESTs//0.58:286:60//Hs.134417:AI336840
F-MAMMA1000084//Human mRNA for KIAA0033 gene, partial cds//1.1e-48:641:70//Hs.22271:D26067
F-MAMMA1000085//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.00013:199:69//Hs.37656:AB011174
F-MAMMA1000092//Homo sapiens telomeric repeat binding factor (TRF1) mRNA, complete cds//1.2e-52:346:77//Hs.90357:U40705
F-MAMMA1000103//Homo sapiens mRNA for extracellular matrix protein, complete cds//1.0:151:64//Hs.35094:AB011792
F-MAMMA1000117
F-MAMMA1000129//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.0015:492:60//Hs.89631:U48508
F-MAMMA1000133//ESTs//1.0:125:67//Hs.118309:AA653402
F-MAMMA1000134//EST//1.2e-08:75:92//Hs.160674:AI248319
F-MAMMA1000139//EST//5.5e-10:139:76//Hs.159121:AI383843
F-MAMMA1000143//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.2e-26:148:97//Hs.153121:AB014585
F-MAMMA1000155//Homo sapiens homeobox transcription factor barx2 (BARX2) mRNA, complete cds//3.3e-31:219:87//Hs.129724:AF031924
F-MAMMA1000163//ESTs//1.2e-59:317:94//Hs.49559:AA401050
F-MAMMA1000171//ESTs//1.7e-09:161:69//Hs.119070:AA629695
F-MAMMA1000173//Human drebrin E2 mRNA (DBN1), complete cds//9.2e-40:686:65//Hs.89434:D17530
F-MAMMA1000175//ESTs//0.65:141:68//Hs.133152:H91657
F-MAMMA1000183//Human mRNA for KIAA0065 gene, partial cds//1.0e-92:904:72//Hs.70617:D31763

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F-MAMMA1000198//ESTs//0.0092:235:62//Hs.98783:AI091739
F-MAMMA1000221//EST//3.3e-16:95:98//Hs.128271:AA973035
F-MAMMA1000227//ESTs//0.010:268:60//Hs.16412:AA506926
F-MAMMA1000241//ESTs//0.13:140:67//Hs.12328:AI377913
F-MAMMA1000251//EST//3.7e-07:118:73//Hs.153116:AA856873
F-MAMMA1000254//ESTs//0.00023:245:59//Hs.150513:AI247587
F-MAMMA1000257//EST//4.2e-10:155:74//Hs.150409:AI003543
F-MAMMA1000264//ESTs//2.0e-18:217:75//Hs.152748:N53015
F-MAMMA1000266//EST//0.14:270:60//Hs.132593:AI031874
F-MAMMA1000270//Human mRNA for KIAA0118 gene, partial cds//2.5e-54:354:87//Hs.154326:D42087
F-MAMMA1000277//Hydroxysteroid (11-beta) dehydrogenase 2//1.0e-07:306:65//Hs.1376:U26726
F-MAMMA1000278//ESTs//4.0e-09:197:67//Hs.157034:AI347361
F-MAMMA1000279//Complement component 5 receptor 1 (C5a ligand)//8.4e-34:341:68//Hs.2161:M62505
F-MAMMA1000284
F-MAMMA1000287//Human mRNA for KIAA0118 gene, partial cds//5.4e-50:245:84//Hs.154326:D42087
F-MAMMA1000302//EST//5.3e-40:213:98//Hs.122363:AA788641
F-MAMMA1000307//Polycystic kidney disease 1 (autosomal dominant)//0.55:510:57//Hs.75813:L33243
F-MAMMA1000309//Apolipoprotein E//9.7e-06:691:58//Hs.76260:M12529
F-MAMMA1000312//EST//0.042:183:63//Hs.158928:AI379519
F-MAMMA1000313
F-MAMMA1000331
F-MAMMA1000339
F-MAMMA1000340//ESTs, Highly similar to HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION [Saccharomyces cerevisiae]//2.9e-11:87:93//Hs.13096:AA180963
F-MAMMA1000348//Homo sapiens KIAA0432 mRNA, complete cds//3.6e-23:270:72//Hs.155174:AB007892
F-MAMMA1000356//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.7e-24:233:72//Hs.158095:AB007953
F-MAMMA1000360//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-75:498:85//Hs.23094:M19503
F-MAMMA1000361//Human mRNA for KIAA0118 gene, partial cds//9.1e-50:304:85//Hs.154326:D42087
F-MAMMA1000372//EST//1.2e-53:376:86//Hs.144295:AA136569
F-MAMMA1000385//ESTs//1.4e-22:220:76//Hs.142552:AA235344
F-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//1.2e-149:710:98//Hs.32170:AB015132
F-MAMMA1000395//Acyl-Coenzyme A dehydrogenase, very long chain//0.74:330:60//Hs.82208:L46590
F-MAMMA1000402//Human Line-1 repeat mRNA with 2 open reading frames//2.4e-58:834:68//Hs.23094:M19503
F-MAMMA1000410//Human NADH:ubiquinone oxidoreductase subunit B13 (B13) mRNA, complete cds//1.2e-08:117:84//Hs.83916:U53468
F-MAMMA1000413//ESTs//3.3e-31:209:88//Hs.146154:AI200725
F-MAMMA1000414//ESTs//0.82:132:62//Hs.124857:AA687092
F-MAMMA1000416//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III [C.elegans]//9.8e-33:267:81//Hs.32370:AA521111
F-MAMMA1000421//ESTs//7.3e-33:320:75//Hs.121659:H02532
F-MAMMA1000422//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//0.98:553:56//Hs.19492:AF061573
F-MAMMA1000423//EST//0.0075:179:63//Hs.162974:AA678459
F-MAMMA1000424//ESTs//1.3e-17:313:67//Hs.139858:AI377641
F-MAMMA1000429//Homo sapiens sorting nexin 3 (SNX3) mRNA, complete cds//5.1e-48:491:72//Hs.12102:AF034546
F-MAMMA1000431//ISLET AMYLOID POLYPEPTIDE PRECURSOR//5.1e-39:320:81//Hs.51048:X68830
F-MAMMA1000444//Homo sapiens mRNA for KIAA0594 protein, partial cds//9.1e-39:342:78//Hs.154872:AB011166
F-MAMMA1000446
F-MAMMA1000458//ESTs, Weakly similar to similar to CCAAT/enhancer-binding protein [C.elegans]//5.1e-08:58:93//Hs.9043:W21827
F-MAMMA1000468//Homo sapiens mRNA for 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, complete cds//0.58:311:63//Hs.66721:D49818
F-MAMMA1000472//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.1e-44:346:80//Hs.51048:X68830
F-MAMMA1000478//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.0017:157:73//Hs.113283:AF018080

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F-MAMMA1000483//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.5e-39:400:75//Hs.51048:X68830
F-MAMMA1000490//ESTs//3.6e-52:331:88//Hs.163686:AA291948
F-MAMMA1000500//EST//9.7e-73:346:99//Hs.98812:AA434482
F-MAMMA1000501//Small inducible cytokine A5 (RANTES)//2.3e-50:325:86//Hs.155464:AF088219
F-MAMMA1000516//Oxytocin receptor//1.6e-29:660:64//Hs.2820:X64878
F-MAMMA1000522//ESTs//2.9e-23:328:70//Hs.125142:AA421352
F-MAMMA1000524//ESTs//1.1e-08:211:65//Hs.33467:R85497
F-MAMMA1000559//EST//4.7e-17:207:71//Hs.162733:AA614352
F-MAMMA1000565
F-MAMMA1000567//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//5.8e-51:404:80//Hs.125231:AF068006
F-MAMMA1000576//ESTs//3.8e-32:236:74//Hs.140039:AA047045
F-MAMMA1000583//ESTs//0.00099:123:70//Hs.135173:AI276780
F-MAMMA1000585//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//8.8e-45:390:78//Hs.159523:AF001622
F-MAMMA1000594//ESTs//8.3e-42:322:81//Hs.161660:AA167744
F-MAMMA1000597//Homo sapiens KIAA0426 mRNA, complete cds//2.6e-37:592:68//Hs.97476:AB007886
F-MAMMA1000605//Homo sapiens 4F5S mRNA, complete cds//5.1e-26:228:73//Hs.32567:AF073519
F-MAMMA1000612//Homo sapiens Gx protein (GX) mRNA, complete cds//0.00091:300:60//Hs.29207:AF071494
F-MAMMA1000616//ESTs//0.41:373:59//Hs.130699:AA621478
F-MAMMA1000621//EST//0.027:146:62//Hs.148305:AA909605
F-MAMMA1000623
F-MAMMA1000625//Homo sapiens ES/130 mRNA, complete cds//0.89:428:56//Hs.98614:AF006751
F-MAMMA1000643//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds//0.092:365:59//Hs.75474:AF023674
F-MAMMA1000664//ESTs//7.6e-07:259:64//Hs.140622:AA844353
F-MAMMA1000669//Human kpni repeat mrna (cdna clone pcd-kpni-4),3' end//9.0e-30:531:64//Hs.139107:K00629
F-MAMMA1000670//ESTs//6.6e-83:389:100//Hs.148595:AI244490
F-MAMMA1000672//Homo sapiens CAGH32 mRNA, partial cds//0.17:109:73//Hs.4316:U80743
F-MAMMA1000684//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds//3.3e-07:249:62//Hs.44481:U13220
F-MAMMA1000696//Interleukin 10//5.6e-47:355:82//Hs.2180:M57627
F-MAMMA1000707//ESTs//1.4e-09:225:65//Hs.138722:N51081
F-MAMMA1000713//Acetylcholinesterase {I4-E5 doman} [human, tumor cell lines, Genomic, 847 nt]//0.16:84:72//Hs.157124:S71129
F-MAMMA1000714//Human clone 23947 mRNA, partial cds//0.97:263:6//Hs.27414:U79275
F-MAMMA1000718//ESTs, Weakly similar to putative p150 [H.sapiens]//5.0e-07:210:66//Hs.71148:AA854648
F-MAMMA1000720//ESTs//1.4e-50:301:83//Hs.138852:AA284247
F-MAMMA1000723//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//8.1e-22:288:72//Hs.114685:AA700024
F-MAMMA1000731//Homo sapiens CHD1 mRNA, complete cds//1.5e-23:292:66//Hs.22670:AF006513
F-MAMMA1000732//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.8e-40:288:78//Hs.158095:AB007953
F-MAMMA1000733//RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1//0.25:467:58//Hs.1742:L33075
F-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.3e-169:802:98//Hs.31575:AF100141
F-MAMMA1000738//EST//1.0:149:63//Hs.136928:AA812580
F-MAMMA1000744//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.3e-51:323:88//Hs.153468:AB011147
F-MAMMA1000746//ESTs//2.3e-42:409:76//Hs.61199:AA024494
F-MAMMA1000752//EST, Weakly similar to putative p150 [H.sapiens]//1.1e-14:285:68//Hs.162011:AA513663
F-MAMMA1000760//Myelin oligodendrocyte glycoprotein {alternative products}//6.2e-47:341:82//Hs.53217:Z48051
F-MAMMA1000761//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//9.8e-19:131:76//Hs.118972:AA761369
F-MAMMA1000775//EST//6.9e-32:424:69//Hs.44554:N34288
F-MAMMA1000776//ESTs//5.5e-43:154:84//Hs.141581:AA315361

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F-MAMMA1000778//EST//4.4e-28:226:80//Hs.128952:AA984114
F-MAMMA1000782//ESTs//0.35:270:60//Hs.29153:AA551137
F-MAMMA1000798//Homo sapiens clone 24407 mRNA sequence//1.6e-23:531:65//Hs.12432:AF070575
F-MAMMA1000802//ESTs//3.1e-67:340:97//Hs.126081:AA459849
F-MAMMA1000824//ESTs//0.98:44:90//Hs.42802:N20130
F-MAMMA1000831//ESTs//0.0081:194:60//Hs.150400:AI298089
F-MAMMA1000839//Small inducible cytokine A5 (RANTES)//4.7e48:241:74//Hs.155464:AF088219
F-MAMMA1000841
F-MAMMA1000842//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds//0.18:483:59//Hs.82210:U47742
F-MAMMA1000843//EST//0.34:113:68//Hs.58415:W74696
F-MAMMA1000845//EST//2.9e-06:56:80//Hs.123243:AA804877
F-MAMMA1000851//EST//0.78:103:65//Hs.135656:AA907022
F-MAMMA1000855
F-MAMMA1000856//Homo sapiens preprocathepsin P mRNA, partial cds//0.14:320:59//Hs.71388:AF032906
F-MAMMA1000859//SOX-3 PROTEIN//0.014:474:57//Hs.157429:X71135
F-MAMMA1000862//EST//1.0:92:66//Hs.157599:AI357342
F-MAMMA1000863//ELK1, member of ETS oncogene family//1.2e-30:214:75//Hs.116549:AL009172
F-MAMMA1000865//ESTs//0.99:127:66//Hs.125230:AA873812
F-MAMMA1000867//EST//0.027:236:60//Hs.147156:AI191777
F-MAMMA1000875//Human mRNA for KIAA0269 gene, complete cds//0.96:245:59//Hs.75850:D87459
F-MAMMA1000876//ESTs//1.5e-39:192:90//Hs.132020:AA704147
F-MAMMA1000877//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.4e-91:484:94//Hs.138938:AA012894
F-MAMMA1000880//EST//0.014:142:66//Hs.137044:AA878812
F-MAMMA1000883//EST//1.0:166:62//Hs.126352:AA894465
F-MAMMA1000897//H.sapiens mRNA for inter-alpha-trypsin inhibitor heavy chain H3//2.6e-06:211:63//Hs.76716:X67055
F-MAMMA1000905//Cartilage matrix protein//0.97:190:64//Hs.150366:M55683
F-MAMMA1000906//ESTs//3.0e-07:145:72//Hs.133556:AA702506
F-MAMMA1000908//ESTs//1.1e-70:484:84//Hs.142497:AA189081
F-MAMMA1000914//Angiopoietin 1//0.14:450:59//Hs.2463:D13628
F-MAMMA1000921//ESTs//6.8e-96:448:99//Hs.135721:AI125239
F-MAMMA1000931//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.0e-25:312:66//Hs.116007:S79267
F-MAMMA1000940//EST//2.9e-42:209:76//Hs.140567:AA825968
F-MAMMA1000941//Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex)//1.8e-38:395:71//Hs.89479:X66785
F-MAMMA1000942//ESTs//1.9e-19:252:71//Hs.141575:AA211734
F-MAMMA1000943//Human mRNA for KIAA0305 gene, complete cds//0.077:236:63//Hs.83790:AB002303
F-MAMMA1000956//Homo sapiens hRVP1 mRNA for RVP1, complete cds//8.8e-33:566:64//Hs.25640:AB000714
F-MAMMA1000957//ESTs//1.0:177:59//Hs.149864:N80474
F-MAMMA1000962//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.1e-56:310:85//Hs.129735:AF010144
F-MAMMA1000968//ESTs//9.2e-18:128:89//Hs.163980:AA715814
F-MAMMA1000975//ESTs//3.8e-08:219:66//Hs.110937:AA137096
F-MAMMA1000979//EST//0.00022:155:65//Hs.101379:Z39802
F-MAMMA1000987//EST//1.1e-48:373:81//Hs.139034:W27062
F-MAMMA1000998//EST//2.0e-07:356:62//Hs.132467:AA922007
F-MAMMA1001003//ESTs//0.47:129:67//Hs.164016:AI003724
F-MAMMA1001008//ESTs//1.9e-17:153:82//Hs.141161:AA210711
F-MAMMA1001021//Homo sapiens beta-dystrobrevin (BDTN) mRNA, complete cds//4.7e-17:100:100//Hs.13451:Y15718
F-MAMMA1001024//ESTs//0.97:251:62//Hs.59389:R93968
F-MAMMA1001030//Homo sapiens orphan G protein-coupled receptor HG38 mRNA, complete cds//3.6e-32:753:61//Hs.98384:AF062006
F-MAMMA1001035//ESTs//6.9e-28:268:77//Hs.139536:AA180857
F-MAMMA1001038

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F-MAMMA1001041//ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM//2.7e-10:357:65//Hs.119000:M95178
F-MAMMA1001050//EST//1.8e-29:321:74//Hs.161240:AI419882
F-MAMMA1001059//ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog//7.9e-87:415:99//Hs.135623:AA134719
F-MAMMA1001067//EST//0.30:166:60//Hs.148441:AI198503
F-MAMMA1001073//ESTs//1.0e-98:476:98//Hs.98321:AA455585
F-MAMMA1001074//ESTs//1.6e-82:396:98//Hs.118923:AA252116
F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA sequence//3.7e-29:559:65//Hs.135251:L09749
F-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//2.7e-99:689:83//Hs.23094:M19503
F-MAMMA1001080//IG ALPHA-2 CHAIN C REGION//5.8e-43:319:81//Hs.32225:AF067420
F-MAMMA1001082//ESTs//6.2e-28:275:77//Hs.152685:AA613896
F-MAMMA1001091//Homo sapiens mRNA for KIAA0711 protein, complete cds//0.0081:586:57//Hs.5333:AB018254
F-MAMMA1001092//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//5.1e-24:328:72//Hs.103948:K00627
F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds//2.1e-24:507:66//Hs.97905:AF016045
F-MAMMA1001110//Human mRNA for KIAA0125 gene, complete cds//0.94:448:57//Hs.38365:D50915
F-MAMMA1001126//Small inducible cytokine A5 (RANTES)//4.6e-18:123:85//Hs.155464:AF088219
F-MAMMA1001133
F-MAMMA1001139
F-MAMMA1001143//ESTs//2.6e-18:121:82//Hs.135117:AI091534
F-MAMMA1001145//ESTs//1.5e-36:442:69//Hs.124712:H90217
F-MAMMA1001154//EST//0.054:208:61//Hs.162088:AA505741
F-MAMMA1001161//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.6e-38:337:77//Hs.153468:AB011147
F-MAMMA1001162//EST//4.7e-16:117:90//Hs.130894:AI014299
F-MAMMA1001181
F-MAMMA1001186//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//6.5e-47:313:81//Hs.97203:U83171
F-MAMMA1001191//ESTs//5.8e-34:197:94//Hs.121575:AA758083
F-MAMMA1001198
F-MAMMA1001202//ESTs//1.5e-37:210:83//Hs.79788:AA527348
F-MAMMA1001203//ESTs//1.2e-29:199:76//Hs.141605:H92974
F-MAMMA1001206//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.5e-25:275:75//Hs.105292:AA504776
F-MAMMA1001215//ESTs//1.9e-06:300:63//Hs.113566:T03200
F-MAMMA1001220//Human mRNA for KIAA0118 gene, partial cds//2.7e-53:367:84//Hs.154326:D42087
F-MAMMA1001222//Homo sapiens mRNA for KIAA0634 protein, partial cds//1.8e-05:435:59//Hs.30898:AB014534
F-MAMMA1001243//ESTs//5.2e-19:118:94//Hs.122830:AA765587
F-MAMMA1001244
F-MAMMA1001249//ESTs//1.3e-89:420:99//Hs.147744:AI220476
F-MAMMA1001256//ESTs//2.1e-34:282:80//Hs.46158:AI160121
F-MAMMA1001259//ESTs//2.9e-07:68:95//Hs.6193:AA045149
F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.8e-41:659:64//Hs.65238:AB014561
F-MAMMA1001268//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-33:336:74//Hs.23094:M19503
F-MAMMA1001271//Homo sapiens CAGH3 mRNA, complete cds//3.4e-06:487:59//Hs.21858:U80747
F-MAMMA1001274//Human mRNA for KIAA0080 gene, partial cds//5.1e-62:396:76//Hs.74554:D38522
F-MAMMA1001280//ESTs//7.3e-14:273:67//Hs.126503:AA913832
F-MAMMA1001292//Human mRNA for KIAA0176 gene, partial cds//5.6e-54:616:71//Hs.4935:D79998
F-MAMMA1001296//ESTs//4.8e-34:136:85//Hs.70279:AA757426
F-MAMMA1001298//ESTs//0.021:73:80//Hs.114233:N91305
F-MAMMA1001305//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat//1.9e-58:295:97//Hs.102336:Z83838

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F-MAMMA1001322//ESTs//9.4e-18:221:74//Hs.139132:AA211087
F-MAMMA1001324//Human endogenous retrovirus pHE.1 (ERV9)//6.7e-75:745:73//Hs.93174:X57147
F-MAMMA1001330//ESTs//2.6e-26:169:91//Hs.4209:AA205806
F-MAMMA1001341//ESTs//0.10:267:62//Hs.155922:AI147197
F-MAMMA1001343//ESTs//0.0024:323:62//Hs.119238:AA476267
F-MAMMA1001346//Homo sapiens mRNA for KIAA0715 protein, partial cds//0.94:89:75//Hs.109358:AB018258
F-MAMMA1001383//Putative mismatch repair/binding protein hMSH3//7.3e-49:273:80//Hs.42674:U61981
F-MAMMA1001388//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR//4.6e-09:415:58//Hs.839:M86826
F-MAMMA1001397//Prostaglandin I2 (prostacyclin) synthase //1.3e-26:358:67//Hs.61333:D83402
F-MAMMA1001408//ESTs//7.2e-06:123:72//Hs.26753:R60763
F-MAMMA1001411//Autosomal dominant polycystic kidney disease type II//1.0:176:64//Hs.82001:U50928
F-MAMMA1001419//Homo sapiens KIAA0395 mRNA, partial cds//4.1e-45:409:80//Hs.43681:AL022394
F-MAMMA1001420//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//0.00042:125:75//Hs.46328:D87942
F-MAMMA1001435//Human HsLIM15 mRNA for HsLim15, complete cds//8.2e-43:543:71//Hs.37181:D64108
F-MAMMA1001442//ESTs//7.9e-15:103:92//Hs.25780:R51321
F-MAMMA1001446//ESTs//3.5e-44:292:73//Hs.111583:AA463590
F-MAMMA1001452//ESTs//0.73:152:65//Hs.163766:AI424040
F-MAMMA1001465//ESTs//1.0e-15:201:75//Hs.8836:AA181053
F-MAMMA1001476//Human mRNA for 5'-terminal region of UMK, complete cds//2.0e-24:273:72//Hs.75939:D78335
F-MAMMA1001487//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//3.2e-25:397:68//Hs.116874:AA524909
F-MAMMA1001501//CALPAIN 1, LARGE//3.1e-53:438:81//Hs.2575:X04366
F-MAMMA1001502//Human p120E4F transcription factor mRNA, complete cds//0.99:258:61//Hs.154196:U87269
F-MAMMA1001510//ESTs//8.7e-09:380:61//Hs.118701:AA420795
F-MAMMA1001522//ESTs//7.1e-44:321:80//Hs.120170:AI018506
F-MAMMA1001547
F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 protein, partial cds//7.5e-130:614:98//Hs.129937:AB007931
F-MAMMA1001575//ESTs, Weakly similar to zinc finger protein C2H2-171 [H.sapiens]//0.71:181:62//Hs.118866:AI017072
F-MAMMA1001576//Tubulin, gamma polypeptide//5.7e-97:529:91//Hs.150785:M61764
F-MAMMA1001590//EST//1.7e-13:94:92//Hs.95900:AA160339
F-MAMMA1001600//EST/1.0e-08:81:87//Hs.149220:AI247132
F-MAMMA1001604//EST//0.0070:157:62//Hs.162516:AA583375
F-MAMMA1001606//Human clone 23627 mRNA, complete cds//0.64:336:58//Hs.23642:U79266
F-MAMMA1001620//ESTs//6.8e-16:99:79//Hs.164052:AA836152
F-MAMMA1001627//Pregnancy-associated plasma protein A//0.27:379:58//Hs.158229:U28727
F-MAMMA1001630//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055//1.4e-40:447:73//Hs.154353:AL022165
F-MAMMA1001633//Human zinc finger protein (LD5-1) mRNA, complete cds//3.6e-44:611:67//Hs.57679:U57796
F-MAMMA1001635
F-MAMMA1001649//ESTs//1.4e-47:238:99//Hs.124063:T75524
F-MAMMA1001654//Homo sapiens retinal rod Na-Ca+K exchanger (NCKX1) mRNA, complete cds//0.00069:140:68//Hs.59829:AB014602
F-MAMMA1001663//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.015:135:71//Hs.27349:AB007917
F-MAMMA1001670//ESTs, Highly similar to 52 KD RO PROTEIN [Homo sapiens]//0.064:472:60//Hs.110819:AI027548
F-MAMMA1001671
F-MAMMA1001679//ESTs//0.94:55:83//Hs.152506:AA573317
F-MAMMA1001683//ESTs//1.6e-92:480:96//Hs.118496:AA036889
F-MAMMA1001686//ESTs//0.00019:171:66//Hs.140402:AI138765

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F-MAMMA1001692//ESTs//0.97:104:70//Hs.27596:AI188549
F-MAMMA1001711//Human G protein-coupled receptor (STRL22) mRNA, complete cds//8.0e-45:323:83//Hs.46468:U45984
F-MAMMA1001715//ESTs//1.3e-14:188:72//Hs.130815:AA936548
F-MAMMA1001730//ESTs//0.048:198:65//Hs.116412:AA506926
F-MAMMA1001735//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//1.5e-111:725:84//Hs.159154:U47634
F-MAMMA1001740//EST//0.77:119:65//Hs.148140:AA887098
F-MAMMA1001743//ESTs//6.5e-27:195:72//Hs.163688:H48768
F-MAMMA1001744//EST//0.00019:134:70//Hs.146863:AI161245
F-MAMMA1001745//Human Line-1 repeat mRNA with 2 open reading frames//4.7e-67:822:69//Hs.23094:M19503
F-MAMMA1001751//Homo sapiens two P domain potassium channel subunit (HOHO1) mRNA, complete cds//1.0e-36:583:65//Hs.79351:U33632
F-MAMMA1001754//ESTs//5.1e-97:456:99//Hs.157928:AA775822
F-MAMMA1001757//EST//0.042:177:63//Hs.144436:R07109
F-MAMMA1001760//Homo sapiens RET finger protein-like 1 antisense transcript, partial//6.6e-41:309:84//Hs.102576:AJ010230
F-MAMMA1001764//ESTs//0.057:290:60//Hs.68647:AA524072
F-MAMMA1001768//Human transcription factor, forkhead related activator 4 (FREAC-4) mRNA, complete cds//2.2e-05:504:60//Hs.96028:AF042832
F-MAMMA1001769//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-85:686:79//Hs.113283:AF018080
F-MAMMA1001771//Human semaphorin III family homolog mRNA, complete cds//0.00071:392:60//Hs.32981:U38276
F-MAMMA1001783//ESTs//8.8e-23:206:79//Hs.142524:H02940
F-MAMMA1001785//ESTs//1.3e-52:270:97//Hs.61809:AA503549
F-MAMMA1001788//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//6.7e-21:212:77//Hs.103948:K00627
F-MAMMA1001790//Homo sapiens KIAA0409 mRNA, partial cds//2.2e-06:139:72//Hs.5158:AB007869
F-MAMMA1001806//ESTs//6.4e-44:373:79//Hs.105665:H78987
F-MAMMA1001812//ESTs//4.8e-83:407:97//Hs.98613:D83884
F-MAMMA1001815//EST//2.1e-56:374:85//Hs.141488:N47096
F-MAMMA1001817//EST//8.6e-39:336:78//Hs.162236:AA551582
F-MAMMA1001818//EST//0.32:375:58//Hs.72729:AA167589
F-MAMMA1001820//Homo sapiens cytokine-like factor-1 precursor (CLF-1) mRNA, complete cds//0.082:153:66//Hs.114948:AF059293
F-MAMMA1001824//EST//0.0013:195:63//Hs.129275:AA992742
F-MAMMA1001836//ESTs//7.4e-52:283:95//Hs.92290:R78691
F-MAMMA1001837/Homo sapiens mRNA for zinc finger protein FPM315, complete cds//2.0e-29:641:62//Hs.56808:D88827
F-MAMMA1001848//ESTs//3.5e-53:264:99//Hs.116430:AA644665
F-MAMMA1001851//ESTs//0.00050:251:64//Hs.163776:AI393028
F-MAMMA1001854
F-MAMMA1001858//EST//1.0:113:68//Hs.132482:AA922218
F-MAMMA1001864//EST//1.3e-06:399:60//Hs.161500:N68060
F-MAMMA1001868//Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete cds//0.084:672:58//Hs.152455:AF044209
F-MAMMA1001874//ESTs//0.97:292:58//Hs.24553:AI150687
F-MAMMA1001878
F-MAMMA1001880//ESTs//9.2e-09:277:62//Hs.15776:T91944
F-MAMMA1001890//EST//1.7e-85:440:97//Hs.128842:AA977576
F-MAMMA1001907//EST//2.7e-26:294:74//Hs.98794:AA434078
F-MAMMA1001908//ESTs//3.2e-109:505:100//Hs.146145:AI391521
F-MAMMA1001931//ESTs//1.0:108:67//Hs.126624:AA768874
F-MAMMA1001956//Apolipoprotein E//1.0:322:59//Hs.76260:M12529
F-MAMMA1001963//ESTs//0.84:320:60//Hs.6523:AA218859
F-MAMMA1001969//Homo sapiens clone 23892 mRNA sequence//3.6e-79:423:81//Hs.91916:AF035317
F-MAMMA1001970//Oxytocin receptor//9.7e-31:626:64//Hs.2820:X64878
F-MAMMA1001992//EST. Weakly similar to reverse transcriptase [H.sapiens]//7.9e-09:150:72//Hs.118222:

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N91115
F-MAMMA1002009//ESTs//2.2e-18:234:69//Hs.21978:AA009633
F-MAMMA1002011//ESTs//0.91:276:59//Hs.141196:AA704826
F-MAMMA1002032//ESTs//7.8e-40:344:77//Hs.141658:N77915
F-MAMMA1002033//ESTs//2.5e-30:293:76//Hs.139158:AA226159
F-MAMMA1002041//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.2e-54:455:70//Hs.158095:AB007953
F-MAMMA1002042//ESTs//1.4e-20:199:79//Hs.140913:R44580
F-MAMMA1002047//EST//4.2e-14:170:75//Hs.124348:AA830225
F-MAMMA1002056//EST//2.1e-49:414:80//Hs.162335:AA564256
F-MAMMA1002058//EST//4.7e-26:268:78//Hs.140520:AA809305
F-MAMMA1002068//Human Line-1 repeat mRNA with 2 open reading frames//8.5e-36:382:75//Hs.23094:M19503
F-MAMMA1002078
F-MAMMA1002082
F-MAMMA1002084//EST//0.37:351:59//Hs.46576:N46012
F-MAMMA1002093//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//0.54:388:57//Hs.99423:AJ010840
F-MAMMA1002108//Loricrin//0.00066:410:56//Hs.155657:M61120
F-MAMMA1002118//EST//0.50:202:64//Hs.126872:AA932932
F-MAMMA1002125//Small inducible cytokine A5 (RANTES)//2.4e-39:272:86//Hs.155464:AF088219
F-MAMMA1002132//EST//6.4e-05:245:60//Hs.149361:AI272963
F-MAMMA1002140//ESTs//5.8e-33:212:77//Hs.141203:H52638
F-MAMMA1002143//SERUM PROTEIN MSE55//1.9e-12:192:70//Hs.148101:M88338
F-MAMMA1002145//EST//0.12:204:60//Hs.160983:AI392837
F-MAMMA1002153
F-MAMMA1002155//ESTs, Weakly similar to p40 [H.sapiens]//3.6e-67:335:97//Hs.88424:AA281385
F-MAMMA1002156//Integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)//0.99:310:58//Hs.87149:M35999
F-MAMMA1002158//EST//0.015:278:58//Hs.162666:AA605196
F-MAMMA1002170//40S RIBOSOMAL PROTEIN S2//6.9e-82:573:82//Hs.119389:X17206
F-MAMMA1002174//Human NOF1 mRNA, complete cds//2.2e-42:375:78//Hs.75859:U39400
F-MAMMA1002198//H.sapiens mRNA for thiol-specific antioxidant//3.3e-36:121:98//Hs.146354:Z22548
F-MAMMA1002209//ESTs//1.1e-84:409:98//Hs.139235:AA278362
F-MAMMA1002215//Loricrin//0.0024:369:57//Hs.155657:M61120
F-MAMMA1002219//ESTs, Weakly similar to coded for by C. elegans cDNA yk52b10.3 [C.elegans]//9.5e-41:202:100//Hs.118849:AA215645
F-MAMMA1002230//ESTs//0.92:253:60//Hs.4222:AI024063
F-MAMMA1002236//ESTs, Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]//4.6e-69:344:90//Hs.76822:AI359536
F-MAMMA1002243//Homo sapiens serine threonine kinase 11 (STK11) mRNA, complete cds//0.99:454:56//Hs.122755:AF032986
F-MAMMA1002250//Human involucrin mRNA//0.0037:396:62//Hs.157091:M13903
F-MAMMA1002267//ESTs//2.0e-12:296:62//Hs.155686:AI308841
F-MAMMA1002268//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//1.2e-06:427:61//Hs.69949:M94172
F-MAMMA1002269
F-MAMMA1002282//ESTs//5.9e-65:342:95//Hs.13962:T72715
F-MAMMA1002292//EST//0.0050:346:58//Hs.97639:AA398440
F-MAMMA1002293//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//2.8e-60:387:75//Hs.133089:AF064019
F-MAMMA1002294//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//4.3e-07:349:64//Hs.92614:M62302
F-MAMMA1002297//EST//0.98:98:68//Hs.148207:AA897460
F-MAMMA1002298//Paired basic amino acid cleaving system 4//0.0061:471:57//Hs.77234:AB001914
F-MAMMA1002299//ESTs//1.0:162:68//Hs.134132:AA205935
F-MAMMA1002308//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.9e-41:293:83//Hs.105292:AA504776
F-MAMMA1002310//Homo sapiens serine protease-like protease (nes1) mRNA, complete cds//0.0037:173:67//Hs.69423:AF055481

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F-MAMMA1002311//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.8e-41:473:65//Hs.92381:AB007956
F-MAMMA1002312//ESTs//0.0017:279:60//Hs.163773:AA806291
F-MAMMA1002317//ESTs//1.0:131:64//Hs.66075:F08908
F-MAMMA1002319//Homo sapiens clone 24566 mRNA sequence//1.2e-28:410:68//Hs.133342:AF070536
F-MAMMA1002322//ESTs//1.2e-47:356:82//Hs.152413:AA780515
F-MAMMA1002329//Homo sapiens clone 24444 RaP2 interacting protein 8 (RPIP8) mRNA, complete cds//0.0079:143:67//Hs.6755:AF055026
F-MAMMA1002332//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//1.2e-26:342:72//Hs.103948:K00627
F-MAMMA1002333//Homo sapiens mRNA for KIAA0711 protein, complete cds//6.8e-07:669:58//Hs.5333:AB018254
F-MAMMA1002339//H.sapiens mRNA for retrotransposon//3.2e-40:348:73//Hs.6940:Z48633
F-MAMMA1002347//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.9e-14:146:81//Hs.163073:R02591
F-MAMMA1002351//ESTs//1.2e-74:371:96//Hs.111429:W28907
F-MAMMA1002352//EST//1.7e-09:198:68//Hs.149218:AI247086
F-MAMMA1002353//ESTs//7.4e-15:163:77//Hs.157253:AI357539
F-MAMMA1002355//Homo sapiens KIAA0441 mRNA, complete cds//7.7e-47:307:78//Hs.32511:AB007901
F-MAMMA1002356//ESTs//0.012:380:58//Hs.105349:AA779733
F-MAMMA1002359//EST//1.1e-44:264:77//Hs.141095:H23818
F-MAMMA1002360//ESTs//7.6e-15:200:70//Hs.19770:AA447830
F-MAMMA1002361//ESTs//2.5e-29:277:79//Hs.155115:AA669923
F-MAMMA1002362//EST//0.25:304:58//Hs.1.62427:AA576345
F-MAMMA1002380//FACTOR VIII INTRON 22 PROTEIN//0.29:485:59//Hs.83363:M34677
F-MAMMA1002384//ESTs//1.1 e-05:220:65//Hs.141388:R52022
F-MAMMA1002385//ESTs, Moderately similar to T11G6.8 [C.elegans]//8.4e-118:578:97//Hs.25516:AI086362
F-MAMMA1002392//EST//0.85:319:57//Hs.126484:AA913624
F-MAMMA1002411//ESTs//0.00044:89:76//Hs.141685:AI142632
F-MAMMA1002413//ESTs//0.0020:303:61//Hs.94903:W85737
F-MAMMA1002417//ESTs//1.4e-06:223:65//Hs.143695:AA662745
F-MAMMMA1002427//ESTs//5.4e-48:356:82//Hs.146811:AA410788
F-MAMMA1002428//EST//1.0:96:71//Hs.105130:AA482030
F-MAMMA1002434//Human mRNA for KIAA0118 gene, partial cds//2.2e-52:370:83//Hs.154326:D42087
F-MAMMA1002446
F-MAMMA1002454//ESTs//9.1e-50:163:100//Hs.80162:AA534809
F-MAMMA1002461//Human diacylglycerol kinase (DAGK) mRNA, complete cds//6.3e-06:595:59//Hs.99932:L38707
F-MAMMA1002470
F-MAMMA1002475//Human MAP kinase activated protein kinase 2 mRNA, complete cds//0.018:417:58//Hs.75074:U12779
F-MAMMA1002480//ESTs//0.0015:258:62//Hs.132082:N67059
F-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//9.4e-120:560:98//Hs.155223:AF055460
F-MAMMA1002494//ESTs//2.4e-68:359:95//Hs.124652:AA857628
F-MAMMA1002498//ESTs, Weakly similar to hypothetical protein [H.sapiens]//4.0e-07:257:63//Hs.133013:AA604920
F-MAMMA1002524//Huntingtin (Huntington disease)//0.0085:215:65//Hs.79391:L12392
F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//4.5e-162:775:97//Hs.18858:AF065214
F-MAMMA1002545//ESTs//6.4e-46:351:81//Hs.146811:AA410788
F-MAMMA1002554
F-MAMMA1002556//Human beige-like protein (BGL) mRNA, partial cds//0.96:187:62//Hs.62354:M83822
F-MAMMA1002566//ESTs//0.0033:130:68//Hs.117018:AA832421
F-MAMMA1002571//EST//0.28:115:66//Hs.156768:AI351368
F-MAMMA1002573//ESTs//2.1e-4.8:265:94//Hs.155128:AI224516
F-MAMMA1002585
F-MAMMA1002590//ESTs//3.2e-11:280:63//Hs.36049:AA436831

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F-MAMMA1002597//ESTs//4.8e-10:118:77//Hs.156166:AI334107
F-MAMMA1002598//Ribosomal protein L7//3.6e-23:123:100//Hs.153:X57958
F-MAMMA1002603//EST//0.070:99:71//Hs.122387:AA789220
F-MAMMA1002612//ESTs, Moderately similar to hCDC10 protein [H.sapiens]//8.3e-18:353:65//Hs.60895: AA428463
F-MAMMA1002617//B94 PROTEIN//0.0097:229:62//Hs.75522:M92357
F-MAMMA1002618
F-MAMMA1002619
F-MAMMA1002622//Homo sapiens advillin mRNA, complete cds//4.7e-22:157:90//Hs.47344:AF041449
F-MAMMA1002623//EST//1.5e-33:168:81//Hs.141526:N52300
F-MAMMA1002625
F-MAMMA1002629//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//1.1e-35:355:76//Hs. 158241:AB007976
F-MAMMA1002636//Homo sapiens mRNA for KIAA0288 gene, complete cds//1.9e-05:439:61//Hs.91400: AB006626
F-MAMMA1002637//KINESIN LIGHT CHAIN//2.0e-47:367:72//Hs.117977:L04733
F-MAMMA1002646//EST//1.2e-32:302:78//Hs.112540:AA601385
F-MAMMA1002650//TRICHOHYALIN//1.2e-08:570:63//Hs.82276:L09190
F-MAMMA1002655//EST//8.8e-40:198:100//Hs.159724:AI393335
F-MAMMA1002662//EST//0.99:95:63//Hs.144074:AI005489
F-MAMMA1002665//Lysosomal-associated membrane protein 2//1.8e-35:722:64//Hs.8262:U36336
F-MAMMA1002671//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//8.6e-06:272:64//Hs.106070:U22398
F-MAMMA1002673
F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.2e-162:752:99//Hs.3363: D86987
F-MAMMA1002685//ESTs//7.5e-40:373:78//Hs.163937:N69915
F-MAMMA1002698//ESTs//2.5e-09:190:68//Hs.138292:AI220397
F-MAMMA1002699//Homo sapiens epsin 2b mRNA, complete cds//4.7e-56:398:81//Hs.22396:AF062085
F-MAMMA1002701//ESTs//4.3e-10:110:80//Hs.156041:AI274697
F-MAMMA1002708//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//1.1e-51:307:79//Hs. 46328:D87942
F-MAMMA1002711//EST//3.6e-38:186:77//Hs.139715:N25041
F-MAMMA1002721//EST//3.9e-06:110:71//Hs.136758:AA714692
F-MAMMA1002727//EST//0.97:137:63//Hs.145153:AI150165
F-MAMMA1002728//ESTs, Highly similar to PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE [Saccharomyces cerevisiae]//2.6e-12:129:81//Hs.154181:AA193502
F-MAMMA1002744//ESTs//0.0026:420:58//Hs.95793:AA617853
F-MAMMA1002746//ESTs//0.28:117:69//Hs.12925:T66312
F-MAMMA1002748
F-MAMMA1002754//ESTs//1.1e-34:340:77//Hs.163641:R61848
F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partial cds//1.1e-27:151:98//Hs.32168:AB007902
F-MAMMA1002764//ESTs//1.7e-45:323:84//Hs.155243:N70293
F-MAMMA1002765//EST//3.2e-11:145:73//Hs.162551:AA584782
F-MAMMA1002769
F-MAMMA1002775//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene// 7.6e-84:417:97//Hs.77705:U07563
F-MAMMA1002780//EST//0.78:210:63//Hs.149413:AI273988
F-MAMMA1002782
F-MAMMA1002796//ESTs//0.021:122:65//Hs.132221:AI380710
F-MAMMA1002807//EST//1.0e-31:184:71//Hs.161497:N66919
F-MAMMA1002820//ESTs//0.21:292:59//Hs.132513:AI778514
F-MAMMA1002830//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.4e-57:286:88//Hs.15731: AB011135
F-MAMMA1002833//Human mRNA for KIAA0033 gene, partial cds//9.1e-52:583:72//Hs.22271:D26067
F-MAMMA1002835
F-MAMMA1002838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 [Locusta migratoria]//7.7e-38:179:78//Hs.141344:H29951
F-MAMMA1002842//ESTs//1.7e-19:134:89//Hs.111583:AA463590

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F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 protein, partial cds//5.4e-137:635:99//Hs.7531:AB018353
F-MAMMA1002844//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.6e-07:329:58//Hs.107747:AI357868
F-MAMMA1002858
F-MAMMA1002868//EST//4.1e-23:180:77//Hs.163196:AA767643
F-MAMMA1002869//Human PINCH protein mRNA, complete cds//7.0e-88:696:78//Hs.83987:U09284
F-MAMMA1002871//ESTs//3.4e-93:466:96//Hs.11873:T68423
F-MAMMA1002880//EST//2.0e-09:364:59//Hs.145181:AI183632
F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete cds//3.8e-30:680:61//Hs.129732:D45027
F-MAMMA1002886//Long (electrocardiographic) QT syndrome 2//0.00075:504:60//Hs.19944:U04270
F-MAMMA1002887//ESTs//0.044:144:68//Hs.133152:H91657
F-MAMMA1002890//EST//1.7e-05:74:86//Hs.116013:AA612666
F-MAMMA1002892//EST//2.1e-67:383:93//Hs.22815:R44265
F-MAMMA1002895//Human transcription factor ERF-1 mRNA, complete cds//0.00053:382:57//Hs.61796:U85658
F-MAMMA1002908//EST//0.0022:132:68//Hs.161697:AA224952
F-MAMMA1002909//ESTs//9.1e-21:343:70//Hs.142068:AA176125
F-MAMMA1002930//ESTs//0.55:72:72//Hs.132440:AA923730
F-MAMMA1002937//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//7.9e-103:485:99//Hs.102928:AI346344
F-MAMMA1002938//Homo sapiens mRNA for KIAA0698 protein, complete cds//1.6e-194:910:98//Hs.31720:AB014598
F-MAMMA1002941//ESTs//9.5e-19:196:67//Hs.137945:AI423389
F-MAMMA1002947//ESTs//1.2e-96:460:99//Hs.156001:AI313418
F-MAMMA1002964//Homo sapiens KIAA0424 mRNA, partial cds//0.48:250:60//Hs.54697:AB007884
F-MAMMA1002970//EST//2.0e-16:132:84//Hs.136518:AA601400
F-MAMMA1002972
F-MAMMA1002973//ESTs//3.2e-43:225:74//Hs.155179:AA223932
F-MAMMA1002982//ESTs//0.0017:162:66//Hs.152669:AA604944
F-MAMMA1002987//EST//0.044:254:59//Hs.135014:AI095645
F-MAMMA1003003//Coagulation factor III (thromboplastin, tissue factor)//3.9e-22:185:83//Hs.62192:J02931
F-MAMMA1003004//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.0e-16:343:61//Hs.159897:AB007970
F-MAMMA1003007//EST//6.6e-10:265:66//Hs.144389:AA530979
F-MAMMA1003011//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.2e-51:620:69//Hs.75258:AF054174
F-MAMMA1003013//Human HOX4C mRNA for a homeobox protein//0.73:347:58//Hs.74061:X59372
F-MAMMA1003015//EST//2.5e-11:137:77//Hs.141312:H73062
F-MAMMA1003019//ESTs//0.0099:182:65//Hs.60787:AI374951
F-MAMMA1003026//EST//1.0:136:67//Hs.9123:T50137
F-MAMMA1003031//EST//1.3e-11:244:67//Hs.136611:AA669549
F-MAMMA1003035
F-MAMMA1003039//ESTs//1.4e-23:265:74//Hs.33393:R83391
F-MAMMA1003040//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.5e-93:339:85//Hs.5247:AF029750
F-MAMMA1003044//Cyclin D2//1.0:234:61//Hs.75586:D13639
F-MAMMA1003047//H.sapiens mRNA for F25B3.3 kinase like protein from C.elegans//1.0:209:60//Hs.99491:Y12336
F-MAMMA1003049//EST//0.99:126:67//Hs.162634:AA601742
F-MAMMA1003055//ESTs//0.00011:130:70//Hs.130539:R68518
F-MAMMA1003056
F-MAMMA1003057//ESTs, Moderately similar to hypothetical protein MD6 [M.musculus]//1.3e-88:334:97//Hs.96500:AI206781
F-MAMMA1003066//ESTs//0.77:88:71//Hs.143618:AI022618
F-MAMMA1003089//Homo sapiens mRNA for KIAA0631 protein, partial cds//4.5e-51:329:71//Hs.75154:AB014531
F-MAMMA1003099//Homo sapiens actin-binding protein homolog ABP-278 mRNA, complete cds//8.5e-44:288:88//Hs.81008:AF043045
F-MAMMA1003104//H.sapiens mRNA for ASM-like phosphodiesterase 3a//1.0:213:60//Hs.42945:Y08136

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F-MAMMA1003113//Homo sapiens mRNA for hair keratin acidic 3-II//0.99:200:64//Hs.32950:X82634
F-MAMMA1003127//Homo sapiens brush border myosin I (BBMI) mRNA, complete cds//5.4e-27:421:66//Hs.5394:AF105424
F-MAMMA1003135//Envoplakin//0.56:250:62//Hs.25482:U53786
F-MAMMA1003140
F-MAMMA1003146//Homo sapiens mRNA for GalT3 protein//7.2e-82:397:97//Hs.151344:Y15062
F-MAMMA1003150//Homo sapiens mRNA for KIAA0515 protein, partial cds//0.00019:297:61//Hs.108945:AB011087
F-MAMMA1003166//Glycoprotein Ib (platelet), beta polypeptide//1.2e-31:487:65//Hs.3847:U59632
F-NT2RM1000001//Human plectin (PLEC1) mRNA, complete cds//0.16:244:63//Hs.79706:U53204
F-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds//1.5e-66:385:92//Hs.82510:D31886
F-NT2RM1000032
F-NT2RM1000035//Human mRNA for KIAA0199 gene, partial cds//4.1e-110:849:81//Hs.78442:D83782
F-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.5e-108:542:95//Hs.60103:AB014590
F-NT2RM1000039//Human plectin (PLEC1) mRNA, complete cds//0.11:545:57//Hs.79706:U53204
F-NT2RM1000055//ESTs, Highly similar to TIP120 [R.norvegicus]//3.2e-69:353:96//Hs.154980:AA948067
F-NT2RM1000059//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA, complete cds//0.029:281:59//Hs.46465:U45285
F-NT2RM1000062//ESTs//0.30:368:59//Hs.131675:AA843210
F-NT2RM1000080//Homo sapiens chromosome 9, P1 clone 11659//2.8e-102:493:97//Hs.3439:AC004472
F-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds//5.8e-116:550:97//Hs.65238:AB014561
F-NT2RM1000092//Murine leukemia viral (bmi-1) oncogene homolog//0.42:190:63//Hs.431:L13689
F-NT2RM1000118//Homo sapiens clone 23763 unknown mRNA, partial cds//0.00086:126:70//Hs.92693:AF007155
F-NT2RM1000119//Peroxisome receptor 1//0.00055:458:58//Hs.158084:Z48054
F-NT2RM1000127
F-NT2RM1000131
F-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUFS6 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds//3.7e-92:448:97//Hs.49767:AF044959
F-NT2RM1000153//Homo sapiens mRNA for MTG8-related protein MTG16a, complete cds//1.0:546:58//Hs.110099:AB010419
F-NT2RM1000186//Homo sapiens clone 23763 unknown mRNA, partial cds//0.00081:126:70//Hs.92693:AF007155
F-NT2RM1000187//ESTs//3.4e-79:400:96//Hs.54971:AI424382
F-NT2RM1000199//Homo sapiens mRNA for KIAA0722 protein, complete cds//0.87:454:59//Hs.47061:AF045458
F-NT2RM1000242
F-NT2RM1000244//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.97:135:66//Hs.27910:AF049105
F-NT2RM1000252//TRICHOHYALIN//0.030:273:58//Hs.82276:L09190
F-NT2RM1000256//Glutamine-fructose-6-phosphate transaminase//1.5e-13:248:69//Hs.1674:M90516
F-NT2RM1000257//ESTs, Highly similar to similar to mago nashi [H.sapiens]//2.9e-98:530:93//Hs.104650:AI037879
F-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds//2.1e-58:460:80//Hs.23106:D50920
F-NT2RM1000271//ESTs//0.93:224:60//Hs.91226:AA649047
F-NT2RM1000272
F-NT2RM1000280//ESTs, Highly similar to VACUOLAR ATP SYNTHASE SUBUNIT D [Bos taurus]//1.3e-21:308:73//Hs.15071:AA781144
F-NT2RM1000300
F-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds//2.6e-128:708:92//Hs.5719:D63880
F-NT2RM1000318//Human mRNA for ribosomal protein L39, complete cds//1.8e-35:182:99//Hs.9837:D79205
F-NT2RM1000341//ESTs//2.3e-72:381:95//Hs.23070:AA631976
F-NT2RM1000354//EST//5.2e-27:202:84//Hs.151186:AI125798
F-NT2RM1000355//ESTs, Weakly similar to putative [M.musculus]//7.7e-75:387:95//Hs.108619:W28608
F-NT2RM1000365//ESTs//1.7e-99:495:97//Hs.103926:AA165691
F-NT2RM1000377//ESTs, Weakly similar to protein-tyrosine-phosphatase [H.sapiens]//7.4e-91:481:95//Hs.163707:AA137181

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F-NT2RM1000388//65 KD YES-ASSOCIATED PROTEIN//0.36:340:57//Hs.8939:X80507
F-NT2RM1000394//HISTONE H3.3//8.5e-91:474:93//Hs.118838:M11353
F-NT2RM1000399
F-NT2RM1000421
F-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//1.2e-85:418:97//Hs.20815:AF084928
F-NT2RM1000499//ESTs, Weakly similar to KIAA0167 protein [H.sapiens]//1.6e-38:201:97//Hs.106262:AI052382
F-NT2RM1000539//EST//0.070:145:62//Hs.149711:AI284660
F-NT2RM1000553//EST//2.2e-48:265:95//Hs.99230:AA449847
F-NT2RM1000555//ESTs//0.82:193:61//Hs.96944:AI359957
F-NT2RM1000563//Human plectin (PLEC1) mRNA, complete cds//1.0:336:58//Hs.79706:U53204
F-NT2RM1000623//Homo sapiens mRNA for KIAA0287 gene, partial cds//0.98:226:61//Hs.17931:AB006625
F-NT2RM1000648//ESTs, Weakly similar to similar to M. musculus MER5 and other AHPC/TSA proteins [C.elegans]//6.2e-51:254:98//Hs.132096:AA314601
F-NT2RM1000661//Homo sapiens translation initiation factor 4e mRNA, complete cds//8.5e-55:276:97//Hs.19122:AF038957
F-NT2RM1000666//Homo sapiens BAI 1 mRNA, complete cds//0.87:274:60//Hs.113936:AB005297
F-NT2RM1000669//ESTs//5.5e-63:481:85//Hs.90527:AI188279
F-NT2RM1000672
F-NT2RM1000691//Homa sapiens mRNA for HRIHFB2060, partial cds//7.0e-121:582:98//Hs.146282:AB015348
F-NT2RM1000699//ESTs//1.1e-89:435:97//Hs.28964:AA715101
F-NT2RM1000702//ESTs//5.4e-90:429:99//Hs.151001:AA564706
F-NT2RM1000725//Homo sapiens mRNA for neuropathy target esterase//1.5e-66:435:85//Hs.5038:AJ004832
F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cds//2.6e-127:690:92//Hs.147946:AB011139
F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds//8.2e-68:524:83//Hs.112360:AF027208
F-NT2RM1000746//ESTs//2.6e-37:231:89//Hs.94446:AA845465
F-NT2RM1000770//Homo sapiens KIAA0425 mRNA, complete cds//3.3e-09:321:63//Hs.150390:AB007885
F-NT2RM1000772//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.053:271:60//Hs.139745 : U39067
F-NT2RM1000780//Human Line-1 repeat mRNA with 2 open reading frames//6.9e-20:128:94//Hs.23094:M19503
F-NT2RM1000781//ESTs//4.4e-60:346:92//Hs.35089:N50845
F-NT2RM1000800
F-NT2RM1000802
F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds//1.2e-64:490:84//Hs.112360:AF027208
F-NT2RM1000826//ESTs//0.82:193:61//Hs.96944:AI359957
F-NT2RM1000829//Mannose-binding lectin, soluble (opsonic defect)//0.92:283:58//Hs.2314:X15422
F-NT2RM1000833//Hydroxysteroid (11-beta) dehydrogenase 2//0.022:178:67//Hs.1376:U26726
F-NT2RM1000850//Human protein tyrosine kinase related mRNA sequence//3.8e-06:384:59//Hs.90314:L05148
F-NT2RM1000852//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//3.0e-149:726:97//Hs.99423:AJ010840
F-NT2RM1000857//ESTs//0.52:274:60//Hs.112095:AA447643
F-NT2RM1000867//ESTs, Highly similar to signal peptidase:SUBUNIT//5.3e-54:277:96//Hs.11125:AI015619
F-NT2RM1000874//ESTs//0.032:185:64//Hs.97713:AA442239
F-NT2RM1000882//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//4.0e-155:750:97//Hs.132898:AC004770
F-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//8.8e-158:762:97//Hs.26285:AF082516
F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 protein, complete cds//6.3e-19:310:67//Hs.65238:AB014561
F-NT2RM1000894
F-NT2RM1000898
F-NT2RM1000905//EST//4.8e-07:77:84//Hs.148017:AI268701
F-NT2RM1000924//HOMEOBOX PROTEIN HOX-A5//0.00051:458:59//Hs.37034:M26679
F-NT2RM1000927//Homo sapiens mRNA for KIAA0807 protein, partial cds//0.084:386:58//Hs.101474:AB018350
F-NT2RM1000962//Human mRNA for KIAA0252 gene, partial cds//0.98:299:59//Hs.83419:D87440
F-NT2RM1000978
F-NT2RM1001003//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.3e-161:760:98//

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Hs.58488:U97067
F-NT2RM1001008//ESTs//1.3e-12:144:75//Hs.133122:AI025200
F-NT2RM1001043//EST//0.24:117:64//Hs.161536:N80395
F-NT2RM1001044//ESTs, Weakly similar to C43E11.9[C.elegans]//3.0e-98:491:96//Hs.102173:AA045270
F-NT2RM1001059//Human plectin (PLEC1) mRNA, complete cds//0.52:533:57//Hs.79706:U53204
F-NT2RM1001066//ESTs//1.2e-114:538:99//Hs.129020:AI380703
F-NT2RM1001072//Human beige-like protein (BGL) mRNA, partial cds//0.69:586:56//Hs.62354:M83822
F-NT2RM1001074//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.0019:294:64//Hs.30223:X90846
F-NT2RM1001082//Archain//3.9e-37:290:81//Hs.33642:X81198
F-NT2RM1001085
F-NT2RM1001092//Zinc finger protein 43 (HTF6)//1.9e-57:770:68//Hs.74107:X59244
F-NT2RM1001102//ESTs//1.2e-35:638:63//Hs.131737:AI343331
F-NT2RM1001105//WEE1-LIKE PROTEIN KINASE//0.0024:246:63//Hs.75188:U10564
F-NT2RM1001112//ESTs//8.9e-82:437:93//Hs.6330:H38495
F-NT2RM1001115
F-NT2RM1001139//Keratin 9//1.5e-05:518:59//Hs.2783:Z29074
F-NT2RM2000006//ESTs//3.9e-16:96:98//Hs.101117:AA576113
F-NT2RM2000013//RNA polymerase II polypeptide B (140 kD)//6.3e-13:640:59//Hs.148027:X63563
F-NT2RM2000030
F-NT2RM2000032//ESTs//7.1 e-18:138:68//Hs.114031:AA700958
F-NT2RM2000042//ESTs//0.0091:241:61//Hs.147895:AI286243
F-NT2RM2000092
F-NT2RM2000093//ESTs//2.6e-40:226:94//Hs.163521:H42085
F-NT2RM2000101//ESTs//1.0:235:61//Hs.48860:N27428
F-NT2RM2000124//Protein kinase, cAMP-dependent, catalytic, alpha//5.8e-46:287:88//Hs.77271:X07767
F-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds//3.0e-139:566:97//Hs.18953:AF067223
F-NT2RM2000192//EST//3.5e-07:168:65//Hs.163122:AA756999
F-NT2RM2000239//ESTs, Weakly similar to K04G2.6 [C.elegans]//3.6e-93:489:95//Hs.143499:R72672
F-nnnnnnnnnnnn//ESTs//1.0e-70:269:97//Hs.156175:AI334328
F-NT2RM2000250//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.0e-129:615:98//Hs.111862:AB011162
F-NT2RM2000259//ESTs//6.1e-30:172:85//Hs.116406:AA209520
F-NT2RM2000260//ESTs//2.5e-25:133:93//Hs.14169:AA203500
F-NT2RM2000287//ESTs//6.2e-13:97:83//Hs.118523:H98981
F-NT2RM2000322//Interferon regulatory factor 5//0.84:208:61//Hs.54434:U51127
F-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds//2.8e-176:805:99//Hs.129952:AB011132
F-NT2RM2000363//ESTs//1.2e-24:139:96//Hs.48818:N63543
F-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds//3.7e-96:599:86//Hs.75871:U48251
F-NT2RM2000371
F-NT2RM2000374//ESTs//3.2e-13:98:91//Hs.65853:AI050866
F-NT2RM2000395//Growth arrest-specific 1//0.80:129:67//Hs.65029:L13698
F-NT2RM2000402//Human p76 mRNA, complete cds//7.2e-23:714:59//Hs.28757:U81006
F-NT2RM2000407//ESTs//9.4e-92:458:96//Hs.148873:T33582
F-NT2RM2000420//EST//1.8e-61:296:99//Hs.147186:AI193053
F-NT2RM2000422//Solute carrier family 6 (neurotransmitter transporter, serotonin), member 4//1.5e-06:260:61//Hs.553:L05568
F-NT2RM2000452//ESTs//1.0:132:62//Hs.110004:AI097379
F-NT2RM2000469//ESTs//0.34:249:60//Hs.149575:AI281807
F-NT2RM2000490//Homo sapiens mRNA for KIAA0747 protein, partial cds//2.4e-16:386:63//Hs.8309:AB018290
F-NT2RM2000502//Human nicotinamide N-methyltransferase (NNMT) mRNA, complete cds//0.99:272:61//Hs.76669:U08021
F-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//1.6e-172:824:97//Hs.4812:AF061243
F-NT2RM2000522//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.18:313:60//Hs.129725:AF047487
F-NT2RM2000540//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//2.7e-41:231:94//Hs.7049:

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AI141736
F-NT2RM2000556//ESTs//3.1e-33:183:96//Hs.136990:AA769220
F-NT2RM2000566//Integrin, alpha 7B//2.0e-155:751:97//Hs.74369:AF032108
F-NT2RM2000567//RYANODINE RECEPTOR, SKELETAL MUSCLE//6.3e-09:689:59//Hs.89631:U48508
F-NT2RM2000569//ESTs//5.4e-17:170:77//Hs.158277:H09128
F-NT2RM2000577//ESTs, Highly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [Saccharomyces cerevisiae]//1.4e-33:214:92//Hs.55609:W37993
F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.8e-175:820:98//Hs.3363:D86987
F-NT2RM2000588//ESTs//1.5e-33:183:97//Hs.136990:AA769220
F-NT2RM2000594
F-NT2RM2000599//Homo sapiens Mad4 homolog (Mad4) mRNA, complete cds//0.017:253:65//Hs.102402:AF040963
F-NT2RM2000609//ESTs//1.0:220:59//Hs.110155:AA007313
F-NT2RM2000612//ESTs//0.97:208:59//Hs.73217:AA846548
F-NT2RM2000623//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.024:326:59//Hs.6150:AB011093
F-NT2RM2000624//ESTs//2.3e-118:557:99//Hs.145904:AA203258
F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds//2.0e-143:664:98//Hs.19542:AB018272
F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds//2.4e-139:664:98//Hs.7278:AB014558
F-NT2RM2000639//ESTs//0.98:144:65//Hs.154364:AI189702
F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.4e-169:518:99//Hs.115763:AB014576
F-NT2RM2000669//ESTs//1.3e-56:283:98//Hs.156342:AI337371
F-NT2RM2000691//Homo sapiens actin-related protein Arp3 (ARP3) mRNA, complete cds//6.7e-86:746:74//Hs.5321:AF006083
F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds//2.2e-50:748:64//Hs.7938:D86984
F-NT2RM2000718//Homa sapiens mRNA for HRIHFB2436, partial cds//7.6e-126:594:98//Hs.136058:AB015342
F-NT2RM2000735//Zinc finger protein 43 (HTF6)//2.7e-112:756:82//Hs.74107:X59244
F-NT2RM2000740//ESTs, Highly similar to HYPOTHETICAL 132.7 KD HELICASE IN ALG7-ENP1 INTERGENIC REGION [Saccharomyces cerevisiae]//4.2e-85:464:91//Hs.161551:W24286
F-NT2RM2000795//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.0e-82:640:81//Hs.5247:AF029750
F-NT2RM2000821//Human mRNA for KIAA0340 gene, partial cds//0.32:679:59//Hs.105919:AB002338
F-NT2RM2000837//ESTs//2.3e-105:501:98//Hs.101514:AI346701
F-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds//2.8e-185:847:99//Hs.137580:AB015046
F-NT2RM2000952//ESTs, Weakly similar to lethal(2)denticleless [D.melanogaster]//6.2e-94:441:99//Hs.59075:AI023761
F-NT2RM2000984//Human mRNA for KIAA0246 gene, partial cds//0.94:351:62//Hs.84753:D87433
F-NT2RM2001004//ESTs//5.0e-10:247:64//Hs.36049:AA436831
F-NT2RM2001035//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//2.9e-48:282:93//Hs.17035:AI080471
F-NT2RM2001065
F-NT2RM2001100//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//1.7e-08:449:62//Hs.75111:D87258
F-NT2RM2001105//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.00079:274:59//Hs.102732:U88153
F-NT2RM2001131//TRICHOHYALIN//2.5e-20:684:62//Hs.82276:L09190
F-NT2RM2001141
F-NT2RM2001152//ESTs//0.53:333:58//Hs.153087:AA649042
F-NT2RM2001177
F-NT2RM2001194//ESTs, Weakly similar to T28H10.2 [C.elegans]//2.4e-23:149:93//Hs.10618:AI288739
F-NT2RM2001196//ESTs//4.0e-98:486:97//Hs.59628:W91959
F-NT2RM2001201//Human mRNA for KIAA0005 gene, complete cds//2.8e-44:554:69//Hs.155291:D13630
F-NT2RM2001221//Homo sapiens mRNA for KIAA0806 protein, complete cds//0.97:165:64//Hs.24279:AB018349
F-NT2RM2001238//EST//6.8e-67:420:89//Hs.130586:AI004766
F-NT2RM2001243//V-jun avian sarcoma virus 17 oncogene homolog//0.87:125:64//Hs.75889:U65928
F-NT2RM2001247//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.0066:321:61//Hs.132206:

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AF039694
F-NT2RM2001256
F-NT2RM2001291//ESTs//1.1e-86:459:93//Hs.10267:W27845
F-NT2RM2001306//Homo sapiens paraoxonase (PON2) mRNA, complete cds//1.0:182:65//Hs.75221:AF001601
F-NT2RM2001312//ESTs//2.0e-35:338:70//Hs.141440:N21615
F-NT2RM2001319//ESTs, Weakly similar to No definition line found [C.elegans]//5.2e-30:277:77//Hs.25347:AI138605
F-NT2RM2001324//Homo sapiens mRNA for beta-spectrin III, complete cds//0.031:245:62//Hs.26915:AB008567
F-NT2RM2001345//ESTs//9.2e-91:428:99//Hs.151001:AA564706
F-NT2RM2001360//ESTs//0.98:45:80//Hs.133520:AA878905
F-NT2RM2001370//Human transportin (TRN) mRNA, complete cds//0.72:224:61//Hs.82925:U70322
F-NT2RM2001393//Mannosidase, alpha B, lysosomal//0.42:383:57//Hs.108969:U68382
F-NT2RM2001420//EST//1.0:287:62//Hs.125285:AA830378
F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e-97:453:99//Hs.155218:AJ007509
F-NT2RM2001499//Ecotropic retroviral receptor//5.4e-47:589:68//Hs.2928:X57303
F-NT2RM2001504//Homo sapiens agrin precursor mRNA, partial cds//0.25:328:60//Hs.68900:AF016903
F-NT2RM2001524//ESTs//1.0e-11:93:90//Hs.33687:R85969
F-NT2RM2001544//ESTs//1.0e-25:157:92//Hs.137451:AA351459
F-NT2RM2001547//ESTs//2.0e-29:168:96//Hs.116392:AA936262
F-NT2RM2001575//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro)//6.9e-28:582:64//Hs.1042:M62800
F-NT2RM2001582//ESTs, Moderately similar to red-1 [M.musculus]//0.0032:57:89//Hs.114722:AA448077
F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds//2.3e-11:282:65//Hs.32168:AB007902
F-NT2RM2001592//ESTs//4.8e-73:372:95//Hs.163801:AI391729
F-NT2RM2001605//Homo sapiens clone 23592 mRNA sequence//7.3e-87:749:75//Hs.76272:S66431
F-NT2RM2001613//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073
F-NT2RM2001632//EST//8.7e-18:222:76//Hs.160402:AI393918
F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds//3.0e-154:740:98//Hs.15832:AB014518
F-NT2RM2001637//ESTs//2.2e-06:386:61//Hs.145198:AI276952
F-NT2RM2001641//ESTs, Highly similar to NADH-CYTOCHROME B5 REDUCTASE [Bos taurus]//3.5e-13:94:92//Hs.22142:AA814725
F-NT2RM2001648//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073
F-NT2RM2001652//ESTs//2.5e-06:82:80//Hs.128203:AA972301
F-NT2RM2001659//ESTs//2.8e-15:92:98//Hs.123321:AA810287
F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//1.2e-173:802:99//Hs.31323:AF044195
F-NT2RM2001668//ESTs, Weakly similar to DNA MISMATSCH REPAIR PROTEIN MSH6 [H.sapiens]//1.1e-136:671:97//Hs.27721:U17907
F-NT2RM2001670//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.1e-25:352:70//Hs.101414:AB011129
F-NT2RM2001671//ESTs//1.8e-08:63:98//Hs.158069:AI365356
F-NT2RM2001675
F-NT2RM20016811/ESTs//0.16:197:63//Hs.20585:R10305
F-NT2RM2001688//ESTs//1.8e-24:130:100//Hs.162504:AA668211
F-NT2RM2001695//EST//5.6e-51:189:89//Hs.162197:AA535216
F-NT2RM2001696//ESTs, Highly similar to gene ERCC5 protein [H.sapiens]//5.8e-16:144:84//Hs.14671:T79937
F-NT2RM2001698//ESTs//0.14:184:63//Hs.148080:AI277415
F-NT2RM2001699//ESTs//6.5e-14:136:79//Hs.127790:AI003817
F-NT2RM2001700//Homo sapiens putative seven pass transmembrane protein (TM7SF1) mRNA, complete cds//0.95:270:61//Hs.15791:AF027826
F-NT2RM2001706//ESTs//2.8e-47:304:86//Hs.146811:AA410788
F-NT2RM2001716//Semenogelin I//0.98:153:64//Hs.1968:M81650
F-NT2RM2001718
F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence//4.4e-28:163:95//Hs.12457:AF052123

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F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.0e-112:530:98//Hs.129937:AB007931
F-NT2RM2001730//Homo sapiens mRNA for KIAA0560 protein, complete cds//0.95:269:58//Hs.129952:AB011132
F-NT2RM2001743
F-NT2RM2001753//Human AF-6 mRNA, complete cds//0.095:350:59//Hs.100469:AB011399
F-NT2RM2001760//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073
F-NT2RM2001768//ESTs//0.61:189:62//Hs.144847:AI222742
F-NT2RM2001771//Zinc finger protein 10 (KOX 1)//1.1e-66:669:71//Hs.2479:X78933
F-NT2RM2001782//YY1 transcription factor//0.094:149:65//Hs.97496:M77698
F-NT2RM2001784//ESTs//8.2e-31:190:92//Hs.144587:AI193595
F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//1.6e-48:476:74//Hs.132898:AC004770
F-NT2RM2001797//Human mRNA for KIAA0065 gene, partial cds//6.1e-66:481:72//Hs.70617:D31763
F-NT2RM2001800//Human mRNA for transcriptional activator hSNF2b, complete cds//0.49:142:66//Hs.78202:U29175
F-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//2.7e-179:827:99//Hs.31323:AF044195
F-NT2RM2001805//EST//1.0:45:80//Hs.159007:AI381341
F-NT2RM2001813//EST//0.41:268:58//Hs.150031:AI292068
F-NT2RM2001823//H.sapiens mRNA for 218kD Mi-2 protein//9.7e-21:554:60//Hs.74441:X86691
F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds//1.2e-132:738:90//Hs.7753:AF013759
F-NT2RM2001840//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.8e-58:329:86//Hs.113283:AF018080
F-NT2RM2001855//ADP-ribosylation factor 5//1.0:301:60//Hs.77541:M57567
F-NT2RM2001867//ESTs, Weakly similar to ZK792.1 [C.elegans]//3.0e-28:421:66//Hs.8763:W30741
F-NT2RM2001879//ESTs//6.3e-43:234:94//Hs.122546:AA186723
F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds//6.1e-189:866:97//Hs.4198:AB014610
F-NT2RM2001896//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin))//3.0e-13:606:57//Hs.23170:AJ005892
F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds//9.4e-178:859:97//Hs.129937:AB007931
F-NT2RM2001930//Homo sapiens semaphorin F homolog mRNA, complete cds//4.2e-08:481:59//Hs.27621:U52840
F-NT2RM2001935//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HOMOLOG 50 [Drosophila melanogaster]//0.37:424:60//Hs.118634:U66688
F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequence//2.2e-139:653:98//Hs.21811:AF091080
F-NT2RM2001950//ESTs//0.12:91:76//Hs.107295:W80392
F-NT2RM2001982
F-NT2RM2001983//Homo sapiens Tax interaction protein 2 mRNA, partial cds//1.2e-21:123:98//Hs.6454:AF089816
F-NT2RM2001989//Homo sapiens mRNA for DRIM protein//0.71:319:59//Hs.104135:AJ006778
F-NT2RM2001997//ESTs//1.7e-25:135:100//Hs.126894:AA932538
F-NT2RM2001998//ESTs, Weakly similar to Mi-2 protein [H.sapiens]//0.99:271:60//Hs.63888:AA203398
F-NT2RM2002004//Homo sapiens mRNA for KIAA0731 protein, partial cds//3.5e-37:509:65//Hs.6214:AB018274
F-NT2RM2002014//Homo sapiens mRNA for CRM1 protein, complete cds//0.79:429:58//Hs.79090:D89729
F-NT2RM2002030//Glutamine-fructose-6-phosphate transaminase//9.0e-89:822:73//Hs.1674:M90516
F-NT2RM2002049//ESTs//0.99:109:71//Hs.19303:AA928427
F-NT2RM2002055//ESTs//1.1e-91:453:98//Hs.158370:AI382154
F-NT2RM2002088//ESTs//6.1e-75:302:96//Hs.153471:AI198377
F-NT2RM2002091//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.69:293:58//Hs.89631:U48508
F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//2.5e-165:776:98//Hs.99423:AJ010840
F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds//7.6e-145:684:98//Hs.26312:AF030435
F-NT2RM2002128

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F-NT2RM2002142//ESTs//0.0031:183:66//Hs.144505:AA757274
F-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//1.4e-144:800:92//Hs.20815:AF084928
F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 protein, partial cds//1.7e-165:787:97//Hs.11147:AB007936
F-NT2RM2002580//Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)//0.064:291:61//Hs.99936:X14487
F-NT2RM4000024//RNA polymerase II polypeptide B (140 kD)//8.0e-10:610:59//Hs.148027:X63563
F-NT2RM4000027//ESTs//1.6e-64:352:94//Hs.21331:H93074
F-NT2RM4000030//ESTs//1.0:115:63//Hs.131055:AI391464
F-NT2RM4000046//ESTs//2.6e-09:207:65//Hs.143533:AI094674
F-NT2RM4000061//ESTs//0.89:207:60//Hs.98445:AI038511
F-NT2RM4000085//ESTs, Weakly similar to The KIAA0134 gene product is related to human RNA helicase A. [H.sapiens]//1.6e-30:369:70//Hs.114623:AI204280
F-NT2RM4000086
F-NT2RM4000104//Homo sapiens chromosome 16 zinc finger protein ZNF210 (ZNF210) mRNA, complete cds//1.3e-24:345:69//Hs.13128:AF060865
F-NT2RM4000139
F-NT2RM4000155
F-NT2RM4000156//ESTs//5.9e-73:345:100//Hs.155958:AA573632
F-NT2RM4000167//Homo sapiens kinesin family member protein KIF3A mRNA, complete cds//9.8e-30:676:61//Hs.159228:AF041853
F-NT2RM4000169//ESTs//2.0e-103:483:99//Hs.43729:AA497044
F-NT2RM4000191//TRICHOHYALIN//0.011:324:60//Hs.82276:L09190
F-NT2RM4000197//ESTs//1.5e-48:311:88//Hs.136144:W27744
F-NT2RM4000199//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.13:322:61//Hs.145088:AI221147
F-NT2RM4000200
F-NT2RM4000202//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.0027:424:60//HS.91400:AB006626
F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//4.4e-184:856:98//Hs.111138:AB018255
F-NT2RM4000215//SET translocation (myeloid leukemia-associated)//0.0013:358:60//Hs.75055:M93651
F-NT2RM4000229//Homo sapiens mRNA for KIAA0722 protein, complete cds//0.65:572:60//Hs.47061:AF045458
F-NT2RM4000233//ESTs//2.0e-37:269:85//Hs.148873:T33582
F-NT2RM4000244//EST//0.83:319:57//Hs.162412:AA573439
F-NT2RM4000251//ESTs, Weakly similar to CUT1 PROTEIN [Schizosaccharomyces pombe]//1.1e-16:112:92//Hs.93841:AA442297
F-NT2RM4000265//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//1.8e-48:229:83//Hs.46328:D87942
F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds//2.5e-154:609:93//Hs.31305:M99438
F-NT2RM4000324//Homo sapiens hCPE-R mRNA for CPE-receptor, complete cds//0.070:460:59//Hs.5372:AB000712
F-NT2RM4000327//ESTs//0.019:269:60//Hs.153697:AI240707
F-NT2RM4000344//ESTs, Highly similar to YME1 PROTEIN [Saccharomyces cerevisiae]//2.7e-83:432:95//Hs.12796:W27884
F-NT2RM4000349//Human mRNA for KIAA0005 gene, complete cds//5.2e-53:666:68//Hs.155291:D13630
F-NT2RM4000354//ESTs, Weakly similar to lethal(2)denticleless [D.melanogaster]//0.0078:55:92//Hs.59075:M023761
F-NT2RM4000356//ESTs//1.0:225:60//Hs.161175:AI418425
F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds//5.3e-135:628:99//Hs.8152:AB014542
F-NT2RM4000368//ESTs//4.9e-13:323:63//Hs.143695:AA662745
F-NT2RM4000386//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//2.0e-72:843:68//Hs.23796:AL022718
F-NT2RM4000395//Nitric oxide synthase 2A (inducible, hepatocytes)//0.63:166:65//Hs.946:X73029

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F-NT2RM4000414//Homo sapiens XYLB mRNA for xylulokinase, complete cds//4.9e-17:114:94//Hs.137580:AB015046
F-NT2RM4000421
F-NT2RM4000425//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.1e-42:432:74//Hs.154872:AB011166
F-NT2RM4000433//Colony stimulating factor 3 receptor (granulocyte)//0.023:543:58//Hs.2175:M59820
F-NT2RM4000457
F-NT2RM4000471//Human transcriptional corepressor hKAP1/TIF1B mRNA, complete cds//0.060:178:631/Hs.66369:U95040
F-NT2RM4000486//ESTs//9.2e-48:237:99//Hs.160685:AI280004
F-NT2RM4000496//ESTs//0.069:252:61//Hs.155958:AA573632
F-NT2RM4000511//EST//0.92:191:58//Hs.61517:AA028915
F-NT2RM4000514
F-NT2RM4000515//ESTs//7.3e-93:450:98//Hs.120975:AA034409
F-NT2RM4000520//ESTs//0.13:183:65//Hs.144828:AI221305
F-NT2RM4000531//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//1.8e-153:756:96//Hs.125870:AI364967
F-NT2RM4000532//ESTs//7.7e-43:388:78//Hs.105665:H78987
F-NT2RM4000534
F-NT2RM4000585
F-NT2RM4000590//Homo sapiens mRNA for KIAA0469 protein, complete cds//1.2e-19:593:62//Hs.7764:AB007938
F-NT2RM4000595//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III [Caenorhabditis elegans]//3.1e-104:532:96//Hs.6092:T75227
F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds//1.7e-15:305:68//Hs.40100:AB002390
F-NT2RM4000611//EST//0.76:268:58//Hs.150031:AI292068
F-NT2RM4000616
F-NT2RM4000674
F-NT2RM4000689
F-NT2RM4000698//Apolipoprotein E//1.0:290:59//Hs.76260:M12529
F-NT2RM4000700
F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//3.5e-91:744:77//Hs.42400:AF022789
F-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//2.6e-163:771:97//Hs.6823:W18181
F-NT2RM4000733//PUTATIVE TACHYKININ RECEPTOR//0.70:257:60//Hs.957:M84605
F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2e-159:743:98//Hs.137168:AB018303
F-NT2RM4000741
F-NT2RM4000751//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//1.1e-75:388:96//Hs.112361:R99396
F-NT2RM4000764//ESTs//3.8e-104:539:95//Hs.24739:H67815
F-NT2RM4000778//ESTs//1.5e-85:419:97//Hs.99838:AA204731
F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//1.8e-173:810:98//Hs.18586:AB007920
F-NT2RM4000787//EST//0.011:182:65//Hs.159928:AA969186
F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216//4.5e-156:736:98//Hs.25817:AC005306
F-NT2RM4000795//ESTs, Highly Similar to LIVER CARBOXYLESTERASE PRECURSOR [Homo sapiens]//6.7e-19:160:80//Hs.124902:AI337820
F-NT2RM4000796//Human K+ channel subunit gene, complete cds//0.96:292:62//Hs.124212:M64676
F-NT2RM4000798//ESTs//1.9e-34:271:82//Hs.128203:AA972301
F-NT2RM4000813//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds//0.052:238:64//Hs:113265:AF032387
F-NT2RM4000820//ESTs//0.053:274:61//Hs.23748:H16568
F-NT2RM4000833
F-NT2RM4000848//Human mRNA for KIAA0324 gene, partial cds//0.97:374:61//Hs.7841:AB002322
F-NT2RM4000852//EST//1.0:222:60//Hs.120354:AA718934
F-NT2RM4000855//ESTs, Highly similar to RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2 [Homo sapi-

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ens]//4.4e-29:164:95//Hs.115095:AI392943
F-NT2RM4000887
F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosamine pyrophosphorylase, complete cds//6.8e-22:407:64//Hs.21293:AB011004
F-NT2RM4000950
F-NT2RM4000971//ESTs//3.6e-27:142:100//Hs.130912:AI014546
F-NT2RM4000979//Homo sapiens KIAA0415 mRNA, complete cds//3.7e-63:571:77//Hs.7289:AB007875
F-NT2RM4000996//Zinc finger protein 3 (A8-51)//8.7e-34:381:67//Hs.2481:X78926
F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.6e-171:803:98//Hs.19542:AB018272
F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//1.1e-126:584:99//Hs.15711:AB014539
F-NT2RM4001032//Homo sapiens mRNA for KIAA0711 protein, complete cds//4.8e-05:469:58//Hs.5333:AB018254
F-NT2RM4001047//ESTs, Moderately similar to MO25 PROTEIN [M.musculus]//7.0e-56:340:92//Hs.87310:AI247543
F-NT2RM4001054//HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR I "A FORM" PRECURSOR//0.79:142:69//Hs.77424:M63835
F-NT2RM4001084
F-NT2RM4001092//Human mRNA for KIAA0050 gene, complete cds//0.045:235:62//Hs.108947:D30758
F-NT2RM4001116
F-NT2RM4001140//Human engrailed protein (EN2) gene, 5' end//0.00029:225:61//Hs.134989:L12701
F-NT2RM4001151//ESTs//1.1e-07:190:65//Hs.151691:AA443730
F-NT2RM4001155//ESTs//2.2e-12:181:74//Hs.128826:AI004145
F-NT2RM4001160//EST//0.83:166:61//Hs.117051:AA677351
F-NT2RM4001187
F-NT2RM4001191//ESTs//1.3e-42:248:93//Hs.13475:R18220
F-NT2RM4001200//Zinc finger protein 10 (KOX 1)//4.0e-68:799:69//Hs.2479:X78933
F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.4e-153:707:99//Hs.14934:AF004828
F-NT2RM4001204//ESTs, Moderately similar to HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III [Caenorhabditis elegans]//0.19:291:62//Hs.31582:AA877205
F-NT2RM4001217//Homo sapiens nuclear matrix protein NRP/B (NRPB) mRNA, complete cds//7.0e-63:715:70//Hs.104925:AF059611
F-NT2RM4001256//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//1.1e-67:208:96//Hs.26676:AA033997
F-NT2RM4001258//Homo sapiens mRNA for KIAA0481 protein, complete cds//0.0019:435:59//Hs.6360:AB007950
F-NT2RM4001309//Human Chromosome 16 BAC clone CIT987SK-254P9//0.019:356:59//Hs.26971:AC003003
F-NT2RM4001313//H.sapiens mRNA for phosphatidylinositol 3-kinase//8.0e-79:474:89//Hs.32971:Z46973
F-NT2RM4001316//ESTs//1.2e-14:126:84//Hs.154344:AA258335
F-NT2RM4001320//Human mRNA for Neuroblastoma, complete cds//3.6e-43:642:66//Hs.87435:D89016
F-NT2RM4001340//EST//0.40:135:70//Hs.161198:AI418988
F-NT2RM4001344//ESTs, Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTERGENIC REGION [Saccharomyces cerevisiae]//0.0096:284:58//Hs.120997:R56714
F-NT2RM4001347//ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-orf7 protein [C.elegans]//3.7e-52:252:100//Hs.15301:AA167818
F-NT2RM4001371//EST//0.52:262:59//Hs.145991:AI277656
F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds//7.2e-169:790:98//Hs.5151:AF098799
F-NT2RM4001384
F-NT2RM4001410//ESTs//1.1e-47:290:91//Hs.72447:AA160575
F-NT2RM4001411//Homo sapiens mRNA for APS, complete cds//2.5e-23:475:64//Hs.105052:AB000520
F-NT2RM4001412
F-NT2RM4001414//ESTs, Moderately similar to 18547_1 [H.sapiens]//5.2e-18:133:87//Hs.28209:AI073817
F-NT2RM4001437//Human mRNA for KIAA0118 gene, partial cds//2.5e-42:611:70//Hs.154326:D42087
F-NT2RM4001444
F-NT2RM4001454//ESTs//3.9e-31:169:96//Hs.117982:AA644658

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F-NT2RM4001455//ESTs//0.0054:48:100//Hs.14920:AA910914
F-NT2RM4001483//ESTs, Weakly similar to ZINC FINGER PROTEIN ZFP-36 [H.sapiens]//1.1e-71:313:99//Hs.163754:AA587784
F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//3.9e-157:724:99//Hs.153121:AB014585
F-NT2RM4001519//ESTs//0.66:264:59//Hs.139891:AA553619
F-NT2RM4001522//ESTs, Weakly similar to D9481.12 gene product [S.cerevisiae]//1.3e-114:536:99//Hs.88820:AA456247
F-NT2RM4001557
F-NT2RM4001565//ESTs//1.7e-107:509:99//Hs.146139:AA731487
F-NT2RM4001566//Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds//1.0:255:60//Hs.14207:U86453
F-NT2RM4001569//ESTs//1.4e-86:417:98//Hs.153044:AI198859
F-NT2RM4001582
F-NT2RM4001592//EST//0.61:142:64//Hs.162900:AA664566
F-NT2RM4001594//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0072:484:60//Hs.129892:AB011094
F-NT2RM4001597//ESTs, Moderately similar to red-1 [M.musculus]//2.3e-72:387:95//Hs.114722:AA448077
F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//1.1e-163:750:99//Hs.23255:AB018334
F-NT2RM4001611//ESTs, Weakly similar to F25H9.6 [C.elegans]//8.6e-05:91:79//Hs.24647:W19739
F-NT2RM4001629//ESTs, Moderately similar to 55 KD ERYTHROCYTE MEMBRANE PROTEIN [Homo sapiens]//0.0042:153:68//Hs.114832:AI147946
F-NT2RM4001650//Human mRNA for KIAA0341 gene, partial cds//0.95:328:60//Hs.101761:AB002339
F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds//8.3e-83:449:93//Hs.153685:AB002320
F-NT2RM4001666//ESTs//2.1e-11:78:96//Hs.152446:AA555323
F-NT2RM4001682//EST//0.027:145:70//Hs.133253:AI052638
F-NT2RM4001710//ESTs//0.098:140:62//Hs.5796:AA767384
F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds//2.2e-86:748:74//Hs.80712:D86957
F-NT2RM4001715//ESTs//1.3e-104:490:99//Hs.127336:AI332905
F-NT2RM4001731//Human involucrin mRNA//0.23:432:59//Hs.157091:M13903
F-NT2RM4001741//Human mRNA for KIAA0320 gene, partial cds//6.9e-80:737:73//Hs.150443:AB002318
F-NT2RM4001746//H.sapiens NF-H gene, exon 1 (and joined CDS)//2.1e-07:418:61//Hs.75735:X15306
F-NT2RM4001754//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//2.0e-27:205:83//Hs.110601:AA206719
F-NT2RM4001758//H.sapiens mRNA for serine/threonine protein kinase EMK//2.1e-86:729:75//Hs.157199:X97630
F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//7.4e-175:803:99//Hs.39871:AB018270
F-NT2RM4001783//ESTs, Weakly similar to T12D8.i [C.elegans]//3.1e-71:376:95//Hs.108396:AA160677
F-NT2RM4001810//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.99:446:58//Hs.27910:AF049105
F-NT2RM4001813//Homo sapiens clone 24820 mRNA sequence//6.6e-14:249:70//Hs.146312:AF070547
F-NT2RM4001819//Cell division cycle 2-like 1 (PITSLRE proteins)//1.4e-35:195:95//Hs.963:M37712
F-NT2RM4001823//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//2.3e-40:252:90//Hs.119294:AI379442
F-NT2RM4001828//Zinc fmger protein 157 (HZF22)//1.8e-75:688:72//Hs.89897:U28687
F-NT2RM4001836//NUCLEOBINDIN PRECURSOR//0.0022:588:59//Hs.953 :M96824
F-NT2RM4001841//ESTs//0.86:156:67//Hs.146276:AI214204
F-NT2RM4001842//ESTs//0.20:191:62//Hs.107657:AA126814
F-NT2RM4001856
F-NT2RM4001858//Human putative cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1) mRNA, complete cds//8.0e-10:244:66//Hs.22138:U49250
F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC//2.3e-150:704:98//Hs.61628:Y17711
F-NT2RM4001876//Human mRNA for KIAA0231 gene, partial cds//9.1e-44:621:66//Hs.7938:D86984
F-NT2RM4001880
F-NT2RM4001905//ESTs//7.5e-11:137:75//Hs.86950:AI204212

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F-NT2RM4001922//ESTs//2.5e-51:291:93//Hs.26660:AI312633
F-NT2RM4001930//Homo sapiens mRNA for putative glucosyltransferase, partial cds//0.98:359:57//Hs.155356:AJ224875
F-NT2RM4001938
F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//3.6e-172:808:98//Hs.118631:AF098162
F-NT2RM4001953//Human mRNA for KIAA0118 gene, partial cds//5.0e-54:362:83//Hs.154326:D42087
F-NT2RM4001965//ESTs, Weakly similar to KIAA0157 gene product is novel. [H.sapiens]//1.8e-65:337:96//Hs.130135:AA905493
F-NT2RM4001969//ESTs//0.00024:261:63//Hs.157579:AI312862
F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.2e-63:527:76//Hs.159277:AB018341
F-NT2RM4001984//EST//7.1e-05:235:61//Hs.105444:AA508082
F-NT2RM4001987//Homo sapiens mRNA for KIAA0467 protein, partial cds//0.73:181:65//Hs.11147:AB007936
F-NT2RM4002013//ESTs//0.97:185:63//Hs.103345:AI302271
F-NT2RM4002018//ESTs//2.5e-76:398:94//Hs.119544:T95601
F-NT2RM4002034
F-NT2RM4002044//ESTs//9.6e-83:410:97//Hs.128162:AA815048
F-NT2RM4002054//EST//8.5e-12:176:71//Hs.137181:R56912
F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.3e-173:803:98//Hs.153026:AB014540
F-NT2RM4002062//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]//7.0e-94:396:94//Hs.59346:AI126802
F-NT2RM4002063
F-NT2RM4002066//Homo sapiens OPA-containing protein mRNA, complete cds//1.1e-74:889:69//Hs.85313:AF071309
F-NT2RM4002067//ESTs//2.3e-34:455:69//Hs.118273:AA626040
F-NT2RM4002073//Insulin-like growth factor binding protein 2//3.2e-10:470:61//Hs.162:X16302
F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//2.9e-24:588:61//Hs.122967:AF059569
F-NT2RM4002093//Polypyrimidine tract binding protein (hnRNP I) {alternative products}//9.2e-34:532:65//Hs.146459:X66975
F-NT2RM4002109//Homo sapiens mitotic centromere-associated kinesin mRNA, complete cds//0.99:408:62//Hs.69360:U63743
F-NT2RM4002128//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.93:202:63//Hs.8152:AB014542
F-NT2RM4002140//Human p300 protein mRNA, complete cds//0.99:320:59//Hs.25272:U01877
F-NT2RM4002145//CARBOXYPEPTIDASE N 83 KD CHAIN//2.7e-06:388:59//Hs.73858:J05158
F-NT2RM4002146//ESTs, Highly similar to similar to mago nashi [H.sapiens]//1.6e-135:646:97//Hs.104650:AI037879
F-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.4e-150:763:95//Hs.22464:AF084535
F-NT2RM4002174
F-NT2RM4002189//Mucin 2, intestinal/tracheal//0.087:298:61//Hs.315:L21998
F-NT2RM4002194//Human semaphorin III family homolog mRNA, complete cds//7.3e-11:454:60//Hs.32981:U38276
F-NT2RM4002205//EST//2.6e-21:270:71//Hs.120013:AA707454
F-NT2RM4002213//Homo sapiens mRNA for KIAA0610 protein, partial cds//0.52:313:61//Hs.118087:AB011182
F-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]//8.4e-125:588:98//Hs.23900:U82984
F-NT2RM4002251//ESTs//1.0:77:74//Hs.155135:AA910966
F-NT2RM4002256//ESTs//7.5e-28:358:74//Hs.13356:AI205764
F-NT2RM4002266//Human kinase Myt1 (Myt1) mRNA, complete cds//0.73:502:57//Hs.77783:AF014118
F-NT2RM4002278//EST//0.33:138:63//Hs.144096:AI032180
F-NT2RM4002281
F-NT2RM4002287//ESTs//0.00037:55:98//Hs.11134:T62979
F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds//6.7e-50:511:72//Hs.31463:D87457
F-NT2RM4002301
F-NT2RM4002323//ESTs//3.6e-09:105:87//Hs.131737:AI343331
F-NT2RM4002339

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F-NT2RM4002344//EST//0.16:166:64//Hs.128600:AA906454
F-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//9.1e-151:708:98//Hs.26163:AB014549
F-NT2RM4002374//Homo sapiens mRNA for KIAA0720 protein, partial cds//0.0040:303:63//Hs.23741:AB018263
F-NT2RM4002383//ESTs//8.0e-16:153:78//Hs.155243:N70293
F-NT2RM4002390
F-NT2RM4002398
F-NT2RM4002409
F-NT2RM4002438//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//1.1e-55:282:96//Hs.26676:AA033997
F-NT2RM4002446//Homo sapiens clone 24574 mRNA sequence//0.59:339:60//Hs.18686:AF052151
F-NT2RM4002452
F-NT2RM4002457//Homo sapiens mRNA for epiregulin, complete cds//3.2e-25:228:81//Hs.115263:D30783
F-NT2RM4002460//EST//1.0:142:65//Hs.145370:AI252780
F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds//8.9e-165:777:98//Hs.8765:AF083255
F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//7.3e-95:464:97//Hs.94781:AB014591
F-NT2RM4002493
F-NT2RM4002499//ESTs//1.3e-44:653:67//Hs.23790:N99347
F-NT2RM4002504//Small inducible cytokine A5 (RANTES)//4.3e-30:225:83//Hs.155464:AF088219
F-NT2RM4002527//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//0.99:290:60//Hs.154968:U02020
F-NT2RM4002532//Human mRNA for KIAA0238 gene, partial cds//1.0:232:61//Hs.82042:D87075
F-NT2RM4002534//Homo sapiens angiotensin/vasopressin receptor AII/AVP mRNA, complete cds//1.0:100:70//Hs.159483:AF054176
F-NT2RM4002558//Homo sapiens amphiphysin II mRNA, complete cds//0.17:393:61//Hs.6619:U84004
F-NT2RM4002565//Homo sapiens mRNA for Asparaginyl tRNA Synthetase, complete cds//1.0:226:60//Hs.84043:D84273
F-NT2RM4002567//ESTs, Weakly similar to C17G10.1 [C.elegans]//3.3e-88:484:93//Hs.105837:AA536054
F-NT2RM4002571//ESTs, Weakly similar to UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase [H.sapiens]//0.059:121:70//Hs.155413:AA429394
F-NT2RM4002593//ESTs//1.0e-15:103:95//Hs.108920:W28151
F-NT2RM4002594//Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds//1.0e-06:499:59//Hs.79357:D78275
F-NT2RM4002623//ESTs//1.2e-11:92:92//Hs.164046:T97402
F-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds//2.0e-102:746:81//Hs.3628:AB014587
F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//3.7e-155:747:96//Hs.159597:AJ012449
F-NT2RP1000040//ESTs//1.3e-58:338:92//Hs.17534:H16907
F-NT2RP1000063//ESTs//0.0013:72:83//Hs.108196:W81647
F-NT2RP1000086//Human mRNA for KIAA0360 gene, partial cds//5.4e-185:548:91//Hs.79971:X98834
F-NT2RP1000101//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0.33:247:61//Hs.30792:AF044924
F-NT2RP1000111
F-NT2RP1000112//TTK protein kinase//3.2e-40:324:81//Hs.2052:M86699
F-NT2RP1000124//ESTs//2.4e-42:268:89//Hs.146078:AI084025
F-NT2RP1000130//ESTs, Moderately similar to HEPATOMA-DERIVED GROWTH FACTOR [H.sapiens]//1.4e-71:382:94//Hs.127842:W38901
F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds//2.1e-06:77:90//Hs.3760:AF011792
F-NT2RP1000170//EST//0.68:130:63//Hs.146994:AI184430
F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence//8.3e-140:679:97//Hs.78019:AF070535
F-NT2RP1000191//ESTs//1.3e-71:405:93//Hs.24054:N46499
F-NT2RP1000202//H.sapiens mRNA for cytokine inducible nuclear protein//2.0e-05:591:58//Hs.74019:X83703
F-NT2RP1000243
F-NT2RP1000259
F-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//5.4e-109:528:97//Hs.

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4214:AF067730
F-NT2RP1000324//ESTs//3.4e-98:499:96//Hs.42530:N41661
F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds//1.3e-148:693:98//Hs.31584:AF053551
F-NT2RP1000333//Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds//0.28:328:60//Hs.22405:AF004231
F-NT2RP1000348//Human plectin (PLEC1) mRNA, complete cds//0.018:337:62//Hs.79706:U53204
F-NT2RP1000357
F-NT2RP1000358//DYNAMIN-1//0.96:273:59//Hs.126:L07807
F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds//3.2e-126:497:86//Hs.77864:AB014538
F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete cds//5.9e-178:877:96//Hs.120360:AF064594
F-NT2RP1000409//ESTs//5.4e-59:415:83//Hs.140578:AA828031
F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.0e-179:710:98//Hs.21862:AB011159
F-NT2RP1000416//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//7.3e-177:857:97//Hs.6823:W18181
F-NT2RP1000418//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.46:222:60//Hs.89230:AF031815
F-NT2RP1000439//EST//0.98:339:56//Hs.137377:AA101603
F-NT2RP1000443//Human SLP-76 associated protein mRNA, complete cds//1.0:356:59//Hs.58435:AF001862
F-NT2RP1000460
F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence//3.7e-134:665:96//Hs.143187:AC002985
F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//6.2e-57:440:80//Hs.159154:U47634
F-NT2RP1000481//ESTs//4.8e-21:154:87//Hs.17392:AA535102
F-NT2RP1000493
F-NT2RP1000513//ESTs//2.2e-71:409:91//Hs.121029:AA480977
F-NT2RP1000522//Homo sapiens clone DT1P1A11 mRNA, CAG repeat region//0.21:255:62//Hs.98834:U92992
F-NT2RP1000547//H.sapiens mRNA for transmembrane protein rnp24//1.9e-06:337:63//Hs.75914:X92098
F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partial cds//1.4e-82:295:92//Hs.104105:AF017418
F-NT2RP1000577//Human sialoprotein mRNA, complete cds//0.014:235:65//Hs.121552:J05213
F-NT2RP1000581//VON WILLEBRAND FACTOR PRECURSOR//1.6e-33:223:89//Hs.110802:X04385
F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//2.2e-49:506:73//Hs.132898:AC004770
F-NT2RP1000629//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//3.6e-19:556:62//Hs.152936:D63475
F-NT2RP1000630
F-NT2RP1000677//Human breast tumor autoantigen mRNA, complete sequence//2.4e-05:389:59//Hs.3844:U24576
F-NT2RP1000688//ESTs, Weakly similar to T06E6.d [C.elegans]//2.5e-43:232:95//Hs.3487:AA425553
F-NT2RP1000695//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//9.2e-53:312:90//Hs.7049:AI141736
F-NT2RP1000701//Myogenic factor 3//0.81:186:63//Hs.2834:AF027148
F-NT2RP1000721//Homo sapiens mRNA for repressor protein, partial cds//4.0e-33:278:78//Hs.58167:D30612
F-NT2RP1000730//ESTs, Weakly similar to putative p150 [H.sapiens]//6.2e-40:297:84//Hs.18122:AI338045
F-NT2RP1000733//G1 to S phase transition 1//1.4e-31:286:78//Hs.2707:X17644
F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds//2.6e-123:604:96//Hs.21771:AF101434
F-NT2RP1000746
F-NT2RP1000767
F-NT2RP1000782//Human globin gene//3.6e-21:140:91//Hs.100090:M69023
F-NT2RP1000796//H.sapiens mRNA for ROX protein//0.17:404:57//Hs.25497:X96401
F-NT2RP1000825//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat//

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2.7e-23:147:91//Hs.102336:Z83838
F-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds//5.4e-143:424:96//Hs.18953:AF067223
F-NT2RP1000834//ESTs//0.18:280:60//Hs.157215:AI332903
F-NT2RP1000836//EST//0.60:103:66//Hs.145708:AI267990
F-NT2RP1000846//EST//1.2e-15:322:65//Hs.149925:AI288838
F-NT2RP1000851//ESTs//6.1e-96:459:98//Hs.121586:AA423875
F-NT2RP1000856//Human globin gene//6.7e-22:140:91//Hs.100090:M69023
F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds//2.2e-107:551:95//Hs.125156:AF064094
F-NT2RP1000902//EST//1.8e-28:218:85//Hs.145258:AI218683
F-NT2RP1000915//ESTs//8.8e-11:102:81//Hs.163740:AI248847
F-NT2RP1000916//ESTs, Weakly similar to coded for by C. elegans cDNA cm04e9 [C.elegans]//2.2e-27:159:94//Hs.122153:AA780270
F-NT2RP1000943//Human hSIAH2 mRNA, complete cds//0.45:130:68//Hs.20191:U76248
F-NT2RP1000944//EST//0.99:116:63//Hs.116633:AA668400
F-NT2RP1000947//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds//2.7e-26:185:87//Hs.108332:U39317
F-NT2RP1000954//Homo sapiens BACH1 mRNA, complete cds//0.81:329:56//Hs.154276:AB002803
F-NT2RP1000958//ESTs//1.3e-20:129:92//Hs.163740:AI248847
F-NT2RP1000959//Ribosomal protein, large, P0//0.36:76:73//Hs.73742:M17885
F-NT2RP1000966//NUCLEOLIN//1.2e-72:353:98//Hs.79110:M60858
F-NT2RP1000980//ESTs//1.6e-109:555:96//Hs.84429:N28866
F-NT2RP1000988//Human chromosome 3p21.1 gene sequence//2.6e-73:665:80//Hs.82837:L13435
F-NT2RP1001011
F-NT2RP1001013//ESTs//3.4e-40:393:74//Hs.120206:AI089163
F-NT2RP1001014
F-NT2RP1001033//Tubulin, gamma polypeptide//0.00041:313:59//Hs.150785:M61764
F-NT2RP1001073//Glucocorticoid receptor//1.0:204:61//Hs.75772:M10901
F-NT2RP1001079//ESTs//1.0:174:62//Hs.158209:AI360531
F-NT2RP1001080//Homo sapiens forkhead protein (FKHRL1) mRNA, complete cds//0.57:215:64//Hs.14845:AF032886
F-NT2RP1001113//ESTs, Weakly similar to coded for by C. elegans cDNA CEESB82F [C.elegans]//1.4e-65:293:95//Hs.32751:H38087
F-NT2RP1001173
F-NT2RP1001177//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.1e-26:259:74//Hs.75258:AF054174
F-NT2RP1001185//EST//1.4e-27:266:77//Hs.122245:AA781524
F-NT2RP1001199//ESTs//0.97:75:73//Hs.131498:AI022150
F-NT2RP1001247//Human endometrial bleeding associated factor mRNA, complete cds//1.6e-19:120:95//Hs.25195:U81523
F-NT2RP1001248//ESTs//3.0e-21:143:93//Hs.157243:AI337094
F-NT2RP1001253//PUTATIVE GLUCOSAMINE-6-PHOSPHATE ISOMERASE//1.2e-89:344:93//Hs.3090:AJ002231
F-NT2RP1001286//H.sapiens mRNA for adenosine triphosphatase, calcium//0.026:392:57//Hs.5541:Y15724
F-NT2RP1001294
F-NT2RP1001302
F-NT2RP1001310//Homo sapiens creatine transporter mRNA, complete cds//3.6e-07:379:61//Hs.154503:U36341
F-NT2RP1001311//ESTs//9.5e-73:403:93//Hs.24739:H67815
F-NT2RP1001313//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//3.1e-87:437:97//Hs.132898:AC004770
F-NT2RP1001361//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [Bos taurus]//6.8e-101:480:94//Hs.75017:AA166853
F-NT2RP1001385//EST//0.86:127:65//Hs.156304:AI336859
F-NT2RP1001395//Homo sapiens stannin mRNA, complete cds//0.75:355:58//Hs.76691:AF070673
F-NT2RP1001410//Thromboxane A2 receptor//1.0:157:63//Hs.89887:D38081
F-NT2RP1001424//ESTs//5.3e-20:118:95//Hs.159792:R60700
F-NT2RP1001432//ESTs//5.3e-20:118:95//Hs.159792:R60700
F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence//5.7e-86:422:97//Hs.21970:AF052149

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F-NT2RP1001457//H.sapiens DAP-kinase mRNA//0.40:231:61//Hs.153924:X76104
F-NT2RP1001466
F-NT2RP1001475//ESTs//1.2e-98:495:97//Hs.14347:AA287742
F-NT2RP1001482
F-NT2RP1001494
F-NT2RP1001543//ESTs//1.2e-38:207:98//Hs.131063:AI016400
F-NT2RP1001546//Homo sapiens mRNA for DAP-1 beta, complete cds//0.00077:254:64//Hs.75814:AB000277
F-NT2RP1001569
F-NT2RP1001616//Homo sapiens Tax interaction protein 1 mRNA, partial cds//2.5e-41:496:74//Hs.12956:U90913
F-NT2RP1001665//ESTs//9.4e-58:311:96//Hs.127391:AA954420
F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence//4.7e-137:685:96//Hs.93677:AF091081
F-NT2RP2000006//ESTs, Weakly similar to B0035.14 [C .elegans]//8.2e-47:300:89//Hs.6473:AA853955
F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds//1.1e-15:241:68//Hs.40100:AB002390
F-NT2RP2000008//Human mRNA for KIAA0065 gene, partial cds//1.5e-29:526:66//Hs.70617:D31763
F-NT2RP2000027//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//2.0e-26:214:82//Hs.140385:AA773359
F-NT2RP2000032//ESTs//0.91:368:57//Hs.131209:AI038867
F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//6.1e-78:383:97//Hs.8309:AB018290
F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//7.8e-97:467:97//Hs.6216:AF061749
F-NT2RP2000054//HOMEOBOX/POU DOMAIN PROTEIN RDC-1//1.0:110:70//Hs.74095:L20433
F-NT2RP2000056//Human HPTP epsilon mRNA for protein tyrosine phosphatase epsilon//1.2e-27:146:100//Hs.155991:X54134
F-NT2RP2000067//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//8.1e-41:767:61//Hs.23796:AL022718 F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence//6.5e-08:344:58//Hs.159402:AC005609
F-NT2RP2000076//H.sapiens mRNA for TFIIAl/0.00023:356:62//Hs.121686:D14887
F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//6.8e-79:278:97//Hs.54877:AF050078
F-NT2RP2000079//ESTs//1.2e-36:202:94//Hs.17606:AI279879
F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//7.1e-160:752:98//Hs.22926:AB018338
F-NT2RP2000091
F-NT2RP2000097
F-NT2RP2000098//ESTs//0.086:92:69//Hs.159389:AI371963
F-NT2RP2000108//Human mRNA for KIAA0392 gene, partial cds//1.4e-18:200:77//Hs.40100:AB002390
F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//1.6e-115:551:97//Hs.17706:AB018356
F-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [C.elegans]//0.019:72:81//Hs.5268:W22670
F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.4e-120:607:96//Hs.159273:AF054177
F-NT2RP2000133//Neuronal pentraxin II//0.00014:401:61//Hs.3281:U29195
F-NT2RP2000147//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//2.2e-18:559:60//Hs.152936:D63475
F-NT2RP2000153//Homo sapiens splicing factor (CC1.3) mRNA, complete cds//0.33:85:70//Hs.256:L10910
F-NT2RP2000157//ESTs//0.53:75:81//Hs.24885:R49291
F-NT2RP2000161//ESTs//2.6e-06:89:84//Hs.21738:AI188190
F-NT2RP2000173
F-NT2RP2000175
F-NT2RP2000183//Homo sapiens mRNA for dihydropyrimidinase related protein 4, complete cds//0.0018:324:58//Hs.100058:AB006713
F-NT2RP2000195//ESTs, Weakly similar to C37E2.2 [C.elegans]//3.6e-37:233:90//Hs.56750:AI148761
F-NT2RP2000205//ESTs//5.6e-58:317:93//Hs.49559:AA401050
F-NT2RP2000208

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F-NT2RP2000224//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds//0.0071:243:61//Hs.143641:AB009462
F-NT2RP2000232//EST//0.0087:187:62//Hs.151024:Z39990
F-NT2RP2000233//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.17:342:59//Hs.8546:U97669
F-NT2RP2000239//Human mRNA for KIAA0380 gene, complete cds//1.0:227:60//Hs.47822:AB002378
F-NT2RP2000248//EST//0.49:117:70//Hs.61016:AA019719
F-NT2RP2000257//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.51:227:60//Hs.30223:X90846
F-NT2RP2000258//ESTs//3.1e-48:261:94//Hs.128230:AA972691
F-NT2RP2000270//ESTs//2.9e-38:357:75//Hs.140329:AA714011
F-NT2RP2000274//ESTs//1.1e-106:508:98//Hs.47646:AA307599
F-NT2RP2000283//EST//1.0:139:63//Hs.128256:AA972910
F-NT2RP2000288
F-NT2RP2000289
F-NT2RP2000297//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//4.2e-60:744:70//Hs.37138:U35376
F-NT2RP2000298//ESTs//6.1e-46:322:85//Hs.159490:AI123467
F-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds//4.3e-13:140:80//Hs.58218:U82381
F-NT2RP2000327//ESTs//4.3e-18:108:98//Hs.126212:AI417006
F-NT2RP2000328//ESTs//6.3e-88:437:96//Hs.127336:AI332905
F-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//6.6e-41:607:66//Hs.101642:X60673
F-NT2RP2000337//Homo sapiens neurocan (CSPG3) mRNA, complete cds//0.96:126:69//Hs.153706:AF026547
F-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds//1.2e-130:627:97//Hs.76556:U83981
F-NT2RP2000369//Homo sapiens mRNA for KIAA0630 protein, partial cds//0.56:464:57//Hs.12259:AB014530
F-NT2RP2000412//ESTs//1.0:214:60//Hs.91226:AA649047
F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//1.6e-67:375:93//Hs.808:L28010
F-NT2RP2000420//ESTs, Moderately similar to zinc finger protein [H.sapiens]//3.9e-75:413:92//Hs.36779:AA626790
F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//6.7e-128:609:96//Hs.5819:AF102265
F-NT2RP2000438//ESTs//1.3e-05:50:98//Hs.156532:AA913381
F-NT2RP2000448//EST//1.1e-24:136:98//Hs.160402:AI393918
F-NT2RP2000459//H.sapiens mRNA for imogen 38//1.9e-22:158:87//Hs.154655:Z68747
F-NT2RP2000498//ESTs//1.0e-17:181:79//Hs.155243:N70293
F-NT2RP2000503//ESTs//4.5e-41:205:100//Hs.62751:AA765702
F-NT2RP2000510
F-NT2RP2000516
F-NT2RP2000523//ESTs, Highly similar to APOLIPOPROTEIN B MRNA EDITING PROTEIN [Rattus norvegicus]//3.2e-15:167:75//Hs.10984:AA806768
F-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//5.6e-38:196:98//Hs.14409:AB011144
F-NT2RP2000617//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//1.0:242:57//Hs.114001:Z20656
F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//4.2e-151:732:97//Hs.7314:AB014514
F-NT2RP2000644//ESTs//0.035:276:60//Hs.43660:N33174
F-NT2RP2000656
F-NT2RP2000658//ESTs//0.032:281:59//Hs.124853:AA420602
F-NT2RP2000668
F-NT2RP2000678//ESTs//2.9e-16:310:65//Hs.126867:AI093453
F-NT2RP2000704//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//2.4e-31:233:78//Hs.114905:AA088442
F-NT2RP2000710
F-NT2RP2000715
F-NT2RP2000731
F-NT2RP2000758//EST//1.0e-14:199:71//Hs.162409:AA573242
F-NT2RP2000764//ESTs, Weakly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//1.6e-74:445:89//Hs.21421:AA911739

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F-NT2RP2000809//ESTs//1.2e-36:235:89//Hs.154580:N34101
F-NT2RP2000812//Homo sapiens pendrin (PDS) mRNA, complete cds//0.22:351:58//Hs.159275:AF030880
F-NT2RP2000814
F-NT2RP2000816//Homo sapiens mRNA for KIAA0610 protein, partial cds//1.0:311:61//Hs.118087:AB011182
F-NT2RP2000819
F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds//3.4e-28:390:70//Hs.20695:AB002292
F-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds//9.5e-29:167:94//Hs.75794:U80811
F-NT2RP2000845//ESTs//1.0e-83:403:98//Hs.156828:AI336850
F-NT2RP2000863//ESTs, Highly similar to HYPOTHETICAL 36.7 KD PROTEIN C2F7.02C IN CHROMOSOME I [Schizosaccharomyces pombe]//6.4e-34:207:92//Hs.135235:AI081880
F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//7.7e-142:732:94//Hs.3615:AB018284
F-NT2RP2000892//ESTs, Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]//0.50:189:65//Hs.46146:AA418097
F-NT2RP2000931//MATRIN3//1.1e-130:610:98//Hs.78825:AB018266
F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from 7p21//5.5e-66:326:97//Hs.15144:AC005014
F-NT2RP2000938//ESTs//1.8e-28:296:75//Hs.22822:H06408
F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//1.9e-113:533:98//Hs.19822:AB018298
F-NT2RP2000965//ESTs//5.3e-59:328:94//Hs.35575:R96494
F-NT2RP2000970
F-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION [Saccharomyces cerevisiae]//7.3e-76:385:96//Hs.21875:AA243700
F-NT2RP2000987//ESTs//5.6e-11:177:72//Hs.15776:T91944
F-NT2RP2001036//ESTs//2.0e-55:352:88//Hs.122131:AA789292
F-NT2RP2001044//EST//0.069:267:60//Hs.102808:N67117
F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-145:696:97//Hs.67619:AB007957
F-NT2RP2001065
F-NT2RP2001070//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//Hs.3989:AB002313
F-NT2RP2001081
F-NT2RP2001094//ESTs//0.0071:262:64//Hs.128115:AI356560
F-NT2RP2001119//Small inducible cytokine A5 (RANTES)//2.2e-34:311:78//Hs.155464:AF088219
F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds//3.5e-33:519:63//Hs.80358:U52191
F-NT2RP2001137//ESTs, Highly similar to RAB GDP DISSOCIATION INHIBITOR ALPHA [Bos taurus]//6.4e-34:201:91//Hs.118470:AI336362
F-NT2RP2001149//EST//3.9e-27:244:78//Hs.162236:AA551582
F-NT2RP2001168//ESTs//0.0023:216:62//Hs.134938:AI091361
F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//7.4e-114:567:96//Hs.26247:AB007949
F-NT2RP2001174//H.sapiens ZNF81 gene//0.21:256:59//Hs.104020:X68011
F-NT2RP2001196
F-NT2RP2001218//ESTs//1.1e-65:337:96//Hs.115710:AA524598
F-NT2RP2001226//Guanylate cyclase 1, soluble, alpha 2//0.030:395:59//Hs.2685:Z50053
F-NT2RP2001233//Zinc finger protein 136 (clone pHZ-20)//4.4e-58:656:70//Hs.69740:U09367
F-NT2RP2001245//EST//0.018:228:62//Hs.116798:AA633813
F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//8.1e-108:514:97//Hs.7531:AB018353
F-NT2RP2001277//EST//0.42:127:66//Hs.42834:N20277
F-NT2RP2001290//Homo sapiens alpha SNAP mRNA, complete cds//1.8e-62:527:76//Hs.75848:U39412
F-NT2RP2001295//ESTs//3.4e-29:90:100//Hs.123321:AA810287
F-NT2RP2001312//ESTs//1.0:121:61//Hs.160261:AI146387
F-NT2RP2001327//Human B12 protein mRNA, complete cds//1.9e-30:359:71//Hs.76090:M80783
F-NT2RP2001328//ESTs//5.2e-103:532:94//Hs.69476:AA628522
F-NT2RP2001347//ESTs//4.3e-28:217:82//Hs.31775:H41883
F-NT2RP2001366//ESTs, Weakly similar to ZK1058.5 [C.elegans]//1.8e-72:418:91//Hs.107039:W27244
F-NT2RP2001378
F-NT2RP2001381//ESTs//0.59:235:62//Hs.118569:AI377558

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F-NT2RP2001392//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence//0.28:225:62//Hs.159402:AC005609
F-NT2RP2001394//ESTs//8.3e-22:133:78//Hs.109655:AI189767
F-NT2RP2001397//ESTs//0.090:265:60//Hs.152775:AA633088
F-NT2RP2001420
F-NT2RP2001423//ESTs, Weakly similar to hypothetical protein [H.sapiens]//0.030:443:59//Hs.140506:AA308018
F-NT2RP2001427//EST//1.9e-19:174:79//Hs.132635:AI032875
F-NT2RP2001436//EST//0.16:132:66//Hs.128265:AA972966
F-NT2RP2001440//Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide//9.8e-56:603:72//Hs.75544:Z82248
F-NT2RP2001445//ESTs//2.2e-26:193:86//Hs.128610:AA504218
F-NT2RP2001449
F-NT2RP2001450
F-NT2RP2001467
F-NT2RP2001506
F-NT2RP2001511//ESTs, Weakly similar to F48F7.1 [C.elegans]//3.2e-83:409:98//Hs.156161:AI333779
F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1//6.4e-138:657:97//Hs.4277:Y14494
F-NT2RP2001526//EST//1.0:180:61//Hs.136311:AA437134
F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//5.2e-105:384:94//Hs.99742:AF035586
F-NT2RP2001560
F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.4e-124:590:98//Hs.67619:AB007957
F-NT2RP2001576//Erythrocyte membrane protein band 4.9 (dematin)//0.046:521:60//Hs.75936:U28389
F-NT2RP2001581//EST//1.0:28:96//Hs.148002:AI264876
F-NT2RP2001597//Casein kinase 2, alpha prime polypeptide//0.069:165:65//Hs.82201:M55268
F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.3e-138:647:98//Hs.27197:AB018340
F-NT2RP2001613
F-NT2RP2001628//ESTs//4.9e-45:238:96//Hs.135222:AI082229
F-NT2RP2001634//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//4.9e-124:604:96//Hs.58488:U97067
F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds//1.3e-145:687:97//Hs.159558:AF058718
F-NT2RP2001663//Enolase 1, (alpha)//4.2e-38:372:74//Hs.675:M14328
F-NT2RP2001675//X-LINKED HELICASE II//0.040:454:58//Hs.96264:U72936
F-NT2RP2001677//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.028:285:63//Hs.6162:AB018314
F-NT2RP2001678//Homo sapiens semaphorin F homolog mRNA, complete cds//1.7e-34:328:76//Hs.27621 : U52840
F-NT2RP2001699//EST//0.029:94:68//Hs.125936:AA889091
F-NT2RP2001720//ESTs, Highly similar to Rap2 interacting protein 8 [M.musculus]//1.0:173:62//Hs.107361:AI197870
F-NT2RP2001721
F-NT2RP2001740//Homo sapiens Rigui (RIGUI) mRNA, complete cds//0.58:403:57//Hs.8114:AF022991
F-NT2RP2001748//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)//1.2e-19:151:86//Hs.77393:D14697
F-NT2RP2001762//Homo sapiens exonuclease 1a (EXO1a) mRNA, complete_cds//5.2e-34:191:96//Hs.47504:AF091754
F-NT2RP2001813//EST//0.46:183:57//Hs.144096:AI032180
F-NT2RP2001839//EST//2.5e-12:86:94//Hs.133226:AI052250
F-NT2RP2001861//Homo sapiens mRNA for paraplegin//0.068:146:71//Hs.78497:Y16610
F-NT2RP2001869//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//0.0013:174:62//Hs.9443:AF027219
F-NT2RP2001876//Allograft inflammatory factor 1//2.2e-08:162:67//Hs.76364:Y14768
F-NT2RP2001883
F-NT2RP2001898//75 KD INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR//3.0e-113:633:90//Hs.142189:M74161

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F-NT2RP2001900//EST//1.9e-14:132:84//Hs.130049:AA902650
F-NT2RP2001907//ESTs, Weakly similar to ankyrin 3, long form [H.sapiens]//0.37:263:62//Hs.106377:H29757
F-NT2RP2001926//ESTs//1.1e-87:430:97//Hs.133487:AI393754
F-NT2RP2001936
F-NT2RP2001943
F-NT2RP2001946//ESTs//1.0:110:69//Hs.7941:AA894797
F-NT2RP2001947
F-NT2RP2001969//ESTs//3.3e-93:433:93//Hs.9622:W44489
F-NT2RP2001976//Homo sapiens KIAA0432 mRNA, complete cds//0.20:238:63//Hs.155174:AB007892
F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds//7.4e-05:235:62//Hs.129943:AB011117
F-NT2RP2001991//EST//0.0027:163:68//Hs.162458:AA579196
F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds//3.2e-62:314:97//Hs.116604:AB018299
F-NT2RP2002032
F-NT2RP2002033//EST//1.2e-16:224:74//Hs.150409:AI003543
F-NT2RP2002041//EST//0.022:139:69//Hs.127219:AA939336
F-NT2RP2002046//ESTs//1.1e-35:218:92//Hs.130678:R51509
F-NT2RP2002047//ESTs//0.43:131:64//Hs.153939:AI284198
F-NT2RP2002058//Homo sapiens mRNA for KIAA0741 protein, complete cds//0.96:137:71//Hs.3615:AB018284
F-NT2RP2002066//Homo sapiens transmembrane receptor UNC5C (UNC5C) mRNA, complete cds//3.1e-36:509:66//Hs.44553:AF055634
F-NT2RP2002070//ESTs//0.00027:107:72//Hs.4852:R84241
F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//3.4e-129:643:96//Hs.11039:AF052183
F-NT2RP2002078//EST//1.0:83:65//Hs.115996:AA609014
F-NT2RP2002079//ESTs//6.2e-06:326:60//Hs.134202:AI313156
F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein//3.2e-112:533:97//Hs.155218:AJ007509
F-NT2RP2002105//Homo sapiens serine threonine kinase 11 (STK11) mRNA, complete cds//6.1e-07:408:60//Hs.122755:AF032986
F-NT2RP2002124//ESTs//1.3e-90:459:96//Hs.142053:AA224286
F-NT2RP2002137//ATPase, Ca++ transporting, plasma membrane 4//0.0032:319:59//Hs.995:M83363
F-NT2RP2002154//Homo sapiens mRNA for C17orf1 protein//1.0:149:65//Hs.100217:AJ008112
F-NT2RP2002172//EST//4.4e-14:276:67//Hs.148392:AI085314
F-NT2RP2002185//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//6.8e-61:354:91//Hs.109966:C06057
F-NT2RP2002192//Human 75-kD autoantigen (PM-Sc1) mRNA, complete cds//3.7e-37:194:97//Hs.91728:M58460
F-NT2RP2002193//Homo sapiens protein inhibitor of activated STAT protein PIASx-alpha mRNA, complete cds//6.8e-15:228:67//Hs.111323:AF077954
F-NT2RP2002208
F-NT2RP2002219//ESTs//0.0059:247:61//Hs.36495:AA151628
F-NT2RP2002231//ESTs//0.29:167:63//Hs.112013:AI394318
F-NT2RP2002235//H.sapiens mRNA for PHAPI2b protein//0.86:67:82//Hs.84264:U70439
F-NT2RP2002252//Homo sapiens mRNA for KIAA0527 protein, partial cds//0.79:264:59//Hs.129748:AB011099
F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds//2.1e-51:315:89//Hs.150595:AF005418
F-NT2RP2002259//Human L-myc protein gene, complete cds//1.2e-26:343:71//Hs.92137:M19720
F-NT2RP2002270//ESTs, Weakly similar to AF-9 PROTEIN [H.sapiens]//1.3e-31:206:88//Hs.4029:Z78373
F-NT2RP2002292//ESTs//1.3e-07:153:67//Hs.13533:H23079
F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//5.0e-95:467:96//Hs.24812:AF069532
F-NT2RP2002316//ESTs//0.95:194:63//Hs.157214:AA805445
F-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds//1.3e-124:640:95//Hs.31034:AB015594
F-NT2RP2002333//Protein-tyrosine kinase tyk2 (non-receptor)//1.0:257:60//Hs.75516:X54637
F-NT2RP2002373
F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds//3.1e-139:673:

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97//Hs.109051:AF038958
F-NT2RP2002394//Human clone 23695 mRNA sequence//0.16:456:59//Hs.90798:U79289
F-NT2RP2002408//HOMEOBOX/POU DOMAIN PROTEIN RDC-1//0.00069:265:65//Hs.74095:L20433
F-NT2RP2002426//EST//4.3e-33:271:79//Hs.145743:AI269098
F-NT2RP2002439//ESTs//0.0041:129:68//Hs.146064:AA714326
F-NT2RP2002442//ESTs, Weakly similar to similar to molybdoterin biosynthesis MOEB proteins [C.elegans]//5.6e-26:169:89//Hs.25198:AA904265
F-NT2RP2002457//ESTs//0.00031:121:71//Hs.134860:AI091436
F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds//0.0013:207:63//Hs.1560:D42045
F-NT2RP2002475//ESTs//1.0:85:75//Hs.155371:AI139929
F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds//7.6e-125:607:96//Hs.125856:AB005289
F-NT2RP2002498
F-NT2RP2002503//Human zinc finger protein (FDZF2) mRNA, complete cds//2.2e-89:314:87//Hs.102681:U95044
F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.8e-159:761:97//Hs.23255:AB018334
F-NT2RP2002520//RAB6, member RAS oncogene family//0.99:216:59//Hs.107563:M28212
F-NT2RP2002537
F-NT2RP2002546//EST//0.81:161:65//Hs.120562:AA741096
F-NT2RP2002549//ESTs//0.76:228:61//Hs.146313:AA594979
F-NT2RP2002591//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.9e-33:285:78//Hs.159277:AB018341
F-NT2RP2002595//Adenylate cyclase 8 (brain)//0.39:377:59//Hs.2522:Z35309
F-NT2RP2002606//Human Line-1 repeat mRNA with 2 open reading frames//6.4e-24:144:95//Hs.23094:M19503
F-NT2RP2002609//Human guanine nucleotide regulatory protein (tim1) mRNA, complete cds//1.0:120:68//Hs.334:U02082
F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, splice variant, 1262 bp//4.3e-28:460:63//Hs.20521:Y10805
F-NT2RP2002621
F-NT2RP2002643//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0022:210:64//Hs.155302:U57317
F-NT2RP2002672//ESTs//7.4e-30:226:84//Hs.94694:W52493
F-NT2RP2002701//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]//8.3e-56:278:97//Hs.109857:AA088385
F-NT2RP2002706//CEREBELLIN 1 PRECURSOR//0.00042:367:61//Hs.662:M58583
F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds//8.0e-42:631:65//Hs.6336:AB014572
F-NT2RP2002727
F-NT2RP2002736//ESTs//3.2e-67:336:97//Hs.86583:AA761217
F-NT2RP2002740//EST//1.0e-70:352:97//Hs.145168:AI150297
F-NT2RP2002741//Human mRNA for Neuroblastoma, complete cds//2.4e-30:628:62//Hs.87435:D89016
F-NT2RP2002750//Human mRNA for KIAA0331 gene, complete cds//2.1e-29:285:75//Hs.146395:AB002329
F-NT2RP2002752//EST//2.2e-06:126:74//Hs.159913:AA862709
F-NT2RP2002753//ESTs//4.3e-14:137:81//Hs.133478:T79705
F-NT2RP2002769//Human plectin (PLEC1) mRNA, complete cds//0.017:507:57//Hs.79706:U53204
F-NT2RP2002778//EST//1.6e-57:319:93//Hs.147519:AI216407
F-NT2RP2002800
F-NT2RP2002839//ESTs//0.075:177:62//Hs.132445:AA921763
F-NT2RP2002857//ESTs//0.99:88:69//Hs.132104:AI382142
F-NT2RP2002862
F-NT2RP2002880
F-NT2RP2002891//Homo sapiens mRNA for KIAA0673 protein, partial cds//1.0:237:62//Hs.106487:AB014573
F-NT2RP2002925//ESTs//1.6e-33:318:77//Hs.16808:W22606
F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds//3.9e-136:623:99//Hs.116674:AF038392
F-NT2RP2002929//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.24:158:65//Hs.108447:AJ000517
F-NT2RP2002939
F-NT2RP2002954

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F-NT2RP2002959//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds//6.4e-21:135:91//Hs.108332:U39317
F-NT2RP2002979
F-NT2RP2002980
F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.8e-11:272:61//Hs.122967:AF059569
F-NT2RP2002987//ESTs//8.2e-20:99:82//Hs.138965:AI004740
F-NT2RP2002993
F-NT2RP2003000//Small inducible cytokine A5 (RANTES)//2.1e-46:353:81//Hs.155464:AF088219
F-NT2RP2003034//ESTs//1.6e-08:263:66//Hs.164048:AA811741
F-NT2RP2003073//Human clone 230971 defective mariner transposon Hsmar2 mRNA sequence//4.6e-43:381:78//Hs.159176:U92019
F-NT2RP2003099//TRICHOHYALIN//0.98:183:62//Hs.82276:L09190
F-NT2RP2003108//H.sapiens nek2 mRNA for protein kinase//0.025:185:67//Hs.153704:U11050
F-NT2RP2003117//ESTs//7.6e-30:219:88//Hs.153408:AA416633
F-NT2RP2003121//ESTs//1.9e-13:158:73//Hs.129998:AI291379
F-NT2RP2003125//Serum response factor (c-fos serum response element-binding transcription factor)//4.5e-06:556:57//Hs.155321:J03161
F-NT2RP2003129//ESTs//0.095:218:63//Hs.70836:AA121544
F-NT2RP2003137
F-NT2RP2003157//Homo sapiens mRNA for KIAA0620 protein, partial cds//0.40:227:61//Hs.105958:AB014520
F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds//5.7e-113:581:93//Hs.9736:D67025
F-NT2RP2003161//ESTs//0.0095:120:65//Hs.163532:AI424170
F-NT2RP2003164//EST//0.11:179:63//Hs.163299:AA853944
F-NT2RP2003165//Human mRNA for KIAA0355 gene, complete cds//1.0e-39:342:79//Hs.153014:AB002353
F-NT2RP2003177//ESTs//3.6e-80:414:96//Hs.4767:N91123
F-NT2RP2003194//ESTs//5.4e-20:119:95//Hs.149531:AI393223
F-NT2RP2003206//EST//0.095:182:60//Hs.88461:AA278594
F-NT2RP2003228//CDC21 HOMOLOG//9.3e-138:726:93//Hs.154443:X74794
F-NT2RP2003230//ESTs//3.0e-10:239:62//Hs.163720:AA526947
F-NT2RP2003237//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.3e-62:543:77//Hs.108966:U48696
F-NT2RP2003243//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.52:200:62//Hs.102732:U88153
F-NT2RP2003265
F-NT2RP2003272//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//5.8e-57:313:93//Hs.109966:C06057
F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.9e-147:714:96//Hs.154919:AB014525
F-NT2RP2003280
F-NT2RP2003286//Homo sapiens mRNA for KIAA0587 protein, complete cds//0.0097:243:65//Hs.21862:AB011159
F-NT2RP2003293//ESTs//5.5e-28:418:70//Hs.146227:AI269334
F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds//2.0e-86:416:97//Hs.7943:AB006572
F-NT2RP2003297//EST//0.99:240:60//Hs.133228:AI052312
F-NT2RP2003307//ESTs//5.6e-15:137:81//Hs.90020:AA442752
F-NT2RP2003308
F-NT2RP2003329//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III [Caenorhabditis elegans]//1.8e-102:532:95//Hs.6092:T75227
F-NT2RP2003339//ESTs//0.13:166:63//Hs.149649:AI346765
F-NT2RP2003347//ESTs//0.96:185:59//Hs.125003:H85963
F-NT2RP2003367//Human HsLIM15 mRNA for HsLim15, complete cds//0.99:243:60//Hs.37181:D64108
F-NT2RP2003391
F-NT2RP2003393
F-NT2RP2003394//Homo sapiens Ran-GTP binding protein mRNA, partial cds//0.86:416:57//Hs.4976:AF039023
F-NT2RP2003401

BNSDOCID: <EP___1074617A2_I_>

F-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//3.7e-33:303:77//Hs.14038:R06800
F-NT2RP2003445//EST//1.7e-06:154:65//Hs.142843:R36893
F-NT2RP2003446//Prostaglandin receptor, ep1 subtype//0.81:273:61//Hs.159360:L22647
F-NT2RP2003456//EST//0.17:95:65//Hs.147190:AI193320
F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//4.3e-53:339:78//Hs.132874:AC004770
F-NT2RP2003480//Calpain, small polypeptide//1.1e-06:154:66//Hs.74451:X04106
F-NT2RP2003499//Homo sapiens delta-catenin mRNA, complete cds//3.1e-10:481:60//Hs.80220:U96136
F-NT2RP2003506
F-NT2RP2003511//Spectrin, beta, non-erythrocytic 1//0.76:189:62//Hs.107164:M96803
F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//8.3e-78:403:94//Hs.78482:Y16270
F-NT2RP2003517//Platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)//1.3e-24:151:95//Hs.1976:M12783
F-NT2RP2003522//Zinc finger protein 148 (pHZ-52)//1.1e-17:512:60//Hs.112180:AF039019
F-NT2RP2003533//ESTs//1.8e-76:373:98//Hs.140402:AI138765
F-NT2RP2003543//ESTs//9.3e-65:363:92//Hs.70643:AA030010
F-NT2RP2003559//ESTs//0.00037:93:77//Hs.157564:AI356513
F-NT2RP2003564//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro)//2.9e-28:664:63//Hs.1042:M62800
F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds//1.3e-114:541:98//Hs.129937:AB007931
F-NT2RP2003581//EST//1.0:59:76//Hs.158575:AI368947
F-NT2RP2003596//ESTs, Weakly similar to No definition line found [C.elegans]//1.3e-63:224:95//Hs.34627:AA126463
F-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.7e-124:585:98//Hs.58488:U97067
F-NT2RP2003629//ESTs//2.0e-103:535:95//Hs.105633:AA479166
F-NT2RP2003643//Kallmann syndrome 1 sequence//0.85:216:61//Hs.89591:M97252
F-NT2RP2003668//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//9.4e-47:371:80//Hs.125231:AF068006
F-NT2RP2003687//EST//2.9e-14:134:80//Hs.132635:AI032875
F-NT2RP2003691//ESTs//8.2e-47:296:83//Hs.138852:AA284247
F-NT2RP2003702//DNA POLYMERASE EPSILON, CATALYTIC SUBUNIT A//0.85:190:61//Hs.18366:L09561
F-NT2RP2003704//ESTs, Weakly similar to putative p150 [H.sapiens]//5.1e-44:269:91//Hs.139757:N95271
F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.3e-110:518:98//Hs.78494:AB011097
F-NT2RP2003713
F-NT2RP2003714//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//2.7e-56:252:83//Hs.86371:AF054180
F-NT2RP2003727//EST//0.52:277:59//Hs.69507:AA111879
F-NT2RP2003737//Human E2 ubiquitin conjugating enzyme UbcH5C (UBCH5C) mRNA, complete cds//4.0e-55:584:71//Hs.118797:U39318
F-NT2RP2003751
F-NT2RP2003760
F-NT2RP2003764
F-NT2RP2003769
F-NT2RP2003770//RETINOBLASTOMA BINDING PROTEIN 3//0.58:247:59//Hs.96055:U47677
F-NT2RP2003777
F-NT2RP2003781//ESTs, Weakly similar to C47D12.3 [C.elegans]//3.7e-63:356:92//Hs.16131:AA568689
F-NT2RP2003793//ESTs//4.8e-68:392:92//Hs.93949:AA782955
F-NT2RP2003825//ESTs//7.6e-79:232:98//Hs.14347:AA287742
F-NT2RP2003840//DNAJ PROTEIN HOMOLOG HSJ1//0.95:300:59//Hs.77768:X63368
F-NT2RP2003857//EST//1.0:112:62//Hs.139216:AA244425
F-NT2RP2003859
F-NT2RP2003871//ESTs//2.5e-44:222:99//Hs.146295:AA935780
F-NT2RP2003885
F-NT2RP2003912//ESTs, Weakly similar to G2-SPECIFIC PROTEIN KINASE NIMA [Emericella nidulans]//2.2e-

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113:632:92//Hs.50072:AI378221
F-NT2RP2003952//ESTs, Moderately similar to 60S RIBOSOMAL PROTEIN L32 [H.sapiens]//1.0:146:67//Hs.156920:AA489296
F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//6.8e-30:165:96//Hs.35086:AB014458
F-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//7.9e-116:610:94//Hs.7302:AB007916
F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//3.2e-161:783:96//Hs.7316:AB018347
F-NT2RP2003984
F-NT2RP2003986//ESTs//1.3e-39:296:83//Hs.152482:AI050036
F-NT2RP2003988//Thiopurine S-methyltransferase//7.1e-44:532:70//Hs.51124:AF019369
F-NT2RP2004013//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo sapiens]//7.0e-104:556:93//Hs.111081:AI380378
F-NT2RP2004014
F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127//6.0e-11:120:80//Hs.10116:AC004780
F-NT2RP2004042
F-NT2RP2004066//Homo sapiens zinc finger protein (ZnF20) mRNA, complete cds//0.80:292:61//Hs.1147:AF011573
F-NT2RP2004081//ESTs//5.7e-87:427:96//Hs.102296:AI217942
F-NT2RP2004098//Homo sapiens leucine-rich repeat protein SHOC-2 (SHOC-2) mRNA, complete cds//0.15:199:60//Hs.104315:AF054828
F-NT2RP2004124//Homo sapiens mRNA for ephrin-A2//0.98:233:59//Hs.158306:AJ007292
F-NT2RP2004142
F-NT2RP2004152//ESTs//5.7e-35:187:96//Hs.98977:AA625872
F-NT2RP2004165//Homo sapiens serine kinase SRPK2 mRNA, complete cds//0.69:176:63//Hs.78353:U88666
F-NT2RP2004170//ESTs//3.9e-05:380:61//Hs.143748:AI419966
F-NT2RP2004172//ESTs//5.8e-18:104:99//Hs.157031:AI343501
F-NT2RP2004187//ESTs, Moderately similar to zinc finger protein [H.sapiens]//1.7e-16:276:67//Hs.36779:AA626790
F-NT2RP2004194//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//1.0:124:69//Hs.155302:U57317
F-NT2RP2004196
F-NT2RP2004207//ESTs//3.8e-11:92:88//Hs.22678:AA604756
F-NT2RP2004226//ESTs, Weakly Similar to teg292 protein [M.musculus]//1.8e-80:386:98//Hs.68791:AA527270
F-NT2RP2004232//Protein kinase C, mu//3.9e-36:448:67//Hs.2891:X75756
F-NT2RP2004239//ESTs//0.12:196:61//Hs.127209:AA976680
F-NT2RP2004240//EST//1.0:134:63//Hs.104466:AA282536
F-NT2RP2004242//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.27:313:59//Hs.129725:AF047487
F-NT2RP2004245//ESTs, Weakly similar to No definition line found [C.elegans]//8.2e-51:474:74//Hs.108990:N25951
F-NT2RP2004270//MUELLERIAN INHIBITING FACTOR PRECURSOR//1.6e-06:490:60//Hs.12432:AC005263
F-NT2RP2004300//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 3//0.35:157:67//Hs.37121:Z37544
F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds//1.5e-151:735:97//Hs.61152:AF000416
F-NT2RP2004321//ESTs//2.6e-64:385:88//Hs.133128:W27735
F-NT2RP2004339//ESTs//3.3e-46:338:83//Hs.145091:AA814510
F-NT2RP2004347//ESTs//1.0:184:61//Hs.134469:AA731632
F-NT2RP2004364//ESTs//2.9e-70:366:95//Hs.14928:AA256202
F-NT2RP2004365
F-NT2RP2004366//Homo sapiens mRNA for DFFRY protein, abundant transcript//0.60:295:57//Hs.39163:AF000986
F-NT2RP2004373
F-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III [Caenorhabditis elegans]//3.3e-97:477:98//Hs.30490:AA146916
F-NT2RP2004392//ESTs//2.6e-61:305:98//Hs.43100:AA186588
F-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21//1.4e-174:875:95//Hs.152759:AC005164
F-NT2RP2004399//ESTs, Weakly similar to K01H12.1 [C.elegans]//1.2e-92:519:91//Hs.13275:AI341468

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F-NT2RP2004400//EST//0.018:150:65//Hs.158739:AI375367
F-NT2RP2004412
F-NT2RP2004425//EST//0.049:145:64/Hs.160759:R36944
F-NT2RP2004463//ESTs//1.5e-40:207:98//Hs.98057:C15687
F-NT2RP2004476//Homo sapiens TWIK-related acid-sensitive K+ channel (TASK) mRNA, complete cds//0.45:208:61//Hs.24040:AF006823
F-NT2RP2004490
F-NT2RP2004512//ESTs//0.0012:330:61//Hs.70258:AI091203
F-NT2RP2004523//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.3e-29:270:79//Hs.73614:U83460
F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cds//4.6e-139:687:96//Hs.129908:AB011163
F-NT2RP2004551//ESTs//0.0075:285:62//Hs.149442:AI346891
F-NT2RP2004568//Homo sapiens antigen NY-CO-16 mRNA, complete cds//8.8e-06:291:61//Hs.132206:AF039694
F-NT2RP2004580//Small inducible cytokine A5 (RANTES)//1.2e-45:334:82//Hs.155464:AF088219
F-NT2RP2004587//Homo sapiens mRNA for KIAA0766 protein, complete cds//0.98:136:64//Hs.28020:AB018309
F-NT2RP2004594//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//1.0:104:68//Hs.125729:N99898
F-NT2RP2004600//Homo sapiens mRNA for Hrs, complete cds//0.20:260:60//Hs.24756:U43895
F-NT2RP2004602//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-59:273:93//Hs.12845:N28835
F-NT2RP2004614//EST//0.99:103:68//Hs.148738:AI224908
F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//8.4e-104:496:98//Hs.5198:AJ006291
F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds//5.2e-155:728:98//Hs.29956:AB007929
F-NT2RP2004675//EST//0.65:151:62//Hs.130504:AI003839
F-NT2RP2004681
F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.1e-61:327:94//Hs.154919:AB014525
F-NT2RP2004709//ESTs//2.2e-05:98:77//Hs.161898:AA286942
F-NT2RP2004710//ESTs//0.0035:76:82//Hs.108470:R93780
F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds//2.1e-118:582:96//Hs.4236:AB007947
F-NT2RP2004743//EST//0.11:170:64//Hs.112670:AA609242
F-NT2RP2004767//EST//1.5e-09:303:65//Hs.148374:AA948183
F-NT2RP2004768//ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE PAK [Rattus norvegicus]//3.7e-110:548:96//Hs.85768:W16504
F-NT2RP2004775//Homo sapiens transcriptional regulatory protein p54 mRNA, complete cds//0.025:547:57//Hs.107474:AF045451
F-NT2RP2004791//Human endosome-associated protein (EEA1) mRNA, complete cds//0.99:121:64//Hs.2864:L40157
F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//4.9e-118:594:95//Hs.40820:AF058953
F-NT2RP2004802//ESTs//5.6e-16:116:91//Hs.153841:N36043
F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//6.8e-103:495:97//Hs.67052:AF054179
F-NT2RP2004841//Human transposon-like element mRNA//3.0e-70:519:83//Hs.84775:M23161
F-NT2RP2004861//ESTs//6.7e-89:427:98//Hs.132980:AI290258
F-NT2RP2004897//ESTs//6.4e-81:431:94//Hs.130961:N79111
F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds//6.5e-84:418:95//Hs.25619:AB007144
F-NT2RP2004936
F-NT2RP2004959
F-NT2RP2004961//Human mRNA for KIAA0065 gene, partial cds//7.2e-26:456:66//Hs.70617:D31763
F-NT2RP2004962//EST//2.8e-15:242:69//Hs.146794:AI149478
F-NT2RP2004967//ESTs//0.0022:218:63//Hs.131987:AI239735
F-NT2RP2004978//Homo sapiens mRNA for KIAA0458 protein, complete cds//1.0:218:61//Hs.7414:AB007927
F-NT2RP2004982//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds//0.13:260:60//Hs.41723:U37426

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F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds//4.8e-22:431:65//Hs.8127:D63478
F-NT2RP2004999
F-NT2RP2005000//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//0.99:269:58//Hs.124161:AF065164
F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//1.9e-160:782:97//Hs.155972:AB014515
F-NT2RP2005003//H.sapiens Staf50 mRNA//9.9e-44:430:75//Hs.68054:X82200
F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds//4.5e-100:501:96//Hs.31575:AF100141
F-NT2RP2005018//Arachidonate 5-lipoxygenase//1.0:232:58//Hs.89499:J03600
F-NT2RP2005020//ESTs//1.2e-06:61:100//Hs.106160:AA527433
F-NT2RP2005022//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.095:271:60//Hs.139745:U39067
F-NT2RP2005031//Homo sapiens mRNA for SCP-1, complete cds//0.99:338:61//Hs.112743:D67035
F-NT2RP2005037//Homo sapiens mRNA for repressor protein, partial cds//0.098:217:60//Hs.58167:D30612
F-NT2RP2005038//Homo sapiens protease-activated receptor 4 mRNA, complete cds//0.22:498:59//Hs.137574:AF055917
F-NT2RP2005108//ESTs//0.74:145:63//Hs.116557:AA657838
F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//6.4e-105:495:98//Hs.22616:AB014564
F-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//9.2e-29:157:98//Hs.100555:X98743
F-NT2RP2005139//ESTs//2.6e-91:479:95//Hs.125037:W42803
F-NT2RP2005140//ESTs//0.81:308:59//Hs.27308:AA534947
F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds//8.3e-91:447:96//Hs.132226:AF045583
F-NT2RP2005147
F-NT2RP2005159//ESTs//1.5e-44:242:94//Hs.109819:AI357582
F-NT2RP2005162//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.97:80:73//Hs.107747:AI357868
F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein//4.4e-127:633:96//Hs.155218:AJ007509
F-NT2RP2005204//H.sapiens 5T4 gene for 5T4 Oncofetal antigen//0.0034:187:66//Hs.82128:AJ012159
F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-66:340:95//Hs.8173:AC005189
F-NT2RP2005239//EST//1.3e-05:215:66//Hs.129528:AA994783
F-NT2RP2005254//H.sapiens mRNA for PHAPI2b protein//1.0:101:71//Hs.84264:U70439
F-NT2RP2005270//Homo sapiens creatine transporter mRNA, complete cds//0.56:114:68//Hs.154503:U36341
F-NT2RP2005276//Homo sapiens acyl-CoA synthetase 4 (ACS4) mRNA, complete cds//1.2e-40:594:65//Hs.81452:AF030555
F-NT2RP2005287//ESTs//8.2e-07:175:70//Hs.117134:AI383932
F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.3e-123:604:96//Hs.27007:AF060219
F-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//1.3e-141:670:98//Hs.44766:AJ007590
F-NT2RP2005293//EST//1.9e-50:254:98//Hs.162017:AA505833
F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.6e-97:483:96//Hs.115763:AB014576
F-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds//2.6e-23:166:90//Hs.1569:U11701
F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds//0.016:353:62//Hs.113265:AF032387
F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds//2.8e-30:456:66//Hs.44697:AB011138
F-NT2RP2005354//ESTs//0.71:192:60//Hs.39063:AA708958
F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-100:489:96//Hs.107254:AC005943
F-NT2RP2005360//ESTs//8.2e-35:190:95//Hs.163038:AA700122
F-NT2RP2005393//Homo sapiens CTG26 alternate open reading frame mRNA, complete cds//0.87:244:59//Hs.113252:U80761
F-NT2RP2005407
F-NT2RP2005436//Homo sapiens mRNA for KIAA0561 protein, partial cds//0.28:338:57//Hs.6189:AB011133
F-NT2RP2005441//ESTs//3.3e-45:238:96//Hs.5209:AA780068
F-NT2RP2005453//ESTs//2.1e-20:115:99//Hs.133087:AI091164

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F-NT2RP2005457//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [Bos taurus]//8.5e-48:295:90//Hs.75017:AA166853
F-NT2RP2005464//ESTs//2.0e-99:495:96//Hs.3530:AA808243
F-NT2RP2005465//V-crk avian sarcoma virus CT10 oncogene homolog//0.032:176:64//Hs.16:D10656
F-NT2RP2005472//ESTs//1.4e-34:180:98//Hs.158892:AD78412
F-NT2RP2005476//Homo sapiens mRNA for KIAA0772 protein, complete cds//9.9e-48:432:77//Hs.15519:AB018315
F-NT2RP2005490//ESTs//4.5e-19:165:84//Hs.134382:AA083573
F-NT2RP2005491
F-NT2RP2005495//ESTs//5.6e-96:452:99//Hs.145417:AI084164
F-NT2RP2005496//Human mRNA for KIAA0326 gene, partial cds//4.4e-48:621:68//Hs.6833:AB002324
F-NT2RP2005498//Human protein phosphatase 2A beta subunit mRNA, complete cds//1.6e-63:503:78//Hs.7688:M64930
F-NT2RP2005501//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.56:139:66//Hs.8546:U97669
F-NT2RP2005509//Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)//1.0:291:59//Hs.89709:L35546
F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//1.2e-82:444:92//Hs.119023:AF092563
F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds//2.2e-19:112:99//Hs.6232:AB018307
F-NT2RP2005531//ESTs, Weakly similar to erythrocyte membrane protein 4.1 [H.sapiens]//3.5e-50:366:83//Hs.61833:AA036735
F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//9.4e-155:747:97//Hs.159597:AJ012449
F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.9e-131:618:98//Hs.62515:AB007963
F-NT2RP2005549//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C16C10.10 IN CHROMOSOME III [C.elegans]//2.5e-51:292:93//Hs.105684:H24407
F-NT2RP2005555//EST//0.046:308:57//Hs.145962:AI276822
F-NT2RP2005557//ESTs//4.6e-48:382:79//Hs.125014:AI422839
F-NT2RP2005581//ESTs//6.3e-28:166:93//Hs.87803:AA034436
F-NT2RP2005600//ESTs//1.6e-40:228:93//Hs.160085:AI218627
F-NT2RP2005605//ESTs//5.7e-13:115:86//Hs.37718:H60071
F-NT2RP2005620//Homo sapiens epsin 2b mRNA, complete cds//3.1e-92:447:97//Hs.22396:AF062085
F-NT2RP2005622//ESTs//0.16:242:63//Hs.136395:AA523702
F-NT2RP2005635
F-NT2RP2005637//ESTs//0.055:96:69//Hs.105998:R90905
F-NT2RP2005640//ESTs//4.5e-16:107:92//Hs.150823:AI292145
F-NT2RP2005645//ESTs//2.7e-29:181:90//Hs.121653:AI375440
F-NT2RP2005651//Oxysterol binding protein//0.00011:122:69//Hs.1433065:M86917
F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds//1.5e-08:351:62//Hs.91400:AB006626
F-NT2RP2005669//ESTs//0.016:185:64//Hs.97713:AA442239
F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//7.7e-96:462:98//Hs.25664:AF089814
F-NT2RP2005683//ESTs//0.83:242:62//Hs.136395:AA523702
F-NT2RP2005690//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.5e-11:328:61//Hs.79217:M77836
F-NT2RP2005694
F-NT2RP2005701//Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA, complete cds//0.15:496:55//Hs.79326:L76703
F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//5.1e-126:599:97//Hs.61638:AB018342
F-NT2RP2005719//ESTs//0.58:326:60//Hs.157209:N57527
F-NT2RP2005722//Zinc finger protein 136 (clone pHZ-20)//8.2e-46:415:77//Hs.69740:U09367
F-NT2RP2005723//ESTs//1.0e-15:141:81//Hs.163747:AA174017
F-NT2RP2005726//EST//3.4e-15:96:95//Hs.156170:AI334191
F-NT2RP2005732//ESTs//0.99:162:62//Hs.154914:AA721086
F-NT2RP2005741//Homo sapiens chondroadherin gene, 5'flanking region and//0.80:362:58//Hs.97220:U96769

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F-NT2RP2005748//H.sapiens ZNF33B gene//0.47:99:65//Hs.72991:X68688
F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//2.5e-23:134:96//Hs.159651:AF068868
F-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//4.0e-102:486:98//Hs.26285:AF082516
F-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A-LIKE NUK-34//2.3e-05:425:56//Hs.79768:D21853
F-NT2RP2005767//Homolog 2 of Drosophila large discs//0.085:262:61//Hs.23205:X82895
F-NT2RP2005773//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.0e-16:153:82//Hs.79217:M77836
F-NT2RP2005775//Human thimet oligopeptidase (THOP1) mRNA, complete cds//1.7e-42:645:64//Hs.78769:Z50115
F-NT2RP2005781//ESTs//1.1e-19:132:90//Hs.13550:AI378556
F-NT2RP2005784//Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein//2.9e-06:201:67//Hs.34853:U28368
F-NT2RP2005804//ESTs//1.2e-07:62:93//Hs.125509:AA883820
F-NT2RP2005812
F-NT2RP2005815//ESTs//1.9e-32:173:97//Hs.144587:AI193595
F-NT2RP2005835
F-NT2RP2005841//Homo sapiens retinal rod Na-Ca+K exchanger (NCKX1) mRNA, complete cds//0.94:148:65//Hs.59829:AB014602
F-NT2RP2005853
F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//5.4e-176:829:98//Hs.50758:AF092564
F-NT2RP2005859//ESTs//2.1e-97:537:92//Hs.131915:W22567
F-NT2RP2005868
F-NT2RP2005886//Human putative M phase phosphoprotein 1 (MPP1) mRNA, partial cds//0.26:728:57//Hs.240:L16782
F-NT2RP2005890//ESTs//2.0e-97:453:100//Hs.88671:AA279943
F-NT2RP2005901//ESTs//0.99:188:64//Hs.28639:R78360
F-NT2RP2005908//ESTs//2.5e-43:325:82//Hs.152340:AA521399
F-NT2RP2005933//ESTs, Highly similar to nucleoporin p54 [R.norvegicus]//7.9e-90:326:98//Hs.156882:AA292186
F-NT2RP2005942//H.sapiens PAP mRNA//5.1e-48:618:67//Hs.49007:X76770
F-NT2RP2005980//ESTs//2.8e-22:358:68//Hs.125446:AA883339
F-NT2RP2006023
F-NT2RP2006038//ESTs//8.0e-37:351:74//Hs.128787:AA418382
F-NT2RP2006043//Human novel homeobox mRNA for a DNA binding protein//0.51:271:59//Hs.37035:U07664
F-NT2RP2006052//ESTs//4.0e-05:233:63//Hs.124864:AA663093
F-NT2RP2006069//Human mRNA for KIAA0279 gene, partial cds//0.0082:770:58//Hs.57652:D87469
F-NT2RP2006071//ESTs//2.1e-24:396:65//Hs.104404:AI337416
F-NT2RP2006098//ESTs//0.97:125:67//Hs.97996:AA405970
F-NT2RP2006100
F-NT2RP2006103//ESTs//5.2e-11:102:83//Hs.125656:AA883135
F-NT2RP2006106//ESTs//1.6e-78:456:90//Hs.133496:AA315349
F-NT2RP2006141//ESTs//1.7e-20:262:72//Hs.128677:AA649240
F-NT2RP2006166
F-NT2RP2006184//H.sapiens p63 mRNA for transmembrane protein//1.0:94:73//Hs.74368:X69910
F-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5e-114:567:96//Hs.109299:AB014554
F-NT2RP2006196//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.0e-23:187:85//Hs.15519:AB018315
F-NT2RP2006200//ESTs//1.0:224:62//Hs.144100:AI205503
F-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//4.4e-118:618:93//Hs.153910:X96484
F-NT2RP2006237
F-NT2RP2006238
F-NT2RP2006258//ESTs//0.0034:143:69//Hs.145798:AI269970
F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK//0.019:111:71//Hs.157199:X97630
F-NT2RP2006275//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//2.4e-05:388:60//Hs.75111:D87258

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F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//2.1e-121:598:97//Hs.3404:AF035262
F-NT2RP2006320//ESTs, Moderately similar to maternal transcript Maid [M.musculus]//1.9e-29:151:100//Hs.36794:AI038407
F-NT2RP2006321//ESTs//7.0e-15:141:82//Hs.71241:H09371
F-NT2RP2006323//Homo sapiens mRNA for NBPhox, complete cds//4.7e-06:170:70//Hs.87202:D82344
F-NT2RP2006333//Homo sapiens TRRAP protein (TRRAP) mRNA, complete cds//0.11:43:100//Hs.6892:AF076974
F-NT2RP2006334//Homo sapiens mRNA for KIAA0602 protein, partial cds//3.1e-05:233:65//Hs.37656:AB011174
F-NT2RP2006365//ESTs//8.9e-46:268:93//Hs.58403:AA058501
F-NT2RP2006393//ESTs//1.2e-20:159:86//Hs.146018:AA280341
F-NT2RP2006436//Human homeodomain-containing protein (HANF) mRNA, complete cds//0.59:133:64//Hs.95838:AF059734
F-NT2RP2006441//ESTs//1.6e-82:400:98//Hs.143514:AI221934
F-NT2RP2006454//EST//5.2e-07:172:68//Hs.157742:AI360509
F-NT2RP2006456
F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein/1.1e-149:545:98//Hs.72160:AJ006266
F-NT2RP2006467
F-NT2RP2006472
F-NT2RP2006534//ESTs//5.6e-05:192:66//Hs.135750:AA160048
F-NT2RP2006554//EST//0.60:116:65//Hs.160110:AA922134
F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds//2.1e-115:669:90//Hs.31218:AF038966
F-NT2RP2006571//Cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6//2.1e-24:476:64//Hs.73864:U22029
F-NT2RP2006573
F-NT2RP2006598//ESTs//1.3e-16:137:85//Hs.131350:AA805223
F-NT2RP3000002//ESTs//3.6e-32:215:86//Hs.155446:AA188180
F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//1.9e-137:637:98//Hs.6764:AJ011972
F-NT2RP3000046//Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds//9.1e-07:568:61//Hs.79531:AF000560
F-NT2RP3000047
F-NT2RP3000050//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.2e-58:633:69//Hs.37138:U35376
F-NT2RP3000055//ESTs//1.2e-07:200:66//Hs.127362:AA954961
F-NT2RP3000068
F-NT2RP3000072//EST//0.99:199:63//Hs.8469:T40769
F-NT2RP3000080//Landsteiner-Wiener blood group glycoprotein//4.8e-41:353:78//Hs.108287:L27670
F-NT2RP3000085//Propionyl-coA carboxylase alpha chain//7.9e-30:665:60//Hs.80741:X14608
F-NT2RP3000092//EST//2.0e-15:94:97//Hs.145389:AI253140
F-NT2RP3000109//ESTs//6.8e-11:77:96//Hs.153931:AI243595
F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//5.0e-94:438:100//Hs.8173:AC005189
F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//2.9e-182:849:98//Hs.13273:AB011164
F-NT2RP3000149//Human Line-1 repeat mRNA with 2 open reading frames//4.1e-20:133:94//Hs.23094:M19503
F-NT2RP3000186//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//6.6e-08:152:71//Hs.127338:AB007961
F-NT2RP3000197//ESTs//1.1e-58:301:96//Hs.87461:AA292779
F-NT2RP3000207
F-NT2RP3000220
F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//6.6e-20:509:58//Hs.122967:AF059569
F-NT2RP3000235//ESTs//1.7e-06:220:62//Hs.42771:N26740
F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds//6.7e-111:691:86//Hs.75863:D86972
F-NT2RP3000251//ESTs//6.7e-48:245:97//Hs.28249:AA203733
F-NT2RP3000252
F-NT2RP3000255
F-NT2RP3000267//ESTs//0.14:53:92//Hs.151586:W45568

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F-NT2RP3000299//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds//1.7e-13:214:67//Hs.80261:L43821
F-NT2RP3000312//ESTs//2.6e-50:255:97//Hs.146263:AA255863
F-NT2RP3000320//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.0088:236:63//Hs.102732:U88153
F-NT2RP3000324//ESTs//3.8e-10:102:83//Hs.55495:AI091242
F-NT2RP3000333//ESTs, Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]//0.57:189:65//Hs.46146:AA418097
F-NT2RP3000341//Human mRNA for KIAA0392 gene, partial cds//1.1e-49:442:78//Hs.40100:AB002390
F-NT2RP3000348
F-NT2RP3000350//H.sapiens mRNA for GTP-binding protein//0.93:164:59//Hs.78582:X80754
F-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//1.8e-43:649:66//Hs.101642:X60673
F-NT2RP3000361//ESTs//2.6e-112:531:98//Hs.17672:AA305921
F-NT2RP3000366//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-18A [Lymnaea stagnalis]//4.0e-116:596:95//Hs.21094:AI337016
F-NT2RP3000393//ESTs//2.6e-18:137:89//Hs.115600:AA351639
F-NT2RP3000397//ESTs//8.7e-44:355:73//Hs.121961:AA777873
F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds//1.6e-175:841:97//Hs.28307:AF071185
F-NT2RP3000418//Human Line-1 repeat mRNA with 2 open reading frames//2.7e-33:610:65//Hs.23094:M19503
F-NT2RP3000433//ESTs//1.5e-32:246:69//Hs.120892:AA724948
F-NT2RP3000439//Adenosine A2b receptor//0.44:210:62//Hs.45743:X68487
F-NT2RP3000441
F-NT2RP3000449//ESTs//0.60:177:64//Hs.132605:AI051562
F-NT2RP3000451//Receptor protein-tyrosine kinase EDDR1//0.95:315:58//Hs.75562:U48705
F-NT2RP3000456//ESTs//7.5e-23:140:92//Hs.5209:AA780068
F-NT2RP3000484//EST//2.5e-06:166:67//Hs.149950:AI289822
F-NT2RP3000487//ESTs//1.2e-63:311:98//Hs.143304:AI084058
F-NT2RP3000512//Homeo box B3//3.1e-18:109:97//Hs.49931:X16667
F-NT2RP3000526//ESTs//3.7e-74:424:93//Hs.42991:N21379
F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds//8.0e-36:706:63//Hs.79347:D86966
F-NT2RP3000531//ESTs//9.6e-75:392:95//Hs.144148:H08308
F-NT2RP3000542//ESTs//3.2e-88:448:96//Hs.30622:AA486412
F-NT2RP3000561//EST//0.88:92:64//Hs.148290:AA908404
F-NT2RP3000562//ESTs//1.1e-112:522:99//Hs.125153:AA453723
F-NT2RP3000578
F-NT2RP3000582//ESTs//2.1e-82:413:97//Hs.118544:R17277
F-NT2RP3000584
F-NT2RP3000590//ESTs//1.0:134:64//Hs.12969:N56904
F-NT2RP3000592//Paired basic amino acid cleaving system 4//3.4e-05:502:57//Hs.77234:AB001914
F-NT2RP3000596//ESTs//6.8e-71:361:95//Hs.118741:AA179811
F-NT2RP3000599//ESTs, Weakly similar to T19B10.6 [C.elegans]//9.3e-61:355:92//Hs.114622:AA693492
F-NT2RP3000603//Human mRNA for KIAA0227 gene, partial cds//6.3e-10:553:59//Hs.79170:D86980
F-NT2RP3000605//ESTs//5.8e-51:283:94//Hs.127152:AI421203
F-NT2RP3000622//ESTs//1.7e-10:72:98//Hs.155360:AA984683
F-NT2RP3000624//64 KD AUTOANTIGEN D1//0.99:194:61//Hs.79386:X54162
F-NT2RP3000628//ESTs//0.96:221:61//Hs.131161:AI017333
F-NT2RP3000632//ESTs//4.4e-53:244:77//Hs.143010:AA767904
F-NT2RP3000644//Small inducible cytokine A5 (RANTES)//3.0e-49:343:84//Hs.155464:AF088219
F-NT2RP3000661
F-NT2RP3000665//Homo sapiens putative transcription factor CA150 mRNA, complete cds//0.62:305:59//Hs.13063:AF017789
F-NT2RP3000685
F-NT2RP3000690//EST//1.0:149:64//Hs.140263:AA709001
F-NT2RP3000736//ESTs//5.3e-26:146:97//Hs.98613:D83884
F-NT2RP3000739//ESTs//0.0046:66:87//Hs.6880:W26854
F-NT2RP3000742//ESTs//5.5e-08:311:61//Hs.152224:AI369426

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F-NT2RP3000753//ESTs//2.6e-63:318:97//Hs.153000:AA777765
F-NT2RP3000759//Homo sapiens mRNA for follistain-related protein (FRP), complete cds//1.6e-38:245:91//Hs.2427:D89937
F-NT2RP3000815
F-NT2RP3000825//EST//1.0:220:61//Hs.135944:N45132
F-NT2RP3000826//Homo sapiens deltex (Dx) mRNA, complete cds//0.00040:263:65//Hs.124024:AF053700
F-NT2RP3000836//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 HOMOLOG 2 [H.sapiens]//1.1e-71:363:96//Hs.23803:AA126476
F-NT2RP3000841//EST//0.36:224:60//Hs.162094:AA524012
F-NT2RP3000845//H.sapiens mRNA for serine/threonine protein kinase EMK//6.5e-48:593:68//Hs.157199:X97630
F-NT2RP3000847//ESTs//0.0028:56:92//Hs.116406:AA209520
F-NT2RP3000850//Small inducible cytokine A5 (RANTES)//2.0e-49:323:86//Hs.155464:AF088219
F-NT2RP3000852
F-NT2RP3000859//ESTs//0.39:169:62//Hs.148948:AA699918
F-NT2RP3000865//EST//0.15:236:62//Hs.123366:AA811476
F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds//6.4e-31:766:60//HS.15432:U53445
F-NT2RP3000869//Human plectin (PLEC1) mRNA, complete cds//1.1e-13:701:60//Hs.79706:U53204
F-NT2RP3000875
F-NT2RP3000901//ESTs//8.2e-26:191:87//Hs.18793:R99101
F-NT2RP3000904//EST//2.4e-49:240:100//Hs.160842:AI348374
F-NT2RP3000917
F-NT2RP3000919//MAP KINASE PHOSPHATASE-1//0.19:340:60//Hs.109895:X68277
F-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//7.7e-44:351:83//Hs.2953:X84407
F-NT2RP3000980//ESTs//6.5e-10:102:81//Hs.86950:AI204212
F-NT2RP3000994//ESTs//4.1e-120:571:98//Hs.127295:AA918411
F-NT2RP3001004//ESTs//1.1e-76:438:88//Hs.144554:N92198
F-NT2RP3001007
F-NT2RP3001055//ESTs, Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]//2.9e-121:588:98//Hs.128781:AA160707
F-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN 45 [Homo sapiens]//9.8e-54:282:97//Hs.30303:AI244662
F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.7e-51:534:74//Hs.27007:AF060219
F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds//3.7e-16:474:60//Hs.21264:AB018325
F-NT2RP3001096//Homo sapiens mRNA for cartilage-associated protein (CASP)//4.4e-16:428:60//Hs.155481:AJ006470
F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds//2.8e-34:712:64//Hs.82292:D86969
F-NT2RP3001109//ESTs//1.2e-67:323:99//Hs.134734:AI337050
F-NT2RP3001111
F-NT2RP3001113//EST//1.1e-33:173:99//Hs.112640:AA609088
F-NT2RP3001115//EST//1.3e-22:122:100//Hs.162990:AA688023
F-NT2RP3001116//ESTs//1.1e-15:93:98//Hs.58412:W74779
F-NT2RP3001119//Homo sapiens BC-2 protein mRNA, complete cds//0.96:258:61//Hs.12107:AF042384
F-NT2RP3001120//Zinc finger protein 136 (clone pHZ-20)//2.4e-77:687:75//Hs.69740:U09367
F-NT2RP3001126//Homo sapiens mRNA for KIAA0775 protein, complete cds//0.00018:341:60//Hs.94790:AB018318
F-NT2RP3001133//Homeo box A4//0.00011:484:59//Hs.77637:M74297
F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//1.1e-180:851:98//Hs.5378:AB018305
F-NT2RP3001147
F-NT2RP3001150//PUTATIVE TACHYKININ RECEPTOR//0.97:257:59//Hs.957:M84605
F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//1.7e-191:891:98//Hs.72160:AJ006266
F-NT2RP3001176
F-NT2RP3001214//EST//0.88:218:60//Hs.161147:AI417859
F-NT2RP3001216//ESTs//1.5e-66:340:96//Hs.105994:W19981
F-NT2RP3001221//ESTs, Weakly similar to M05D6.7 [C.elegans]//1.7e-97:512:95//Hs.103816:AA130866
F-NT2RP3001232//EST//0.0016:116:71//Hs.136498:AA594010

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F-NT2RP3001236//ESTs//3.7e-97:455:99//Hs.157488:AI362756
F-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B//1.7e-20:501:62//Hs.103042:L06237
F-NT2RP3001245//ESTs//7.1e-80:434:93//Hs.22587:AA743132
F-NT2RP3001253//Human prepromultimerin mRNA, complete cds//0.99:293:60//Hs.32934:U27109
F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete cds//1.2e-48:761:64//Hs.107809:AB018269
F-NT2RP3001268//Zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide)//1.2e-42:454:72//Hs.41728:L75847
F-NT2RP3001272//ESTs//5.0e-21:162:87//Hs.69149:AA102566
F-NT2RP3001274
F-NT2RP3001281//ESTs//2.1e-39:186:73//Hs.161662:AA836811
F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds//2.4e-48:544:69//Hs.31463:D87457
F-NT2RP3001307//Human homeodomain protein (Prox 1) mRNA, complete cds//0.72:151:68//Hs.159437:U44060
F-NT2RP3001318//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)//0.012:522:56//Hs.904:U84010
F-NT2RP3001325//ESTs//2.9e-80:396:97//Hs.99838:AA204731
F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds//1.6e-30:345:73//Hs.79347:D86966
F-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//6.3e-67:559:80//Hs.18586:AB007920
F-NT2RP3001340//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//0.00019:473:61//Hs.124161:AF065164
F-NT2RP3001355//ESTs, Weakly similar to ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 [H.sapiens]//1.1e-81:421:96//Hs.32508:H29831
F-NT2RP3001356//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.15:313:60//Hs.129725:AF047487
F-NT2RP3001374//ESTs//0.98:269:59//Hs.125303:AA873022
F-NT2RP3001383//Homo sapiens mRNA for Sck, partial cds//0.73:173:65//Hs.30965:AB001451
F-NT2RP3001384//Homa sapiens mRNA for HRIHFB2018, partial cds//2.1e-158:743:98//Hs.146214:AB015332
F-NT2RP3001392//ESTs//0.013:246:63//Hs.95111:AA514595
F-NT2RP3001396//ESTs//5.6e-16:141:85//Hs.97664:H10783
F-NT2RP3001398//Zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide)//1.0e-05:189:66//Hs.41728:L75847
F-NT2RP3001399//Homo sapiens mitochondrial citrate transport protein (CTP) mRNA, 3' end//0.77:132:66//Hs.111024:L77567
F-NT2RP3001407//EST//0.015:167:65//Hs.42217:H96658
F-NT2RP3001420//ESTs//1.0:214:60//Hs.91226:AA649047
F-NT2RP3001426
F-NT2RP3001427
F-NT2RP3001428//Neurotrophic tyrosine kinase, receptor, type 1//1.8e-73:431:91//Hs.85844:X66397
F-NT2RP3001432//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//6.9e-05:195:65//Hs.115868:AA568393
F-NT2RP3001447
F-NT2RP3001449//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.00033:187:68//Hs.89631:U48508
F-NT2RP3001453//ESTs//0.020:260:60//Hs.97882:AA203212
F-NT2RP3001457//ESTs//9.4e-29:165:94//Hs.71749:AA988323
F-NT2RP3001459
F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, complete cds//4.2e-10:168:70//Hs.32317:AF072836
F-NT2RP3001490//ESTs//3.1e-35:198:94//Hs.163665:AA250877
F-NT2RP3001495//ESTs//2.5e-47:239:98//Hs.128045:AA970231
F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds//2.8e-172:804:98//Hs.28285:AF064801
F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-B) mRNA, complete cds//9.4e-139:743:91//Hs.85283:U36500
F-NT2RP3001529//ESTs, Moderately similar to topoisomerase IC-terminal fragment [H.sapiens]//0.28:224:65//Hs.105912:AI431328
F-NT2RP3001538//ESTs//4.1e-05:139:71//Hs.148425:AI198074
F-NT2RP3001554//Microtubule-associated protein 1A//9.8e-16:327:64//Hs.147918:U38291

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F-NT2RP3001580//Insulin-like growth factor binding protein 2//1.9e-06:426:59//Hs.162:X16302
F-NT2RP3001587//Guanine nucleotide binding protein (G protein), alpha 11 (Gq class)//0.049:185:65//Hs.1686:M69013
F-NT2RP3001589//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.6e-51:345:82//Hs.144563:AF057280
F-NT2RP3001607//ESTs//1.3e-07:299:63//Hs.43231:N22688
F-NT2RP3001608//ESTs//5.7e-14:85:98//Hs.161133:AI091349
F-NT2RP3001621//ESTs//1.6e-106:310:96//Hs.128505:AA306435
F-NT2RP3001629
F-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//1.4e-62:276:97//Hs.9899:AF099149
F-NT2RP3001642//ESTs//1.0:148:63//Hs.159495:T70173
F-NT2RP3001646
F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.1e-172:816:98//Hs.159597:AJ012449
F-NT2RP3001672//ESTs//5.0e-16:138:82//Hs.151864:T69027
F-NT2RP3001676//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]//9.0e-53:375:85//Hs.41127:AA555184
F-NT2RP3001678//Human mRNA for KIAA0233 gene, complete cds//0.21:321:65//Hs.79077:D87071
F-NT2RP3001679//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]//4.0e-111:518:99//Hs.20364:AI420022
F-NT2RP3001688//Homo sapiens mRNA expressed in thyroid gland//1.0:230:63//Hs.7486:D83198
F-NT2RP3001690//EST//0.15:291:59//Hs.162336:AA564329
F-NT2RP3001698//ESTs//0.24:134:69//Hs.129551:AA885219
F-NT2RP3001708//ESTs, Weakly similar to TWISTED GASTRULATION PROTEIN PRECURSOR [D.melanogaster]//1.4e-31:191:94//Hs.131279:AA486291
F-NT2RP3001712//Human SLP-76 associated protein mRNA, complete cds//0.41:259:59//Hs.58435:AF001862
F-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//7.6e-159:747:98//Hs.6823:W18181
F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//4.4e-161:565:97//Hs.159273:AF054177
F-NT2RP3001727//ESTs, Highly similar to HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III [Caenorhabditis elegans]//3.5e-116:554:98//Hs.144332:AA046836
F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds//1.3e-105:811:78//Hs.90998:D50918
F-NT2RP3001739
F-NT2RP3001752//ELK1, member of ETS oncogene family//7.2e-35:299:80//Hs.116549:AL009172
F-NT2RP3001753//Human putative cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1) mRNA, complete cds//0.10:528:56//Hs.22138:U49250
F-NT2RP3001764//Human protein-tyrosine phosphatase mRNA, complete cds//2.4e-47:725:64//Hs.41688:U27193
F-NT2RP3001777//Human eukaryotic translation initiation factor (eIF3) mRNA, complete cds//0.42:198:61//Hs.57783:U78525
F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//9.1e-153:710:98//Hs.28169:AB007928
F-NT2RP3001792//Human M4 protein mRNA, complete cds//5.6e-27:358:69//Hs.79024:L03532
F-NT2RP3001799//ESTs//0.0088:178:64//Hs.134938:AI091361
F-NT2RP3001819//Collagen, type IX, alpha 3//0.026:530:58//Hs.53563:L41162
F-NT2RP3001844//Homo sapiens mRNA for hair keratin acidic 3-II//0.90:379:58//Hs.32950:X82634
F-NT2RP3001854//ESTs//1.5e-100:501:96//Hs.72217:AA166729
F-NT2RP3001855//Human homeobox-containing protein mRNA, complete cds//7.8e-35:481:67//Hs.158225:U68727
F-NT2RP3001857//ESTs//2.7e-85:414:98//Hs.151001:AA564706
F-NT2RP3001896//ESTs, Weakly similar to F20D12.3 gene product [C.elegans]//2.9e-94:452:98//Hs.54952:AA872675
F-NT2RP3001898//Homo sapiens mRNA for synaptogyrin 1a//0.65:245:61//Hs.6139:AL022326
F-NT2RP3001915//ESTs//1.1e-83:397:99//Hs.157125:AA723896
F-NT2RP3001926//EST//0.53:362:57//Hs.127917:AA969185
F-NT2RP3001929//ESTs//7.4e-16:141:82//Hs.138852:AA284247
F-NT2RP3001931

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F-NT2RP3001938//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//0.0022:268:61//Hs.106070:U22398
F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds//5.8e-167:815:96//Hs.15869:AB014575
F-NT2RP3001944//ESTs//0.00052:60:91//Hs.131731:AI339335
F-NT2RP3001969
F-NT2RP3001989//EST//0.00016:263:63//Hs.144096:AI032180
F-NT2RP3002002//Small inducible cytokine A5 (RANTES)//4.0e-61:293:83//Hs.155464:AF088219
F-NT2RP3002004//H.sapiens mRNA for FAST kinase//5.2e-28:104:100//Hs.75087:X86779
F-NT2RP3002007//ESTs//0.025:88:69//Hs.163310:AA856946
F-NT2RP3002014//ESTs//4.8e-70:291:98//Hs.123693:AA283821
F-NT2RP3002033//Homo sapiens mRNA for HYA22, complete cds//0.021:175:67//Hs.147189:D88153
F-NT2RP3002045//ESTs, Highly similar to ALPHA-ADAPTIN [M.musculus]//3.8e-48:353:81//Hs.127507:AA993745
F-NT2RP3002054//ESTs, Weakly similar to KIAA0319 [H.sapiens]//3.0e-25:212:83//Hs.71622:AA195155
F-NT2RP3002056//ESTs, Highly similar to RETINOBLASTOMA BINDING PROTEIN 1 [Homo sapiens]//4.2e-82:407:97//Hs.131888:AI091806
F-NT2RP3002057//Human Line-1 repeat mRNA with 2 open reading frames//3.7e-21:168:85//Hs.23094:M19503
F-NT2RP3002062//EST//0.46:198:62//Hs.157711:AI359710
F-NT2RP3002063//Membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)//0.91:194:65//Hs.1298:J03779
F-NT2RP3002081
F-NT2RP3002097//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA partial cds//0.073:297:61//Hs.102732:U88153
F-NT2RP3002102//EST//2.8e-16:237:67//Hs.136255:T70256
F-NT2RP3002108
F-NT2RP3002142//ESTs//4.3e-138:654:98//Hs.5729:AA306018
F-NT2RP3002146//H.sapiens mRNA for RanGTPase activating protein 1//0.27:276:62//Hs.5923:X82260
F-NT2RP3002147//Human DNA sequence from clone 431H6 on chromosome 16. Contains a novel gene with some homology to mouse HN1 (Hematological and Neurological expressed sequence 1) downstream of a putative CpG island. Contains ESTs and GSSs//6.0e-51:204:99//Hs.107256:AL031009
F-NT2RP3002151//G1 to S phase transition 1//2.6e-37:292:81//Hs.2707:X17644
F-NT2RP3002163//Human DNA fragmentation factor-45 mRNA, complete cds//0.46:224:60//Hs.155344:U91985
F-NT2RP3002165//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP [Mus musculus]//3.0e-61:340:93//Hs.11379:AA594140
F-NT2RP3002166//EST//0.039:114:69//Hs.140335:AA737046
F-NT2RP3002173//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//4.0e-39:255:72//Hs.141429:AA631915
F-NT2RP3002181//ESTs//3.6e-111:518:99//Hs.128505:AA30643
F-NT2RP3002244//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic1)//0.98:242:57//Hs.114001:Z20656
F-NT2RP3002248
F-NT2RP3002255//ESTs//8.4e-19:227:75//Hs.122817:AA772261
F-NT2RP3002273//Homo sapiens homeobox protein A10 (HOXA10) gene, complete cds//0.42:189:62//Hs.110637:AC004080
F-NT2RP3002276//ESTs//8.2e-97:463:98//Hs.45120:AA225139
F-NT2RP3002303//ESTs//7.1e-10:96:87//Hs.135700:AA989386
F-NT2RP3002304//Protein phosphatase 1, catalytic subunit, beta isoform//1.3e-05:496:60//Hs.21537:X80910
F-NT2RP3002330//ESTs//1.3e-81:482:90//Hs.121460:AA744871
F-NT2RP3002343//Homo sapiens potassium channel mRNA, complete cds//0.30:462:56//Hs.143624:AF033383
F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE//1.6e-65:588:75//Hs.154672:X16396
F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene//4.2e-166:770:98//Hs.6483:Y16355
F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds//7.5e-161:911:89//Hs.2397:Z70200
F-NT2RP3002399
F-NT2RP3002402//ESTs, Weakly similar to F02E9.6 [C.elegans]//4.3e-41:233:94//Hs.22880:AA056274
F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//3.9e-140:649:99//Hs.12707:AB014578

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F-NT2RP3002484//ESTs//0.95:166:63//Hs.149993:AI291310
F-NT2RP3002501//ESTs//0.92:43:90//Hs.119314:AA432108
F-NT2RP3002512//Homo sapiens mRNA for KIAA0466 protein, partial cds//1.0:173:61//Hs.81234:AB007935
F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, complete cds//4.4e-146:763:93//Hs.57738:U35246
F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//5.9e-180:833:98//Hs.19542:AB018272
F-NT2RP3002549//ESTs, Weakly similar to POLYPOSIS LOCUS PROTEIN 1 [H.sapiens]//1.3e-42:510:70//Hs.96759:AA469984
F-NT2RP3002566//Carnitine acetyltransferase//0.032:226:62//Hs.12068:X78706
F-NT2RP3002587//EST//4.8e-31:330:74//Hs.139415:AA426054
F-NT2RP3002590//EST//1.3e-40:202:100//Hs.144716:AI187919
F-NT2RP3002602//RYANODINE RECEPTOR, SKELETAL MUSCLE//1.3e-06:280:63//Hs.89631:U48508
F-NT2RP3002603
F-NT2RP3002628//Homo sapiens mRNA for MSJ-1, complete cds//1.5e-05:264:61//Hs.3845:AB014888
F-NT2RP3002631//Homo sapiens ADAM 21 mRNA, partial cds//0.97:320:58//Hs.121287:AF029900
F-NT2RP3002650//Homo sapiens mRNA for cartilage-associated protein (CASP)//2.6e-13:441:63//Hs.155481:AJ006470
F-NT2RP3002659//Human TAR RNA loop binding protein (TRP-185) mRNA, complete cds//1.7e-05:615:58//Hs.151518:U38847
F-NT2RP3002660//ESTs//2.9e-32:164:100//Hs.152982:AA584308
F-NT2RP3002663//ESTs, Highly similar to OXYSTEROL-BINDING PROTEIN [Homo sapiens]//4.1e-38:493:70//Hs.41086:AI337400
F-NT2RP3002671//ESTs//3.7e-05:288:59//Hs.161359:AI421991
F-NT2RP3002682//ESTs, Weakly similar to F17C11.8 [C.elegans]//1.6e-61:294:100//Hs.128750:AI367584
F-NT2RP3002687
F-NT2RP3002688//EST//1.0:312:58//Hs.156800:AI352200
F-NT2RP3002701//EST//0.00083:55:87//Hs.159750:AI393657
F-NT2RP3002713//ESTs//0.93:229:61//Hs.150459:AI279514
F-NT2RP3002763//ESTs//1.7e-97:419:96//Hs.121593:W86291
F-NT2RP3002770//Homo sapiens G protein-coupled receptor kinase 6 (GRK6) gene, partial cds//0.91:161:62//Hs.129736:AF040753
F-NT2RP3002785
F-NT2RP3002799//EST//1.7e-17:199:73//Hs.118694:AA148713
F-NT2RP3002810//ESTs, Weakly similar to KIAA0062 [H.sapiens]//1.4e-76:423:93//Hs.41068:AA844350
F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete cds//2.2e-55:615:70//Hs.105940:AF004715
F-NT2RP3002861//ESTs//1.1e-88:468:94//Hs.159821:AA524070
F-NT2RP3002869//ESTs//3.4e-23:132:97//Hs.148873:T33582
F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds//2.7e-90:557:88//Hs.123090:AB001895
F-NT2RP3002877//ESTs//1.1e-19:160:84//Hs.118273:AA626040
F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.8e-181:853:98//Hs.6162:AB018314
F-NT2RP3002911//ESTs//2.8e-07:160:70//Hs.140402:AI138765
F-NT2RP3002948//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//1.4e-133:645:97//Hs.3826:U69560
F-NT2RP3002953//Homo sapiens mRNA for KIAA0588 protein, complete cds//5.2e-13:594:57//Hs.74599:AB011160
F-NT2RP3002955//Homo sapiens mRNA for KIAA0719 protein, complete cds//0.76:412:57//Hs.21198:AB018262
F-NT2RP3002969//EST//3.7e-50:272:94//Hs.162331:AA563870
F-NT2RP3002972//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter//5.1e-35:361:75//Hs.8003:AC004997
F-NT2RP3002978//ESTs//2.8e-46:253:95//Hs.151924:AI287703
F-NT2RP3002985//Human TFIIB related factor hBRF (HBRF) mRNA, complete cds//0.071:550:58//Hs.32935:U28838
F-NT2RP3002988//EST//0.0016:180:63//Hs.147632:AI218308
F-NT2RP3003008//Human DNA-binding protein (HRC1) mRNA, complete cds//0.59:201:63//Hs.72925:M91083
F-NT2RP3003032//ESTs//9.1e-40:241:92//Hs.113363:C06446
F-NT2RP3003059//ESTs//0.0015:399:58//Hs.136895:AA897749
F-NT2RP3003061//Ankyrin 1, erythrocytic//4.5e-14:633:59//Hs.1242:X16609

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F-NT2RP3003068//EST//0.00014:80:83//Hs.121993:AA777928
F-NT2RP3003071//ESTs//1.1e-62:315:98//Hs.16141:W56079
F-NT2RP3003078
F-NT2RP3003101
F-NT2RP3003121//EST, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//0.98:88:68//Hs.99715:AA292700
F-NT2RP3003133//EST//8.0e-17:218:68//Hs.134815:AI090740
F-NT2RP3003138//Homo sapiens vasopressin-activated calcium mobilizing putative receptor protein (VACM-1) mRNA, complete cds//0.013:438:57//Hs.101299:AF017061
F-NT2RP3003139//ESTs//0.020:260:61//Hs.59142:W88975
F-NT2RP3003145//Homo sapiens aortic carboxypeptidase-like protein ACLP mRNA, complete cds//2.2e-20:430:63//Hs.118397:AF053944
F-NT2RP3003150
F-NT2RP3003157//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//2.0e-72:894:68//Hs.37138:U35376
F-NT2RP3003185//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.045:410:59//Hs.6150:AB011093
F-NT2RP3003193//Zinc finger protein 10 (KOX 1)//2.4e-74:737:71//Hs.2479:X78933
F-NT2RP3003197//ESTs//1.8e-24:130:100//Hs.162504:AA668211
F-NT2RP3003203//ESTs//3.5e-30:232:82//Hs.6880:W26854
F-NT2RP3003204//ESTs//3.1e-109:524:98//Hs.152982:AA584308
F-NT2RP3003210//ESTs//3.6e-16:113:91//Hs.121030:AA625325
F-NT2RP3003212//EST//1.0e-52:500:74//Hs.161635:W22525
F-NT2RP3003230//Human mRNA for actin binding protein p57, complete cds//6.0e-55:587:70//Hs.109606:D44497
F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//1.2e-129:617:98//Hs.155223:AF055460
F-NT2RP3003251//H.sapiens Staf50 mRNA//1.1e-68:651:76//Hs.68054:X82200
F-NT2Rp3003264//Human bullous 230 kDa pemphigoid antigen (BPAG1) mRNA, complete cds//0.069:382:59//Hs.620:M69225
F-NT2RP3003278//Homo sapiens hook2 protein (HOOK2) mRNA. complete cds//0.98:261:59//Hs.30792:AF044924
F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//4.2e-133:694:93//Hs.11702:L36983
F-NT2RP3003290//Human mRNA for RTP, complete cds//6.3e-66:662:71//Hs.75789:D87953
F-NT2RP3003301//EST//1.0:58:74//Hs.158575:AI368947
F-NT2RP3003302//Human Line-1 repeat mRNA with 2 open reading frames//3.1e-91:681:80//Hs.23094:M19503
F-NT2RP3003311//ESTs//0.95:308:59//Hs.27308:AA534947
F-NT2RP3003313//ESTs//0.0016:345:61//Hs.143304:AI084058
F-NT2RP3003327//H.sapiens Staf50 mRNA//8.0e-31:253:67//Hs.68054:X82200
F-NT2RP3003330
F-NT2RP3003344
F-NT2RP3003346//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase//1.2e-42:644:66//Hs.2638:Z28339
F-NT2RP3003353//Breast cancer 1, early onset//0.30:145:67//Hs.66746:L78833
F-NT2RP3003377//Human mRNA for cadherin-15, complete cds//0.019:416:60//Hs.148090:D83542
F-NT2RP3003384//ESTs//1.1e-65:346:96//Hs.35012:R92791
F-NT2RP3003385//ESTs, Highly similar to SKD3 [M.musculus]//7.0e-74:384:96//Hs.21263:H16363
F-NT2RP3003403//ESTs//4.9e-12:335:63//Hs.87258:AA463850
F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds//3.2e-22:430:63//Hs.113272:U90653
F-NT2RP3003411//Human metallothionein-le gene (hMT-le)//0.99:116:62//Hs.74170:M10942
F-NT2RP3003427//ESTs//0.24:447:61//Hs.160907:AI422830
F-NT2RP3003433//Protein tyrosine phosphatase, non-receptor type 12//1.0:243:61//Hs.62:M93425
F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.7e-182:853:98//Hs.14934:AF004828
F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//5.2e-175:826:98//Hs.26450:AB018268
F-NT2RP3003491//Ryanodine receptor 2 (cardiac)//1.0:148:66//Hs.90821:X98330
F-NT2RP3003500//ESTs//0.86:211:62//Hs.136037:AA013302
F-NT2RP3003543//Homo sapiens clone 23790 unknown protein mRNA, complete cds//0.64:626:58//Hs.150828:

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AF038169
F-NT2RP3003552
F-NT2RP3003555//ESTs//1.4e-12:81:98//Hs.144487:AI418322
F-NT2RP3003564//EST//4.5e-08:186:69//Hs.116769:AA630365
F-NT2RP3003572//EST//0.27:105:69//Hs.162134:AA526311
F-NT2RP3003576//ESTs//1.2e-57:277:84//Hs.138852:AA284247
F-NT2RP3003589//RAS-RELATED PROTEIN RAB-8//6.3e-38:373:73//Hs.123109:X56741
F-NT2RP3003621//HEPATOCYTE GROWTH FACTOR ACTIVATOR PRECURSOR//8.0e-09:564:61//Hs.104:D14012
F-NT2RP3003625
F-NT2RP3003656
F-NT2RP3003659
F-NT2RP3003665//ESTs//0.015:221:62//Hs.153705:AA527586
F-NT2RP3003672//ESTs//0.70:351:57//Hs.27633:N76184
F-NT2RP3003680//Human Bcl2, p53 binding protein Bbp/53BP2 (BBP/53BP2) mRNA, complete cds//0.013:190:63//Hs.44585:U58334
F-NT2RP3003686//Homo sapiens clone 24519 unknown mRNA, partial cds//0.69:246:62//Hs.118463:AF055000
F-NT2RP3003701//EST//0.93:79:69//Hs.145285:AI249848
F-NT2RP3003716//Homo sapiens KIAA0405 mRNA, complete cds//8.3e-24:478:61//Hs.48998:AB007865
F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//7.4e-150:700:98//Hs.48513:AB018300
F-NT2RP3003746
F-NT2RP3003795//ESTs//7.1e-20:228:74//Hs.159571:AA454230
F-NT2RP3003799
F-NT2RP3003800//Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog//4.7e-41:432:73//Hs.1422:M19722
F-NT2RP3003805//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//0.98:242:57//Hs.114001:Z20656
F-NT2RP3003809//Human transcription factor, forkhead related activator 4 (FREAC-4) mRNA, complete cds//5.1e-07:624:59//Hs.96028:AF042832
F-NT2RP3003819//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//0.84:171:63//Hs.102877:U41315
F-NT2RP3003825
F-NT2RP3003828//ESTs//2.1e-12:434:61//Hs.156864:AI346481
F-NT2RP3003831
F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//2.6e-48:242:98//Hs.25300:AF070611
F-NT2RP3003842//Integrin, beta 8//1.0:345:60//Hs.832:M73780
F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds//1.3e-37:335:68//Hs.26450:AB018268
F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.3e-175:805:99//Hs.118738:AB018343
F-NT2RP3003876//ESTs, Highly similar to Rabin3 [R.norvegicus]//6.8e-39:243:90//Hs.124832:AA846576
F-NT2RP3003914//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]//1.1e-107:499:99//Hs.105794:AA701659
F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds//8.3e-49:404:77//Hs.9006:AF057358
F-NT2RP3003932//ESTs//0.94:278:58//Hs.15661:W02396
F-NT2RP3003989//ESTs//1.0:174:64//Hs.8095:AI359006
F-NT2RP3003992//Cyclic nucleotide gated channel (photoreceptor), cGMP gated 2 (beta)//0.00070:433:58//Hs.93909:AF042498
F-NT2RP3004013//ESTs, Moderately similar to M-phase phosphoprotein 4 [H.sapiens]//2.8e-127:617:97//Hs.142151:AA984061
F-NT2RP3004016//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0086:283:62//Hs.155302:U57317
F-NT2RP3004041//EST//0.98:264:58//Hs.127552:AA953234
F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds//7.0e-63:774:67//Hs.26441:AB002317
F-NT2RP3004070//EST//6.8e-22:163:85//Hs.132635:AI032875
F-NT2RP3004078//Regulatory factor (trans-acting) 2 (influences HLA class II expression)//5.3e-90:520:90//Hs.

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100007:X76091
F-NT2RP3004093
F-NT2RP3004095//Human clone 23732 mRNA, partial cds//3.3e-27:372:69//Hs.81281:U79258
F-NT2RP3004110//Human mRNA for KIAA0392 gene, partial cds//1.2e-20:211:77//Hs.40100:AB002390
F-NT2RP3004125//ESTs, Highly similar to OOCYTE ZINC FINGER PROTEIN XLCOF7.1 [Xenopus laevis]//1.0e-126:590:99//Hs.129888:AI096509
F-NT2RP3004145
F-NT2RP3004148
F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds//2.1e-121:578:98//Hs.157113:AF032900
F-NT2RP3004189//ESTs//1.3e-80:409:97//Hs.151001:AA564706
F-NT2RP3004206//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640
F-NT2RP3004207//Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)//0.095:281:62//Hs.101047:M31523
F-NT2RP3004209//ESTs//5.8e-87:458:94//Hs.155303:AI221835
F-NT2RP3004215//ESTs//0.074:56:80//Hs.163590:H43361
F-NT2RP3004242
F-NT2RP3004246//EST//0.20:219:63//Hs.161920:AA483240
F-NT2RP3004253//ESTs//1.2e-36:204:96//Hs.143588:AI149140
F-NT2RP3004258//Human gene for neurofilament subunit M (NF-M)//7.2e-07:369:59//Hs.71346:Y00067
F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds//1.0e-154:733:98//Hs.158471:AF088982
F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds//4.2e-26:597:61//Hs.19261:AF007871
F-NT2RP3004332
F-NT2RP3004334//ESTs//8.8e-27:142:99//Hs.28068:H06285
F-NT2RP3004341//EST//0.0068:213:64//Hs.153208:X98426
F-NT2RP3004348//ESTs//1.2e-18:126:93//Hs.58595:AA830999
F-NT2RP3004349//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//3.9e-45:337:83//Hs.141429:AA631915
F-NT2RP3004378//ESTs, Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]//4.3e-125:608:98//Hs.128781:AA160707
F-NT2RP3004399//H.sapiens mRNA for leucine-rich primary response protein 1//2.3e-141:804:90//Hs.123122:X97249
F-NT2RP3004424//ESTs, Weakly similar to JTV-1 [H.sapiens]//3.2e-122:609:96//Hs.20132:AA203113
F-NT2RP3004428//Homo sapiens ALR mRNA, complete cds//0.00044:458:60//Hs.153638:AF010403
F-NT2RP3004451//Bone morphogenetic protein 8 (osteogenic protein 2)//0.00023:357:59//Hs.99948:M97016
F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//2.0e-124:583:99//Hs.27349:AB007917
F-NT2RP3004466//Homo sapiens mRNA for KIAA0664 protein, partial cds//0.48:399:58//Hs.22616:AB014564
F-NT2RP3004470//EST//1.3e-56:331:91//Hs.136830:AA769219
F-NT2RP3004472
F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.8e-152:715:98//Hs.5003:AB007925
F-NT2RP3004480//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae]//4.6e-118:547:99//Hs.124768:AA307735
F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds//2.3e-156:752:97//Hs.158311:AB012851
F-NT2RP3004498//ESTs, Moderately similar to ROSA26AS [M.musculus]//3.5e-89:425:99//Hs.126082:AI077718
F-NT2RP3004503//EST//5.3e-49:399:81//Hs.162335:AA564256
F-NT2RP3004504//Homo sapiens mRNA for KIAA0479 protein, partial cds//1.0:370:59//Hs.158244:AB007948
F-NT2RP3004507//Human zinc finger protein (MAZ) mRNA//0.86:129:66//Hs.7647:M94046
F-NT2RP3004527//EST//0.053:260:62//Hs.123314:AA810110
F-NT2RP3004534//ESTs//3.5e-78:370:99//Hs.132808:AI031571
F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds//2.7e-146:679:98//Hs.75970:AB014532
F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds//9.1e-171:793:98//Hs.74750:AB011126
F-NT2RP3004566//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//2.2e-66:362:94//Hs.125870:AI364967
F-NT2RP3004569

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F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF50) mRNA, complete cds//3.3e-181:860:97//Hs.122752:AF026445
F-NT2RP3004578//Homo sapiens mRNA for KIAA0454 protein, partial cds//4.0e-85:422:97//Hs.129928:AB007923
F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein//3.7e-160:796:95//Hs.72160:AJ006266
F-NT2RP3004617//ESTs, Weakly similar to estrogen-responsive finger protein, efp [H.sapiens]//6.4e-13:356:64//Hs.124138:AI266336
F-NT2RP3004618//ESTs//1.5e-42:481:70//Hs.130768:AA909232
F-NT2RP3004669//Human plectin (PLEC1) mRNA, complete cds//0.0099:538:56//Hs.79706:U53204
F-NT2RP3004670//Homo sapiens sox1 gene//0.11:311:58//Hs.144029:Y13436
F-NT2RP4000008//ESTs, Highly similar to CHLORINE CHANNEL PROTEIN P64 [Bos taurus]//8.0e-177:827:98//Hs.118991:AA675919
F-NT2RP4000023//ESTs//1-4e-33:182:96//Hs.122722:AA455668
F-NT2RP4000035//ESTs//1.1e-23:283:72//Hs.142147:AA706495
F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds//6.8e-83:556:85//Hs.129844:AF029761
F-NT2RP4000051//Homo sapiens mRNA for cartilage-associated protein (CASP)//4.9e-13:441:62//Hs.155481:AJ006470
F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.0e-151:720:97//Hs.159597:AJ012449
F-NT2RP4000102//ESTs//8.8e-33:184:82//Hs.93054:H47743
F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.4e-167:774:99//Hs.57929:AB011538
F-NT2RP4000111
F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//1.1e-115:548:98//Hs.64691:AB007952
F-NT2RP4000147//Human mRNA for KIAA0041 gene, partial cds//0.00045:212:63//Hs.75520:D26069
F-NT2RP4000150
F-NT2RP4000151//Homo sapiens chromosome 7q22 sequence//0.98:431:59//Hs.3386:AF053356
F-NT2RP4000159
F-NT2RP4000167
F-NT2RP4000185//ESTs//1.1e-51:240:68//Hs.33020:N31946
F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.6e-175:825:98//Hs.13999:AB014600
F-NT2RP4000212//ESTs//1.6e-10:74:95//Hs.111885:AA422006
F-NT2RP4000214//ESTs//3.9e-11:225:68//Hs.59793:AA451731
F-NT2RP4000218//Human G protein-coupled receptor (STRL22) mRNA, complete cds//6.2e-34:425:71//Hs.46468:U45984
F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP)//8.6e-158:771:97//Hs.155481:AJ006470
F-NT2RP4000246//ESTs, Highly similar to NPC DERIVED PROLINE RICH PROTEIN 1 [M.musculus]//1.9e-62:384:89//Hs.115498:AA436298
F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.4e-130:604:99//Hs.43728:AF091092
F-NT2RP4000263
F-NT2RP4000290//EST//1.0:149:63//Hs.136928:AA812580
F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds//1.5e-42:685:63//Hs.158132:D63481
F-NT2RP4000321//Homo sapiens gene for insulin receptor substrate-2, complete cds//8.6e-05:547:57//Hs.143648:AB000732
F-NT2RP4000323//Human HCF1 gene related mRNA sequence//0.48:589:58//Hs.83634:U52112
F-NT2RP4000355
F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//6.4e-142:654:99//Hs.107479:AB018281
F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//8.5e-137:649:97//Hs.31323:AF044195
F-NT2RP4000370//ESTs, Weakly similar to MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR [S.cerevisiae]//1.2e-09:157:76//Hs.97950:AI382073
F-NT2RP4000376//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//0.098:291:59//Hs.994:M95678
F-NT2RP4000381//Myosin, heavy polypeptide 7, cardiac muscle, beta//0.00025:509:59//Hs.929:M57965

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F-NT2RP4000398//Zinc finger protein 140 (clone pHZ-39)//4.9e-60:469:68//Hs.154205:U09368
F-NT2RP4000415//ESTs//0.85:89:67//Hs.152312:AA485688
F-NT2RP4000417//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//0.014:178:66//Hs.125315:AF027156
F-NT2RP4000424//Human G protein-coupled receptor (STRL22) mRNA, complete cds//2.0e-34:431:73//Hs.46468:U45984
F-NT2RP4000448//Human mRNA for KIAA0118 gene, partial cds//1.9e-37:360:75//Hs.154326:D42087
F-NT2RP4000449//EST//0.84:113:65//Hs.145274:AI249468
F-NT2RP4000455//ALPHA-2C-1 ADRENERGIC RECEPTOR//0.063:221:61//Hs.123022:J03853
F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP)//1.1e-05:532:57//Hs.78683:Z72499
F-NT2RP4000480//Homo sapiens mRNA, complete cds//0.056:655:60//Hs.133151:AB001535
F-NT2RP4000481//Human mRNA for KIAA0268 gene, partial cds//0.46:272:58//Hs.78862:D87742
F-NT2RP4000498//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds//0.94:133:69//Hs.159234:U89995
F-NT2RP4000500//V-myb avian myeloblastosis viral oncogene homolog-like 2//0.60:335:61//Hs.74605:X13293
F-NT2RP4000515//ESTs//2.9e-45:253:95//Hs.104898:AA429594
F-NT2RP4000517//EST//0.043:131:64//Hs.99030:AA443904
F-NT2RP4440518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//2.0e-34:203:93//Hs.99423:AJ010840
F-NT2RP4000519//Human mRNA for KIAA0374 gene, complete cds//0.33:154:66//Hs.100837:AB002372
F-NT2RP4000524
F-NT2RP4000528
F-NT2RP4000541//ESTs//2.1e-51:251:99//Hs.157240:AI348154
F-NT2RP4000556//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.norvegicus]//1.1e-27:162:93//Hs.25597:H93026
F-NT2RP4000560//ESTs//2.5e-09:181:66//Hs.122609:AA778351
F-NT2RP4000588//ESTs//1.4e-46:533:70//Hs.8836:AA181053
F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//1.0e-139:666:98//Hs.4214:AF067730
F-NT2RP4000638//Fibroblast growth factor 2 (basic)//1.0:226:61//Hs.56066:J04513
F-NT2RP4000648//ESTs//2.5e-11:116:80//Hs.115449:AA418396
F-NT2RP4000657//Homo sapiens bone morphogenetic protein 11 (BMP11) mRNA, complete cds//0.00056:367:60//Hs.144626:AF100907
F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone IMAGE:300856//8.0e-167:676:98//Hs.50748:AB004848
F-NT2RP4000713//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//6.9e-07:494:61//Hs.113286:U77783
F-NT2RP4000724//ESTs, Weakly similar to pol/env ORF [H.sapiens]//2.8e-46:411:78//Hs.111817:T80622
F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds//9.9e-43:350:71//Hs.38176:AB011178
F-NT2RP4000737//Human mRNA for KIAA0252 gene, partial cds//0.97:409:60//Hs.83419:D87440
F-NT2RP4000739//DESMOPLAKIN I AND II//0.99:192:63//Hs.74316:AL031058
F-NT2RP4000781//Homo sapiens mRNA for APC 2 protein, complete cds//0.023:351:60//Hs.20912:AB012162
F-NT2RP4000787//Human mRNA for ESP1/CRP2, complete cds//0.0051:276:58//Hs.70327:D42123
F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//4.8e-176:816:98//Hs.25132:AB007939
F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-93:438:99//Hs.8173:AC005189
F-NT2RP4000837//Homo sapiens SALL1 gene, partial//5.9e-05:470:59//Hs.123094:X98833
F-NT2RP4000839//ESTs//5.7e-11:133:82//Hs.103852:W27603
F-NT2RP4000855//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//1.4e-37:680:63//Hs.75875:U49278
F-NT2RP4000865//Zinc finger protein 136 (clone pHZ-20)//2.0e-96:415:78//Hs.69740:U09367
F-NT2RP4000878//ESTs//2.7e-16:390:63//Hs.163451:AI206803
F-NT2RP4000879//ESTs//0.89:184:64//Hs.122333:AA782843
F-NT2RP4000907//Homo sapiens BAC clone RG118D07 from 7q31//4.5e-52:933:61//Hs.3781:AC004142
F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein//3.0e-80:584:78//Hs.109526:AJ224901
F-NT2RP4000918
F-NT2RP4000925//Homo sapiens KIAA0405 mRNA, complete cds//1.9e-47:861:61//Hs.48998:AB007865

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F-NT2RP4000927//ESTs//0.37:159:63//Hs.147949:AI341503
F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//1.1e-164:781:97//Hs.24812:AF069532
F-NT2RP4000929//ESTs//0.88:284:60//Hs.141317:AI281371
F-NT2RP4000955//Human mRNA for cadherin-15, complete cds//0.0019:495:58//Hs.148090:D83542
F-NT2RP4000973//Homo sapiens mRNA for MSJ-1, complete cds//1.2e-05:318:60//Hs.3845:AB014888
F-NT2RP4000975//ESTs//0.0051:345:61//Hs.143304:AI084058
F-NT2RP4000979
F-NT2RP4000984
F-NT2RP4000989//Homo sapiens Tax interaction protein 1 mRNA, partial cds//0.85:257:63//Hs.12956:U90913
F-NT2RP4000996//ESTs//4.3e-10:329:62//Hs.33085:AA258068
F-NT2RP4000997//Human plectin (PLEC1) mRNA, complete cds//1.0:218:58//Hs.79706:U53204
F-NT2RP4001004
F-NT2RP4001006//ESTs, Moderately similar to ROSA26AS [M.musculus]//7.4e-90:425:99//Hs.126082:AI077718
F-NT2RP4001010//Homo sapiens PSD-95/SAP90-associated protein-2 mRNA, partial cds//2.8e-19:689:61//Hs.113287:AF009204
F-NT2RP4001029//Human transcription factor LSF mRNA, complete cds//9.6e-84:778:74//Hs.154970:U03494
F-NT2RP4001041//Human endosome-associated protein (EEA1) mRNA, complete cds//0.95:170:64//Hs.2864:L40157
F-NT2RP4001057//EST//9.6e-05:122:72//Hs.132518:AA928157
F-NT2RP4001064//Homo sapiens mRNA for cartilage-associated protein (CASP)//7.2e-13:441:63//Hs.155481:AJ006470
F-NT2RP4001078//ESTs//1.3e-29:165:95//Hs.113817:AA702497
F-NT2RP4001079//Homo sapiens mRNA for putative Ca^{2+}-transporting ATPase, partial//1.4e-131:634:98//Hs.106778:AJ010953
F-NT2RP4001080//Polypyrimidine tract binding protein (hnRNP I) {alternative products}//0.025:166:66//Hs.146459:X66975
F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.5e-85:604:86//Hs.13273:AB011164
F-NT2RP4001095
F-NT2RP4001100//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.4e-93:448:98//Hs.105837:AA536054
F-NT2RP4001117//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//2.2e-26:171:92//Hs.14038:R06800
F-NT2RP4001122//Human mRNA for histone H1x, complete cds//0.99:185:66//Hs.109804:D64142
F-NT2RP4001126//ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]//5.8e-37:185:100//Hs.126925:AA931237
F-NT2RP4001138//ESTs//3.4e-09:125:77//Hs.1433 82:AA476266
F-NT2RP4001143//ESTs//1.0:282:57//Hs.157423:AI358261
F-NT2RP4001148//ESTs//0.82:206:62//Hs.129259:AA992207
F-NT2RP4001149//EST//1.3e-17:140:88//Hs.101727:H16171
F-NT2RP4001150//AXONIN-1 PRECURSOR//7.7e-07:562:59//Hs.2998:X67734
F-NT2RP4001159//EST//0.26:125:66//Hs.152092:AA377324
F-NT2RP4001174//ESTs//2.9e-103:502:98//Hs.125886:AA884264
F-NT2RP4001206//EST//0.33:125:66//Hs.152092:AA377324
F-NT2RP4001207
F-NT2RP4001210//ESTs//3.1e-95:460:97//Hs.46913:AI017636
F-NT2RP4001213//KRAB zinc finger protein {alternative products}//1.1e-45:187:74//Hs.22556:U37251
F-NT2RP4001219//ESTs//1.4e-69:352:96//Hs.116392:AA936262
F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.2e-28:855:60//Hs.122967:AF059569
F-NT2RP4001235//Homo sapiens Jagged 2 mRNA, complete cds//1.0:257:59//Hs.106387:AF029778
F-NT2RP4001256//Human mRNA for KIAA0273 gene, complete cds//0.96:247:62//Hs.75899:D87463
F-NT2RP4001260//Syntrophin, alpha (dystrophin-associated protein A1, 59kD, acidic component)//0.015:246:62//Hs.31121:U40571
F-NT2RP4001274//Homo sapiens clone 24674 mRNA sequence//1.2e-06:259:64//Hs.71168:AF070578
F-NT2RP4001276//Homo sapiens CAGF9 mRNA, partial cds//7.6e-06:266:62//Hs.110826:U80736
F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding mitochondrial protein, complete cds//2.3e-31:535:65//Hs.30928:AF043250
F-NT2RP4001315//EST//9.5e-20:146:88//Hs.158755:AI375917

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F-NT2RP4001336//ESTs//1.0:128:67//Hs.99598:AA603110
F-NT2RP4001339
F-NT2RP4001343
F-NT2RP4001345//Lecithin-cholesterol acyltransferase//8.0e-39:686:64//Hs.112125:M12625
F-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds//2.0e-31:784:62//Hs.15432:U53445
F-NT2RP4001353//Homo sapiens chromosome 7q22 sequence//0.0034:497:57//Hs.125742:AF053356
F-NT2RP4001372
F-NT2RP4001373//Homo sapiens clone Dt1P1b11 mRNA, CAG repeat region//0.43:290:58//Hs.82101:Z50194
F-NT2RP4001375
F-NT2RP4001379//TRICHOHYALIN//8.2e-05:591:58//Hs.82276:L09190
F-NT2RP4001389//EST//5.3e-27:212:84//Hs.160402:AI393918
F-NT2RP4001407//Homo sapiens mRNA for RGS5, complete cds//0.93:218:58//Hs.24950:AB008109
F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds//6.3e-78:818:71//Hs.80712:D86957
F-NT2RP4001433//Zinc finger protein 10 (KOX 1)//1.1e-88:839:73//Hs.2479:X78933
F-NT2RP4001442
F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.0075:218:63//Hs.41153:AB018326
F-NT2RP4001474//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//2.1e-90:460:96//Hs.26676:AA033997
F-NT2RP4001483//Oxoglutarate dehydrogenase (lipoamide)//8.1e-61:480:75//Hs.75533:D10523
F-NT2RP4001498//ESTs, Weakly similar to GA BINDING PROTEIN BETA-2 CHAIN [H.sapiens]//0.25:216:60//Hs.63220:AA522707
F-NT2RP4001502//ESTs//2.6e-41:206:99//Hs.159257:N40395
F-NT2RP4001507//H.sapiens mRNA for RanGTPase activating protein 1//0.51:281:61//Hs.5923:X82260
F-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [C.elegans]//9.4e-30:173:94//Hs.5570:AI377863
F-NT2RP4001529//Human transcription factor LSF mRNA, complete cds//1.3e-35:329:76//Hs.154970:U03494
F-NT2RP4001547//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds//0.0015:221:65//Hs.44481:U13220
F-NT2RP4001551//Human BRCA2 region, mRNA sequence CG003//0.56:428:59//Hs.30649:U50534
F-NT2RP4001555//EST//0.99:225:64//Hs.96863:AA347174
F-NT2RP4001567
F-NT2RP4001568//ESTs, Weakly similar to HYPOTHETICAL 32.6 KD PROTEIN IN MET30-CBR5 INTERGENIC REGION [Saccharomyces cerevisiae]//1.1e-54:252:83//Hs.158208:AA167836
F-NT2RP4001571//ESTs//3.0e-94:475:96//Hs.65322:AA019410
F-NT2RP4001574
F-NT2RP4001575//Homo sapiens mRNA for ARE1-like protein//1.8e-169:796:98//Hs.108826:AL031228
F-NT2RP4001592
F-NT2RP4001610//Human involucrin mRNA//0.94:462:59//Hs.157091:M13903
F-NT2RP4001614//ESTs//0.71:331:58//Hs.116533:AI343952
F-NT2RP4001634
F-NT2RP4001638//ESTs, Weakly similar to HYPOTHETICAL 117.9 KD PROTEIN IN FKH1-STH1 INTERGENIC REGION [S.cerevisiae]//8.6e-57:287:97//Hs.117439:C18436
F-NT2RP4001644//Human mRNA for MNK1, complete cds//1.7e-53:415:80//Hs.5591:AB000409
F-NT2RP4001656//ESTs, Highly similar to PHENYLALANYL-TRNA SYNTHETASE MITOCHONDRIAL PRECURSOR [Saccharomyces cerevisiae]//1.0:311:59//Hs.57969:AA203629
F-NT2RP4001677//Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds//0.19:162:67//Hs.30250:AF055376
F-NT2RP4001679//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.2e-50:332:86//Hs.113283:AF018080
F-NT2RP4001696
F-NT2RP4001725//Galactokinase 1//1.0:202:63//Hs.92357:L76927
F-NT2RP4001730//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//0.0035:247:62//Hs.92614:M62302
F-NT2RP4001739//Complement component 8, gamma polypeptide//0.74:654:56//Hs.1285:U08198
F-NT2RP4001753//Zinc finger protein 84 (HPF2)//4.5e-29:476:67//Hs.9450:M27878
F-NT2RP4001760//ESTs//1.0:411:60//Hs.108548:AA081656
F-NT2RP4001790//Homo sapiens PAC clone DJ0604G05 from 7q22-q31.1//9.1e-34:400:68//Hs.154212:AC004522

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F-NT2RP4001803//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete cds//0.028:580:58//Hs.2363:L36069
F-NT2RP4001822//ESTs//3.4e-50:307:90//Hs.113509:AA132131
F-NT2RP4001823//Human faciogenital dysplasia (FGD1) mRNA, complete cds//3.1e-07:509:59//Hs.1572:U11690
F-NT2RP4001828
F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds//6.9e-55:555:73//Hs.78398:D31888
F-NT2RP4001841//ESTs//0.99:215:60//Hs.136895:AA897749
F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-57:813:65//Hs.6336:AB014572
F-NT2RP4001861//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.8e-12:84:94//Hs.140232:AA705170
F-NT2RP4001889
F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21//4.4e-108:535:97//Hs.15144:AC005014
F-NT2RP4001896
F-NT2RP4001901//ESTs//1.4e-50:291:93//Hs.67991:AA147848
F-NT2RP4001927
F-NT2RP4001938//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//2.8e-54:375:84//Hs.119294:AI379442
F-NT2RP4001946//EST//0.050:268:60//Hs.148341:AA921894
F-NT2RP4001950//EST//7.9e-14:336:63//Hs.112810:AA610063
F-NT2RP4001953//ESTs//0.018:206:65//Hs.130105:AA904868
F-NT2RP4001966//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//1.7e-54:788:65//Hs.23796:AL022718 F-NT2RP4001975//Homo sapiens homeobox protein Six3 (SIX3) gene, complete cds//0.0019:279:65//Hs.159439:AF092047
F-NT2RP4002018//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//0.58:463:55//Hs.3826:U69560
F-NT2RP4002047//EST//2.5e-13:102:90//Hs.148997:AI243139
F-NT2RP4002052
F-NT2RP4002058//ESTs//5.2e-41:347:72//Hs.121961:AA777873
F-NT2RP4002071//Homo sapiens TTAGGG repeat binding factor 2 (hTRF2) mRNA, complete cds//0.97:227:60//Hs.100030:AF002999
F-NT2RP4002075
F-NT2RP4002078//ESTs, Moderately similar to zinc finger protein [H.sapiens]//1.0e-38:243:90//Hs.139115:AA325104
F-NT2RP4002081//TATA box binding protein//0.0059:310:60//Hs.1100:M55654
F-NT2RP4002083//H.sapiens Pur (pur-alpha) mRNA, complete cds//0.0015:152:70//Hs.25180:M96684
F-NT2RP4002408//Human protein kinase C-L (PRKCL) mRNA, complete cds//8.0e-10:401:59//Hs.89616:M55284
F-NT2RP4002791//Ataxin 1//1.0:215:61//Hs.74520:X79204
F-NT2RP4002888
F-NT2RP4002905//ESTs//3.4e-50:280:94//Hs.131697:H14960
F-NT2RP5003459//Glyceraldehyde-3-phosphate dehydrogenase//1.3e-35:193:96//Hs.74456:U34995
F-NT2RP5003461//ESTs//3.6e-104:513:98//Hs.88088:AA521071
F-NT2RP5003477//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.18:271:60//Hs.139745:U39067
F-NT2RP5003492
F-NT2RP5003500//Homo sapiens mRNA for heparan-sulfate 6-sulfotransferase, complete cds//6.1e-56:750:69//Hs.132884:AB006179
F-NT2RP5003506//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5.1e-14:348:62//Hs.154050:AC004131
F-NT2RP5003512//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.94:202:63//Hs.8152:AB014542
F-NT2RP5003522
F-NT2RP5003524//ESTs//8.7e-08:340:62//Hs.152730:AI308943
F-NT2RP5003534
F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.0e-69:373:94//Hs.108258:AB007934
F-OVARC1000004//ESTs//6.0e-38:216:93//Hs.163801:AI391729

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F-OVARC1000006//ESTs, Highly similar to HISTONE H2A [Cairina moschata]//4.4e-75:355:99//Hs.36727:AI051983
F-OVARC1000013//ESTs//0.65:331:58//Hs.146326:AA534304
F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds//1.8e-171:815:98//Hs.81449:AF058922
F-OVARC1000017//Homo sapiens mRNA for NTAK, complete cds//0.50:482:58//Hs.113264:AB005060
F-OVARC1000035//Homo sapiens GA17 protein mRNA, complete cds//2.2e-37:238:89//Hs.69469:AF064603
F-OVARC1000058//ESTs//1.1e-23:132:97//Hs.61809:AA503549
F-OVARC1000060//ESTs, Highly similar to ribonuclease 6 precursor [H.sapiens]//6.7e-60:305:97//Hs.31696:H50008
F-OVARC1000068//ESTs//3.8e-10:69:100//Hs.89048:AA282798
F-OVARC1000071//ESTs//1.9e-36:202:95//Hs.125013:AA400543
F-OVARC1000085
F-OVARC1000087//EST//1.0:199:58//Hs.122919:AA768442
F-OVARC1000091//Homo sapiens Jagged 2 mRNA, complete . cds//0.00017:414:59//Hs.106387:AF029778
F-OVARC1000092//ESTs//4.6e-06:410:60//Hs.152250:AA203600
F-OVARC1000106//ESTs, Weakly similar to C25A1.1 [C.elegans]//2.9e-73:406:92//Hs.109463:AI205174
F-OVARC1000109
F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//5.3e-135:663:96//Hs.3688:AF069250
F-OVARC1000114//Homo sapiens mRNA for KIAA0562 protein, complete cds//3.4e-43:532:72//Hs.118401:AB011134
F-OVARC1000133//ESTs//9.4e-50:249:98//Hs.159146:AI384010
F-OVARC1000139
F-OVARC1000145//ESTs//1.6e-09:87:90//Hs.25219:AA291293
F-OVARC1000148//ESTs//4.4e-28:146:100//Hs.133223:AA677414
F-OVARC1000151
F-OVARC1000168//ESTs//2.3e-48:264:95//Hs.14539:H67305
F-OVARC1000191//Thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor)//0.10:504:59//Hs.154083:U70136
F-OVARC1000198//ESTs//1.3e-103:505:97//Hs.149341:AI249131
F-OVARC1000209//EST//1.0:73:72//Hs.162600:AA594840
F-OVARC1000212//ESTs//1.7e-17:121:91//Hs.50473:W68834
F-OVARC1000240//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [Homo sapiens]//2.7e-31:264:79//Hs.151895:AA196379
F-OVARC1000241//Homo sapiens clone 23698 mRNA sequence//3.4e-35:466:68//Hs.8136:U81984
F-OVARC1000288//TESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.00084:170:65//Hs.107747:AI357868
F-OVARC1000302//EST//4.1e-05:249:60//Hs.136432:AA555306
F-OVARC1000304//ESTs//1.0:252:64//Hs.12126:AA203287
F-OVARC1000309//ESTs, Highly similar to BRAIN ENRICHED HYALURONAN BINDING PROTEIN PRECURSOR [Felis catus]//0.51:193:66//Hs.6194:AI378579
F-OVARC1000321
F-OVARC1000326//Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds//0.0018:507:60//Hs.122359:AF051946
F-OVARC1000335//ESTs//9.3e-39:202:98//Hs.132849:AA779444
F-OVARC1000347
F-OVARC1000384//Homo sapiens (clone PEBP2aA1) core-binding factor, runt domain, alpha subunit 1 (CBFA1) mRNA, 3' end of cds//3.4e-06:353:62//Hs.121895:AF001450
F-OVARC1000408//Human mRNA for KIAA0140 gene, complete cds//0.94:231:64//Hs.156016:D50930
F-OVARC1000411//EST//0.43:234:59//Hs.124673:AA858162
F-OVARC1000414//EST//5.2e-05:105:72//Hs.98827:AA435682
F-OVARC1000420//Human mRNA for KIAA0140 gene, complete cds//0.86:231:58//Hs.156016:D50930
F-OVARC1000427//ESTs, Moderately similar to ORF1 [H.sapiens]//1.7e-25:190:84//Hs.139513:AA259082
F-OVARC1000431//ESTs//0.041:356:57//Hs.139907:AA621615
F-OVARC1000437//Filamin 1 (actin-binding protein-280)//0.93 :281:60//Hs.76279:X53416
F-OVARC1000440//Human PINCH protein mRNA, complete cds//8.8e-21:116:99//Hs.83987:U09284
F-OVARC1000442//ESTs//2.0e-19:207:78//Hs.134071:AI377423
F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.2e-140:566:99//Hs.12334:AB014583

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F-OVARC1000461//ESTs//1.0e-39:215:95//Hs.131532:AI024524
F-OVARC1000465//Homo sapiens clone 24781 mRNA sequence//1.0:252:58//Hs.108112:AF070640
F-OVARC1000466//ESTs//3.6e-14:189:71//Hs.164041:R51854
F-OVARC1000473//ESTs//0.00012:77:85//Hs.29173:AA134926
F-OVARC1000479
F-OVARC1000486//ESTs//4.2e-07:409:60//Hs.99280:AA453036
F-OVARC1000496//ESTs//6.0e-14:240:69//Hs.131900:AI023327
F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds//6.9e-115:539:99//Hs.111285:AF051850
F-OVARC1000526//ESTs//2.9e-08:368:611/Hs.42771:N26740
F-OVARC1000533//EST//3.4e-14:137:82//Hs.123405:AA813492
F-OVARC1000543//ESTs//0.13:278:61//Hs.54894:N98475
F-OVARC1000556//ESTs//1.4e-31:217:90//Hs.106385:W26667
F-OVARC1000557//ESTs//3.8e-20:208:76//Hs.138919:AA827410
F-OVARC1000564//Human dsRNA adenosine deaminase DRADA2b (DRADA2b) mRNA, complete cds//0.87:135:66//Hs.85302:U76421
F-OVARC1000573//ESTs//2.1e-22:268:76//Hs.121852:AA776358
F-OVARC1000576//ESTs//9.4e-22:124:98//Hs.24220:W22200
F-OVARC1000578//EST//4.7e-31:335:74//Hs.162881:AA652729
F-OVARC1000588//Human BMK1 alpha kinase mRNA, complete cds//0.67:263:63//Hs.3080:U29725
F-OVARC1000605//EST//1.0:148:62//Hs.163346:AA883722
F-OVARC1000622//EST//4.3e-50:313:88//Hs.149580:AI281881
F-OVARC1000640//ESTs//2.6e-55:441:80//Hs.105319:AA470097
F-OVARC1000649//Human squamous cell carcinama of esophagus mRNA for GRB-7 SH2 domain protein, complete cds//1.6e-78:424:93//Hs.86859:D43772
F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.6e-100:536:94//Hs.111862:AB011162
F-OVARC1000678//EST//1.3e-08:131:77//Hs.145970:AI277106
F-OVARC1000679//ESTs//0.66:223:61//Hs.134782:H74279
F-OVARC1000681//EST//0.017:315:61//Hs.147799:AI221639
F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//4.8e-153:549:99//Hs.125315:AF027156
F-OVARC1000689//Homo sapiens clone 24640 mRNA sequence//0.030:479:57//Hs.4764:AB018306
F-OVARC 1000700
F-OVARC1000703//ESTs//0.41:100:68//Hs.160699:AI284320
F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds//1.2e-110:451:91//Hs.13476:AF038661
F-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//2.9e-53:318:91//Hs.7049:AI141736
F-OVARC1000746//ESTs//3.2e-123:570:99//Hs.127295:AA918411
F-OVARC1000769//ESTs//0.072:177:67//Hs.142573:AA601196
F-OVARC1000771//ESTs, Moderately similar to RAS-RELATED PROTEIN RAB-2 [H.sapiens]//1.2e-38:194:99//Hs.157059:W28130
F-OVARC1000781//ESTs//4.0e-14:113:89//Hs.41972:AA626793
F-OVARC1000787//EST//0.92:91:64//Hs.163258:AA828835
F-OVARC1000800//ESTs//1.6e-44:193:81//Hs.163971:N27584
F-OVARC1000802//ESTs//4.6e-43:395:80//Hs.115401:AA400032
F-OVARC1000834//ESTs//1.9e-91:431:99//Hs.154450:AA069390
F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds//1.9e-151:432:100//Hs.155995:AB014543
F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//3.3e-137:632:99//Hs.18910:AF045584
F-OVARC1000862//ESTs, Highly similar to gene Fif protein [M.musculus]//6.1e-31:183:93//Hs.108620:AA418155
F-OVARC1000876//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds//0.54:133:69//Hs.159234:U89995
F-OVARC1000883//ESTs//0.44:154:63//Hs.98183:AA417143
F-OVARC1000885//EST//0.91:152:63//Hs.160765 :AI313323
F-OVARC1000886//ESTs//4.6e-08:375:61//Hs.131653:AI025777
F-OVARC 1000890
F-OVARC1000891

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F-OVARC1000897//ESTs//1.1e-07:145:69//Hs.119878:AA706818
F-OVARC1000912//EST//3.6e-08:376:61//Hs.158782:AI376601
F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds//2.3e-85:419:97//Hs.9028:AF039691
F-OVARC1000924//ESTs//3.6e-113:540:98//Hs.66058:AA424456
F-OVARC1000936//Human endogenous retrovirus envelope region mRNA (PL1)//4.3e-64:623:72//Hs.114440:M11119
F-OVARC1000937//EST//2.4e-39:170:96//Hs.129138:AA988078
F-OVARC1000945//ESTs, Weakly similar to protein tyrosine phosphatase [H.sapiens]//2.4e-29:157:97//Hs.136243:AA307843
F-OVARC 1000948
F-OVARC1000959//EST//0.65:293:55//Hs.134725:AI088986
F-OVARC1000960//Ley I-L//1.4e-41:425:72//Hs.37062:AC005952
F-OVARC1000964//ESTs//1.4e-95:486:96//Hs.57079:D45288
F-OVARC1000971//ESTs//0.19:198:62//Hs.153429:AI283069
F-OVARC1000984//Breakpoint cluster region protein BCR//0.26:365:56//Hs.2557:Y00661
F-OVARC1000996//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//6.8e-10:312:65//Hs.155302:U57317
F-OVARC1000999//Homo sapiens mRNA for chemokine LEC precursor, complete cds//0.0056:209:62//Hs.10458:AF088219
F-OVARC1001000//EST//4.2e-24:242:77//Hs.128952:AA984114
F-OVARC1001004
F-OVARC1001010
F-OVARC1001011//ESTs, Moderately similar to Tera [M.musculus]//3.8e-47:234:99//Hs.110327:AA205866
F-OVARC1001032//HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2//0.0076:624:57//Hs.75063:AL023584
F-OVARC1001034//ESTs, Highly similar to mitogen-induced [M.musculus]//3.9e-97:578:89//Hs.111974:AI050735
F-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//8.6e-152:733:97//Hs.9899:AF099149
F-OVARC 1001040//ESTs//2.2e-38:204:96//Hs.128927:AI168074
F-OVARC1001044//EST//0.036:304:61//Hs.137342:AA017385
F-OVARC1001051
F-OVARC1001055//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//1.1e-46:381:81//Hs.154968:U02020
F-OVARC1001062//ESTs//0.020:265:60//Hs.146226:AI312873
F-OVARC1001065//ESTs, Weakly similar to C50F4.12 [C.elegans]//1.4e-21:183:84//Hs.46680:AA809451
F-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds//6.6e-132:620:98//Hs.3426:AF082657
F-OVARC1001072//ESTs//1.1e-24:289:74//Hs.139614:AA709013
F-OVARC1001074//ESTs//0.059:198:63//Hs.59974:AA001937
F-OVARC1001085//H.sapiens mRNA for sortilin//0.99:142:67//Hs.104247:X98248
F-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))//1.3e-75:289:95//Hs.21753:AJ005897
F-OVARC1001107//Homo sapiens SKB1Hs mRNA, complete cds//1.2e-73:351:86//Hs.12912:AF015913
F-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds//2.1e-151:710:98//Hs.26584:AF051782
F-OVARC1001117//ESTs//3.8e-73:347:99//Hs.116029:AA813102
F-OVARC1001118
F-OVARC1001129
F-OVARC1001154//Granulin//2.4e-94:686:83//Hs.75451:AF055008
F-OVARC1001161//ESTs//2.2e-40:208:97//Hs.113006:AA621725
F-OVARC1001162
F-OVARC1001167
F-OVARC1001169//ESTs//0.81:158:63//Hs.48527:AI078279
F-OVARC1001170//ESTs//9.0e-87:412:99//Hs.116550:AA813287
F-OVARC1001171//ESTs//4.9e-26:167:79//Hs.139158:AA226159
F-OVARC1001173//ESTs, Moderately similar to GLUTAMATE DEHYDROGENASE 1 PRECURSOR [Homo sapiens]//1.8e-11:192:69//Hs.130020:AA887581
F-OVARC1001176//Homo sapiens chromosome 19, cosmid R26529//0.61:387:58//Hs.91103:AC005551
F-OVARC1001180//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//1.5e-13:199:71//Hs.109966:

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C06057
F-OVARC1001188//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.4e-52:324:90//Hs.114673:W72675
F-OVARC1001200//ESTs//3.9e-16:104:94//Hs.125520:AA883889
F-OVARC1001232//Cyclin A//0.95:124:67//Hs.85137:X51688
F-OVARC1001240//EST//0.017:351:60//Hs.120655:AA745676
F-OVARC1001243//ESTs//0.78:291:59//Hs.132458:AI424825
F-OVARC1001244//RING3 PROTEIN//2.8e-19:118:95//Hs.75243:D42040
F-OVARC1001261//EST//1.9e-42:225:96//Hs.158854:AI377837
F-OVARC1001268//ESTs//0.66:239:61//Hs.132525:AA576821
F-OVARC1001270//ESTs//0.99:204:60//Hs.144647:AA625224
F-OVARC1001271//Homo sapiens mRNA for KIAA0643 protein, partial cds//6.8e-144:644:96//Hs.155995:AB014543
F-OVARC1001282//ESTs, Weakly similar to Ydr438wp [S.cerevisiae]//0.11:355:60//Hs.108812:AA044835
F-OVARC1001296//ESTs//1.1e-46:237:98//Hs.33746:N78172
F-OVARC1001306//Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete cds//0.20:188:64//Hs.152455:AF044209
F-OVARC1001329//ESTs//1.4e-97:486:97//Hs.125886:AA884264
F-OVARC1001330
F-OVARC1001339//Solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)//0.021:232:62//Hs.79410:U62531
F-OVARC1001341//ESTs, Weakly similar to C17G10.1 [C.elegans]//2.5e-76:363:99//Hs.105837:AA536054
F-OVARC1001342//EST//0.98:97:65//Hs.148210:AA897493
F-OVARC1001344//EST//5.3e-10:241:64//Hs.138777:N67251
F-OVARC1001357//Homo sapiens jerky gene product homolog mRNA, complete cds//0.64:198:61//Hs.105940:AF004715
F-OVARC1001360//ESTs//4.9e-87:429:97//Hs.130145:AI264633
F-OVARC1001369//ESTs//6.3e-07:371:62//Hs.131653:AI025777
F-OVARC1001372//Homo sapiens mRNA for KIAA0654 protein, partial cds//1.4e-69:533:74//Hs.109299:AB014554
F-OVARC1001376//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//2.5e-49:365:73//Hs.129735:AF010144
F-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL//4.1e-149:683:99//Hs.151428:AJ224819
F-OVARC1001391//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//0.097:235:65//Hs.25674:AF072242
F-OVARC1001399//ESTs//1.1e-35:264:83//Hs.59379:W28225
F-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//1.3e-150:707:98//Hs.21586:AB006651
F-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds//1.6e-49:586:69//Hs.74597:U52426
F-OVARC1001425//ESTs//2.4e-11:258:67//Hs.119197:T83651
F-OVARC1001436
F-OVARC1001442
F-OVARC1001453
F-OVARC1001476//ESTs, Weakly similar to HYPOTHETICAL 38.6 KD PROTEIN IN TIF4631-KRE11 INTERGENIC REGION [S.cerevisiae]//1.9e-125:581:99//Hs.110950:AI041823
F-OVARC1001480//ESTs//0.95:125:72//Hs.152584:AA584568
F-OVARC1001489//EST//4.9e-72:341:100//Hs.148191:AA897343
F-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds//2.6e-86:479:92//Hs.6534:AF016507
F-OVARC1001506//Polycystic kidney disease 1 (autosomal dominant)//1.1e-97:538:92//Hs.75813:L33243
F-OVARC1001525
F-OVARC1001542//Envoplakin//0.34:258:60//Hs.25482:U53786
F-OVARC1001547//EST//0.0046:237:62//Hs.54638:N90595
F-OVARC1001555
F-OVARC1001577//Homo sapiens SRp46 splicing factor retropseudogene mRNA//6.8e-57:275:98//Hs.155160:AF031166
F-OVARC1001600//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.0035:271:60//Hs.108465:AI144299

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F-OVARC1001610//ESTs, Weakly similar to F22E10.5 [C.elegans]//1.4e-43:216:99//Hs.120002:AI038398
F-OVARC1001611
F-OVARC1001615//EST//0.99:135:68//Hs.129410:AA993500
F-OVARC1001668//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.3e-37:217:94//Hs.14409:AB011144
F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds//5.9e-49:393:81//Hs.95582:AB006867
F-OVARC1001703//EST//1.7e-24:172:88//Hs.121198:AA757229
F-OVARC1001711//Fms-related tyrosine kinase 3 ligand//0.049:353:61//Hs.428:U03858
F-OVARC1001713//ESTs//8.9e-37:263:86//Hs.110298:AA621807
F-OVARC1001726//ESTs//2.0e-12:121:82//Hs.153332:AA236863
F-OVARC1001731//Tropomyosin beta chain (skeletal muscle)//1.7e-83:617:80//Hs.155652:X06825
F-OVARC1001745//EST//0.75:174:64//Hs.146778:AI148588
F-OVARC1001762
F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//1.4e-150:706:98//Hs.155377:U97670
F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds//9.8e-117:580:96//Hs.15869:AB014575
F-OVARC 1001768//ESTs//0.035:179:64//Hs.87279:AI218697
F-OVARC1001791
F-OVARC1001795//ESTs//0.19:68:76//Hs.37699:AA062830
F-OVARC1001802//EST//3.7e-45:254:92//Hs.130620:AI005102
F-OVARC1001805//Homo sapiens mRNA for KIAA0744 protein, complete cds//0.77:362:58//Hs.116753:AB018287
F-OVARC1001809//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//2.2e-07:435:62//Hs.69949:M94172
F-OVARC1001812//ESTs//3.0e-47:360:83//Hs.141756:AA700825
F-OVARC1001813//EST//1.8e-57:277:100//Hs.162414:AA573453
F-OVARC1001820//ESTs//1.4e-64:310:99//Hs.137398:AA164567
F-OVARC1001828//EST//1.0e-09:184:66//Hs.130435:AA923537
F-OVARC1001846//ESTs//1.8e-80:410:97//Hs.114539:N54973
F-OVARC1001861
F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence//3.9e-20:122:95//Hs.25300:AF070611
F-OVARC1001879//Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel subunit mRNA, complete cds//0.042:199:67//Hs.127436:AF040709
F-OVARC1001880//Interferon regulatory factor 5//1.1e-06:489:60//Hs.54434:U51127
F-OVARC1001883//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//9.5e-33:509:68//Hs.158095:AB007953
F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//2.6e-57:300:96//Hs.6216:AF061749
F-OVARC1001901//ESTs//2.3e-07:185:69//Hs.145630:AI263834
F-OVARC1001911//EST//0.88:101:66//Hs.162622:AA601261
F-OVARC1001916//H.sapiens mRNA for prepronociceptin//1.0:540:58//Hs.89040:U48263
F-OVARC1001928
F-OVARC1001942//Human plectin (PLEC1) mRNA, complete cds//0.038:290:62//Hs.79706:U53204
F-OVARC1001943//ESTs, Weakly similar to HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III [C.elegans]//2.3e-119:565:98//Hs.5392:AA313794
F-OVARC1001949//KRAB zinc finger protein {alternative products}//1.8e-17:294:67//Hs.22556:U37251
F-OVARC1001950//ESTs//1.5e-15:300:65//Hs.138501:AI051228
F-OVARC1001987//ESTs//6.7e-34:202:92//Hs.115600:AA351639
F-OVARC1001989//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-23:213:78//Hs.105292:AA504776
F-OVARC1002044//EST//0.26:164:66//Hs.161094:N30417
F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//6.6e-160:739:98//Hs.108258:AB007934
F-OVARC1002066//ESTs//1.8e-103:482:99//Hs.124923:AI375865
F-OVARC1002082//EST//2.5e-09:213:67//Hs.112810:AA610063
F-OVARC1002107

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F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds//2.7e-101:498:96//Hs.75258:AF054174
F-OVARC1002127//ESTs//1.6e-76:397:96//Hs.33432:R83913
F-OVARC1002138//Homo sapiens p60 katanin mRNA, complete cds//3.5e-20:399:62//Hs.112725:AF056022
F-OVARC1002143//EST//4.2e-09:240:65//Hs.140547:AA812795
F-OVARC1002156//EST//0.35:112:66//Hs.136761:AA738097
F-OVARC1002158//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//7.4e-07:329:58//Hs.107747:AI357868
F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase//0.00010:300:64//Hs.118929:X79568
F-OVARC1002182//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.19:178:64//Hs.108447:AJ000517
F-PLACE1000004//ESTs//0.79:332:59//Hs.120221:AA731230
F-PLACE1000005//ESTs//1.8e-10:89:87//Hs.158913:AI378928
F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//1.2e-52:550:72//Hs.42400:AF022789
F-PLACE1000014
F-PLACE1000031
F-PLACE1000040//ESTs//3.1e-18:123:91//Hs.138387:AA873088
F-PLACE1000048//ESTs//1.2e-43:387:78//Hs.61199:AA024494
F-PLACE1000050//ESTs//1.8e-84:421:96//Hs.128632:AI076755
F-PLACE1000061//Ribosomal protein L37a//5.5e-29:177:93//Hs.1946:L06499
F-PLACE1000066//ESTs, Weakly similar to coded for by C. elegans cDNA yk10c10.3 [C.elegans]//1.4e-47:266:93//Hs.30026:AI356771
F-PLACE1000078//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.sapiens]//6.4e-15:203:70//Hs.157422:R85366
F-PLACE1000081//Human transporter protein (g17) mRNA, complete cds//0.30:324:60//Hs.76460:U49082
F-PLACE1000094
F-PLACE1000133//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo sapiens]//6.2e-82:476:92//Hs.111081:AI380378
F-PLACE1000142//ESTs, Weakly similar to enoyl-CoA hydratase [H.sapiens]//7.7e-27:205:85//Hs.9670:AA632135
F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds//2.5e-151:737:97//Hs.151017:AF058291
F-PLACE1000185
F-PLACE1000213
F-PLACE1000214//ESTs//0.00059:335:59//Hs.143849:AI167255
F-PLACE1000236//Fanconi anemia, complementation group A//0.44:306:61//Hs.86297:X99226
F-PLACE1000246//ESTs//7.3e-80:457:89//Hs.57209:W22022
F-PLACE1000292//ESTs//1.8e-05:323:60//Hs.59962:AI278202
F-PLACE1000308//EST//0.0024:253:62//Hs.144238:W52294
F-PLACE1000332//EST//5.6e-18:223:74//Hs.99532:AA461047
F-PLACE1000347//ESTs//6.4e-33:169:99//Hs.122975:AA428675
F-PLACE1000374//Human CCAAT-box-binding factor (CBF) mRNA, complete cds//0.26:45:95//Hs.147991:M37197
F-PLACE1000380//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//1.0:262:58//Hs.102732:U88153
F-PLACE1000383//Myotubular myopathy 1//1.1e-50:669:67//Hs.75302:U46024
F-PLACE1000401//Homo sapiens mRNA for KIAA0616 protein, partial cds//0.036:471:58//Hs.6051:AB014516
F-PLACE1000406//ESTs, Highly similar to PTB-ASSOCIATED SPLICING FACTOR [Homo sapiens]//8.7e-63:346:93//Hs.19501:AA742260
F-PLACE1000420//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.0023:216:65//Hs.37656:AB011174
F-PLACE1000421//Human lipid-activated protein kinase PRK1 mRNA, complete cds//0.55:212:63//Hs.2499:U33053
F-PLACE1000424
F-PLACE1000435//Homo sapiens mRNA for XPR2 protein//0.58:674:55//Hs.44766:AJ007590
F-PLACE1000444//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//2.7e-52:421:80//Hs.69747:M35531
F-PLACE1000453//Human mRNA for MTG8a protein, complete cds//0.026:240:60//Hs.31551:D43638
F-PLACE1000481//Oxytocin receptor//1.6e-25:347:71//Hs.2820:X64878

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F-PLACE1000492//Human mRNA for KIAA0355 gene, complete cds//0.58:302:60//Hs.153014:AB002353
F-PLACE1000540//EST//0.32:229:59//Hs.163011:AA700573
F-PLACE1000547//Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds//0.0046:223:65//Hs.75578:M85289
F-PLACE1000562
F-PLACE1000564//ESTs//8.0e-35:247:89//Hs.12999:AA278538
F-PLACE1000583//Homo sapiens clone 23939 mRNA sequence//6.6e-47:525:72//Hs.21838:AF038179
F-PLACE1000588//Guanylate binding protein 1, interferon-inducible, 67kD//2.3e-85:503:88//Hs.62661:M55542
F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.2e-165:798:97//Hs.159597:AJ012449
F-PLACE1000599//ESTs//0.65:201:58//Hs.98216:AA758751
F-PLACE1000610//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.98:215:60//Hs.8152:AB014542
F-PLACE1000611//ESTs//7.2e-20:406:64//Hs.128966:AA620986
F-PLACE1000636
F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//5.0e-154:747:96//Hs.5819:AF102265
F-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin))//7.5e-158:775:97//Hs.29595:AJ005896
F-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds//1.0e-57:675:69//Hs.128763:AF009353
F-PLACE1000712//EST//0.56:171:61//Hs.112790:AA609949
F-PLACE1000716//Human mRNA for KIAA0258 gene, complete cds//6.1e-38:426:70//Hs.47313:D87447
F-PLACE1000748//ESTs//2.6e-43:233:95//Hs.110754:AA112288
F-PLACE1000749//Human MAGE-9 antigen (MAGE9) gene, complete cds//0.72:331:57//Hs.37110:U10694
F-PLACE1000755//NUCLEOLIN//0.0038:186:66//Hs.79110:M60858
F-PLACE1000769
F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds//1.1e-139:663:98//Hs.31921:AB014548
F-PLACE1000786//Myosin, heavy polypeptide 9, non-muscle//8.5e-06:362:59//Hs.44782:Z82215
F-PLACE1000793//ESTs//2.7e-62:315:97//Hs.16141:W56079
F-PLACE1000798//ESTs//1.4e-55:316:93//Hs.139119:N32189
F-PLACE1000841//EST//0.47:143:61//Hs.144096:AI032180
F-PLACE1000849//Homo sapiens CAGF9 mRNA, partial cds//1.6e-06:266:63//Hs.110826:U80736
F-PLACE1000856//ESTs//2.6e-60:319:96//Hs.25994:AA470000
F-PLACE1000863//EST//9.4e-29:249:78//Hs.121919:AA777428
F-PLACE1000909//ESTs//0.97:214:60//Hs.128601:AA906455
F-PLACE1000931//ESTs//2.1e-46:592:70//Hs.154244:AA195201
F-PLACE1000948
F-PLACE1000972//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds//7.9e-10:294:66//Hs.80261:L43821
F-PLACE1000977//ESTs, Weakly similar to coded for by C. elegans cDNA yk28h2.5 [C.elegans]//9.3e-45:309:88//Hs.13531:R61789
F-PLACE1000979//Zinc finger protein 91 (HPF7, HTF10)//0.0034:229:62//Hs.8597:L11672
F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds//2.6e-141:694:96//Hs.158497:AB018267
F-PLACE1001000//ESTs//0.0035:116:73//Hs.144532:H39913
F-PLACE1001007//Guanylate cyclase 2D, membrane (retina-specific)//0.050:338:61//Hs.1974:M92432
F-PLACE1001010//H.sapiens mRNA for retrotransposon//1.6e-45:371:80//Hs.6940:Z48633
F-PLACE1001015//ESTs//8.6e-27:211:71//Hs.88040:AA256876
F-PLACE1001024
F-PLACE1001036//EST//1.0:133:65//Hs.161424:AI424741
F-PLACE1001054//Human plectin (PLEC1) mRNA, complete cds//0.98:284:59//Hs.79706:U53204
F-PLACE1001062
F-PLACE1001076//EST//0.84:223:59//Hs.161147:AI417859
F-PLACE1001088
F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds//1.0e-96:489:96//Hs.95448:AF065485
F-PLACE1001104//ESTs//0.19:249:64//Hs.152627:AA595817
F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds//8.2e-66:676:

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71//Hs.150406:AF022158
F-PLACE1001136//Amphiregulin (schwannoma-derived growth factor)//1.5e-16:122:91//Hs.1257:M30704
F-PLACE1001168
F-PLACE1001171//ESTs//4.3e-12:214:72//Hs.141392:R95135
F-PLACE1001185//ESTs, Weakly similar to ZK792.1 [C.elegans]//1.6e-28:421:66//Hs.8763:W30741
F-PLACE1001238
F-PLACE1001241//ESTs//1.1e-22:225:79//Hs.159786:R49494
F-PLACE1001257//ESTs//1.9e-23:165:89//Hs.126518:AA913929
F-PLACE1001272//COATOMER BETA'SUBUNIT//0.012:50:96//Hs.75724:X70476
F-PLACE1001279//ESTs//0.97:377:59//Hs.152628:N51283
F-PLACE1001280//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.2e-08:586:58//Hs.124161:AF065164
F-PLACE1001294//Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)//0.91:221:61//Hs.16533:D87930
F-PLACE1001304//Human zinc finger protein mRNA, complete cds//8.6e-08:370:60//Hs.42672:AF016052
F-PLACE1001311//ESTs//1.7e-44:480:73//Hs.155384:Z78385
F-PLACE1001323//ESTs//1.1e-25:151:95//Hs.134120:AA699591
F-PLACE1001351
F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cds//2.8e-26:155:95//Hs.61638:AB018342
F-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//3.4e-44:393:79//Hs.152005:AF009615
F-PLACE1001383//ESTs//1.0:159:65//Hs.128501:AA973748
F-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//2.6e-09:117:84//Hs.21301:AF093419
F-PLACE1001387//ESTs, Weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 [H.sapiens]//0.00083:187:64//Hs.5399:N30646
F-PLACE1001395//Homo sapiens mRNA for putative DNA methyltransferase, complete CDS//0.0038:496:57//Hs.97681:AJ223333
F-PLACE1001399//Human melanoma antigen recognized by T-cells (MART-1) mRNA//7.0e-45:456:75//Hs.154069:U06452
F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//6.5e-71:365:96//Hs.110404:AF091087
F-PLACE1001414//EST//1.2e-75:364:98//Hs.136622:AA633232
F-PLACE1001440//ESTs//2.8e-05:163:66//Hs.141082:H18987
F-PLACE1001456//EST//0.95:132:61//Hs.20373:R09510
F-PLACE1001468//ESTs//0.00019:184:66//Hs.126536:AI379455
F-PLACE1001484//EST//8.6e-18:190:76//Hs.160992:H52716
F-PLACE1001502//Apolipoprotein E//2.5e-05:306:60//Hs.76260:M12529
F-PLACE1001503
F-PLACE1001517//ESTs//1.9e-12:138:78//Hs.120352:AA718914
F-PLACE1001534//EST//0.015:121:65//Hs.144156:R85753
F-PLACE1001545
F-PLACE1001551
F-PLACE1001570//EST//0.58:286:59//Hs.120202:AA728835
F-PLACE1001602//Human POU domain protein (Brn-3b) mRNA, complete cds//0.013:159:66//Hs.266:U06233
F-PLACE1001603//Homo sapiens nitrilase 1 (NIT1) mRNA, complete cds//1.1e-10:133:77//Hs.146406:AF069987
F-PLACE1001608//ESTs//0.022:187:60//Hs.145915:AI342230
F-PLACE1001610//ESTs//1.4e-77:377:97//Hs.115700:AA808005
F-PLACE1001611//Human faciogenital dysplasia (FGD1) mRNA, complete cds//0.96:141:66//Hs.1572:U11690
F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.4e-76:702:75//Hs.159277:AB018341
F-PLACE1001634//ESTs//1.2e-43:260:92//Hs.134064:AI276198
F-PLACE1001640
F-PLACE1001672//EST//2.8e-21:201:82//Hs.123341:AA810927
F-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//2.8e-148:726:96//Hs.3688:AF069250
F-PLACE1001692//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN [Rattus norvegicus]//1.1e-95:481:92//Hs.24309:AI125696

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F-PLACE1001705//Human RNA polymerase III subunit (RPC39) mRNA, complete cds//6.0e-30:347:76//Hs.101555:U93869
F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds//2.1e-69:369:73//Hs.12413:D83776
F-PLACE1001720//ESTs//1.2e-27:146:99//Hs.106432:AI391686
F-PLACE1001729//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0084:484:60//Hs.129892:AB011094
F-PLACE1001739//Histidine-rich calcium binding protein//0.14:240:64//Hs.1480:M60052
F-PLACE1001740//ESTs//4.9e-32:343:74//Hs.139158:AA226159
F-PLACE1001745
F-PLACE1001746//ESTs//7.0e-15:168:80//Hs.46601:N78361
F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//2.8e-160:773:97//Hs.4812:AF061243
F-PLACE1001756//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.7e-35:269:83//Hs.5247:AF029750
F-PLACE1001761//ESTs//6.9e-27:159:93//Hs.78277:AA131283
F-PLACE1001771//Human putative calcium influx channel (htrp3) mRNA, complete cds//3.4e-52:548:72//Hs.150981:U47050
F-PLACE1001781
F-PLACE1001799//EST//5.4e-07:145:70//Hs.121840:AA776115
F-PLACE1001810//ESTs//0.024:134:67//Hs.43134:AA766138
F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//3.6e-110:546:96//Hs.40820:AF058953
F-PLACE1001821
F-PLACE1001844//ESTs//5.4e-45:387:79//Hs.61199:AA024494
F-PLACE1001845//ESTs//2.5e-47:232:100//Hs.120809:AA150214
F-PLACE1001869//EST//1.0:139:59//Hs.122285:AA781906
F-PLACE1001897//ESTs//0.29:348:57//Hs.139993:AI343257
F-PLACE1001912//ESTs//4.0e-10:95:89//Hs.13475:R18220
F-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//4.0e-153:685:95//Hs.17839:AF099936
F-PLACE1001928//H.sapiens HUMM9 mRNA//0.063:196:66//Hs.2750:X74837
F-PLACE1001983//Homo sapiens Jagged 2 mRNA, complete cds//9.8e-06:431:58//Hs.106387:AF029778
F-PLACE1001989
F-PLACE1002004
F-PLACE1002046
F-PLACE1002052//Human mRNA for phospholipase C, complete cds//0.0092:465:58//Hs.153322:D42108
F-PLACE1002066//EST//0.49:307:61//Hs.150652:AA908555
F-PLACE1002072//EST//1.0:103:65//Hs.116488:F13707
F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds//4.2e-39:635:64//Hs.38176:AB011178
F-PLACE1002090//Homo sapiens signal recognition particle 72 (SRP72) mRNA, complete cds//4.3e-83:388:99//Hs.5171:AF069765
F-PLACE1002115//EST//0.18:215:62//Hs.135747:AI002637
F-PLACE1002119//Human transcription factor ETR101 mRNA, complete cds//6.2e-13:384:61//Hs.737:M62831
F-PLACE1002140//EST, Moderately similar to ALPHA-1-ANTITRYPSIN PRECURSOR [Homo sapiens]//0.89:60:75//Hs.144290:T61747
F-PLACE1002150//ESTs//0.56:245:64//Hs.24119:AA115631
F-PLACE1002157//Human mRNA for KIAA0392 gene, partial cds//2.8e-51:440:79//Hs.40100:AB002390
F-PLACE1002163//ESTs//0.76:212:61//Hs.112494:AI366891
F-PLACE1002170//ESTs//6.5e-09:108:76//Hs.41418:H90627
F-PLACE1002171//ESTs//3.5e-81:493:89//Hs.122553:H66674
F-PLACE1002205//Human clone 23695 mRNA sequence//0.00080:472:60//Hs.90798:U79289
F-PLACE1002213//ESTs//0.041:146:67//Hs.119162:AA399989
F-PLACE1002227//ESTs//9.4e-06:173:66//Hs.127882:AI024442
F-PLACE1002256//ESTs//1.8e-93:440:99//Hs.128700:AA970935
F-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-75:434:83//Hs.23094:M19503
F-PLACE1002319//ESTs//0.82:188:62//Hs.50918:AA036675
F-PLACE1002342//EST//0.61:148:66//Hs.144319:AA280279
F-PLACE1002395//ESTs//1.2e-18:168:83//Hs.3853:AA034291
F-PLACE1002399//EST//0.0011:166:65//Hs.137500:AA436710
F-PLACE1002433//ESTs//1.2e-14:151:80//Hs.161837:AA421067

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F-PLACE1002437//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//2.6e-23:458:66//Hs.40993:AF000148
F-PLACE1002438//EST//0.81:48:77//Hs.158575:AI368947
F-PLACE1002450//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds//7.1e-07:270:66//Hs.150406:AF022158
F-PLACE1002465
F-PLACE1002474//Homo sapiens mRNA for matrilin-4, partial//1.3e-14:369:63//Hs.129361:AJ007581
F-PLACE1002477//ESTs//3.5e-13:125:71//Hs.145032:AA343523
F-PLACE1002493
F-PLACE1002499
F-PLACE1002500//Human putative zinc transporter ZnT-3 (ZnT-3) mRNA, complete cds//4.3e-19:708:59//Hs.111967:U76010
F-PLACE1002514//ESTs//3.1e-07:178:66//Hs.70932:AA126482
F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//2.9e-144:583:95//Hs.88756:AB018256
F-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//3.1e-115:566:96//Hs.99348:AC004774
F-PLACE1002537//Thiopurine S-methyltransferase//1.9e-28:198:86//Hs.51124:AF019369
F-PLACE1002571//Homo sapiens mRNA for TP55, complete cds//0.99:274:59//Hs.138202:AF027866
F-PLACE1002578//ESTs//7.3e-10:185:73//Hs.41418:H90627
F-PLACE1002583//EST//0.0028:348:61//Hs.160396:AI393725
F-PLACE1002591//Human mRNA for actin binding protein p57, complete cds//2.8e-27:279:74//Hs.109606:D44497
F-PLACE1002598//EST//0.011:209:62//Hs.131470:AI024187
F-PLACE1002604//EST//0.47:220:61//Hs.145434:AI198915
F-PLACE1002625
F-PLACE1002655//GELSOLIN PRECURSOR, PLASMA//1.7e-36:693:62//Hs.80562:X04412
F-PLACE1002665//EST//0.15:156:65//Hs.161793:AA380706
F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//1.1e-187:804:97//Hs.124903:AF068180
F-PLACE1002714//Human involucrin mRNA//3.6e-08:509:60//Hs.157091:M13903
F-PLACE1002722//Human protease-activated receptor 3 (PAR3) mRNA, complete cds//0.34:230:58//Hs.159196:U92971
F-PLACE1002768//EST//0.37:126:69//Hs.125353:AA877080
F-PLACE1002772//ESTs//0.0017:147:69//Hs.132439:AA923728
F-PLACE1002775//EST//5.5e-09:129:75//Hs.135336:AI049827
F-PLACE1002782//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0.0031:298:62//Hs.26285:AF082516
F-PLACE1002794//ESTs//0.71:125:66//Hs.97441:AI368926
F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds//5.8e-46:567:70//Hs.77546:D79994
F-PLACE1002815
F-PLACE1002816//Homo sapiens mRNA for KIAA0600 protein, partial cds//4.3e-70:687:73//Hs.9028:AF039691
F-PLACE1002834//ESTs//2.6e-41:393:74//Hs.120206:AI089163
F-PLACE1002839//ESTs//0.26:177:63//Hs.149013:AI334167
F-PLACE1002851//EST//0.0034:102:72//Hs.129630:AI000405
F-PLACE1002853//ESTs//1.1e-20:136:90//Hs.125895:AA889024
F-PLACE1002881//Interleukin 10//1.1e-41:454:72//Hs.2180:M57627
F-PLACE1002908//ESTs//3.8e-48:325:88//Hs.54702:AI040029
F-PLACE1002941//ESTs//5.0e-18:128:88//Hs.17376:AA855056
F-PLACE1002962
F-PLACE1002968//ESTs, Highly similar to trg gene product [R.norvegicus]//0.031:372:59//Hs.8021:AI041815
F-PLACE1002991
F-PLACE1002993
F-PLACE1002996//ESTs, Weakly similar to T20D3.3 [C.elegans]//1.3e-12:104:86//Hs.124808:T86959
F-PLACE1003025//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0510//0.99:192:64//Hs.92660:AB007979
F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds//2.0e-131:632:97//Hs.129872:AB011088

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F-PLACE1003044//Homo sapiens mRNA for KIAA0667 protein, partial cds//2.7e-14:555:58//Hs.154740:AB014567
F-PLACE1003045
F-PLACE1003092//ESTs//1.1e-108:506:99//Hs.22119:AA885491
F-PLACE1003100//Human Hep27 protein mRNA, complete cds//2.9e-66:650:73//Hs.102137:U31875
F-PLACE1003108//EST//0.016:181:65//Hs.119762:AA703419
F-PLACE1003136
F-PLACE1003145
F-PLACE1003153//ESTs//3.1e-09:209:65//Hs.111583:AA463590
F-PLACE1003174//ESTs//0.073:97:69//Hs.12992:W01997
F-PLACE1003176//ESTs//3.3e-60:296:90//Hs.58239:AA215797
F-PLACE1003190//Homo sapiens C19steroid specific UDP-glucuronosyltransferase mRNA, complete cds//0.98:221:60//Hs.139756:U59209
F-PLACE1003200//EST//0.0021:309:60//Hs.140561:AA765532
F-PLACE1003205//EST//1.2e-07:204:65//Hs.147372:AI208770
F-PLACE1003238//ESTs//7.4e-62:343:94//Hs.121302:AA758208
F-PLACE1003249//Insulin-like growth factor 1 (somatomedia C)//0.99:175:62//Hs.85112:X57025
F-PLACE1003256
F-PLACE1003258//H.sapiens mRNA for ZYG homologue//0.00020:217:64//Hs.29285:X99802
F-PLACE1003296//ESTs//2.6e-14:80:86//Hs.155441:AA533106
F-PLACE1003302//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//4.3e-51:700:67//Hs.37138:U35376
F-PLACE1003334
F-PLACE1003342//ESTs//0.94:310:57//Hs.131502:AI023308
F-PLACE1003343//EST//1.2e-09:114:77//Hs.103418:AA035568
F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds//2.6e-144:773:92//Hs.6564:U92715
F-PLACE1003361//ESTs, Weakly similar to ATP SYNTHASE A CHAIN [Trypanosoma brucei brucei]//8.9e-35:332:78//Hs.163820:H71277
F-PLACE1003366//Homo sapiens dysferlin mRNA, complete cds//7.9e-06:502:57//Hs.143897:AF075575
F-PLACE1003369//NUCLEOLIN//0.00037:282:60//Hs.79110:M60858
F-PLACE1003373//EST//1.1e-11:420:63//Hs.156592:AI343009
F-PLACE1003375//EST//0.75:119:68//Hs.160270:AI149069
F-PLACE1003383
F-PLACE1003394//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-14 [Rattus norvegicus]//8.9e-113:590:94//Hs.125175:AI142546
F-PLACE1003401//ESTs//0.55:176:66//Hs.154292:AA886178
F-PLACE1003420//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.40:206:62//Hs.30223:X90846
F-PLACE1003454//ESTs//0.98:74:72//Hs.127131:AA150912
F-PLACE1003478//EST//5.0e-06:183:69//Hs.127524:AA952874
F-PLACE1003493//Protein-tyrosine kinase 7//0.98:232:63//Hs.90572:U33635
F-PLACE1003516//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//3.4e-85:357:86//Hs.103948:K00627
F-PLACE1003519//ESTs//1.6e-33:288:72//Hs.159510:AA297145
F-PLACE1003521//H.sapiens mRNA for retrotransposon//1.4e-45:269:76//Hs.6940:Z48633
F-PLACE1003528//ESTs//0.65:120:68//Hs.162376:AA570248
F-PLACE1003537//ESTs, Weakly similar to ZK858.6 [C.elegans]//3.6e-110:543:97//Hs.120416:AA057428
F-PLACE1003553
F-PLACE1003566//ESTs//0.0015:508:59//Hs.5724:AA156780
F-PLACE1003575//Homo sapiens cdc14 homolog mRNA, complete cds//4.4e-05:499:58//Hs.65993:AF000367
F-PLACE1003583//ESTs//5.5e-19:448:63//Hs.161701:AA225932
F-PLACE1003584//EST//1.6e-46:263:94//Hs.147412:AI209194
F-PLACE1003592//ESTs, Moderately similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//1.4e-50:287:93//Hs.154799:AA130620
F-PLACE1003593//ESTs//0.0025:318:61//Hs.106771:AA806965
F-PLACE1003596//Integral transmembrane protein 1//1.9e-54:685:68//Hs.89650:L38961
F-PLACE1003602//Homo sapiens mRNA expressed in placenta//3.4e-140:679:97//Hs.56851:D83200
F-PLACE1003605//Homo sapiens Cdc14B2 phosphatase mRNA, partial cds//0.00065:236:64//Hs.22116:AF064104

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F-PLACE1003611//EST//0.00015:318:59//Hs.28788:R66896
F-PLACE1003618//Human Line-1 repeat mRNA with 2 open reading frames//1.3e-122:737:87//Hs.23094:M19503
F-PLACE1003625//ESTs//1.6e-16:103:96//Hs.111223:N51105
F-PLACE1003638//ESTs//0.60:305:57//Hs.19104:W07762
F-PLACE1003669//ESTs, Weakly similar to 3-7 gene product [H.sapiens]//0.021:445:58//Hs.158275:AI365413
F-PLACE1003704//Human mRNA for KIAA0301 gene, partial cds//0.014:622:56//Hs.76730:AB002299
F-PLACE1003709//Homo sapiens protein kinase (BUB1) mRNA, complete cds//1.4e-133:669:95//Hs.98658:AF053305
F-PLACE1003711//ESTs//2.2e-14:178:77//Hs.114831:T57101
F-PLACE1003723//Homo sapiens mRNA for T lymophocyte specific adaptor protein//8.5e-09:393:60//Hs.103527:AJ000553
F-PLACE1003738//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//1.8e-53:260:99//Hs.102928:AI346344
F-PLACE1003760//ESTs//5.1e-08:334:63//Hs.43675:AA805648
F-PLACE1003762//ESTs//1.0:59:83//Hs.29863:W28983
F-PLACE1003768//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//2.7e-40:608:68//Hs.139107:K00629
F-PLACE1003771//ESTs//6.6e-10:226:65//Hs.15776:T91944
F-PLACE1003783
F-PLACE1003784//Homo sapiens mRNA for KIAA0765 protein, partial cds//1.0:457:57//Hs.62318:AB018308
F-PLACE1003795//Human homologue of yeast sec7 mRNA, complete cds//0.85:314:60//Hs.1050:M85169
F-PLACE1003833//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.00059:201:68//Hs.40806:AA018786
F-PLACE1003850//ESTs//0.0088:220:61//Hs.145504:AI254165
F-PLACE1003858//EST//0.77:137:61//Hs.146935:AI168124
F-PLACE1003864//ESTs//0.11:225:59//Hs.160910:AI370359
F-PLACE1003870//EST//7.2e-18:283:69//Hs.135497:AI091257
F-PLACE1003885//H.sapiens PAP mRNA//2.4e-75:759:72//Hs.49007:X76770
F-PLACE1003886
F-PLACE1003888//Human mRNA for phospholipase C, complete cds//8.4e-55:702:67//Hs.153322:D42108
F-PLACE1003892//ESTs//2.4e-13:258:67//Hs.28039:H24050
F-PLACE1003900//ESTs//3.5e-14:271:66//Hs.28589:AI004944
F-PLACE1003903//CTP synthetase//1.6e-49:528:71//Hs.84112:X52142
F-PLACE1003915//ESTs, Highly similar to ARGINYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR [Saccharomyces cerevisiae]//1.2e-49:251:98//Hs.65831:F03069
F-PLACE1003923//Interferon, alpha 16//0.48:278:60//Hs.56303:M28585
F-PLACE1003932//EST//0.00060:221:63//Hs.163044:AA707537
F-PLACE1003936//ESTs//0.86:211:62//Hs.150751:AI123536
F-PLACE1003968//Human 5'-AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds//2.0e-47:522:71//Hs.3136:U42412
F-PLACE1004103//ESTs//8.6e-35:226:89//Hs.78973:AI026812
F-PLACE1004104//ESTs//1.0:179:61//Hs.163935:AA506940
F-PLACE1004114//ESTs//1.3e-52:323:89//Hs.35156:AA148516
F-PLACE1004118//Spleen focus forming virus (SFFV) proviral integration oncogene spi1//0.85:164:64//Hs.153045:X52056
F-PLACE1004128//Guanine nucleotide binding protein (G protein), beta polypeptide 1//3.1e-41:422:74//Hs.3620:X04526
F-PLACE1004149//ESTs, Weakly similar to F48F7.1 [C.elegans]//8.2e-82:418:96//Hs.156161:AI333779
F-PLACE1004156//ESTs//0.10:166:63//Hs.133279:AI053552
F-PLACE1004161//Human mRNA for KIAA0200 gene, complete cds//0.85:269:64//Hs.76986:D83785
F-PLACE1004183//EST//1.3e-40:224:94//Hs.156603:AI343666
F-PLACE1004197//ESTs//2.8e-91:441:98//Hs.97269:AA292201
F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds//1.3e-145:695:98//Hs.24640:AF069493
F-PLACE1004242//ESTs//0.99:213:60//Hs.117311:AA699722
F-PLACE1004256//EST//0.019:364:58//Hs.122395:AA789273
F-PLACE1004257//ESTs//0.77:154:64//Hs.112582:AA608689
F-PLACE1004258//ESTs, Weakly similar to vanilloid receptor subtype 1 [R.norvegicus]//1.1e-98:479:97//Hs.31718:N29128
F-PLACE1004270//Homo sapiens CAGF9 mRNA, partial cds//0.00010:369:63//Hs.110826:U80736

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F-PLACE1004274//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.085:573:56//Hs.154139:AB007914
F-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds//2.0e-157:756:97//Hs.127007:AF084830
F-PLACE1004284//ESTs//3.6e-71:344:99//Hs.145870:AI271884
F-PLACE1004289//ESTs//2.6e-57:370:85//Hs.16740:AA586576
F-PLACE1004302//FACTOR VIII INTRON 22 PROTEIN//0.032:513:59//Hs.83363:M34677
F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//9.3e-152:797:94//Hs.11171:Y11588
F-PLACE1004336
F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//1.9e-140:688:97//Hs.16232:AF100153
F-PLACE1004376//ESTs, Weakly similar to F27D4.4 [C.elegans]//3.9e-109:521:98//Hs.14079:AA306552
F-PLACE1004384//Human HsLIM15 mRNA for HsLiml5, complete cds//2.0e-49:466:76//Hs.37181:D64108
F-PLACE1004388
F-PLACE1004405//EST//0.010:191:64//Hs.147600:AI217871
F-PLACE1004425//ESTs//2.1e-20:124:80//Hs.94195:W03579
F-PLACE1004428//H.sapiens mRNA for Branched chain Acyl-CoA Oxidase//1.0:552:58//Hs.9795:X95190
F-PLACE1004437//Human NAD^+-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds//9.9e-131:536:99//Hs.155410:U49283
F-PLACE1004451//ESTs//5.9e-18:203:73//Hs.156097:AI348867
F-PLACE1004460
F-PLACE1004467//ESTs//8.0e-17:345:66//Hs.112993:AA824363
F-PLACE1004471//EST//9.3e-69:463:84//Hs.116391:AA644085
F-PLACE1004473//ESTs//0.93:358:58//Hs.33263:AA724416
F-PLACE1004491//EST//2.5e-58:285:99//Hs.97603:AA398163
F-PLACE1004506//CD81 ANTIGEN//7.2e-06:228:63//Hs.54457:M33680
F-PLACE1004510//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds//2.5e-147:699:97//Hs.122752:AF026445
F-PLACE1004516//EST//1.0e-26:343:71//Hs.142595:N24150
F-PLACE1004518
F-PLACE1004548//EST//0.84:193:62//Hs.99583:AA461314
F-PLACE1004550//ESTs, Weakly similar to No definition line found [C.elegans]//4.0e-120:627:94//Hs.107387:AA058854
F-PLACE1004564//EST//1.0:240:62//Hs.16824:T91371
F-PLACE1004629//Centromere protein B (80kD)//0.0015:242:64//Hs.85004:X05299
F-PLACE1004645
F-PLACE1004646//Retinal pigment epithelium-specific protein (65kD)//1.4e-12:386:63//Hs.2133:U18991
F-PLACE1004658//ESTs//0.52:273:61//Hs.97252:AA291590
F-PLACE1004664
F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene//1.5e-66:357:95//Hs.77705:U07563
F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//1.4e-110:625:91//Hs.80019:AF035606
F-PLACE1004681//EST//0.00092:303:61//Hs.149560:AI281589
F-PLACE1004686//ESTs//3.0e-31:186:76//Hs.139130:AA704561
F-PLACE1004691//Homo sapiens clone 23963 mRNA sequence//0.54:242:61//Hs.48483:AF007131
F-PLACE1004693//ESTs, Weakly similar to pot. ORF III [H.sapiens]//0.56:96:71//Hs.125740:AA884845
F-PLACE1004716//ESTs//2.0e-79:388:98//Hs.150999:AI306542
F-PLACE1004722//ESTs//7.5e-06:105:72//Hs.128796:AA485891
F-PLACE1004736//ESTs//1.7e-27:203:86//Hs.119593:AA700148
F-PLACE1004740//ESTs//1.0e-25:174:89//Hs.29696:AA910680
F-PLACE1004743
F-PLACE1004751//ESTs, Highly similar to CMP-N-ACETYLNEURAMINATE-BETA-1,4-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE [Rattus norvegicus]//2.0e-41:260:90//Hs.6863:W52470
F-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds//1.7e-172:828:97//Hs.104715:AF084367
F-PLACE1004777//Human myosin IXb mRNA, complete cds//1.0e-29:556:63//Hs.159629:U42391
F-PLACE1004793
F-PLACE1004804

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F-PLACE1004813//EST//2.8e-42:296:83//Hs.155725:AI310340
F-PLACE1004814//ESTs, Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus laevis]//2.4e-78:415:95//Hs.80965:AA493284
F-PLACE1004815//Human mRNA for KIAA0364 gene, complete cds//4.3e-14:294:69//Hs.22111:AB002362
F-PLACE1004824//ESTs//0.0072:128:69//Hs.164062:AA934047
F-PLACE1004827//ESTs//0.78:38:100//Hs.18925:W30943
F-PLACE1004836//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.78:338:57//Hs.8546:U97669
F-PLACE1004838
F-PLACE1004840//Protein phosphatase 1, catalytic subunit, beta isoform//0.89:200:66//Hs.21537:X80910
F-PLACE1004868
F-PLACE1004885//ESTs//0.41:181:61//Hs.116796:AA633772
F-PLACE1004900
F-PLACE1004902//ESTs//4.7e-72:367:96//Hs.54971:AI424382
F-PLACE1004913//ESTs//0.031:166:63//Hs.130110:AA904929
F-PLACE1004918//Human tumor susceptiblity protein (TSG101) mRNA, complete cds//4.1e-24:402:64//Hs.118910:U82130
F-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//9.7e-86:519:88//Hs.17839:AF099936
F-PLACE1004934//ESTs//7.2e-43:231:78//Hs.133503:AA628592
F-PLACE1004937//ESTs//0.97:80:68//Hs.144264:C00851
F-PLACE1004969
F-PLACE1004972//Human retinoic acid- and interferon-inducible 58K protein RI58 mRNA, complete cds//0.031:235:60//Hs.27610:U34605
F-PLACE1004979//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-43:331:83//Hs.153468:AB011147
F-PLACE1004982//ESTs//0.020:148:63//Hs.129377:AI218520
F-PLACE1004985//ESTs//7.9e-05:372:61//Hs.87606:AA242831
F-PLACE1005026//ESTs//4.6e-29:212:89//Hs.137451:AA351459
F-PLACE1005027//ESTs//6.5e-91:455:97//Hs.30890:H15159
F-PLACE1005046//ESTs//3.7e-56:250:96//Hs.152730:AI308943
F-PLACE1005052//EST//1.8e-36:370:73//Hs.123424:AA813594
F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds//6.2e-161:761:98//Hs.14687:AB011148
F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//3.0e-11:757:56//Hs.122967:AF059569
F-PLACE1005077//EST//0.79:283:591/Hs.89276:AA283899
F-PLACE1005085//ESTs//3.5e-18:231:72//Hs.142654:AA324740
F-PLACE1005086//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.9e-49:401:80//Hs.153468:AB011147
F-PLACE1005101//Homo sapiens (clone zapl28) mRNA, 3' end of cds//8.2e-20:194:80//Hs.75437:L40401
F-PLACE1005102//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//8.9e-18:538:62//Hs.104640:AF000561
F-PLACE1005108//Treacher Collins syndrome susceptibility protein//0.73:405:57//Hs.73166:U76366
F-PLACE1005111//ESTs//0.66:191.63//Hs.106446:N93227
F-PLACE1005128//Breakpoint cluster region protein BCR//5.6e-08:291:63//Hs.2557:Y00661
F-PLACE1005146//ESTs, Weakly similar to hypothetical protein II [H.sapiens]//4.8e-12:360:63//Hs.142177:H11741
F-PLACE1005162//Human mRNA for KIAA0118 gene, partial cds//3.9e-49:563:72//Hs.154326:D42087
F-PLACE1005176//Homo sapiens mRNA for KIAA0641 protein, complete cds//0.82:259:60//Hs.128316:AB014541
F-PLACE1005181//ESTs, Weakly similar to No definition line found [C.elegans]//4.4e-126:583:99//Hs.25347:AI138605
F-PLACE1005187//ESTs//6.2e-34:222:90//Hs.124265:N70417
F-PLACE1005206//EST//0.089:167:62//Hs.140487:AA767009
F-PLACE1005232//ESTs, Weakly similar to synapse-associated protein sap47-1 [D.melanogaster]//0.56:192:60//Hs.47334:W72370
F-PLACE1005243
F-PLACE1005261//ESTs//0.52:245:58//Hs.6682:T76941

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F-PLACE1005266//Kallmann syndrome 1 sequence//7.8e-06:484:60//Hs.89591:M97252
F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds//5.1e-150:706:98//Hs.118087: AB011182
F-PLACE1005287//ESTs//8.1e-107:501:99//Hs.145703:AA447947
F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//4.4e-37:597:66//Hs.101642: X60673
F-PLACE1005308//High-mobility group (nonhistone chromosomal) protein 2//0.83:239:62//Hs.80684:X62534
F-PLACE1005313
F-PLACE1005327//ESTs, Weakly similar to No definition line found [C.elegans]//6.0e-81:459:91//Hs.146177: R51650
F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569//3.7e-66:412:88//Hs.134031:AC004794
F-PLACE1005335//Homo sapiens mRNA for KIAA0754 protein, partial cds//0.96:510:56//Hs.159183:AB018297
F-PLACE1005373
F-PLACE1005374//ESTs//7.5e-77:437:91//Hs.143266:AI141348
F-PLACE1005409//ESTs//2.4e-05:267:63//Hs.163307:AA856751
F-PLACE1005453//ESTs//0.12:333:58//Hs.134672:AI087951
F-PLACE1005467//HOMEOBOX/POU DOMAIN PROTEIN RDC-1//0.0043:148:67//Hs.74095:L20433
F-PLACE1005471//ESTs//3.4e-24:135:97//Hs.49275:N66925
F-PLACE1005477//Human Line-1 repeat mRNA with 2 open reading frames//3.5e-126:744:87//Hs.23094:M19503
F-PLACE1005480//ESTs//3.7e-26:184:70//Hs.113198:N39323
F-PLACE1005481//EST//0.27:153-:64//Hs.120066:AA707973
F-PLACE1005494//ESTs//2.4e-50:257:98//Hs.159003:AA633029
F-PLACE1005502//ESTs//0.15:408:57//Hs.45106:AA504105
F-PLACE1005526//ESTs//3.2e-61:305:98//Hs.122574:AA776747
F-PLACE1005528//ESTs//9.9e-32:249:78//Hs.142531:N91572
F-PLACE1005530//ESTs//1.0e-94:491:95//Hs.131731:AI339335
F-PLACE1005550//ESTs//0.084:290:58//Hs.157775:AI359385
F-PLACE1005554//EST//0.38:213:58//Hs.102749:N64144
F-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR [Saccharomyces cerevisiae]//4.5e-51:258:97//Hs.7736:W81261
F-PLACE1005574//ESTs//3.2e-09:236:66//Hs.146884:AI160278
F-PLACE1005584//Fragile X mental retardation 2//1.2e-05:151:69//Hs.54472:U48436
F-PLACE1005595//ESTs//2.1e-98:512:95//Hs.118552:W74594
F-PLACE1005603//EST//1.0:90:66//Hs.111204:AA211851
F-PLACE1005611//ESTs, Weakly similar to B0035.14 [C.elegans]//3.5e-32:197:92//Hs.8241:AA283057
F-PLACE1005623//ESTs//3.0e-30:191:92//Hs.77570:N48234
F-PLACE1005630//ESTs//2.3e-32:175:97//Hs.122278:AA781867
F-PLACE1005639//ESTs//0.88:218:58//Hs.117389:AA701991
F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//2.1e-151:721:98//Hs.8765: AF083255
F-PLACE1005656//Ribonucleotide reductase M2 polypeptide//3.9e-53:480:74//Hs.75319:X59618
F-PLACE1005666//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.086:223:59//Hs.27349: AB007917
F-PLACE1005698//Human membrane-associated lectin type-C mRNA//6.1e-65:374:85//Hs.23759:M98457
F-PLACE1005727//ESTs//8.7e-65:330:96//Hs.127027:AA935437
F-PLACE1005730//ESTs//2.9e-14:270:67//Hs.28589:AI004944
F-PLACE1005739//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//0.75:289:59// Hs.75111:D87258
F-PLACE1005755//Insulin-like growth factor binding protein 2//3.6e-05:377:62//Hs.162:X16302
F-PLACE1005763//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN [Rattus norvegicus]//5.7e-49:252:88//Hs.24309:AI125696
F-PLACE1005799//ESTs//5.2e-13:392:58//Hs.110530:AA191493
F-PLACE1005802
F-PLACE1005803
F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//4.5e-128:636:96//Hs.125315: AF027156
F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//8.4e-156:739:98//Hs.11183: AF065482

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F-PLACE1005828//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.1e-42:327:81//Hs.138404:R70986
F-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)//0.038:436:58//Hs.75770:L41870
F-PLACE1005845//ESTs//4.8e-50:309:89//Hs.107149:AI379497
F-PLACE1005850//ESTs//7.1e-40:253:79//Hs.158096:AA186905
F-PLACE1005851//ESTs//7.6e-93:483:95//Hs.135608:AA732242
F-PLACE1005876//ESTs//0.97:282:60//Hs.98664:AI381487
F-PLACE1005884//ESTs//0.070:276:60//Hs.106057:AI031552
F-PLACE1005890//ESTs//1.5e-91:500:93//Hs.136993:AA843300
F-PLACE1005898
F-PLACE1005921
F-PLACE1005923//ESTs//0.50:308:58//Hs.52489:R61504
F-PLACE1005925//ESTs//0.024:93:68//Hs.149868:AI288274
F-PLACE1005932//TYROSINE-PROTEIN KINASE RECEPTOR EPH PRECURSOR//0.97:342:57//Hs.89839:M18391
F-PLACE1005934//ESTs//8.6e-10:74:93//Hs.25092:AA922142
F-PLACE1005936//DNA excision repair protein ERCC5//1.0:144:63//Hs.48576:X69978
F-PLACE1005951//B94 PROTEIN//0.00025:371:61//Hs.75522:M92357
F-PLACE1005953//ESTs//2.8e-06:290:61//Hs.140996:R73468
F-PLACE1005955//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.15:136:66//Hs.107747:AI357868
F-PLACE1005966//Human zinc fmger/leucine zipper protein (AF10) mRNA, complete cds//1.0:215:63//Hs.7885:U13948
F-PLACE1005968
F-PLACE1005990
F-PLACE1006002//Putative mismatch repair/binding protein hMSH3//1.9e-48:312:77//Hs.42674:U61981
F-PLACE1006003//EST//0.00018:171:67//Hs.138882:W73256
F-PLACE1006011
F-PLACE1006017//ESTs//3.1e-21:159:88//Hs.142173:AA757743
F-PLACE1006037//Homo sapiens mRNA for KIAA0789 protein, complete cds//0.021:202:64//Hs.158319:AB018332
F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine//1.1e-148:719:97//Hs.98782:X99906
F-PLACE1006076//EST//0.29:92:64//Hs.161536:N80395
F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds//4.1e-147:679:99//Hs.4976:AF039023
F-PLACE1006129
F-PLACE1006139
F-PLACE1006143//Human mRNA for KIAA0355 gene, complete cds//9.3e-43:357:79//Hs.153014:AB002353
F-PLACE1006157//ESTs, Weakly similar to ETX1 {alternatively spliced} [H.sapiens]//2.9e-12:119:84//Hs.23153:R92857
F-PLACE1006159//ESTs//2.3e-87:443:96//Hs.23740:H17868
F-PLACE10061641/ESTs//0.099:223:60//Hs.8108:AA902721
F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//1.1e-68:333:92//Hs.152894:AC005239
F-PLACE1006170//ESTs//0.081:171:67//Hs.135187:AI074005
F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//1.2e-150:694:99//Hs.30464:AF091433
F-PLACE1006195//ESTs//8.9e-14:229:70//Hs.141470:N49608
F-PLACE1006196//ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog//3.5e-59:369:88//Hs.135623:AA134719
F-PLACE1006205
F-PLACE1006223//ESTs, Weakly similar to TERATOCARCINOMA-DERIVED GROWTH FACTOR 1 [H.sapiens]//0.0089:166:63//Hs.127179:AI279486
F-PLACE1006225
F-PLACE1006236//EST//0.060:89:69//Hs.136977:AA830668
F-PLACE1006239//ESTs//0.028:105:66//Hs.142336:AA358185
F-PLACE1006246//ESTs//0.060:330:60//Hs.105695:AI085802
F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//7.3e-168:791:98//Hs.31921:AB014548
F-PLACE1006262
F-PLACE1006288//Homo sapiens mRNA for Pex3 protein//4.8e-37:186:100//Hs.7277:AJ001625

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F-PLACE1006318
F-PLACE1006325//ESTs//3.7e-25:206:83//Hs.102319:AI246503
F-PLACE1006335//ESTs//2.0e-27:161:95//Hs.163529:AI361492
F-PLACE1006357//ESTs//0.013:268:61//Hs.105775:AA526249
F-PLACE1006360//ESTs//4.8e-27:146:98//Hs.100739:Z98481
F-PLACE1006368//Homo sapiens clone 24540 mRNA sequence//0.65:272:59//Hs.153529:AF070581
F-PLACE1006371//Homo sapiens jerky gene product homolog mRNA, complete cds//2.6e-07:403:61//Hs.105940:AF004715
F-PLACE1006382//EST//0.98:77:68//Hs.136933:AA814693
F-PLACE1006385//Homo sapiens epsin 2b mRNA, complete cds//1.6e-111:539:97//Hs.22396:AF062085
F-PLACE1006412//Human mRNA for KIAA0298 gene, complete cds//1.0e-36:424:74//Hs.21560:AB002296
F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds//4.3e-111:525:98//Hs.131846:AF069735
F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds//2.2e-24:531:65//Hs.101414:AB011129
F-PLACE1006445//Homo sapiens chromosome 16 zinc finger protein ZNF200 (ZNF200) mRNA, complete cds//1.0:248:60//Hs.88219:AF060866
F-PLACE1006469//Human SA mRNA for SA gene product, complete cds//0.24:210:62//Hs.89659:AC004381
F-PLACE1006470
F-PLACE1006482//Homo sapiens basic-leucine zipper transcription factor MafK (MAFK) mRNA, complete cds//5.0e-46:520:71//Hs.131953:AF059194
F-PLACE1006488//ESTs//6.2e-47:239:97//Hs.158161:AA312511
F-PLACE1006492//ESTs//0.82:37:100//Hs.160417:AA488493
F-PLACE1006506//HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2//0.98:505:56//Hs.75063:AL023584
F-PLACE1006521//ESTs//0.032:222:63//Hs.23171:AA706542
F-PLACE1006531//EST//2.1e-53:258:100//Hs.117316:AA699358
F-PLACE1006534//EST//1.8e-07:78:89//Hs.157551:AI356219
F-PLACE1006540//Homo sapiens mRNA for cadherin-6, complete cds//0.96:383:58//Hs.32963:D31784
F-PLACE1006552//Human (clone N5-4) protein p84 mRNA, complete cds//0.058:464:57//Hs.1540:L36529
F-PLACE1006598//Homo sapiens mRNA for KIAA0737 protein, complete cds//4.1e-17:372:65//Hs.17630:AB018280
F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//2.2e-168:781:99//Hs.155377:U97670
F-PLACE1006617//ESTs//6.0e-08:354:60//Hs.42624:H99088
F-PLACE1006626//NUCLEOLIN//0.0044:186:66//Hs.79110:M60858
F-PLACE1006629//Homo sapiens (clone s22i71) mRNA fragment//0.097:229:63//Hs.26956:L40396
F-PLACE1006640//ESTs//0.00019:380:59//Hs.13672:AI131473
F-PLACE1006673//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//1.6e-12:113:83//Hs.3385:N25917
F-PLACE1006678
F-PLACE1006704//Homo sapiens ALR mRNA, complete cds//0.16:284:60//Hs.153638:AF010403
F-PLACE1006731//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//1.6e-05:382:63//Hs.43627:U35612
F-PLACE1006754//Biliary glycoprotein//8.9e-27:305:72//Hs.50964:X16354
F-PLACE1006760//ESTs//0.10:207:62//Hs.152589:AA954152
F-PLACE1006779//Kallmann syndrome 1 sequence//0.00025:251:64//Hs.89591:M97252
F-PLACE1006782//ESTs//1.2e-90:423:100//Hs.132826:AI075783
F-PLACE1006792//ESTs//1.5e-10:439:58//Hs.138501:AI051228
F-PLACE1006795//TYROSINE-PROTEIN KINASE RECEPTOR ETK1 PRECURSOR//4.5e-10:84:95//Hs.123642:M83941
F-PLACE1006800//ESTs//0.00068:360:61//Hs.157876:AI422017
F-PLACE1006805//ESTs//4.6e-103:491:98//Hs.140465:AA769892
F-PLACE1006815//Homo sapiens mRNA for KIAA0618 protein, complete cds//0.47:403:56//Hs.15832:AB014518
F-PLACE1006819//Human Line-1 repeat mRNA with 2 open reading frames//3.7e-103:619:87//Hs.23094:M19503
F-PLACE1006829//ESTs//1.5e-22:141:94//Hs.142988:AA142876
F-PLACE1006860//EST//0.0062:206:65//Hs.158793:AI376773
F-PLACE1006867//ESTs//0.068:218:62//Hs.91166:AA551273
F-PLACE1006878//Homo sapiens mRNA for KIAA0711 protein, complete cds//1.0:268:58//Hs.5333:AB018254

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F-PLACE1006883//ESTs//1.6e-75:398:94//Hs.119544:T95601
F-PLACE1006901//ESTs//1.9e-13:87:96//Hs.134737:AI089187
F-PLACE1006904//EST//1.0:91:70//Hs.148270:AA906443
F-PLACE1006917
F-PLACE1006932//ESTs//0.98:110:70//Hs.100855:AI423913
F-PLACE1006935//EST//1.0:92:65//Hs.124554:AA847211
F-PLACE1006956//PERIPHERIN//0.13:443:57//Hs.37044:L14565
F-PLACE1006958//Heat shock 70kD protein 4//6.4e-40:456:70//Hs.127:L12723
F-PLACE1006961//ESTs, Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae]//3.2e-07:67:98//Hs.21806:AA630312
F-PLACE1006962//H.sapiens ir1B mRNA//2.3e-16:202:71//Hs.135202:X63417
F-PLACE1006966//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds//0.14:191:67//Hs.8813:AF032922
F-PLACE1006989//Cyclin B1//0.99:224:59//Hs.23960:M25753
F-PLACE1007014//Homo sapiens NBMPR-insensitive nucleoside transporter ei (ENT2) mRNA, complete cds//3.1e-05:594:58//Hs.32951:AF034102
F-PLACE1007021//ESTs//7.2e-89:446:96//Hs.7111:U55971
F-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//1.0e-117:775:84//Hs.23094:M19503
F-PLACE1007053//Homo sapiens mRNA for ARNO3 protein//0.35:63:82//Hs.129811:AJ223957
F-PLACE1007068//Polycystic kidney disease 1 (autosomal dominant)//0.22:361:60//Hs.75813:L33243
F-PLACE1007097//ESTs//2.9e-25:197:83//Hs.105665:H78987
F-PLACE1007105//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)//0.18:268:63//Hs.904:U84010
F-PLACE1007111//EST//0.0066:260:60//Hs.147903:AI223385
F-PLACE1007112
F-PLACE1007132//ESTs//3.1e-30:195:76//Hs.46158:AI160121
F-PLACE1007140//TRANSCRIPTION ELONGATION FACTOR S-II//0.13:302:60//Hs.78869:M81601
F-PLACE1007178//ESTs//9.6e-54:289:95//Hs.12251:H12965
F-PLACE1007226//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.00090:412:59//Hs.8546:U97669
F-PLACE1007238//Human plectin (PLEC1) mRNA, complete cds//1.4e-07:492:64//Hs.79706:U53204
F-PLACE1007239//Human mRNA for transcription elongation factor S-II, hS-II-T1, complete cds//2.0e-58:405:87//Hs.80598:D50495
F-PLACE1007242//EST//0.014:55:89//Hs.88432:AA262141
F-PLACE1007243//ESTs//2.0e-43:227:97//Hs.124775:AA648467
F-PLACE1007257//Homo sapiens mRNA for dia-156 protein//3.7e-144:677:98//Hs.121556:Y15909
F-PLACE1007274
F-PLACE1007276//ATPase, Cu++ transporting, alpha polypeptide (Menkes syndrome)//0.94:167:64//Hs.606:L06133
F-PLACE1007282
F-PLACE1007286//ESTs//1.0e-25:333:71//Hs.134860:AI091436
F-PLACE1007301//EST//0.78:171:61//Hs.160990:H52412
F-PLACE1007317//Homo sapiens oxysterol 7alpha-hydroxylase (CYP7b1) mRNA, complete cds//0.88:298:58//Hs.144877:AF029403
F-PLACE1007342
F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds//1.7e-121:567:98//Hs.76596:AF096870
F-PLACE1007367//H.sapiens mRNA for MACH-alpha-2 protein//2.2e-55:532:77//Hs.19949:X98173
F-PLACE1007375
F-PLACE1007386//ESTs//0.00066:61:91//Hs.149318:AI248642
F-PLACE1007402//EST//1.7e-06:193:65//Hs.132124:AI041287
F-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence//3.8e-18:128:92//Hs.14387:AF093771
F-PLACE1007416
F-PLACE1007450//ESTs//2.6e-36:194:97//Hs.22359:AI024436
F-PLACE1007452//EST//1.8e-34:197:94//Hs.134795:AI090359
F-PLACE1007454//Homo sapiens (clone s153) mRNA fragment//2.6e-53:317:93//Hs.6445:L40391
F-PLACE1007460//ESTs//0.0012:168:64//Hs.151708:AA554714
F-PLACE1007478//ESTs//1.0e-42:440:74//Hs.141722:AA769103

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F-PLACE1007484//ESTs//7.1e-18:127:91//Hs.100251:AA535975
F-PLACE1007488
F-PLACE1007507//ESTs//1.2e-99:274:98//Hs.123462:AA903385
F-PLACE1007511//Keratin 19//4.2e-31:586:64//Hs.23761:Y00503
F-PLACE1007524//ESTs//6.8e-71:356:97//Hs.163067:AA897296
F-PLACE1007525//ESTs//0.073:242:59//Hs.128711:AA856979
F-PLACE1007537//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.93:468:57//Hs.113283:AF018080
F-PLACE1007544//ESTs//1.7e-74:360:98//Hs.128632:AI076755
F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete cds//1.0e-70:733:71//Hs.65238:AB014561
F-PLACE1007557//EST//0.58:80:72//Hs.130267:AI001863
F-PLACE1007583//ESTs//1.8e-46:234:98//Hs.155071:AA584257
F-PLACE1007598//ESTs//1.7e-83:400:99//Hs.120206:AI089163
F-PLACE1007618//Homo sapiens mRNA for KIAA0633 protein, partial cds//7.2e-12:778:56//Hs.33010:AB014533
F-PLACE1007621
F-PLACE1007632//ESTs//1.7e-32:175:97//Hs.122278:AA781867
F-PLACE1007645
F-PLACE1007649
F-PLACE1007677//ESTs//3.0e-13:125:82//Hs.143382:AA476266
F-PLACE1007688//ESTs//6.8e-06:311:61//Hs.132926:AI027055
F-PLACE1007690//ESTs//1.9e-13:83:98//Hs.150088:AI348503
F-PLACE1007697//TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR//0.99:216:63//Hs.1103:X02812
F-PLACE1007705//Human mRNA for RTP, complete cds//4.8e-58:637:70//Hs.75789:D87953
F-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//4.1e-149:709:97//Hs.4812:AF061243
F-PLACE1007725//ESTs, Weakly similar to No definition line found [C.elegans]//4.5e-36:233:89//Hs.108797:AA476815
F-PLACE1007729//ESTs, Moderately similar to RETRO VIRUS-RELATED PROTEASE [H.sapiens]//0.00033:270:64//Hs.104129:AA923278
F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.6e-156:728:98//Hs.153121:AB014585
F-PLACE1007737//Coagulation factor II (thrombin) receptor//1.1e-18:364:68//Hs.159347:M62424
F-PLACE1007743//ESTs//0.029:421:58//Hs.106090:AA457030
F-PLACE1007746//ESTs//6.7e-55:330:89//Hs.153392:AI089469
F-PLACE1007791//EST//0.39:261:62//Hs.145991:AI277656
F-PLACE1007807//ESTs//2.0e-54:385:83//Hs.163930:AA640504
F-PLACE1007810//ESTs//6.1e-53:416:81//Hs.152395:AA533107
F-PLACE1007829//EST//0.28:271:61//Hs.125514:AA883841
F-PLACE1007843//EST//0.020:307:59//Hs.145535:AI261635
F-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//6.3e-38:396:77//Hs.23094:M19503
F-PLACE1007852
F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//1.3e-190:894:98//Hs.28020:AB018309
F-PLACE1007866//ESTs//3.0e-50:333:86//Hs.15792:AI038387
F-PLACE1007877
F-PLACE1007897//EST//1.0:59:72//Hs.138770:N70943
F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//7.3e-156:755:97//Hs.92381:AB007956
F-PLACE1007946//ESTs//8.9e-16:250:68//Hs.88527:N24002
F-PLACE1007954//ESTs//1.6e-05:76:90//Hs.63314:AA056538
F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//8.9e-173:813:98//Hs.5671:AF084530
F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//8.2e-155:730:98//Hs.78106:AF079529
F-PLACE1007969//ESTs, Weakly similar to hnRNA-binding protein M4 [H.sapiens]//5.1e-45:264:92//Hs.42222:W28567
F-PLACE1007990//ESTs//1.2e-104:493:99//Hs.118445:AI097043
F-PLACE1008000//Homo sapiens veli 1 mRNA, complete cds//5.7e-63:578:74//Hs.150380:AF087693

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F-PLACE1008002//ESTs//0.52:236:59//Hs.134292:AA603031
F-PLACE1008044
F-PLACE1008045//COL10A1//0.29:221:58//Hs.37075:X60382
F-PLACE1008080//Human homeodomain protein (Prox 1) mRNA, complete cds//0.00037:151:71//Hs.159437:U44060
F-PLACE1008095//Human hybrid receptor gp250 precursor mRNA, complete cds//1.0:461:58//Hs.155494:U60975
F-PLACE1008111//Homo sapiens B lymphocyte chemoattractant BLC mRNA, complete cds//0.034:497:58//Hs.100431:AF044197
F-PLACE1008122//ESTs//0.95:198:60//Hs.126776:N28769
F-PLACE1008129//ESTs//1.1e-99:499:96//Hs.131807:AA778874
F-PLACE1008132//EST//3.3e-27:218:83//Hs.145258:AI218683
F-PLACE1008177//ESTs, Moderately similar to meiosis-specific nuclear structural protein 1 [M.musculus]//5.1e-20:124:95//Hs.146238:AI263135
F-PLACE1008181//ESTs//0.018:285:61//Hs.88843:AA281427
F-PLACE1008198//ESTs//5.9e-07:410:60//Hs.63348:AA643524
F-PLACE1008201
F-PLACE1008209
F-PLACE1008231//ESTs//0.40:188:61//Hs.130266:AI001856
F-PLACE1008244//Miller-Dieker syndrome chromosome region//0.22:247:61//Hs.77318:L13385
F-PLACE1008273
F-PLACE1008275//EST//0.77:74:71//Hs.145907:AI275113
F-PLACE1008280//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.6e-25:389:70//Hs.159897:AB007970
F-PLACE1008309//Homo sapiens serine phosphatase FCP1a (FCP1) mRNA, complete cds//0.16:263:63//Hs.4076:AF081287
F-PLACE1008329//EST//1.3e-09:94:85//Hs.144135:R82071
F-PLACE1008330//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.5e-45:291:83//Hs.101414:AB011129
F-PLACE1008331//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5.4e-74:356:98//Hs.105382:AA496362
F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//3.4e-139:659:98//Hs.5734:AB014579
F-PLACE1008368//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.011:355:60//Hs.122967:AF059569
F-PLACE1008369//ESTs//0.00074:443:61//Hs.102756:AA526911
F-PLACE1008392//EST//7.4e-08:324:60//Hs.149930:AI289171
F-PLACE1008398
F-PLACE1008401//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//2.5e-09:461:62//Hs.25674:AF072242
F-PLACE1008402//Homo sapiens mRNA for p115, complete cds//1.4e-149:711:98//Hs.7763:D86326
F-PLACE1008405//ESTs//2.8e-102:529:95//Hs.116278:AA628943
F-PLACE1008424//Human DNA sequence from clone 753P9 on chromosome Xq25-26.1. Contains the gene coding for Aminopeptidase P (EC 3.4.11.9, XAA-Pro/X-Pro/Proline/Aminoacylproline Aminopeptidase) and a novel gene. Contains ESTs, STSs, GSSs and a gaaa repeat polymorphism//0.98:113:67//Hs.57922:AL023653
F-PLACE1008426//ESTs//3.2e-77:393:95//Hs.37585:W28499
F-PLACE1008429//Orf1 5' to PD-ECGF/TP...orf2 5' to PD-ECGF/TP [human, epidermoid carcinoma cell line A431, mRNA, 3 genes, 1718 nt]//0.019:530:58//Hs.72248:S72487
F-PLACE1008437
F-PLACE1008455//ESTs//0.51:279:61//Hs.122319:AA782335
F-PLACE1008457//ESTs//3.0e-30:229:75//Hs.60740:AA053901
F-PLACE1008465//Human mRNA for KIAA0383 gene, partial cds//0.0084:210:63//Hs.27590:AB002381
F-PLACE1008488//Human density enhanced phosphatase-1 mRNA, complete cds//6.8e-07:469:60//Hs.1177:U10886
F-PLACE1008524//Homo sapiens TWIK-related acid-sensitive K+ channel (TASK) mRNA, complete cds//1.0:304:60//Hs.24040:AF006823
F-PLACE1008531//ESTs//1.1e-17:190:76//Hs.156041:AI274697
F-PLACE1008532//Thromboxane A2 receptor//5.6e-17:231:71//Hs.89887:D38081
F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter//1.1e-45:507:71//Hs.8003:AC004997
F-PLACE1008568//Homo sapiens mRNA for neuronatin alpha, complete cds//1.0:95:71//Hs.117546:U31767

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F-PLACE1008584//ESTs//1.4e-13:252:68//Hs.153429:AI283069
F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.9e-175:812:98//Hs.23255:AB018334
F-PLACE1008621//ESTs, Weakly similar to reverse transcriptase [H.sapiens]//1.2e-15:350:66//Hs.151087:AA649326
F-PLACE1008625//ESTs//0.86:269:57//Hs.94998:N26794
F-PLACE1008626//ESTs//0.55:69:71//Hs.92096:F10560
F-PLACE1008627//ESTs//3.0e-62:302:99//Hs.120766:H82458
F-PLACE1008629//EST//0.0012:174:67//Hs.121195:AA757211
F-PLACE1008630//ESTs//4.5e-77:371:99//Hs.132960:AA252394
F-PLACE1008643//Human mRNA for PK-120//4.7e-25:299:64//Hs.76415:D38535
F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//3.5e-135:622:99//Hs.147967:AF044333
F-PLACE1008693//EST//0.19:36:94//Hs.138817:N93728
F-PLACE1008696//Human mitochondrial NADH dehydrogenase-ubiquinone Fe-S protein 8, 23 kDa subunit precursor (NDUFS8) nuclear mRNA encoding mitochondrial protein, complete cds//8.3e-25:137:97//Hs.90443:AF038406
F-PLACE1008715//Homo sapiens mRNA for matrilin-3//0.99:183:63//Hs.119534:AJ224741
F-PLACE1008748//ESTs//0.88:204:63//Hs.15139:AA527080
F-PLACE1008757//ESTs, Weakly similar to unknown protein [R.norvegicus]//4.3e-17:285:69//Hs.35460:H65503
F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds//1.4e-121:503:97//Hs.6458:AF060543
F-PLACE1008798//ESTs, Weakly similar to putative p150 [H.sapiens]//0.30:127:68//Hs.111380:AA258772
F-PLACE1008807//ESTs//0.81:346:58//Hs.116901:AA663542
F-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 mRNA, complete cds//6.7e-104:376:98//Hs.7179:AF011905
F-PLACE1008813//Glutamate decarboxylase 1 (brain, 67kD)//0.17:318:61//Hs.75668:M81883
F-PLACE1008851//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 2 HOMOLOG [Plasmodium falciparum (isolate k1 / thailand)]//0.73:354:59//Hs.26322:AA156858
F-PLACE1008854//ESTs//3.0e-26:391:66//Hs.133260:AI052728
F-PLACE1008867//ESTs//5.9e-08:64:93//Hs.91115:AI221563
F-PLACE1008887//Human Line-1 repeat mRNA with 2 open reading frames//5.5e-51:701:68//Hs.23094:M19503
F-PLACE1008902//EST//0.85:425:60//Hs.140573:AA826323
F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.1e-159:753:98//Hs.62318:AB018308
F-PLACE1008925//ESTs//0.025:133:67//Hs.103218:W84771
F-PLACE1008934//ESTs//0.27:307:59//Hs.135168:AI394026
F-PLACE1008941//ESTs//3.3e-53:266:98//Hs.108677:AA488937
F-PLACE1008947//Human TBP-associated factor (hTAFII130) mRNA, partial cds//2.4e-13:625:58//Hs.24644:U75308
F-PLACE1009020//ESTs//3.3e-11:122:81//Hs.131777:AI024950
F-PLACE1009027//Homo sapiens mRNA for doublecortin//1.2e-151:763:96//Hs.34780:AJ003112
F-PLACE1009039//EST//0.76:111:63//Hs.160997:H55762
F-PLACE1009045//ESTs//2.2e-76:399:95//Hs.114919:AA457689
F-PLACE1009048//GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR//2.6e-16:93:100//Hs.119689:S70585
F-PLACE1009050//ESTs//1.4e-92:451:98//Hs.66373:AI239698
F-PLACE1009060//ESTs//1.4e-14:86:100//Hs.131725:AI090525
F-PLACE1009090//ESTs//2.7e-20:198:78//Hs.110044:AA181800
F-PLACE1009091//ESTs//0.99:342:57//Hs.46903:AI093091
F-PLACE1009094//ESTs//1.0:225:63//Hs.120374:AI337031
F-PLACE1009099//H.sapiens ZNF81 gene//2.2e-79:733:74//Hs.104020:X68011
F-PLACE1009110//ESTs//2.6e-91:453:96//Hs.143756:AI040890
F-PLACE1009111//ESTs//2.7e-15:159:77//Hs.146811:AA410788
F-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//1.1e-139:671:97//Hs.99742:AF035586
F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds//1.1e-24:718:59//Hs.35804:D25215
F-PLACE1009150//Human HsLIM15 mRNA for HsLim15, complete cds//1.7e-50:440:78//Hs.37181:D64108

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F-PLACE1009155//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.0e-46:440:69//Hs.158095:AB007953
F-PLACE1009158//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//0.28:245:61//Hs.92614:M62302
F-PLACE1009166//EST//0.98:114:67//Hs.137706:AA977250
F-PLACE1009172//EST//6.2e-34:257:84//Hs.161081:N22770
F-PLACE1009174//ESTs//6.0e-24:234:77//Hs.155196:AI282821
F-PLACE1009183//EST//0.021:261:62//Hs.144222:N90100
F-PLACE1009186//ESTs, Weakly similar to No definition line found [C.elegans]//3.6e-117:588:95//Hs.54943:Z78396
F-PLACE1009190//EST//0.046:95:70//Hs.131646:AI025689
F-PLACE1009200//EST//2.5e-41:195:78//Hs.162404:AA573131
F-PLACE1009230//CARCINOEMBRYONIC ANTIGEN PRECURSOR//5.3e-29:157:77//Hs.146403:M29540
F-PLACE1009246//EST//0.13:178:62//Hs.23298:R22575
F-PLACE1009298//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae]//1.9e-21:121:98//Hs.124768:AA307735
F-PLACE1009308//SERUM PROTEIN MSE55//0.44:195:62//Hs.148101:M88338
F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mRNA, complete cds//9.7e-08:411:59//Hs.23731:U83192
F-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-91:594:86//Hs.23094:M19503
F-PLACE1009335//EST//0.037:169:63//Hs.148875:AI240767
F-PLACE1009338//ESTs//5.7e-22:123:98//Hs.66783:AA059473
F-PLACE1009368
F-PLACE1009375
F-PLACE1009388//Homo sapiens KIAA0395 mRNA, partial cds//1.7e-41:317:81//Hs.43681:AL022394
F-PLACE1009398//Zinc finger protein 84 (HPF2)//1.4e-79:730:74//Hs.9450:M27878
F-PLACE1009404//MICROTUBULE-ASSOCIATED PROTEIN TAU//0.099:207:61//Hs.101174:AF047863
F-PLACE1009410//Homo sapiens BAF57 (BAF57) gene, complete cds//1.4e-27:210:86//Hs.3404:AF035262
F-PLACE1009434//Human mRNA for KIAA0005 gene, complete cds//2.8e-45:599:68//Hs.155291:D13630
F-PLACE1009443//H.sapiens 5T4 gene for 5T4 Oncofetal antigen//0.11:350:58//Hs.82128:AJ012159
F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//1.5e-22:146:93//Hs.76987:AF012872
F-PLACE1009459//H.sapiens garp gene mRNA, complete CDS//1.0:241:60//Hs.151641:Z24680
F-PLACE1009468//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//0.00039:347:60//Hs.994:M95678
F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67AI//4.1e-91:464:96//Hs.155049:AC004531
F-PLACE1009477//ESTs//0.30:221:61//Hs.107287:AI308839
F-PLACE1009493//Homo sapiens mRNA for LAK-4p, complete cds//1.6e-30:608:63//Hs.16165:AB002405
F-PLACE1009524//Human Sec7p-like protein mRNA, partial cds//2.3e-68:526:78//Hs.8517:U70728
F-PLACE1009539//ESTs//3.3e-18:186:83//Hs.71922:AA148417
F-PLACE1009542//EST//7.8e-11:265:65//Hs.159692:AI416956
F-PLACE1009571//ESTs//6.1e-15:94:97//Hs.151458:AA600866
F-PLACE1009581//Microtubule-associated protein 1A//1.0:196:59//Hs.147918:U38291
F-PLACE1009595//EST//1.8e-28:179:92//Hs.60090:AA004806
F-PLACE1009596//ESTs, Weakly similar to LIS-1 protein [H.sapiens]//4.1e-16:281:66//Hs.13889:AI341394
F-PLACE1009607//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.9e-52:313:79//Hs.113283:AF018080
F-PLACE1009613//ESTs//0.50:297:60//Hs.25114:AI074011
F-PLACE1009621//ESTs//1.4e-98:470:98//Hs.124695:AI094085
F-PLACE1009622//ESTs//9.8e-14:94:93//Hs.117227:AA682773
F-PLACE1009637//ESTs//4.9e-92:440:98//Hs.126587:AA917087
F-PLACE1009639
F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//4.4e-173:816:98//Hs.21862:AB011159
F-PLACE1009665//ESTs//9.1e-45:383:79//Hs.61199:AA024494
F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//8.1e-149:701:98//Hs.109590:AF062534
F-PLACE1009708//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN HXT14-PHA2 INTERGENIC REGION [S.cerevisiae]//7.5e-51:295:92//Hs.48541:AA827926
F-PLACE1009721//EST//0.18:467:58//Hs.124358:AA830650

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F-PLACE1009731//ESTs//1.0:207:63//Hs.60440:AA195789
F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//1.3e-126:602:98//Hs.154320:AF046024
F-PLACE1009794//ESTs//4.0e-41:252:91//Hs.42927:N20989
F-PLACE1009798//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs//5.5e-130:600:95//Hs.16411:AL030996
F-PLACE1009845
F-PLACE1009861
F-PLACE1009879//ESTs//6.3e-12:293:66//Hs.147071:AI200021
F-PLACE1009886
F-PLACE1009888//EST//0.044:255:58//Hs.160695:AI282889
F-PLACE1009908
F-PLACE1009921//Apoptosis (APO-1) antigen 1//0.62:407:57//Hs.82359:X63717
F-PLACE1009924//EST//2.9e-29:155:99//Hs.162937:AA634379
F-PLACE1009925
F-PLACE1009935//CATHEPSIN K PRECURSOR//0.43:153:66//Hs.83942:X82153
F-PLACE1009947//ESTs//1.8e-07:56:100//Hs.149940:AI306446
F-PLACE1009971//Acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain//0.89:243:61//Hs.127610:Z80345
F-PLACE1009992//ESTs//0.99:123:68//Hs.91202:AI139114
F-PLACE1009995//ESTs, Weakly similar to C01A2.4 [C.elegans]//3.3e-24:174:88//Hs.11449:AI201540
F-PLACE1009997//Homo sapiens mRNA for KIAA0629 protein, partial cds//3.7e-36:196:96//Hs.153545:AB014529
F-PLACE1010023
F-PLACE1010031//ESTs//1.3e-16:132:87//Hs.46847:W02878
F-PLACE1010053//ESTs, Moderately similar to M-phase phosphoprotein 4 [H.sapiens]//5.2e-63:312:98//Hs.142151:AA984061
F-PLACE1010069//ESTs//6.6e-33:171:98//Hs.128844:AA977596
F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//5.9e-168:792:98//Hs.11183:AF065482
F-PLACE1010076//ESTs//0.88:379:55//Hs.5884:N21424
F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.6e-154:727:98//Hs.5003:AB007925
F-PLACE1010089//ESTs, Highly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE [Mus musculus]//1.8e-38:212:95//Hs.98067:AA236822
F-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.norvegicus]//1.8e-08:100:89//Hs.11469:U69567
F-PLACE1010102//Homo sapiens stimulator of Fe transport mRNA, complete cds//0.0035:339:60//Hs.129683:AF020761
F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//1.2e-26:728:60//Hs.122967:AF059569
F-PLACE1010106//EST//8.5e-28:394:70//Hs.142044:AA166682
F-PLACE1010134//H.sapiens hbrm mRNA//1.2e-14:380:64//Hs.77590:X72889
F-PLACE1010148//Human trans-Golgi p230 mRNA, complete cds//0.26:708:57//Hs.158245:U41740
F-PLACE1010152
F-PLACE1010181//EST//1.3e-21:312:71//Hs.141501:N50792
F-PLACE1010194//ESTs//2.6e-55:284:97//Hs.155940:AA459582
F-PLACE1010202//ESTs, Weakly similar to No definition line found [C.elegans]//2.3e-72:391:94//Hs.35225:H69637
F-PLACE1010231
F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.9e-146:693:97//Hs.27349:AB007917
F-PLACE1010270//ESTs//2.0e-104:514:98//Hs.124062:H04590
F-PLACE1010274//ESTs, Weakly similar to C01A2.4 [C.elegans]//6.8e-25:149:93//Hs.11449:AI201540
F-PLACE1010293//EST//4.5e-36:358:74//Hs.162398:AA572813
F-PLACE1010310//HOMEOBOX/POU DOMAIN PROTEIN RDC-1//2.1e-10:352:62//Hs.74095:L20433
F-PLACE1010321//Human hSIAH2 mRNA, complete cds//0.071:604:58//Hs.20191:U76248
F-PLACE1010324//ESTs//0.22:286:58//Hs.130853:AI367875

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F-PLACE1010329//EST//5.7e-05:351:60//Hs.120644:AA742659
F-PLACE1010341//EST//4.5e-16:255:72//Hs.141206:H53117
F-PLACE1010362//ESTs//1.9e-41:246:92//Hs.128771:AA236855
F-PLACE1010364//EST//0.11:292:58//Hs.135771:AI005648
F-PLACE1010383//EST//6.1e-08:107:76//Hs.136441:AA564986
F-PLACE1010401
F-PLACE1010481//Human BLu protein (BLu) mRNA, complete cds//0.94:254:61//Hs.125257:U70824
F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds//7.2e-152:702:99//Hs.13313:AF039081
F-PLACE1010492//ESTs//1.0:201:60//Hs.146036:AI038500
F-PLACE1010522//ESTs//3.9e-52:263:97//Hs.125149:AI302100
F-PLACE1010529//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.0:175:64//Hs.159273:AF054177
F-PLACE1010547//ESTs//0.96:288:57//Hs.87156:AA233472
F-PLACE1010562//EST//1.0:164:66//Hs.147868:AI222979
F-PLACE1010579//EST//0.39:279:58//Hs.158960:AI380148
F-PLACE1010580//ESTs, Moderately similar to PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06 [Schizosaccharomyces pombe]//3.8e-31:193:91//Hs.145229:N44661
F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14p (PEX14) mRNA, complete cds//9.9e-148:707:97//Hs.19851:AF045186
F-PLACE1010616//EST//3.1e-43:213:100//Hs.128215:AA972394
F-PLACE1010622//NUCLEOLIN//0.00040:282:60//Hs.79110:M60858
F-PLACE1010624//Homo sapiens Jagged 2 mRNA, complete cds//1.2e-05:516:61//Hs.106387:AF029778
F-PLACE1010628//EST, Weakly similar to line-1 protein ORF2 [H.sapiens]//0.012:258:62//Hs.144375:AA484200
F-PLACE1010629//EST//8.3e-23:218:79//Hs.161975:AA501461
F-PLACE1010630//EST//0.29:319:58//Hs.137277:N62225
F-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//9.5e-66:363:95//Hs.10801:AB011102
F-PLACE1010661//ESTs//3.9e-89:504:92//Hs.122666:W27076
F-PLACE1010662
F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.1e-74:697:74//Hs.37138:U35376
F-PLACE1010714//EST//0.018:253:59//Hs.148028:AI270027
F-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//6.1e-77:393:96//Hs.50758:AF092564
F-PLACE1010739//Homo sapiens mRNA for Sec24 protein (Sec24A isoform), partial//0.97:314:59//Hs.14574:AJ131244
F-PLACE1010743//Human myosin-IXb mRNA, complete cds//2.4e-56:409:86//Hs.159629:U42391
F-PLACE1010761//ESTs, Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus laevis]//5.1e-80:407:96//Hs.80965:AA493284
F-PLACE1010771//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP [Mus musculus]//6.0e-45:251:94//Hs.11379:AA594140
F-PLACE1010786
F-PLACE1010800
F-PLACE1010802//EST//0.94:128:64//Hs.120366:AA719157
F-PLACE1010811//ESTs//0.89:339:59//Hs.127314:N48085
F-PLACE1010833//ESTs, Weakly similar to allograft inflammatory factor-1 [H.sapiens]//2.9e-28:245:79//Hs.132736:AA583494
F-PLACE1010856//ESTs//1.5e-06:95:87//Hs.17401:W81048
F-PLACE1010857//ESTs, Weakly similar to KIAA0157 gene product is novel. [H.sapiens]//5.8e-67:336:97//Hs.130135:AA905493
F-PLACE1010870//Zinc finger protein 43 (HTF6)//9.7e-40:498:69//Hs.74107:X59244
F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//3.7e-149:694:98//Hs.118087:AB011182
F-PLACE1010891//ESTs//6.9e-54:377:87//Hs.24453:R31671
F-PLACE1010896//Human homologue of yeast sec7 mRNA, complete cds//0.64:167:65//Hs.1050:M85169
F-PLACE1010900
F-PLACE1010916//EST//0.55:151:66//Hs.145800:AI269981
F-PLACE1010917

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F-PLACE1010925//ESTs//2.6e-81:437:94//Hs.5876:H26537
F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//3.1e-139:653:98//Hs.74750: AB011126
F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds//2.9e-91:437:98//Hs.66392: AF064244
F-PLACE1010944//ESTs//1.3e-17:117:91//Hs.29444:W30985
F-PLACE1010947//EST//0.97:93:72//Hs.162299:AA555154
F-PLACE1010954//Apolipoprotein B (including Ag(x) antigen)//0.28:444:59//Hs.585:X04506
F-PLACE1010960//ESTs//0.98:238:60//Hs.163674:AA506632
F-PLACE1010965//ESTs//3.1e-74:376:96//Hs.115679:AI379721
F-PLACE1011026//EST//0.022:222:60//Hs.47154:N50931
F-PLACE1011032//EST//1.1e-05:88:79//Hs.118024:N34032
F-PLACE1011041//Human density enhanced phosphatase-1 mRNA, complete cds//0.28:179:67//Hs.1177: U10886
F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//6.2e-11:207:68//Hs.994:M95678
F-PLACE1011054//H.sapiens OBF-1 mRNA for octamer binding factor 1//6.1e-35:310:78//Hs.2407:Z49194
F-PLACE1011056//Human putative serine/threonine protein kinase PRK (prk) mRNA, complete cds//0.74:228:61// Hs.153640:U56998
F-PLACE1011057//EST//2.5e-80:388:98//Hs.126466:AA913320
F-PLACE1011090//ESTs//1.4e-94:469:97//Hs.106448:R76663
F-PLACE1011109//ESTs//0.13:303:62//Hs.49294:AA418037
F-PLACE1011114//ESTs//5.8e-12:75:100//Hs.147422:AI214317
F-PLACE1011133//ESTs//0.17:225:62//Hs.132853:AI370857
F-PLACE1011143//ESTs//0.013:264:63//Hs.115368:AA629949
F-PLACE1011160
F-PLACE1011165//Galactokinase 2//2.7e-32:194:92//Hs.129228:M84443
F-PLACEL011185//EST//1.4e-34:261:83//Hs.140250:AA708114
F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyltransferase mRNA, complete cds//6.9e-124:576:99//Hs.159140:AF038664
F-PLACE1011214//ESTs, Weakly similar to B0035.14 [C.elegans]//9.7e-101:469:99//Hs.8241:AA283057
F-PLACE1011219//ESTs, Weakly similar to coded for by C. elegans cDNA CEESL70F [C.elegans]//2.6e-62:221: 88//Hs.101821:W27452
F-PLACE1011221//ESTs//0.46:238:62//Hs.32853:AA015751
F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds//1.4e-147:675:99//Hs.23168: AB011101
F-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21//5.9e-71:350:98//Hs.15144:AC005014
F-PLACE1011273//ESTs//1.0:222:59//Hs.35274:AA495803
F-PLACE1011291//Homo sapiens clone 24712 unknown mRNA, partial cds//3.4e-09:191:65//Hs.140950: AF070637
F-PLACE1011296//ESTs//0.019:137:63//Hs.140654:AA865915
F-PLACE1011310//EST//0.066:336:58//Hs.162529:AA584160
F-PLACE1011325//ESTs//7.4e-43:229:96//Hs.21081:H08310
F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.8e-151:696: 99//Hs.5819:AF102265
F-PLACE1011340//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.5e-20:120:81//Hs. 159897:AB007970
F-PLACE1011371//Human mRNA for PK-120//9.5e-35:684:63//Hs.76415:D38535
F-PLACE1011375//ESTs, Moderately similar to potassium channel protein Raw3 [R.norvegicus]//6.7e-68:325:99// Hs.107245:AA627053
F-PLACE1011399//ESTs//8.6e-05:285:61//Hs.130105:AA904868
F-PLACE1011419//ESTs//0.70:240:62//Hs.159650:N95552
F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds//1.5e-158:743:98//Hs.10801: AB011102
F-PLACE1011452//Human Line-1 repeat mRNA with 2 open reading frames//1.9e-53:557:72//Hs.23094:M19503
F-PLACE1011465//EST//3.1e-58:380:85//Hs.131605:AI025204
F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.5e-152:703:99//Hs.111138: AB018255

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F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.7e-146:675:99//Hs.11183:AF065482
F-PLACE1011492//ESTs//2.0e-35:186:98//Hs.125886:AA884264
F-PLACE1011503//EST//0.67:149:65//Hs.149774:AI285997
F-PLACE1011520//ESTs//0.00014:213:64//Hs.119889:AA705319
F-PLACE1011563//ESTs//2.2e-61:394:86//Hs.117718:AA883476
F-PLACE1011567//Homo sapiens DEC-205 mRNA, complete cds//3.1e-46:325:84//Hs.153563:AF011333
F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//4.3e-67:268:86//Hs.86371:AF054180
F-PLACE1011586//Homo sapiens hLRpl05 mRNA for LDL receptor related protein 105, complete cds//0.98:153:65//Hs.143641:AB009462
F-PLACE1011635//Homo sapiens Jagged 2 mRNA, complete cds//0.00029:585:57//Hs.106387:AF029778
F-PLACE1011641
F-PLACE1011643//Homo sapiens mRNA for KIAA0293 gene, partial cds//0.00058:499:58//Hs.12784:AB006631
F-PLACE1011646//EST//3.2e-26:201:68//Hs.140349:AA757661
F-PLACE1011649//ESTs//0.25:145:64//Hs.23033:R46086
F-PLACE1011650//ESTs//0.041:96:77//Hs.119351:AA447745
F-PLACE1011664//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640
F-PLACE1011675//Cell division cycle 27//0.098:448:57//Hs.73151:S78234
F-PLACE1011682//EST//9.6e-06:119:72//Hs.93664:N23366
F-PLACE1011719//Human mRNA for KIAA0352 gene, complete cds//0.92:365:60//Hs.17262:AB002350
F-PLACE1011725
F-PLACE1011729//EST//0.56:304:58//Hs.86378:AA210853
F-PLACE1011749//ESTs//4.3e-88:443:96//Hs.132850:AA779891
F-PLACE1011762//ESTs//0.012:149:68//Hs.145075:AI208240
F-PLACE1011778//ESTs//0.00016:199:64//Hs.160395:AI393693
F-PLACE1011783//EST//1.0:119:66//Hs.162191:AA534660
F-PLACE1011858//Human novel homeobox mRNA for a DNA binding protein//8.9e-05:477:59//Hs.37035:U07664
F-PLACE1011874//EST//0.20:118:66//Hs.127351:AA954775
F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cds//5.3e-110:526:98//Hs.22572:AB011152
F-PLACE1011891//ESTs//1.8e-58:397:88//Hs.84698:AA725913
F-PLACE1011896//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//9.4e-09:478:56//Hs.107747:AI357868
F-PLACE1011922//ESTs//0.49:249:62//Hs.152627:AA595817
F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//3.7e-140:664:98//Hs.3838:AF059617
F-PLACE1011962//EST//1.7e-07:81:85//Hs.104333:AA250763
F-PLACE1011964//EST//6.6e-38:412:74//Hs.140562:AA826514
F-PLACE1011982//ESTs//0.40:405:60//Hs.127743:AI261591
F-PLACE1011995//ESTs//1.7e-22:486:64//Hs.105157:AA527514
F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//4.0e-148:690:98//Hs.88756:AB018256
F-PLACE2000003//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//6.5e-54:290:81//Hs.92381:AB007956
F-PLACE2000006//ESTs//0.067:224:62//Hs.144100:AI205503
F-PLACE2000007//ESTs//8.1e-23:147:91//Hs.128530:AA325330
F-PLACE2000011//Interleukin 10//4.2e-42:362:78//Hs.2180:M57627
F-PLACE2000014//EST//0.10:214:61//Hs.160247:AI138831
F-PLACE2000015//Interleukin 10//1.4e-44:393:78//Hs.2180:M57627
F-PLACE2000017
F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, partial cds//5.7e-85:844:72//Hs.7928:AF082557
F-PLACE2000030
F-PLACE2000033//Human adhesion molecule ninjurin mRNA, complete cds//0.85:234:66//Hs.11342:U91512
F-PLACE2000034//Homo sapiens mRNA for KIAA0607 protein, partial cds//0.058:348:62//Hs.94653:AB011179
F-PLACE2000039//Human plectin (PLEC1) mRNA, complete cds//0.0058:473:59//Hs.79706:U53204
F-PLACE2000047//ESTs//4.9e-32:328:75//Hs.141024:H07128
F-PLACE2000050//ESTs//3.0e-36:270:83//Hs.155512:AA663966
F-PLACE2000061

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F-PLACE2000062//Human membrane-associated lectin type-C mRNA//2.9e-114:662:86//Hs.23759:M98457
F-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//7.1e-135:631:98//Hs.9443:AF027219
F-PLACE2000097//ESTs//0.021:117:70//Hs.132811:AI034333
F-PLACE2000100
F-PLACE2000103//ESTs//1.1e-56:284:98//Hs.144786:AI219219
F-PLACE2000111//H.sapiens mRNA for l-acylglycerol-3-phosphate O-acyltransferase//0.76:215:65//Hs.6587:U56417
F-PLACE2000115
F-PLACE2000124//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:400:79//Hs.153014:AB002353
F-PLACE2000132
F-PLACE2000136//ESTS, Moderately similar to hypothetical protein [H.sapiens]//1.2e-08:245:64//Hs.140343:AA718911
F-PLACE2000140//Adenylate kinase 2 (adk2)//3.7e-24:162:90//Hs.83833:U54645
F-PLACE2000164
F-PLACE2000170
F-PLACE2000172//ESTs//0.64:239:62//Hs.31175:AI219179
F-PLACE2000176
F-PLACE2000187
F-PLACE2000216
F-PLACE2000223//EST//0.0092:171:60//Hs.162830:AA643933
F-PLACE2000235//Human mRNA for KIAA0298 gene, complete cds//1.6e-38:792:63//Hs.21560:AB002296
F-PLACE2000246//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.5e-74:367:98//Hs.22926:AB018338
F-PLACE2000264//Homo sapiens mRNA for KIAA0792 protein, complete cds//2.0e-29:366:73//Hs.119387:AB007958
F-PLACE2000274//Homo sapiens mRNA for dynein heavy chain//1.0e-23:650:62//Hs.144672:AJ000522
F-PLACE2000302//ESTs//1.7e-05:66:89//Hs.55572:W37560
F-PLACE2000305//ESTs//1.6e-78:382:98//Hs.136731:AA745869
F-PLACE2000317
F-PLACE2000335//Fc fragment of IgE, high affinity I, receptor for; beta polypeptide//6.1e-24:295:76//Hs.30:M89796
F-PLACE2000341//Human sodium iodide symporter mRNA, complete cds//6.8e-21:593:61//Hs.103983:U66088
F-PLACE2000342//Centromere protein B (80kD)//1.4e-06:326:61//Hs.85004:X05299
F-PLACE2000347//ESTs, Moderately similar to F18547_1 [H.sapiens]//3.7e-16:139:82//Hs.28209:AI073817
F-PLACE2000359//ESTs//5.0e-19:251:71//Hs.58272:W76645
F-PLACE2000366//ESTs//1.7e-37:399:75//Hs.136646:AA748045
F-PLACE2000371//EST//0.65:107:65//Hs.157677:AI358861
F-PLACE2000373//ESTs//0.30:207:59//Hs.143902:AI131032
F-PLACE2000379//ESTs//1.3e-64:402:87//Hs.146307:AA584638
F-PLACE2000394//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.0e-87:694:80//Hs.158095:AB007953
F-PLACE2000398
F-PLACE2000399
F-PLACE2000404
F-PLACE2000411
F-PLACE2000419//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.0e-52:463:74//Hs.113283:AF018080
F-PLACE2000425//EST//0.44:168:62//Hs.44677:N34966
F-PLACE2000427
F-PLACE2000433//ESTs//4.7e-18:213:74//Hs.110187:AA699719
F-PLACE2000435//EST//4.7e-05:159:64//Hs.123604:AA815257
F-PLACE2000438//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T2)//1.9e-20:418:64//Hs.130181:X85019
F-PLACE2000450//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.0e-83:324:81//Hs.113283:AF018080
F-PLACE2000455//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//4.0e-05:100:73//Hs.104239:AA488082
F-PLACE2000458//H.sapiens mRNA for hFat protein//0.0010:545:57//Hs.91107:X87241
F-PLACE2000465//ESTs//4.4e-38:377:75//Hs.55855:AA621381
F-PLACE2000477//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.8e-68:520:81//Hs.113283:AF018080

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F-PLACE3000004//Human EYA3 homolog (EYA3) mRNA, complete cds//3.9e-14:204:73//Hs.46925:Y10262 ,
F-PLACE3000009//Human mRNA for KIAA0386 gene, complete cds//4.8e-59:696:69//Hs.101359:AB002384
F-PLACE3000020//Prostaglandin 12 (prostacyclin) receptor (IP)//0.00081:500:61//Hs.393:D38128
F-PLACE3000029
F-PLACE3000059//ESTs//0.0026:49:100//Hs.42913:AI082248
F-PLACE3000070//ESTs//5.6e-15:202:74//Hs.154993:AA142842
F-PLACE3000103//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds//1.0:186:62//Hs.122752:AF026445
F-PLACE3000119//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.8e-48:283:83//Hs.23711:AB018295
F-PLACE3000121
F-PLACE3000124//Thromboxane A2 receptor//1.1e-55:195:83//Hs.89887:D38081
F-PLACE3000136//Homo sapiens mRNA for KIAA0703 protein, complete cds//1.0:194:59//Hs.6168:AB014603
F-PLACE3000142//EST//0.41:179:59//Hs.137438:AA282243
F-PLACE3000145//ESTs//3.5e-25:145:96//Hs.163950:AA683016
F-PLACE3000147//EST//5.0e-43:285:86//Hs.160895:AI365871
F-PLACE3000148
F-PLACE3000155//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-80:382:99//Hs.6336:AB014572
F-PLACE3000156//ESTs//0.00015:277:62//Hs.156834:AI336023
F-PLACE3000157//Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit//0.54:320:60//Hs.96253:U79666
F-PLACE3000158//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-66:319:88//Hs.153468:AB011147
F-PLACE3000160
F-PLACE3000169//Small inducible cytokine A5 (RANTES)//1.3e-64:501:80//Hs.155464:AF088219
F-PLACE3000194
F-PLACE3000197
F-PLACE3000199//EST//1.0:108:68//Hs.98488:AA426546
F-PLACE3000207//EST//1.0e-32:184:75//Hs.160146:AI049975
F-PLACE3000208//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR//1.0:271:61//Hs.77522:X62744
F-PLACE3000218//EST//1.3e-46:317:84//Hs.162197:AA535216
F-PLACE3000220//EST//9.3e-95:443:99//Hs.112702:AA609377
F-PLACE3000221//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//9.2e-56:200:85//Hs.133089:AF064019
F-PLACE3000226
F-PLACE3000230//EST//6.1e-16:173:72//Hs.148578:AI201568
F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//1.2e-54:434:80//Hs.4943:Z98046
F-PLACE3000244
F-PLACE3000254//NUCLEOLIN//2.6e-05:445:60//Hs.79110:M60858
F-PLACE3000271//ESTs//1.6e-25:195:72//Hs.108452:H78650
F-PLACE3000276//ESTs//1.0e-13:274:66//Hs.28589:AI004944
F-PLACE3000304//EST//0.043:210:61//Hs.132378:AI026770
F-PLACE3000310
F-PLACE3000320//EST//1.2e-12:188:70//Hs.145771:AI269586
F-PLACE3000322//Small inducible cytokine A5 (RANTES)//4.7e-29:252:80//Hs.155464:AF088219
F-PLACE3000331
F-PLACE3000339//Homo sapiens mRNA for KIAA0645 protein, complete cds//0.91:222:61//Hs.155987:AB014545
F-PLACE3000341//EST//1.8e-05:394:58//Hs.112894:AA620741
F-PLACE3000350//ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE SULU [Caenorhabditis elegans]//2.9e-59:474:77//Hs.125850:AA885355
F-PLACE3000352//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.5e-48:442:78//Hs.2407:Z49194
F-PLACE3000353//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T1)//0.78:234:63//Hs.7498:U41514

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F-PLACE3000362//EST//6.5e-25:302:73//Hs.140504:AA810441
F-PLACE3000363
F-PLACE3000365//ESTs//0.81:200:60//Hs.141556:N49928
F-PLACE3000373//ESTs//0.0071:82:73//Hs.136310:AA442641
F-PLACE3000388//ESTs//7.9e-16:235:71//Hs.44701:AA830432
F-PLACE3000399//Clathrin, light polypeptide (Lcb)//5.2e-70:391:81//Hs.73919:X81637
F-PLACE3000400//ESTs//0.53:162:66//Hs.49303:AA810785
F-PLACE3000401//EST//2.3e-35:178:100//Hs.162851:AA632270
F-PLACE3000402//ESTs//2.4e-84:425:96//Hs.148962:AI219715
F-PLACE3000405//EST//2.1e-39:452:73//Hs.140414:AA778541
F-PLACE3000406//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-07:116:78//Hs.77579:AF013263
F-PLACE3000413//ESTs, Weakly similar to methyl sterol oxidase [H.sapiens]//1.6e-51:260:98//Hs.122512:H61502
F-PLACE3000416//Homo sapiens mRNA for KIAA0801 protein, complete cds//0.00020:630:57//Hs.17585:AB018344
F-PLACE3000425//EST//3.8e-34:286:79//Hs.135301:AI039161
F-PLACE3000455//Homo sapiens mRNA for cytochrome b small subunit of complex II, complete cds//3.6e-32:183:93//Hs.108326:AB006202
F-PLACE3000475//ESTs//1.9e-09:422:61//Hs.145783:AA081874
F-PLACE3000477//H.sapiens mRNA for chemokine receptor D6//1.0:426:54//Hs.117572:U94888
F-PLACE4000009//TRICHOHYALIN//3.1e-09:692:60//Hs.82276:L09190
F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//3.6e-118:331:100//Hs.105399:AB018352
F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//1.1e-06:244:63//Hs.154050:AC004131
F-PLACE4000049//Homo sapiens clone 24619 mRNA sequence//4.3e-45:371:79//Hs.139088:AF070533
F-PLACE4000052//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//1.4e-53:669:67//Hs.40993:AF000148
F-PLACE4000063
F-PLACE4000089//ESTs//2.2e-10:121:85//Hs.49391:W00713
F-PLACE4000093//ESTs//0.0053:273:60//Hs.136952:AA825819
F-PLACE4000100//ESTs//8.0e-21:246:73//Hs.140207:N32058
F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//3.8e-147:684:99//Hs.129937:AB007931
F-PLACE4000128//Homo sapiens ES/130 mRNA, complete cds//0.23:398:60//Hs.98614:AF006751
F-PLACE4000129
F-PLACE4000131//ESTs//2.4e-13:194:72//Hs.41418:H90627
F-PLACE4000147//ESTs//0.0060:324:60//Hs.85640:AA535856
F-PLACE4000156//Zinc finger protein 136 (clone pHZ-20)//2.3e-89:764:76//Hs.69740:U09367
F-PLACE4000192
F-PLACE4000211
F-PLACE4000222//EST//1.9e-15:317:66//Hs.149206:AI246594
F-PLACE4000230//Human mRNA for KIAA0331 gene, complete cds//0.0048:258:60//Hs.146395:AB002329
F-PLACE4000233//ESTs//4.4e-38:240:80//Hs.114605:AI304317
F-PLACE4000247//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding mitochondrial protein, complete cds//0.0095:156:69//Hs.30928:AF043250
F-PLACE4000250//ESTs//3.8e-72:377:94//Hs.124234:T89609
F-PLACE4000252//ESTs//1.0:196:64//Hs.144869:AA493886
F-PLACE4000259//Homo sapiens mRNA for KIAA0788 protein, partial cds//6.2e-27:191:87//Hs.2397:Z70200
F-PLACE4000261
F-PLACE4000269//ESTs, Weakly similar to coded for by C. elegans cDNA yk52b10.3 [C.elegans]//9.5e-41:202:100//Hs.118849:AA215645
F-PLACE4000270
F-PLACE4000300
F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN//4.5e-23:135:96//Hs.155952:U88966
F-PLACE4000323//EST//6.7e-09:180:68//Hs.116769:AA630365
F-PLACE4000326//ESTs//2.1e-94:453:98//Hs.103177:W72798

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F-PLACE4000344//EST//6.4e-05:135:67//Hs.146729:AI147292
F-PLACE4000367
F-PLACE4000369
F-PLACE4000379//EST//3.9e-42:381:79//Hs.162335:AA564256
F-PLACE4000387//ESTs//0.19:93:69//Hs.154173:AI379823
F-PLACE4000392//ESTs//0.0015:381:59//Hs.120172:AA709046
F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1e-47:605:71//Hs.153026:AB014540
F-PLACE4000411//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//4.7e-33:159:81//Hs.154257:AI275982
F-PLACE4000431//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.3e-45:263:92//Hs.2397:Z70200
F-PLACE4000445
F-PLACE4000450
F-PLACE4000465//ESTs//1.5e-11:273:65//Hs.145783:AA081874
F-PLACE4000487//Sialophorin (gpL115, leukosialin, CD43)//3.0e-14:189:71//Hs.80738:X52075
F-PLACE4000489//ESTs//0.94:104:68//Hs.125119:R38951
F-PLACE4000494//ESTs//1.0:185:60//Hs.143053:AI126289
F-PLACE4000521//ESTs//0.0027:161:70//Hs.135740:AA651731
F-PLACE4000522//ESTs, Highly similar to NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG 1 PRECURSOR [Homo sapiens]//0.047:119:65//Hs.129053:AA767022
F-PLACE4000548
F-PLACE4000558//Homo sapiens mRNA for DFFRY protein, abundant transcript//0.0035:510:59//Hs.39163:AF000986
F-PLACE4000581
F-PLACE4000590//ESTs, Highly similar to POL POLYPROTEIN [Friend murine leukemia virus (isolate 57)]//3.4e-13:275:68//Hs.113980:AI034080
F-PLACE4000593//ESTS, Weakly similar to F25D7.1 [C.elegans]//5.2e-28:239:79//Hs.109084:AI004675
F-PLACE4000612//Keratin 9//0.27:207:64//Hs.2783:Z29074
F-PLACE4000638//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//3.5e-47:562:69//Hs.129685:AB002446
F-PLACE4000650
F-PLACE4000654
F-PLACE4000670//ESTs//6.1e-88:411:100//Hs.130688:AI028132
F-SKNMC1000011//Centromere protein B (80kD)//0.0013:243:62//Hs.85004:X05299
F-SKNMC1000013//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HOMOLOG 50 [Drosophila melanogaster]//2.5e-36:197:96//Hs.118634:U66688
F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5e-148:706:98//Hs.109299:AB014554
F-SKNMC1000050//Calpain, large polypeptide L2//4.1e-53:330:90//Hs.76288:M23254
F-SKNMC1000091//ESTs//3.3e-64:420:88//Hs.90997:AA946877
F-THYRO1000017//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//Hs.3989:AB002313
F-THYRO1000026//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.9e-35:299:81//Hs.2407:Z49194
F-THYRO1000034
F-THYRO1000035//ESTs//4.1e-37:317:79//Hs.141254:AI334099
F-THYRO1000040//ESTs//0.30:331:59//Hs.87176:AI148326
F-THYRO1000070//Human mRNA for KIAA0347 gene, complete cds//0.069:278:63//Hs.101996:AB002345
F-THYRO1000072//Homo sapiens clone 23584 mRNA sequence//8.7e-86:722:77//Hs.6654:AB014557
F-THYRO1000085
F-THYRO1000092//ESTs//3.1e-100:469:99//Hs.132207:AI148065
F-THYRO1000107
F-THYRO1000111//Human Line-1 repeat mRNA with 2 open reading frames//6.8e-106:690:86//Hs.23094:M19503
F-THYRO1000121
F-THYRO1000124//Human mRNA for alanine aminotransferase//0.0026:420:58//Hs.103502:U70732
F-THYRO1000129//Homo sapiens TED protein (TED).mRNA, complete cds//2.8e-155:732:98//Hs.87619:AF087142
F-THYRO1000132//ESTs//1.9e-35:164:79//Hs.139179:AA650203
F-THYRO1000156//EST//0.32:102:68//Hs.139634:AA478416
F-THYRO1000163//Small inducible cytokine A5 (RANTES)//5.2e-50:331:85//Hs.155464:AF088219
F-THYRO1000173//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//1.1e-05:261:61//Hs.

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152936:D63475
F-THYRO1000186//H.sapiens mRNA for phosphoinositide 3-kinase//3.7e-41:270:87//Hs.101238:Y11312
F-THYRO1000187//EST//0.11:227:62//Hs.101773:H23270
F-THYRO1000190//ESTs//0.82:194:63//Hs.128818:AA976883
F-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//2.4e-175:805:99//Hs.43445:AJ005698
F-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.0e-88:616:84//Hs.79672:AB014552
F-THYRO1000206//EST//0.96:291:61//Hs.104962:AA443848
F-THYRO1000221//Human clone 23589 mRNA sequence//0.035:242:62//Hs.11506:U79297
F-THYRO1000241//EST//0.48:102:69//Hs.160764:AI313322
F-THYRO1000242//Zinc finger protein 84 (HPF2)//1.2e-42:534:64//Hs.9450:M27878
F-THYRO1000253//Homo sapiens mRNA for KIAA0690 protein, partial cds//0.61:211:64//Hs.60103:AB014590
F-THYRO1000270
F-THYRO1000279//ESTs//0.0020:104:72//Hs.121476:AI215500
F-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds//1.3e-180:848:98//Hs.25846:AB016068
F-THYRO1000320//ESTs, Weakly similar to Similar to glutamate decarboxylase [C.elegans]//7.6e-92:431:99//Hs.122719:AA777803
F-THYRO1000327//Autocrine motility factor receptor//2.8e-52:290:93//Hs.80731:M63175
F-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//7.2e-164:763:98//Hs.12002:AB018333
F-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds//6.9e-34:177:84//Hs.7833:U29091
F-THYRO1000368//ESTs//0.0011:55:96//Hs.34994:AA252919
F-THYRO1000381//Homo sapiens mRNA for KIAA0562 protein, complete cds//0.081:240:62//Hs.118401:AB011134
F-THYRO1000387//EST//3.6e-14:197:71//Hs.139399:AA416855
F-THYRO1000394//ESTs, Weakly similar to No definition line found [C.elegans]//5.8e-39:245:91//Hs.119095:T79413
F-THYRO1000395//EST//5.8e-69:333:99//Hs.156524:AA724572
F-THYRO1000401//ESTs//1.8e-24:132:98//Hs.54852:W26238
F-THYRO1000438//EST//1.9e-05:217:63//Hs.115930:AA579773
F-THYRO1000452//B cell lymphoma protein 6 (zinc finger protein 51)//0.096:306:60//Hs.155024:U00115
F-THYRO1000471//Tyrosine aminotransferase//5.6e-44:403:77//Hs.2999:X52520
F-THYRO1000484//EST, Weakly similar to putative p150 [H.sapiens]//8.9e-22:248:76//Hs.162011:AA513663
F-THYRO1000488
F-THYRO1000501//H.sapiens Staf50 mRNA//3.2e-75:615:77//Hs.68054:X82200
F-THYRO1000502//ESTs//1.0:350:57//Hs.119749:AA689298
F-THYRO1000505//Interleukin 13//0.95:245:60//Hs.845:U31120
F-THYRO1000558//EST//1.3e-24:351:64//Hs.142326:AA351877
F-THYRO1000569//Homo sapiens mRNA for dihydropyrimidinase related protein 4, complete cds//0.28:229:61//Hs.100058:AB006713
F-THYRO1000570//EST//0.80:171:61//Hs.112790:AA609949
F-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds//2.4e-168:808:97//Hs.151411:AF075587
F-THYRO1000596//EST//9.5e-94:461:96//Hs.135397:AI056322
F-THYRO1000602//EST//4.9e-06:80:80//Hs.162135:AA526331
F-THYRO1000605//Guanylate cyclase 1, soluble, alpha 2//0.44:182:62//Hs.2685:Z50053
F-THYRO1000625//Thromboxane A2 receptor//4.5e-45:323:82//Hs.89887:D38081
F-THYRO1000637//ESTs//4.4e-24:255:75//Hs.101014:AA194941
F-THYRO1000641//ESTs//0.00017:375:58//Hs.32703:AA054125
F-THYRO1000658//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.8e-09:127:77//Hs.116007:S79267
F-THYRO1000662
F-THYRO1000666//ESTs//1.9e-28:149:99//Hs.105187:AI394157
F-THYRO1000676//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//5.7e-49:281:77//Hs.116007:S79267
F-THYRO1000684//ESTs, Weakly similar to band-6-protein [H.sapiens]//0.46:368:57//Hs.26557:AA480380

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F-THYRO1000699//ESTs//1.6e-10:314:65//Hs.139212:AA243452
F-THYRO1000712//ESTs//3.3e-42:211:99//Hs.69330:AI056324
F-THYRO1000715//Human plectin (PLEC1) mRNA, complete cds//2.9e-06:631:59//Hs.79706:U53204
F-THYRO1000734//ESTs//8.4e-08:226:64//Hs.125754:AA806085
F-THYRO1000748//Homo sapiens KIAA0411 mRNA, complete cds//3.1e-35:339:74//Hs.7977:AB007871
F-THYRO1000756//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//1.0:209:62//Hs.19492:AF061573
F-THYRO1000777//Human mRNA for KIAA0147 gene, partial cds//0.00069:636:57//Hs.158132:D63481
F-THYRO1000783//Homo sapiens Arp2/3 protein complex subunit p41-Arc (ARC41) mRNA, complete cds//0.70:452:58//Hs.11538:AF006084
F-THYRO1000787
F-THYRO1000793
F-THYRO1000796
F-THYRO1000805//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//9.4e-36:561:68//Hs.129685:AB002446
F-THYRO1000815//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:465:75//Hs.154326:D42087
F-THYRO1000829//ESTs//1.7e-66:361:95//Hs.7906:H16339
F-THYRO1000843
F-THYRO1000852//ESTs//6.2e-23:204:81//Hs.144452:AA838788
F-THYRO1000855//ESTs//0.049:159:64//Hs.163532:AI424170
F-THYRO1000865//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-33:190:75//Hs.133526:N21103
F-THYRO1000895//ESTs//3.8e-24:191:84//Hs.132722:AA618531
F-THYRO1000916//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.8e-43:318:79//Hs.92381:AB007956
F-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//3.0e-179:839:98//Hs.78106:AF079529
F-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE//1.1e-33:759:63//Hs.79217:M77836
F-THYRO1000951//MUELLERIAN INHIBITING FACTOR PRECURSOR//0.055:662:56//Hs.112432:AC005263
F-THYRO1000952//Human mRNA for KIAA0208 gene, complete cds//0.98:177:65//Hs.83558:D86963
F-THYRO1000974//Homo sapiens putative ATP-dependent mitochondrial RNA helicase (SUV3) mRNA, nuclear gene encoding mitochondrial protein, complete cds//2.7e-15:123:90//Hs.106469:AF042169
F-THYRO1000975//EST//0.45:172:62//Hs.105449:AA513907
F-THYRO1000983
F-THYRO1000984//EST//0.0075:119:65//Hs.150347:AA984646
F-THYRO1000988//ESTs//0.056:99:71//Hs.153409:AI224307
F-THYRO1001003
F-THYRO1001031//Thiopurine S-methyltransferase//3.8e-44:568:71//Hs.51124:AF019369
F-THYRO1001033//H.sapiens mRNA for cylicin II//0.0061:287:60//Hs.3232:Z46788
F-THYRO1001062//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.2e-45:394:79//Hs.51048:X68830
F-THYRO1001093//Human mRNA for KIAA0355 gene, complete cds//3.4e-33:421:72//Hs.153014:AB002353
F-THYRO1001100//Human DNA-binding protein mRNA, 3'end//2.1e-74:741:74//Hs.159249:Z99130
F-THYRO1001120//Homo sapiens deltex (Dx) mRNA, complete cds//4.5e-18:447:62//Hs.124024:AF053700
F-THYRO1001121//ESTs//0.92:257:61//Hs.118246:N95416
F-THYRO1001133//EST//1.1e-38:367:75//Hs.144175:H70425
F-THYRO1001134//ESTs//1.4e-28:186:91//Hs.109468:W52074
F-THYRO1001142//ESTs//1.8e-44:332:82//Hs.146811:AA410788
F-THYRO1001173
F-THYRO1001177//ESTs//7.7e-40:240:84//Hs.155384:Z78385
F-THYRO1001189//ESTs//2.1e-36:323:76//Hs.120206:AI089163
F-THYRO1001204
F-THYRO1001213//Small inducible cytokine A5 (RANTES)//3.1e-43:256:81//Hs.155464:AF088219
F-THYRO1001262//ESTs//7.9e-44:279:87//Hs.138856:H47461
F-THYRO1001271//Homo sapiens mRNA for synaptogyrin 3//0.0045:273:60//Hs.6467:AJ002309
F-THYRO1001287//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//0.014:178:66//Hs.125315:AF027156
F-THYRO1001290//ESTs//3.9e-43:145:99//Hs.147797:AA069836
F-THYRO1001313//ESTs//1.0:244:61//Hs.127488:AA528182

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F-THYRO1001320//ESTs//0.062:126:67//Hs.133296:AI311872
F-THYRO1001321//Homo sapiens DEC-205 mRNA, complete cds//2.5e-35:560:68//Hs.153563:AF011333
F-THYRO1001322//ESTs//0.12:238:61//Hs.29169:N66545
F-THYRO1001347//ESTs//7.5e-61:293:99//Hs.129962:AA927207
F-THYRO1001363//ESTs//1.0e-16:178:78//Hs.163954:N57939
F-THYRO1001365//Homo sapiens KIAA0417 mRNA, complete cds//3.6e-18:187:79//Hs.12385:AB007877
F-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds//7.4e-157:740:97//Hs.138488:AB014607
F-THYRO1001401//EST//4.6e-14:171:76//Hs.157587:AI356993
F-THYRO1001403//ESTs//2.2e-50:464:79//Hs.118046:N49946
F-THYRO1001405//ESTs//1.7e-44:226:98//Hs.156667:AI347694
F-THYRO1001406//Hydroxysteroid (17-beta) dehydrogenase 3//2.8e-20:459:62//Hs.477:U05659
F-THYRO1001411//ESTs//1.9e-41:342:78//Hs.146811:AA410788
F-THYRO1001426//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//4.6e-33:153:81//Hs.102877:U41315
F-THYRO1001434//ESTs//1.1e-07:274:60//Hs.151093:AI224099
F-THYRO1001458//Myosin, heavy polypeptide 9, non-muscle//6.2e-60:653:71//Hs.44782:Z82215
F-THYRO1001480//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.3e-42:370:78//Hs.51048:X68830
F-THYRO1001487//EST//1.0:88:71//Hs.160760:AI311943
F-THYRO1001534//ESTs//1.2e-94:457:98//Hs.125523:AA883904
F-THYRO1001537//ESTs//3.5e-94:469:97//Hs.106448:R76663
F-THYRO1001541//EST//1.4e-10:158:65//Hs.145159:AI150211
F-THYRO1001559//ESTs//1.4e-07:91:81//Hs.43507:N24046
F-THYRO1001570//ESTs//2.3e-41:280:80//Hs.119752:AA703335
F-THYRO1001573//Homo sapiens clone 24778 unknown mRNA//2.7e-105:546:95//Hs.25306:AF070572
F-THYRO1001584//Human RGP3 mRNA, complete cds//0.14:335:58//Hs.82294:U27655
F-THYRO1001595//Human RSU-1/RSP-1 mRNA, complete cds//3.6e-35:165:84//Hs.75551:L12535
F-THYRO1001602//ESTs//3.1e-42:350:80//Hs.138384:R72849
F-THYRO1001605//EST//0.11:426:57//Hs.151206:AI126071
F-THYRO1001617//ESTs//5.2e-43:345:81//Hs.8710:W07046
F-THYRO1001637//ESTs, Weakly similar to anion exchanger [H.sapiens]//5.2e-13:108:86//Hs.141045:AA191659
F-THYRO1001656//Solute carrier family 2 (facilitated glucose transporter), member 4//0.099:540:55//Hs.95958:M91463
F-THYRO1001661//ESTs//0.12:53:92//Hs.151586:W45568
F-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform//8.0e-166:780:98//Hs.118633:AJ225089
F-THYRO1001673//Von Hippel-Lindau syndrome//4.6e-25:212:73//Hs.78160:AF010238
F-THYRO1001703//Homo sapiens clone 24767 mRNA sequence//0.27:421:57//Hs.122908:AF070552
F-THYRO1001706//ESTs//1.8e-24:142:95//Hs.112536:AI147691
F-THYRO1001721//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//2.5e-51:296:92//Hs.3826:U69560
F-THYRO100173 8//EST//6.9e-30:180:94//Hs.58641:W81229
F-THYRO1001745//ESTs//6.1e-49:244:98//Hs.97534:AA398813
F-THYRO1001746//EST//0.96:119:63//Hs.144107:AI053590
F-THYRO1001772//ESTS, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-21:182:81//Hs.118053:N75725
F-THYRO1001793//ESTs//1.9e-93:439:99//Hs.150116:AI299324
F-THYRO1001809//Human mRNA for KIAA0297 gene, partial cds//0.47:168:67//Hs.11711:AB002295
F-THYRO1001828
F-THYRO1001854//EST//0.038:128:67//Hs.160649:AI241823
F-THYRO1001895//Intercellular adhesion molecule 1 (CD54), human rhinovirus receptor//9.6e-13:288:65//Hs.51061:M24283
F-THYRO1001907//EST//1.9e-12:126:80//Hs.139296:AA350198
F-VESEN1000122
F-Y79AA1000013//ESTs//1.7e-72:369:96//Hs.97176:AA447885
F-Y79AA1000033
F-Y79AA1000037//Murine leukemia viral (bmi-1) oncogene homolog//7.8e-21:230:66//Hs.431:L13689
F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, complete cds//7.3e-40:629:64//Hs.75305:

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U78521
F-Y79AA1000065//CD81 ANTIGEN//0.0050:241:60//Hs.54457:M33680
F-Y79AA1000131//Guanylate cyclase 1, soluble, alpha 2//0.078:477:58//Hs.2685:Z50053
F-Y79AA1000181//Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt]// 0.0022:684:58//Hs.83190:U29344
F-Y79AA1000202//ESTs//2.5e-17:143:86//Hs.76925:AA211860
F-Y79AA1000214//Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds//3.9e-73:345:100//Hs.9242:AF081192
F-Y79AA1000230//Polymeric immunoglobulin receptor//0.98:335:59//Hs.842:X73079
F-Y79AA1000231//ESTs//0.11:209:66//Hs.132184:AI278623
F-Y79AA1000258//Homo sapiens metase (MET-1) mRNA, complete cds//0.30:444:61//Hs.99941:L23134
F-Y79AA1000268//Human mRNA for KIAA0367 gene, partial cds//9.1e-11:300:64//Hs.23311:AB002365
F-Y79AA1000313//Human mRNA for KIAA0129 gene, complete cds//0.89:744:56//Hs.44361:D50919
F-Y79AA1000328
F-Y79AA1000342//Homo sapiens OPA-containing protein mRNA, complete cds//8.4e-15:223:75//Hs.85313:AF071309
F-Y79AA1000346
F-Y79AA1000349//ALPHA-2C-1 ADRENERGIC RECEPTOR//8.3e-06:180:73//Hs.123022:J03853
F-Y79AA1000355
F-Y79AA1000368//ESTs//0.0062:235:64//Hs.114777:AA782908
F-Y79AA1000405//ESTs//0.76:244:62//Hs.153027:AA648897
F-Y79AA1000410//Small inducible cytokine A5 (RANTES)//8.1e-31:229:83//Hs.155464:AF088219
F-Y79AA1000420//ESTs//1.1e-53:271:87//Hs.13056:AA181018
F-Y79AA1000469//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0.0047:315:66//Hs.26285:AF082516
F-Y79AA1000480
F-Y79AA1000538//ESTs//5.7e-09:110:77//Hs.98790:AA284871
F-Y79AA1000539//ESTs//2.6e-52:412:77//Hs.81648:W26521
F-Y79AA1000540//Homo sapiens chromosome 7q22 sequence//0.70:133:69//Hs.151555:AF053356
F-Y79AA1000560//Homo sapiens gamma2-adaptin (G2AD) mRNA, complete cds//1.2e-07:371:63//Hs.8991:AF068706
F-Y79AA1000574//Human mRNA for GC box bindig protein, complete cds//0.95:258:62//Hs.150557:D31716
F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence//2.8e-154:755:97//Hs.21811:AF091080
F-Y79AA10006277//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//1.7e-136:644:98//Hs.60580:AF060503
F-Y79AA1000705//Homo sapiens CHD1 mRNA, complete cds//0.0023:523:59//Hs.22670:AF006513
F-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds//1.6e-181:850:98//Hs.83023:AF093670
F-Y79AA1000748//ESTs//4.2e-12:95:90//Hs.33687:R85969
F-Y79AA1000752//ESTs//8.1e-114:551:97//Hs.153471:AI198377
F-Y79AA1000774//ESTs//2.9e-59:296:98//Hs.150536:W20067
F-Y79AA1000782//EST//0.97:78:69//Hs.147351:AI208468
F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds//1.1e-178:847:97//Hs.5151:AF098799
F-Y79AA1000794//G-rich RNA sequence binding factor 1//0.83:228:61//Hs.79295:U07231
F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds//0.12:244:60//Hs.12307:AF056085
F-Y79AA1000802//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.87:466:59//Hs.122967:AF059569
F-Y79AA1000805
F-Y79AA1000824//Titin//1.0:437:58//Hs.83049:X90568
F-Y79AA1000827//Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt]// 0.0048:630:57//Hs.83190:U29344
F-Y79AA1000833//TUBULIN ALPHA-4 CHAIN//6.9e-107:603:90//Hs.75318:X06956
F-Y79AA1000850//ESTs, Weakly similar to T22C1.7 [C.elegans]//6.0e-77:368:99//Hs.86660:AA398644
F-Y79AA1000962//Homo sapiens orphan nuclear hormone receptor BD73 mRNA, 3' end//0.14:499:58//Hs.37288:D16815
F-Y79AA1000966//ESTs//0.80:52:86//Hs.6671:AI341699

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F-Y79AA1000968//ESTs, Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]//6.9e-69:310:94//Hs.76822:AI359536
F-Y79AA1000969//LYMPHOTOXIN-BETA RECEPTOR PRECURSOR//1.0:150:64//Hs.1116:L04270
F-Y79AA1000976//Arachidonate 15-lipoxygenase//0.87:174:66//Hs.73809:M23892
F-Y79AA1000985//Human plectin (PLEC1) mRNA, complete cds//0.091:385:58//Hs.79706:U53204
F-Y79AA1001023
F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds//0.99:37:100//Hs.78489:U63329
F-Y79AA1001048//Acyl-Coenzyme A dehydrogenase, very long chain//8.7e-30:772:60//Hs.82208:L46590
F-Y79AA1001061//ESTs//6.3e-41:303:84//Hs.55855:AA621381
F-Y79AA1001068//EST//3.0e-23:165:90//Hs.157607:AI357511
F-Y79AA1001077//ESTs//4.9e-40:237:94//Hs.11197:AA309047
F-Y79AA1001078
F-Y79AA1001105//Homo sapiens homeodomain protein (OG12) mRNA, complete cds//6.5e-11:247:66//Hs.55967:AF022654
F-Y79AA1001145//ESTs//1.3e-20:234:75//Hs.55855:AA621381
F-Y79AA1001167//Homo sapiens mRNA for KIAA0750 protein, complete cds//1.0:155:63//Hs.5444:AB018293
F-Y79AA1001177//Human hSIAH2 mRNA, complete cds//6.5e-09:299:65//Hs.20191:U76248
F-Y79AA1001185//ESTs//1.7e-56:318:93//Hs.102991:AA639646
F-Y79AA1001211//ESTs//9.1e-108:503:99//Hs.100605:AA305965
F-Y79AA1001216//Peroxisome receptor 1//0.00028:458:57//Hs.158084:Z48054
F-Y79AA1001228//Fragile X mental retardation 2//0.040:207:64//Hs.54472:U48436
F-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1//6.5e-25:731:60//Hs.85279:U34879
F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin))//4.0e-135:441:97//Hs.23170:AJ005892
F-Y79AA1001281//ESTs//2.7e-21:157:88//Hs.163825:AI393240
F-Y79AA1001299//Human Ini1 mRNA, complete cds//2.2e-116:323:93//Hs.155626:U04847
F-Y79AA1001312//ESTs//3.7e-95:448:99//Hs.104469:W38395
F-Y79AA1001323//ESTs//8.9e-50:340:86//Hs.144198:AI017555
F-Y79AA1001384
F-Y79AA1001391//Human Hoxb-13 mRNA, complete cds//8.6e-42:505:70//Hs.66731:U81599
F-Y79AA1001394//ESTs, Weakly similar to F54B3.3 [C.elegans]//1.5e-90:424:96//Hs.154221:H23167
F-Y79AA1001402//ESTs//1.0:245:62//Hs.134695:AI088489
F-Y79AA1001493//SRY (sex determining region Y)-box 4//0.38:311:61//Hs.83484:X70683
F-Y79AA1001511//ESTs//9.9e-105:487:99//Hs.153581:AA630465
F-Y79AA1001533//ESTs, Highly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Homo sapiens]//0.95:256:63//Hs.29974:AI360447
F-Y79AA1001541//EST//0.96:202:61//Hs.99141:AA447744
F-Y79AA1001548//ESTs//2.6e-25:166:90//Hs.164036:AA845659
F-Y79AA1001555//ESTs//1.6e-35:191:97//Hs.52885:H29851
F-Y79AA1001581//Cyclin-dependept kinase inhibitor 1C (p57, Kip2)//2.5e-05:272:64//Hs.106070:U22398
F-Y79AA1001585//ESTs//1.1e-84:473:93//Hs.42547:AA210783
F-Y79AA1001594//ESTs//1.7e-08:169:71//Hs.97366:AA393109
F-Y79AA1001603//ESTs//4.6e-07:429:59//Hs.160422:AI363426
F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds//0.00078:520:57//Hs.12334:AB014583
F-Y79AA1001647//ESTs, Weakly similar to ZK1058.5 [C.elegans]//9.4e-79:421:94//Hs.107039:W27244
F-Y79AA1001665//VON WILLEBRAND FACTOR PRECURSOR//1.0:386:60//Hs.110802:X04385
F-Y79AA1001679//Guanine nucleotide binding protein (G protein), beta polypeptide 1//0.88:243:61//Hs.3620:X04526
F-Y79AA1001692//Insulin-like growth factor binding protein 2//1.9e-06:426:59//Hs.162:X16302
F-Y79AA1001696//ESTs//2.3e-44:249:94//Hs.163665:AA250877
F-Y79AA1001705//Homo sapiens interleukin-1 receptor-associated kinase (IRAK) mRNA, complete cds//0.19:609:58//Hs.77297:L76191
F-Y79AA1001711//ESTs//5.2e-29:224:83//Hs.100461:AI018620
F-Y79AA1001781//Homo sapiens KIAA0443 mRNA, complete cds//0.49:183:66//Hs.113082:AB007903
F-Y79AA1001805//ESTs//1.1e-62:315:98//Hs.16141:W56079
F-Y79AA1001827//ESTs, Weakly similar to Similar to S.cerevisiae YD9335.03c protein [H.sapiens]//2.9e-62:313:98//Hs.15709:W81213

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F-Y79AA1001846//ESTs//9.4e-16:146:82//Hs.140588:H60533
F-Y79AA1001848//ESTs, Weakly similar to KIAA0390 [H.sapiens]//1.6e-19:142:90//Hs.103349:AI141124
F-Y79AA1001866//Homo sapiens mRNA for zinc finger protein 10//5.1e-09:215:67//Hs.104115:X52332
F-Y79AA1001874//Homo sapiens Jagged 2 mRNA, complete cds//5.4e-06:412:62//Hs.106387:AF029778
F-Y79AA1001875//ESTs//6.8e-09:198:67//Hs.138036:AI343173
F-Y79AA1001923//Homo sapiens growth-arrest-specific protein (gas) mRNA, complete cds//0.98:430:58//Hs.78501:L13720
F-Y79AA1001963//ESTs//8.1e-131:642:97//Hs.54971:AI424382
F-Y79AA1002027//ESTs//0.00042:58:91//Hs.5375:AA620611
F-Y79AA1002083//ESTs//2.5e-51:285:95//Hs.117205:W88943
F-Y79AAI002089//ESTs, Weakly similar to putative p150 [H.sapiens]//8.3e-53:348:88//Hs.18122:AI338045
F-Y79AA1002093
F-Y79AA1002103//ESTs//1.5e-15:223:71//Hs.97427:AA411865
F-Y79AA1002115
F-Y79AA1002125//ESTs//6.5e-41:206:99//Hs.159257:N40395
F-Y79AA1002139//ESTs, Weakly similar to B0035.14 [C.elegans]//1.2e-24:165:90//Hs.6473:AA853955
F-Y79AA1002204//Homo sapiens mRNA for KIAA0638 protein, partial cds//9.5e-05:393:62//Hs.77864:AB014538
F-Y79AA1002208//ESTs//2.7e-13:211:69//Hs.112469:AA598515
F-Y79AA1002209//ESTs, Weakly similar to TYROSYL-TRNA SYNTHETASE [Bacillus caldotenax]//2.3e-113:568:96//Hs.111637:AA305890
F-Y79AA1002210//ESTs, Weakly similar to D2045.8 [C.elegans]//8.6e-33:338:73//Hs.26662:U55984
F-Y79AA1002211//ESTs//2.6e-15:121:75//Hs.159584:AA524477
F-Y79AA1002220//EST//0.010:360:60//Hs.136341:AA482508
F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds//0.0041:203:63//Hs.1560:D42045
F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//4.1e-176:821:98//Hs.100729:AB014592
F-Y79AA1002246//Human involucrin mRNA//5.6e-05:525:59//Hs.157091:M13903
F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.2e-160:748:98//Hs.96731:AB014555
F-Y79AA1002298//ESTs//2.5e-05:115:77//Hs.87164:T84489
F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//2.1e-130:622:97//Hs.30898:AB014534
F-Y79AA1002311//ESTs//4.9e-19:126:94//Hs.58595:AA830999
F-Y79AA1002351//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete cds//0.028:587:58//Hs.2363:L36069
F-Y79AA1002361//ESTs//8.7e-29:149:100//Hs.156074:AA824377
F-Y79AA1002399
F-Y79AA1002407//ESTs//1.5e-25:183:89//Hs.110031:T52569
F-Y79AA1002416//CTP synthetase//9.1e-51:489:72//Hs.84112:X52142
F-Y79AA1002431
F-Y79AA1002433//EST//0.0037:94:71//Hs.136780:AA772318
F-Y79AA1002472//Homo sapiens DNA from chromosome 19, BAC 33152//1.1e-37:263:69//Hs.55452:AC003973
F-Y79AA1002482//ESTs//1.4e-49:313:80//Hs.132590:AI160765
F-Y79AA1002487//Insulin-like growth factor binding protein 2//0.43:249:61//Hs.162:X16302

Homology Search Result Data 5.

[0310] The result of the homology search of the Human Unigene using the clone sequence of 3'-end.

[0311] Data include

the name of clone,
title of the top hit data,
the P-value: the length of the compared sequence: identity (%), and
the Accession No. of the top hit data, as in the order separated by //.

[0312] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

[0313] Data are not shown for the clones in which the P-value was higher than 1.

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R-HEMBA1000005//ESTs, Highly similar to HYPOTHETICAL 31.6 KD PROTEIN F54F2.9 IN CHROMOSOME III [Caenorhabditis elegans]//5.6e-93:501:93//Hs.13015:AA628434
R-HEMBA1000030//Human POU domain protein (Brn-3b) mRNA, complete cds//0.83:314:61//Hs.266:U06233
R-HEMBA1000042//Archain//1:4e-45:282:89//Hs.33642:X81198
R-HEMBA1000046//Human mRNA for KIAA0118 gene, partial cds//8.3e-52:528:72//Hs.154326:D42087
R-HEMBA1000050//EST//0.043:155:63//Hs.149031:AI243340
R-HEMBA1000076//ESTs//3.1e-77:394:97//Hs.111742:R39329
R-HEMBA1000111//ESTs//1.7e-33:228:85//Hs.146811:AA410788
R-HEMBA1000129//ESTs, Weakly similar to contains similarity to helicases [C.elegans]//4.4e-90:502:90//Hs.55918:AA151667
R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.1e-100:514:94//Hs.27197:AB018340
R-HEMBA1000150//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1e-45:435:77//Hs.153026:AB014540
R-nnnnnnnnnnnn//ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]//7.7e-92:428:100//Hs.126925:AA931237
R-HEMBA1000158
R-nnnnnnnnnnnn//ESTs, Weakly similar to F13B12.1 [C.elegans]//1.3e-05:58:91//Hs.5570:AI377863
R-HEMBA1000180//ESTs//7.7e-90:461:95//Hs.159200:N50545
R-HEMBA1000185//ESTs//1.3e-72:371:96//Hs.134506:AA308366
R-HEMBA1000193//ESTs//4.2e-103:481:99//Hs.143251:AA769927
R-HEMBA1000201//Human Ini1 mRNA, complete cds//3.0e-25:137:99//Hs.155626:U04847
R-HEMBA1000213//ESTs//5.4e-85:465:94//Hs.23412:AA133311
R-HEMBA1000216//ESTs//3.0e-37:311:79//Hs.137875:AA993532
R-nnnnnnnnnnnn//EST//2.2e-100:498:96//Hs.161570:W80404
R-HEMBA1000231//Homo sapiens KIAA0414 mRNA, partial cds//2.7e-34:287:70//Hs.127649:AB007874
R-HEMBA1000243//Homo sapiens mRNA for KIAA0475 protein, complete cds//1.3e-23:276:75//Hs.5737:AB007944
R-HEMBA1000244//ESTs//2.3e-88:455:96//Hs.8929:AA719019
R-HEMBA1000251//ESTs//0.96:411:56//Hs.120277:AI243808
R-HEMBA1000264//ESTs//3.7e-97:487:96//Hs.29258:W37424
R-nnnnnnnnnnnn//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//4.9e-14:208:73//Hs.93332:AA811920
R-HEMBA1000282//ESTs//2.5e-38:216:94//Hs.120757:R92485
R-HEMBA1000288//ESTs//2.6e-43:289:86//Hs.151365:AA643962
R-HEMBA1000290//ESTs//5.1e-110:543:96//Hs.139068:AA516409
R-HEMBA1000302//Homo sapiens mRNA for KIAA0527 protein, partial cds//1.0:122:67//Hs.129748:AB011099
R-nnnnnnnnnnnn//ESTs//7.4e-76:386:97//Hs.22276:AA191323
R-nnnnnnnnnnnn//Human Ca^{2+}-dependent activator protein for secretion mRNA, complete cds//8.8e-30:160:98//Hs.151301:U36448
R-HEMBA1000307//ESTs, Highly similar to 8A-2V protein [M.musculus]//1.1e-103:489:99//Hs.108881:AI018024
R-nnnnnnnnnnnn//ESTs//9.3e-99:472:98//Hs.163512:AA903238
R-HEMBA1000338//EST//5.1e-49:278:92//Hs.150815:AI302560
R-HEMBA1000351//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.1e-42:270:88//Hs.73614:U83460
R-HEMBA1000355//ESTs//1.0e-105:531:96//Hs.61762:AI422243
R-HEMBA1000357//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//9.4e-89:432:87//Hs.139107:K00629
R-HEMBA1000366//ESTs//1.1e-99:524:95//Hs.11785:T65857
R-HEMBA1000369//ESTs//6.5e-70:355:96//Hs.124847:AA843938
R-HEMBA1000376//Human mRNA for KIAA0205 gene, complete cds//3.6e-44:388:77//Hs.3610:D86960
R-HEMBA1000387//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.5e-47:337:83//Hs.73614:U83460
R-HEMBA1000390//Oxytocin receptor//2.4e-16:428:62//Hs.2820:X64878
R-HEMBA1000392//ESTs//3.9e-105:531:96//Hs.130661:AI340248
R-HEMBA1000396//ESTs, Weakly similar to line-1 protein ORF2 [H.sapiens]//1.1e-44:447:75//Hs.42849:N31920
R-HEMBA1000411//ESTs, Weakly similar to ankyrin 3, long form [H.sapiens]//6.1e-92:373:99//Hs.48675:AI005282

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R-HEMBA1000418//ESTs//3.1e-66:315:100//Hs.94133:AI270700
R-HEMBA1000422//ESTs//1.6e-99:464:99//Hs.33024:AA002140
R-HEMBA1000428//Homo sapiens mRNA for oligophrenin 1//4.9e-85:535:87//Hs.158122:AJ001189
R-HEMBA1000434//ESTs//3.7e-53:266:99//Hs.22782:Z38143
R-HEMBA1000442//ESTs//0.93:322:57//Hs.144763:AI218014
R-HEMBA1000456//ESTs//4.1e-48:277:93//Hs.6937:AA524349
R-HEMBA1000459//ESTs//0.010:184:63//Hs.128797:AI246316
R-HEMBA1000460
R-HEMBA1000464//EST//0.082:87:70//Hs.147977:AI262370
R-HEMBA1000469//Small inducible cytokine A5 (RANTES)//1.4e-65:494:81//Hs.155464:AF088219
R-HEMBA1000488//ESTs, Weakly similar to The KIAA0132 gene product is related to Drosophila melanogaster ring canel protein. [H.sapiens]//1.1e-31:181:94//Hs.61454:AA312449
R-HEMBA1000490//ESTs//6.4e-17:132:86//Hs.32855:N25528
R-HEMBA1000491//ESTs//2.2e-22:171:85//Hs.8035:AA195087
R-HEMBA1000504//ESTs//0.016:282:58//Hs.130778:AI077571
R-HEMBA1000505//EST//6.1e-15:116:87//Hs.162783:AA627318
R-HEMBA1000508//ESTs//1.1e-28:244:81//Hs.132722:AA618531
R-HEMBA1000518//EST//0.60:141:60//Hs.97831:AA400885
R-HEMBA1000519//ESTs//2.8e-64:334:96//Hs.97885:AA402414
R-HEMBA1000520//ESTs//6.9e-104:503:97//Hs.18370:AA947280
R-HEMBA1000523//Cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD//4.0e-55:203:92//Hs.155510:U15782
R-HEMBA1000531//ESTs, Weakly similar to HEAT SHOCK 70 KD PROTEIN 1 [H.sapiens]//1.3e-117:550:99//Hs.99722:AI422277
R-HEMBA1000540//ESTs//4.7e-72:350:98//Hs.109755:AA180809
R-HEMBA1000545//Homo sapiens clone 23892 mRNA sequence//3.7e-68:549:80//Hs.91916:AF035317
R-nnnnnnnnnnnn//ESTs//2.3e-66:342:97//Hs.71916:AA219699
R-HEMBA1000557//EST//1.5e-49:297:90//Hs.149580:AI281881
R-HEMBA1000561//ESTs, Moderately similar to zinc finger protein [R.norvegicus]//1.8e-108:550:96//Hs.26799:W74481
R-HEMBA1000563//Adenosine kinase//0.16:367:58//Hs.94382:U50196
R-HEMBA1000568//ESTs//5.1e-42:321:82//Hs.141024:H07128
R-nnnnnnnnnnn
R-HEMBA1000575//ESTs//3.8e-45:352:80//Hs.146811:AA410788
R-HEMBA1000588//ESTs//0.18:122:67//Hs.140507:AA761944
R-HEMBA1000591//Homo sapiens mRNA for EIB-55kDa-associated protein//3.9e-113:591:94//Hs.155218:AJ007509
R-HEMBA1000592//TYROSINE-PROTEIN KINASE ITK/TSK//0.024:309:61//Hs.89519:L10717
R-HEMBA1000594//ESTs//8.6e-07:172:68//Hs.160289:AI168041
R-HEMBA1000604//Human telomerase-associated protein TP-1 mRNA, complete cds//1.5e-19:129:93//Hs.158334:U86136
R-HEMBA1000608//ESTs//2.2e-95:506:94//Hs.6103:AA496424
R-HEMBA1000622//ESTs//3.8e-10:440:61//Hs.137538:AA769438
R-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//1.4e-86:422:97//Hs.26252:AA643235
R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.7e-99:443:97//Hs.60103:AB014590
R-HEMBA1000655//Human mRNA for KIAA0392 gene, partial cds//1.3e-50:426:79//Hs.40100:AB002390
R-HEMBA1000657//ESTs//3.0e-74:419:93//Hs.109477:AA477929
R-HEMBA1000662//EST//1.1e-90:425:99//Hs.122144:AA780136
R-HEMBA1000673//ESTs//1.2e-101:473:99//Hs.138215:AI123922
R-HEMBA1000682//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403
R-HEMBA1000686//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//6.8e-18:137:86//Hs.7049:AI141736
R-HEMBA1000702//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//7.4e-52:345:84//Hs.144563:AF057280
R-HEMBA1000705//EST//0.21:139:63//Hs.132687:AI033672

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R-HEMBA1000719//ESTs//8.4e-90:484:94//Hs.29005:AA477213
R-HEMBA1000722//ESTs, Weakly similar to similar to enoyl-COA hydratases/isomerases [C.elegans]//7.2e-113:572:95//Hs.28644:AI018612
R-HEMBA1000726//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//2.8e-40:449:75//Hs.74478:U33931
R-HEMBA1000727//ESTs//0.0047:267:60//Hs.133095:AA927777
R-HEMBA1000747//EST//3.9e-20:160:85//Hs.99048:AA446110
R-HEMBA1000749//Small inducible cytokine A5 (RANTES)//4.7e-37:286:82//Hs.155464:AF088219
R-HEMBA1000752//EST//0.041:39:94//Hs.127772:AA961131
R-HEMBA1000769//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.6e-32:309:75//Hs.10458:AF088219
R-HEMBA1000773//EST//7.5e-05:201:63//Hs.122887:AA767612
R-HEMBA1000774//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//1.3e-48:284:90//Hs.103458:X53795
R-HEMBA1000791//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:291:87//Hs.154326:D42087
R-HEMBA1000817//ESTs//8.3e-95:445:99//Hs.107357:AA983939
R-HEMBA1000822//ESTs//1.1e-107:522:97//Hs.92832:AA631027
R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRM160) mRNA, complete cds//2.2e-44:228:98//Hs.18192:AF048977
R-HEMBA1000843//Homo sapiens LIM protein mRNA, complete cds//6.6e-46:410:77//Hs.154103:AF061258
R-HEMBA1000851
R-HEMBA1000852//Aldehyde dehydrogenase 10 (fatty aldehyde dehydrogenase)//3.7e-33:284:80//Hs.159608:U46689
R-HEMBA1000867//EST//2.0c-17:211:74//Hs.145670:AI265794
R-HEMBA1000869//ESTs//3.1e-16:237:71//Hs.116518:AA653202
R-HEMBA1000870//ESTs//1.6e-43:222:98//Hs.69564:AA203608
R-HEMBA1000872//ESTs//1.9e-93:453:98//Hs.152622:AA594951
R-HEMBA1000876//Small inducible cytokine A5 (RANTES)//3.0e-41:329:79//Hs.155464:AF088219
R-HEMBA1000908//ESTs//1.6e-51:291:92//Hs.12247:AI203154
R-HEMBA1000910//EST//0.98:139:64//Hs.132687:AI033672
R-HEMBA1000918//EST//9.6e-30:152:84//Hs.162136:AA526508
R-HEMBA1000919
R-HEMBA1000934//ESTs//4.1e-38:254:89//Hs.87784:AA460597
R-HEMBA1000942//ESTs//3.5e-20:172:69//Hs.160065:AI018619
R-HEMBA1000943//Homo sapiens mRNA for KIAA0748 protein, complete cds//1.3e-44:281:78//Hs.33187:AB018291
R-HEMBA1000946//ESTs//1.6e-68:352:96//Hs.21331:H93074
R-HEMBA1000960//Homo sapiens tapasin (NGS-17) mRNA, complete cds//4.0e-61:347:81//Hs.5247:AF029750
R-HEMBA1000968//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//6.8e-51:362:84//Hs.159187:AB007977
R-HEMBA1000971//ESTs//2.8e-41:246:91//Hs.104287:AI363498
R-HEMBA1000972//Homo sapiens mRNA for XPR2 protein//7.3e-44:341:81//Hs.44766:AJ007590
R-HEMBA1000974//ESTs//1.4e-32:166:100//Hs.149274:AI018170
R-HEMBA1000975//Oxytocin receptor//2.7e-46:563:73//Hs.2820:X64878
R-HEMBA1000985//ESTs//4.4e-05:125:69//Hs.147434:AI214464
R-HEMBA1000986//ESTs//7.8e-44:266:84//Hs.163784:N54902
R-HEMBA1000991//EST//1.4e-42:162:86//Hs.149580:AI281881
R-HEMBA1001007
R-HEMBA1001008//ESTs//2.3e-82:463:92//Hs.10339:AA058764
R-HEMBA1001009//ESTs, Weakly similar to non-lens beta gamma-crystallin like protein [H.sapiens]//2.6e-58:280:100//Hs.128738:AA970836
R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//3.3e-115:587:95//Hs.158287:AB007937
R-HEMBA1001019//Cell division cycle 2, G1 to S and G2 to M//1.1e-24:140:95//Hs.58393:X05360
R-HEMBA1001020//ESTs//0.52:86:72//Hs.69683:AA115292
R-HEMBA1001022//ESTs//3.4e-18:102:100//Hs.63243:AI123912
R-HEMBA1001024//ESTs//1.9e-07:262:61//Hs.124399:AA832336
R-HEMBA1001026//ESTs//0.0017:142:67//Hs.144109:AI345543

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R-nnnnnnnnnnnn//Ankyrin G//0.23:244:60//Hs.75893:U13616
R-HEMBA1001051//Homo sapiens mRNA for KIAA0621 protein, partial cds//6.4e-21:186:79//Hs.132942:AB014521
R-HEMBA1001052//ESTs//5.4e-107:497:99//Hs.121773:AI357886
R-HEMBA1001060//ESTs//1.1e-31:298:80//Hs.24821:AA044813
R-HEMBA1001071//Alpha-1 type 3 collagen//9.1e-34:179:98//Hs.119571:X14420
R-HEMBA1001077//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//2.7e-21:417:64//Hs.127338:AB007961
R-HEMBA1001080
R-HEMBA1001085//ESTs//1.9e-47:385:79//Hs.146811:AA410788
R-HEMBA1001088//ESTs//2.8e-102:548:93//Hs.127273:AA522674
R-HEMBA1001094
R-HEMBA1001099//ESTs//0.24:41:97//Hs.18612:T99245
R-HEMBA1001109//Small inducible cytokine A5 (RANTES)//2.4e-46:396:80//Hs.155464:AF088219
R-HEMBA1001121//ESTs//1.7e-15:216:71//Hs.141605:H92974
R-HEMBA1001122//ESTs//2.0e-90:474:94//Hs.107884:AA131320
R-HEMBA1001123//B-CELL GROWTH FACTOR PRECURSOR//2.7e-45:319:84//Hs.99879:M15530
R-HEMBA1001133//ESTs//1.2e-92:443:99//Hs.99626:AA632341
R-HEMBA1001137//ESTs//2.0e-86:426:97//Hs.157103:W60265
R-HEMBA1001140//Small inducible cytokine A5 (RANTES)//2.9e-45:323:83//Hs.155464:AF088219
R-HEMBA1001172//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.1e-39:309:82//Hs.96337:AA225358
R-HEMBA1001174//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.21:238:60//Hs.127338:AB007961
R-HEMBA1001197//ESTs//0.010:388:61//Hs.14881:R91896
R-HEMBA1001208//ESTs, Highly similar to Similar to S.cerevisiae hypothetical protein 5 [H.sapiens]//0.27:305:62//Hs.100238:U69194
R-HEMBA1001226//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.0e-54:333:81//Hs.113283:AF018080
R-HEMBA1001235//EST//2.3e-07:42:92//Hs.141620:N63316
R-HEMBA1001247//ESTs, Weakly similar to WWP2 [H.sapiens]//2.9e-20:160:87//Hs.103102:W55932
R-HEMBA1001257//ESTs//3.3e-112:544:97//Hs.128749:AA779728
R-HEMBA1001265//ESTs//8.7e-116:564:98//Hs.155150:AI061435
R-nnnnnnnnnnnn//ESTs, Weakly similar to Lpa8p [S.cerevisiae]//2.4e-35:239:87//Hs.103919:AA159181
R-HEMBA1001286//ESTs//1.4e-97:507:95//Hs.26244:AI352674
R-HEMBA1001289//ESTs//8.2e-44:122:96//Hs.76267:AA877534
R-HEMBA1001294//ESTs//1.0:140:65//Hs.149638:AI298324
R-HEMBA1001299//Small inducible cytokine A5 (RANTES)//1.1e-45:307:84//Hs.155464:AF088219
R-HEMBA1001302//Homo sapiens mRNA for APC 2 protein, complete cds//0.53:89:68//Hs.20912:AB012162
R-HEMBA1001303//EST//0.00053:271:60//Hs.156148:AI333214
R-HEMBA1001310//ESTs//1.4e-91:486:93//Hs.86228:AA206019
R-HEMBA1001319//ESTs//0.051:228:61//Hs.99404:AA953977
R-HEMBA1001323//ESTs//6.2e-83:401:98//Hs.47343:AI282950
R-HEMBA1001326//ESTs, Weakly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION [S.cerevisiae]//1.3e-77:458:92//Hs.9398:N41838
R-HEMBA1001327//ESTs//0.60:251:58//Hs.117162:AA701259
R-HEMBA1001330//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-46:249:78//Hs.113283:AF018080
R-HEMBA1001351//ESTs//0.13:230:57//Hs.138510:R94816
R-HEMBA1001361//ESTs//3.5e-107:570:94//Hs.7727:AA142837
R-HEMBA1001375//ESTs//1.1e-96:454:99//Hs.59584:AA587334
R-HEMBA1001377//ESTs//8.5e-91:459:95//Hs.61859:AA628550
R-HEMBA1001383//ESTs//0.077:381:58//Hs.163093:AA745458
R-HEMBA1001387//ESTs//2.0e-85:405:99//Hs.152127:AI246482
R-HEMBA1001388//ESTs//1.5e-83:395:99//Hs.105191:AA133439
R-HEMBA1001391//ESTs//7.7e-90:455:96//Hs.120905:R22204
R-HEMBA1001398//Thromboxane A2 receptor//4.0e-46:279:89//Hs.89887:D38081
R-HEMBA1001405//ESTs//1.2e-98:485:97//Hs.73287:W16714
R-HEMBA1001407//ESTs//2.2e-76:365:99//Hs.110128:AA584364
R-HEMBA1001411//ESTs//1.2e-102:476:100//Hs.143162:AI380343

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R-HEMBA1001413//ESTs//3.7e-66:321:98//Hs.152472:AA041199
R-HEMBA1001415
R-HEMBA1001432//Putative mismatch repair/binding protein hMSH3//7.9e-42:183:82//Hs.42674:U61981
R-HEMBA1001433//ESTs//1.4e-34:240:77//Hs.95611:U51704
R-HEMBA1001435//ESTs//5.6e-23:292:70//Hs.116315:AA629263
R-HEMBA1001442//ESTs//0.76:414:58//Hs.156189:AI419982
R-HEMBA1001446//ESTs//2.2e-95:447:99//Hs.154091:AA767546
R-HEMBA1001450//ESTs//1.0e-93:491:94//Hs.16130:AA195077
R-HEMBA1001454//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-47:304:88//Hs.23094:M19503
R-HEMBA1001455//ESTs//7.1e-103:482:99//Hs.97407:AI417220
R-HEMBA1001463
R-HEMBA1001476//Human mRNA for KIAA0186 gene, complete cds//2.0e-25:409:66//Hs.36232:D80008
R-HEMBA1001478
R-HEMBA1001497
R-HEMBA1001510//ESTs//3.3e-44:381:78//Hs.139882:AA864426
R-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//5.9e-79:528:84//Hs.23094:M19503
R-HEMBA1001517//ESTs//5.8e-32:272:81//Hs.119512:AA487269
R-HEMBA1001522//ESTs//1.7e-84:364:95//Hs.117858:AA-702493
R-HEMBA1001526//ESTs//1.8e-93:527:93//Hs.10624:N64723
R-HEMBA1001533//ESTs//1.9e-42:211:100//Hs.55830:AA580270
R-HEMBA1001557//ESTs//4.2e-83:413:97//Hs.47546:AA181348
R-HEMBA1001566//Small inducible cytokine A5 (RANTES)//3.4e-50:304:88//Hs.155464:AF088219
R-HEMBA1001569//POU domain, class 3, transcription factor 4//2.3e-06:259:62//Hs.2229:X82324
R-HEMBA1001570//Homo sapiens pendrin (PDS) mRNA, complete cds//3.5e-47:456:77//Hs.159275:AF030880
R-HEMBA1001579//ESTs//0.11:299:60//Hs.106090:AA457030
R-HEMBA1001581//ESTs//0.016:350:61//Hs.124664:AI015652
R-HEMBA1001585//Human mRNA for KIAA0331 gene, complete cds//0.30:251:63//Hs.146395:AB002329
R-HEMBA1001589
R-HEMBA1001595//ESTs, Weakly similar to SEPTIN 2 [D.melanogaster]//6.9e-71:431:88//Hs.26625:W25874
R-HEMBA1001608//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//1.3e-73:533:82//Hs.103948:K00627
R-HEMBA1001620//ESTs, Highly similar to MYO-INOSITOL-1-PHOSPHATE SYNTHASE [Arabidopsis thaliana]//4.5e-93:537:90//Hs.20218:AA628530
R-nnnnnnnnnnnn//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.054:362:60//Hs.132206:AF039694
R-HEMBA1001636//ESTs//4.9e-53:267:97//Hs.47459:AA700158
R-HEMBA1001640//ESTs//2.9e-27:299:72//Hs.65236:AA927623
R-nnnnnnnnnnnn//ESTs, Weakly similar to Mi-2 protein [H.sapiens]//1.2e-86:442:95//Hs.63888:AA203398
R-HEMBA1001655//ESTs//1.5e-101:516:95//Hs.86541:AA214554
R-HEMBA1001658
R-HEMBA1001661//Homo sapiens protocadherin 68 (PCH68) mRNA, complete cds//1.3e-16:427:61//Hs.106511:AF029343
R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-93:493:92//Hs.107254:AC005943
R-HEMBA1001675
R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA, complete cds//4.2e-103:534:94//Hs.7381:AF038962
R-HEMBA1001681//ESTs//6.0e-49:292:92//Hs.65588:AA523424
R-HEMBA1001702//ESTs//9.0e-98:478:97//Hs.28661:AA805916
R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete cds//6.3e-98:483:96//Hs.31720:AB014598
R-HEMBA1001711//ESTs//5.8e-83:398:98//Hs.34804:AA514960
R-HEMBA1001712//ESTs//0.028:202:63//Hs.105790:AA528095
R-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]//1.8e-46:236:98//Hs.132948:AA194452
R-HEMBA1001718//Small inducible cytokine A5 (RANTES)//8.6e-43:166:88//Hs.155464:AF088219
R-HEMBA1001723//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisiae]//7.1e-88:431:96//Hs.29203:AI344105
R-HEMBA1001731//EST//0.25:100:68//Hs.149171:AI245712

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R-HEMBA1001734//Human mRNA for KIAA0355 gene, complete cds//2.6e-39:366:77//Hs.153014:AB002353
R-HEMBA1001744
R-HEMBA1001745//ESTs//6.6e-05:244:62//Hs.157663:AI358623
R-HEMBA1001746//EST//4.9e-65:409:88//Hs.124673:AA858162
R-HEMBA1001761//ESTs//1.9e-44:315:84//Hs.159510:AA297145
R-HEMBA1001781//ESTs//3.0e-98:462:99//Hs.60059:AI057306
R-HEMBA1001784//EST//1.0e-12:250:68//Hs.152366:AA486721
R-HEMBA1001791//EST//1.4e-47:292:89//Hs.163333:AA879053
R-HEMBA1001800//ESTs//8.4e-37:314:79//Hs.105151:AA970243
R-HEMBA1001803//ESTs//4.5e-99:465:99//Hs.135159:AI095823
R-nnnnnnnnnnnn//Zinc finger protein 148 (pHZ-52)//0.78:232:57//Hs.112180:AF039019
R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//9.0e-114:548:98//Hs.118164:AB007969
R-HEMBA1001809//EST//3.8e-63:292:89//Hs.158591:AI369334
R-HEMBA1001815//Calcium modulating ligand//1.1e-47:299:87//Hs.13572:AF068179
R-HEMBA1001819//ZINC FINGER PROTEIN HF.12//1.2e-16:259:69//Hs.155470:X07290
R-HEMBA1001820//ESTs//2.6e-86:404:100//Hs.112881:AA620707
R-nnnnnnnnnnnn//ESTs//2.2e-101:480:99//Hs.159940:AA971578
R-HEMBA1001824//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//6.2e-27:147:97//Hs.23476:AA401210
R-HEMBA1001835//EST//0.79:216:64//Hs.47437:N52250
R-HEMBA1001844//ESTs//4.7e-62:319:95//Hs.55200:N98513
R-HEMBA1001847//ESTs//2.3e-102:522:95//Hs.20879:AA845446
R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//1.1e-109:553:96//Hs.78946:AB014517
R-HEMBA1001864//ESTs//7.4e-94:449:99//Hs.132776:AI142853
R-HEMBA1001866//Myelin oligodendrocyte glycoprotein {alternative products}//1.9e-37:357:76//Hs.53217:Z48051
R-nnnnnnnnnnnn//ESTs, Weakly similar to trithorax homolog HTX, version 2 [H.sapiens]//2.3e-32:193:94//Hs.9489:R84329
R-HEMBA1001888//H.sapiens mRNA for urea transporter//2.0e-47:425:78//Hs.66710:X96969
R-HEMBA1001896//ESTs//3.5e-56:274:99//Hs.129018:H03128
R-HEMBA1001910
R-HEMBA1001912//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.5e-73:347:100//Hs.30991:AA994438
R-HEMBA1001913//ESTs, Highly similar to GCN20 PROTEIN [Saccharomyces cerevisiae]//5.1e-57:320:91//Hs.91251:U66685
R-HEMBA1001915//ESTs//4.9e-88:459:95//Hs.122810:AI273706
R-HEMBA1001918//ESTs//1.2e-106:505:99//Hs.98518:AI027125
R-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//5.5e-107:534:96//Hs.154934:AF000145
R-HEMBA1001939//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.9e-99:482:98//Hs.96849:AA879470
R-HEMBA1001940//Human mRNA for KIAA0392 gene, partial cds//5.6e-45:336:82//Hs.40100:AB002390
R-HEMBA1001942//EST//2.6e-84:397:99//Hs.145444:AI203668
R-HEMBA1001945//ESTs//1.4e-92:437:99//Hs.144565:AI192452
R-HEMBA1001950//ESTs//3.9e-43:280:88//Hs.84429:N28866
R-HEMBA1001960//ESTs//0.040:243:62//Hs.29567:AA640421
R-HEMBA1001962//ESTs//0.0071:113:69//Hs.49792:N70048
R-HEMBA1001964//ESTs//3.0e-38:239:87//Hs.158126:W26825
R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs//1.8e-106:517:97//Hs.11050:AL031178
R-HEMBA1001979//EST//0.039:167:63//Hs.129451:AA993932
R-HEMBA1001987//ESTs//3.1e-44:320:83//Hs.136839:H93717
R-HEMBA1001991//Human mRNA for KIAA0355 gene, complete cds//9.5e-47:303:88//Hs.153014:AB002353
R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase 2C (beta)//1.6e-91:448:97//Hs.5687:AJ005801
R-HEMBA1002008//ESTs//9.2e-47:297:87//Hs.142314:AA347930
R-HEMBA1002018//ESTs//9.4e-21:118:97//Hs.7871:AI041837

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R-HEMBA1002022//Human mRNA for KIAA0075 gene, partial cds//0.25:196:63//Hs.1189:D38550
R-HEMBA1002035//ESTs//7.7e-101:475:99//Hs.8858:AI131538
R-HEMBA1002039//H.sapiens mRNA for phosphoinositide 3-kinase//0.68:256:64//Hs.101238:Y11312
R-HEMBA1002049//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.4e-51:254:85//Hs.15731:AB011135
R-HEMBA1002084//EST//0.31:219:60//Hs.162396:AA572764
R-HEMBA1002092//EST//6.4e-72:342:99//Hs.148533:AI200996
R-HEMBA1002100//EST//5.6e-38:258:85//Hs.103094:W52354
R-HEMBA1002102//Thiopurine S-methyltransferase//1.4e-46:403:79//Hs.51124:AF019369
R-HEMBA1002113//Prostaglandin 12 (prostacyclin) synthase //1.4e-76:280:90//Hs.61333:D83402
R-HEMBA1002119//Homo sapiens OR7E12P pseudogene, complete sequence//1.4e-87:362:94//Hs.103443:AF065854
R-HEMBA1002125//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.7e-16:94:100//Hs.107747:AI357868
R-HEMBA1002139//H.sapiens mRNA for nebulin//0.0019:68:88//Hs.83870:X83957
R-HEMBA1002144//ESTs//3.1e-30:259:72//Hs.141575:AA211734
R-HEMBA1002150//ESTs//7.1e-105:543:95//Hs.32275:AA595199
R-HEMBA1002151//ESTs//2.2e-35:178:100//Hs.77703:W19642
R-HEMBA1002153//EST//4.5e-49:458:77//Hs.141708:W44337
R-HEMBA1002160//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds//1.4e-36:400:75//Hs.75474:AF023674
R-HEMBA1002161//Homo sapiens EVI5 homolog mRNA, complete cds//1.9e-33:294:77//Hs.26929:AF008915
R-HEMBA1002162//ESTs//1.0e-47:317:85//Hs.48919:N64043
R-HEMBA1002166//Thromboxane A2 receptor//6.8e-46:296:81//Hs.89887:D38081
R-HEMBA1002177//EST//2.6e-42:215:99//Hs.116880:AA662457
R-HEMBA1002185//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//6.0e-42:419:73//Hs.159523:AF001622
R-HEMBA1002189//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.4e-29:244:72//Hs.119387:AB007958
R-HEMBA1002191//ESTs//2.6e-31:275:66//Hs.133852:AI076357
R-HEMBA1002199//Human Line-1 repeat mRNA with 2 open reading frames//4.3e-84:557:84//Hs.23094:M19503
R-HEMBA1002204//EST//0.00057:113:71//Hs.144868:AI202342
R-HEMBA1002212//ESTs//1.5e-48:277:93//Hs.104741:AI393315
R-HEMBA1002215//ESTs//1.1e-23:158:90//Hs.152529:AA897151
R-HEMBA1002226//Homo sapiens mRNA for KIAA0706 protein, complete cds//5.1e-21:230:75//Hs.139648:AB014606
R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//1.5e-47:238:98//Hs.25664:AF089814
R-HEMBA1002237//ESTs//6.9e-35:357:76//Hs.116518:AA653202
R-HEMBA1002253//EST//6.0e-19:125:81//Hs.140596:AA829426
R-HEMBA1002257
R-HEMBA1002267//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.3e-31:201:91//Hs.114673:W72675
R-HEMBA1002270//ESTs//4.6e-100:483:97//Hs.34940:AI264314
R-HEMBA1002321//ESTs//2.3e-85:403:99//Hs.120388:AA723595
R-HEMBA1002328//ESTs//1.3e-90:423:100//Hs.117936:AI280818
R-HEMBA1002337//ESTs//8.7e-24:147:93//Hs.9893:AA007679
R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8e-130:642:96//Hs.6162:AB018314
R-HEMBA1002348//ESTs//5.0e-71:387:93//Hs.30494:H04822
R-HEMBA1002349//ESTs//9.7e-88:420:98//Hs.132972:AA543094
R-nnnnnnnnnnnn//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//3.9e-123:661:93//Hs.119023:AF092563
R-HEMBA1002381//ESTs//1.3e-73:352:99//Hs.56121:AA781435
R-HEMBA1002389//EST//2.3e-05:132:69//Hs.37558:H58237
R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//3.9e-63:358:91//Hs.25527:AC005954
R-HEMBA1002419//ESTs, Weakly similar to APK1 antigen [H.sapiens]//5.6e-87:429:96//Hs.13209:AI417849
R-HEMBA1002430//ESTs//0.10:388:57//Hs.119238AA476267
R-HEMBA1002439//Human mRNA for KIAA0080 gene, partial cds//2.0e-22:181:80//Hs.74554:D38522

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R-HEMBA1002458//ESTs//1.8e-88:448:95//Hs.97914:AA769069
R-HEMBA1002460//Catalase//0.67:314:60//Hs.76359:X04085
R-HEMBA1002462//EST//0.032:44:88//Hs.161536:N80395
R-nnnnnnnnnnnn//ESTs, Weakly similar to F08G12.1 [C.elegans]//5.4e-95:488:95//Hs.108115:AA582193
R-HEMBA1002477//Homo sapiens KIAA0395 mRNA, partial cds//2.5e-37:281:80//Hs.43681:AL022394
R-HEMBA-1002486//Small inducible cytokine A5 (RANTES)//1.1e-49:311:88//Hs.155464:AF088219
R-HEMBA1002495//ESTs//1.2e-94:457:98//Hs.42140:AI188995
R-HEMBA1002498//ESTs//1.7e-35:240:78//Hs.119871:AA705133
R-HEMBA1002503//ESTs//2.3e-14:64:85//Hs.140190:AA701449
R-HEMBA1002508//ESTs//0.00057:160:62//Hs.149661:AA872990
R-nnnnnnnnnnnn//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//2.3e-113:456:92//Hs.6764:AJ011972
R-HEMBA1002515//EST//1.0:153:63//Hs.118045:N51715
R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds//5.1e-106:564:93//Hs.129928:AB007923
R-HEMBA1002542//ESTs//1.0e-101:539:93//Hs.93872:AA524700
R-HEMBA1002547//EST//8.7e-27:151:96//Hs.132145:AI041804
R-HEMBA1002552//EST//5.9e-49:335:85//Hs.149580:AI281881
R-HEMBA1002555//ESTs//1.1e-77:461:91//Hs.38750:N30012
R-HEMBA1002558//Homo sapiens 4F5S mRNA, complete cds//1.3e-42:264:89//Hs.32567:AF073519
R-HEMBA1002561//Small inducible cytokine A5 (RANTES)//6.4e-40:196:78//Hs.155464:AF088219
R-nnnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds//1.4e-120:587:97//Hs.151411:AF075587
R-HEMBA1002583//ESTs//7.1e-79:410:95//Hs.21599:AA478904
R-HEMBA1002590//EST//3.3e-54:278:97//Hs.138637:N20838
R-HEMBA1002592//ESTs//2.6e-44:500:74//Hs.110934:N26055
R-HEMBA1002621
R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//2.2e-77:380:97//Hs.91338:AB018351
R-HEMBA1002628//ESTs//0.0020:167:66//Hs.140605:AA830881
R-HEMBA1002629//ESTs//0.00014:50:100//Hs.119132:AA398715
R-HEMBA1002645//EST//2.1e-37:285:82//Hs.141728:W73041
R-HEMBA1002651//EST//2.2e-23:374:69//Hs.139357:AA420970
R-HEMBA1002659//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.5e-53:406:81//Hs.108966:U48696
R-HEMBA1002661//Homo sapiens mRNA for KIAA0764 protein, complete cds//1.1e-41:296:84//Hs.6232:AB018307
R-HEMBA1002666//EST//4.4e-09:79:88//Hs.72015:AA151945
R-HEMBA1002678//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//7.6e-104:560:92//Hs.161748:T64896
R-nnnnnnnnnnnn//EST//0.15:136:69//Hs.129570:AA995396
R-HEMBA1002688//T-CELL SURFACE PROTEIN TACTILE PRECURSOR//0.16:247:62//Hs.142023:M88282
R-HEMBA1002696//ESTs//3.5e-94:529:92//Hs.16725:AA196477
R-HEMBA1002712//Homo sapiens mRNA for KIAA0772 protein, complete cds//6.0e-46:302:86//Hs.15519:AB018315
R-HEMBA1002716//ESTs//1.3e-109:555:96//Hs.9812:AA147884
R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.8e-37:287:81//Hs.132942:AB014521
R-HEMBA1002730//ESTs//1.2e-95:488:95//Hs.22030:AA521168
R-HEMBA1002742//ESTs//1.0e-91:437:99//Hs.139987:AA652163
R-HEMBA1002746//ESTs//4.4e-97:468:98//Hs.129903:AA576526
R-HEMBA1002748//ESTs//5.0e-98:475:98//Hs.125461:AI375792
R-HEMBA1002750//ESTs//1.6e-42:223:97//Hs.40460:N36090
R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//4.0e-106:545:95//Hs.74750:AB011126
R-HEMBA1002770//EST//0.34:294:59//Hs.43091:N22127
R-HEMBA1002777//ESTs//3.0e-85:316:98//Hs.17537:C06491
R-HEMBA1002779//Human mRNA for KIAA0013 gene, complete cds//0.25:342:58//Hs.48824:D87717

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R-HEMBA1002780//Homo sapiens DEC-205 mRNA, complete cds//4.2e-46:449:75//Hs.153563:AF011333
R-HEMBA1002794//ESTs//1.2e-115:559:97//Hs.79741:AI279709
R-HEMBA1002801//EST//0.00049:287:60//Hs.126466:AA913320
R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//1.4e-116:559:97//Hs.28307:AF071185
R-HEMBA1002816//Human plectin (PLEC1) mRNA, complete cds//0.28:281:62//Hs.79706:U53204
R-HEMBA1002826//EST//6.7e-25:134:99//Hs.134683:AI092013
R-HEMBA1002833//ESTs, Highly similar to ribosome-binding protein p34 [R.norvegicus]//4.3e-25:137:98//Hs.5337:AA243757
R-HEMBA1002850//ESTs//0.010:323:57//Hs.18282:W67514
R-HEMBA1002863//ESTs//1.1e-67:359:94//Hs.124699:W27830
R-HEMBA1002876//ESTs//0.72:202:62//Hs.144816:AI220827
R-HEMBA1002886//EST//3.2e-85:401:99//Hs.96580:AA405670
R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds//1.2e-107:541:95//Hs.33787:AF037261
R-HEMBA1002921//Human mRNA for KIAA0189 gene, complete cds//0.84:103:71//Hs.95140:D80011
R-HEMBA1002924//ESTs//3.5e-86:423:98//Hs.27513:N34820
R-HEMBA1002934//Human mRNA for KIAA0118 gene, partial cds//2.1e-50:308:88//Hs.154326:D42087
R-HEMBA1002935//ESTs//1.0e-73:384:95//Hs.118193:N74481
R-HEMBA1002937//ESTs//0.052:167:65//Hs.145504:AI254165
R-HEMBA1002939//ESTs//1.6e-94:467:97//Hs.9893:AA007679
R-HEMBA1002944//ESTs//2.7e-17:176:80//Hs.143768:AA229732
R-HEMBA1002951//ESTs//3.7e-119:565:98//Hs.16218:AI190892
R-HEMBA1002954//EST//0.076:285:58//Hs.98706:AA431085
R-HEMBA1002968//Thiopurine S-methyltransferase//1.9e-46:314:85//Hs.51124:AF019369
R-HEMBA1002970//EST//0.00050:164:64//Hs.129630:AI000405
R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.3e-30:162:99//Hs.5734:AB014579
R-HEMBA1002973//Small inducible cytokine A5 (RANTES)//5.7e-42:318:81//Hs.155464:AF088219
R-nnnnnnnnnnnn//ESTs//3.2e-18:102:100//Hs.146255:AA197064
R-HEMBA1002999//ESTs, Moderately similar to lamina associated polypeptide 1C [R.norvegicus]//7.9e-113:560:96//Hs.125749:AI377682
R-HEMBA1003021//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.3e-42:290:85//Hs. 113283:AF018080
R-HEMBA1003033//ESTs//2.8e-77:417:94//Hs.138860:W47480
R-HEMBA1003034//ESTs//3.7e-42:429:74//Hs.132818:AI038577
R-HEMBA1003035//ESTs//0.025:156:64//Hs.8473:T40827
R-HEMBA1003037//ESTs//0.69:381:57//Hs.47312:AI240366
R-HEMBA1003041//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//5.6e-34:280:79//Hs.114905:AA088442
R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds//1.3e-119:578:97//Hs.44097:AF054182
R-HEMBA1003064//ESTs//7.8e-85:419:96//Hs.87020:AA706627
R-HEMBA1003067//Von Hippel-Lindau syndrome//2.0e-30:299:75//Hs.78160:AF010238
R-HEMBA1003071//ESTs//2.3e-74:360:98//Hs.17270:AA701903
R-HEMBA1003077//ESTs, Weakly similar to KIAA0405 [H.sapiens]//1.1e-90:434:99//Hs.14146:W92235
R-HEMBA1003078//ESTs//5.9e-16:156:77//Hs.142684:AA902402
R-HEMBA1003079//ESTs//0.16:341:58//Hs.95923:AI075249
R-HEMBA1003083//Small inducible cytokine A5 (RANTES)//1.9e-39:284:83//Hs.155464:AF088219
R-HEMBA1003086//EST//1.0e-48:372:82//Hs.161917:AA483223
R-HEMBA1003096//ESTs, Weakly similar to Mouse 19.5 mRNA, complete cds [M.musculus]//4.2e-100:531:94//Hs.104800:AA709155
R-HEMBA1003098//ESTs//4.2e-107:537:96//Hs.107213:AA121624
R-HEMBA1003117//ESTs//2.4e-67:331:97//Hs.157158:AI150058
R-HEMBA1003129//Human nucleolar fibrillar center protein (ASE-1) mRNA, complete cds//2.1e-13:109:88//Hs.118717:U86751
R-HEMBA1003133//ESTs//1.1e-34:180:98//Hs.159387:AI370845
R-HEMBA1003136//ESTs, Weakly similar to MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE [Saccharomyces cerevisiae]//9.2e-114:577:95//Hs.27059:AI088615
R-HEMBA1003142//Small inducible cytokine A5 (RANTES)//1.1e-45:285:88//Hs.155464:AF088219

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R-HEMBA1003148//Homo sapiens mRNA for dachshund protein//3.6e-118:586:96//Hs.63931:AJ005670
R-HEMBA1003166//ESTs//1.6e-96:479:96//Hs.119940:AA705933
R-HEMBA1003175//ESTs//2.7e-74:407:92//Hs.139167:AA715389
R-HEMBA1003197//ESTs//1.6e-68:384:94//Hs.120969:W92000
R-HEMBA1003199//Sjogren syndrome antigen B (autoantigen La)//0.19:328:57//Hs.83715:X69804
R-HEMBA1003202//Homo sapiens mRNA for KIAA0640 protein, partial cds//1.3e-40:290:83//Hs.153026:AB014540
R-HEMBA1003204//ESTs//1.1e-34:215:91//Hs.108090:AA424943
R-HEMBA1003212//ESTs//1.9e-81:441:93//Hs.28471:W20265
R-HEMBA1003220//ESTs, Weakly similar to MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S28 PRECURSOR [S.cerevisiae]//1.6e-40:232:93//Hs.107707:N32817
R-HEMBA10032227/ESTs, Weakly similar to weak similarity to HSP90 [C.elegans]//1.1e-42:310:85//Hs.23294:W27666
R-HEMBA1003229//ESTs//4.8e-18:133:90//Hs.61763:AA035305
R-HEMBA1003235//ESTs//7.7e-35:201:78//Hs.163979:AA828834
R-HEMBA1003250//Homo sapiens p21-activated kinase 3 (PAK3) mRNA, complete cds//7.4e-05:534:58//Hs.152663:AF068864
R-HEMBA1003257//EST//1.4e-95:473:97//Hs.32443:H28929
R-HEMBA1003273//Small inducible cytokine A5 (RANTES)//2.6e-38:253:86//Hs.155464:AF088219
R-HEMBA1003276//ESTs//7.6e-55:269:99//Hs.23817:AA526392
R-HEMBA1003278//ESTs//2.6e-45:301:71//Hs.51652:AI084785
R-HEMBA1003281
R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//9.7e-117:551:99//Hs.12836:AB011109
R-HEMBA1003296//ESTs//4.8e-17:210:72//Hs.44451:AA203266
R-HEMBA1003304//ESTs//2.8e-98:468:98//Hs.120849:AI148353
R-HEMBA1003309//ESTs//1.8e-97:455:99//Hs.11571:AA713504
R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//8.9e-113:545:97//Hs.124224:AB001872
R-HEMBA1003322//ESTs//4.9e-79:419:95//Hs.138760:N66869
R-HEMBA1003327//Homo sapiens clone 23622 mRNA sequence//1.4e-16:177:78//Hs.151608:AF052119
R-HEMBA1003328//H.sapiens mRNA for MACH-alpha-2 protein//2.1e-43:269:88//Hs.19949:X98173
R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds//0.66:64:76//Hs.117176:AF026029
R-HEMBA1003348//ESTs//1.4e-35:185:78//Hs.117879:H77357
R-HEMBA1003369//ESTs, Weakly similar to F59C6.9 [C.elegans]//3.2e-113:553:97//Hs.65539:AI148540
R-HEMBA1003370//ESTs//2.0e-46:319:86//Hs.37573:H59651
R-HEMBA1003373//ESTs//1.6e-31:136:81//Hs.114849:AI139588
R-HEMBA1003376//ESTs//3.0e-47:383:80//Hs.138852:AA284247
R-HEMBA1003380//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.8e-11:261:65//Hs.87578:AI125363
R-HEMBA1003384//EST//0.00013:82:75//Hs.141237:H57847
R-HEMBA1003395//ESTs//5.2e-78:379:98//Hs.162208:AA536127
R-HEMBA1003402//ESTs//8.6e-14:108:89//Hs.55424:AA774204
R-nnnnnnnnnnnn//ESTs//1.7e-24:188:85//Hs.70266:Z78309
R-HEMBA1003417//ESTs//4.2e-74:396:94//Hs.55220:D11563
R-HEMBA1003418//ESTs//3.1e-107:545:95//Hs.3494:AI421013
R-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//3.2e-115:544:98//Hs.25812:AF058696
R-HEMBA1003461//ESTs//2.8e-62:304:99//Hs.148747:AI225121
R-HEMBA1003463//ESTs//2.3e-112:549:97//Hs.104627:AA885516
R-HEMBA1003480//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.7e-76:529:84//Hs.113283:AF018080
R-HEMBA1003528//ESTs//2.1e-59:312:96//Hs.22505:R41688
R-HEMBA1003531//ESTs//2.2e-17:116:93//Hs.140217:AA702760
R-HEMBA1003538//Complement component C1r//4.7e-25:333:68//Hs.1279:M14058
R-HEMBA1003545//ESTs//8.7e-89:432:98//Hs.99497:AA776817
R-HEMBA1003548//EST//0.0091:274:60//Hs.148336:AA911673
R-HEMBA1003555//ESTs, Weakly similar to NUCLEOTIDE-BINDING PROTEIN [H.sapiens]//2.8e-93:495:93//Hs.91619:AA552351

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R-HEMBA1003556//ESTs//7.1e-44:406:77//Hs.141575:AA211734
R-HEMBA1003560//ESTs//4.0e-34:182:97//Hs.14811:AA434522
R-HEMBA1003568//ESTs//2.0e-101:486:98//Hs.118570:AI342058
R-HEMBA1003569//ESTs, Moderately similar to metastasis-associated gene [H.sapiens]//4.0e-63:343:93//Hs.58598:AA625440
R-HEMBA1003571//Homo sapiens clone 23632 mRNA sequence//3.7e-47:338:84//Hs.46918:AF052099
R-HEMBA1003579//EST//0.00057:239:60//Hs.162828:AA643892
R-HEMBA1003581//ESTs//2.6e-10:118:79//Hs.44856:N37065
R-HEMBA1003591//ESTs//2.4e-96:460:98//Hs.128741:AI244212
R-HEMBA1003595//Human mRNA for KIAA0118 gene, partial cds//1.7e-48:421:78//Hs.154326:D42087
R-HEMBA1003597//EST//1.6e-38:313:80//Hs.160911:AI371042
R-HEMBA1003598//ESTs//0.0085:273:61//Hs.145333:AI251374
R-HEMBA1003615
R-HEMBA1003617//ESTs//1.0e-111:574:95//Hs.4552:W68167
R-HEMBA1003621//EST//1.7e-31:288:78//Hs.140909:R49387
R-HEMBA1003622//EST//1.1e-46:468:75//Hs.139093:AA166888
R-HEMBA1003630//ESTs//1.4e-21:411:69//Hs.128729:AA973021
R-HEMBA1003637//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]//9.3e-24:189:84//Hs.142208:AA209438
R-HEMBA1003640//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.5e-42:332:81//Hs.51048:X68830
R-HEMBA1003645//ESTs//2.4e-77:423:94//Hs.99539:R59010
R-HEMBA1003646//ESTs//2.6e-98:549:91//Hs.96427:AA151783
R-HEMBA1003656//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//5.6e-44:245:77//Hs.67619:AB007957
R-HEMBA1003662//Human TBX2 (TXB2) mRNA, complete cds//2.6e-17:144:84//Hs.32931:U28049
R-HEMBA1003667//Farnesyltransferase, CAAX box, beta//1.3e-22:170:88//Hs.117596:L00635
R-HEMBA1003679//ESTs, Weakly similar to trithorax homolog HTX, version 2 [H.sapiens]//4.1e-87:434:97//Hs.9489:R84329
R-HEMBA1003680//Human DNA-binding protein (HRC1) mRNA, complete cds//0.86:315:61//Hs.72925:M91083
R-HEMBA1003684//ESTs, Highly similar to ZINC FINGER PROTEIN 7 [Homo sapiens]//1.1e-101:528:95//Hs.22934:AA581379
R-HEMBA1003690//ESTs//0.0021:119:69//Hs.98641:AA429916
R-HEMBA1003692//Human cytochrome P450-IIB (hIIB3) mRNA, complete cds//2.0e-43:360:80//Hs.110194:M29873
R-HEMBA1003711//ESTs//1.0e-70:375:94//Hs.150407:AI279064
R-HEMBA1003714//VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR//0.94:367:62//Hs.1139:X77777
R-HEMBA1003715//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.1e-77:299:85//Hs.113283:AF018080
R-HEMBA1003720//Homo sapiens TWIK-related acid-sensitive K+ channel (TASK) mRNA, complete cds//1.2e-33:377:74//Hs.24040:AF006823
R-HEMBA1003725//ESTs//3.8e-103:481:99//Hs.122518:AA778847
R-HEMBA1003729//ESTs//2.5e-51:277:95//Hs.26270:AA258839
R-HEMBA1003733//ESTs//1.9e-69:350:96//Hs.139278:AA702592
R-HEMBA1003742//ESTs, Moderately similar to T13H5.2 [C.elegans]//4.6e-70:348:96//Hs.11282:AI147040
R-HEMBA1003758//ESTs//1.7e-52:306:85//Hs.138852:AA284247
R-HEMBA1003760//ESTs//7.4e-76:420:93//Hs.26501:H05089
R-HEMBA1003773//ESTs, Highly similar to SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT [Mus musculus]//1.9e-77:364:100//Hs.12152:AA156214
R-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]//2.1e-101:558:93//Hs.18171:AA524327
R-HEMBA1003784//EST//0.83:127:62//Hs.144002:F01600
R-HEMBA1003799//EST//9.7e-30:362:71//Hs.156577:AA860236
R-HEMBA1003803//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//2.8e-16:93:100//Hs.107747:AI357868
R-HEMBA1003804//Interleukin 15//0.13:227:62//Hs.111867:AB007295
R-HEMBA1003805//ESTs//0.029:199:65//Hs.91582:T25344
R-HEMBA1003807//EST//2.4e-13:137:81//Hs.145645:AI264163
R-HEMBA1003836//Small inducible cytokine A5 (RANTES)//3.2e-39:284:83//Hs.155464:AF088219
R-HEMBA1003838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 [Paramecium tetraurelia)//6.5e-71:357:96//Hs.107573:AA524333

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R-HEMBA1003856//ESTs//8.2e-20:266:71//Hs.48312:N68161
R-HEMBA1003864//ESTs//1.6e-99:528:93//Hs.26890:AA449033
R-HEMBA1003866//POLYPOSIS LOCUS PROTEIN 1//0.30:146:64//Hs.74648:M73547
R-HEMBA1003879//EST, Weakly similar to DNA-REPAIR PROTEIN COMPLEMENTING XP-A CELLS [Homo sapiens]//2.1e-59:295:98//Hs.161661:AA166911
R-HEMBA1003880//Homo sapiens clone 24760 mRNA sequence//3.8e-34:286:79//Hs.61408:AF070621
R-HEMBA1003885//ESTs//4.6e-50:293:90//Hs.142314:AA347930
R-HEMBA1003893//Calcium modulating ligand//2.1e-43:294:86//Hs.13572:AF068179
R-HEMBA1003902//ESTs//1.8e-43:300:85//Hs.146811:AA410788
R-HEMBA1003908//ESTs//3.5e-91:477:94//Hs.6638:AA536187
R-HEMBA1003926//ESTs//7.9e-44:294:87//Hs.164036:AA845659
R-HEMBA1003937//Homo sapiens mRNA for KIAA0585 protein, partial cds//3.5e-48:276:81//Hs.72660:AB011157
R-HEMBA1003939
R-HEMBA1003942//ESTs//1.6e-81:428:94//Hs.50418:AA524669
R-HEMBA1003950//ESTs//8.1e-54:283:95//Hs.145528:AI261545
R-HEMBA1003953//ESTs//3.8e-30:194:89//Hs.99681:AA504591
R-HEMBA1003958//ESTs//4.0e-45:394:77//Hs.141602:N63562
R-HEMBA1003959//ESTs//5.2e-28:197:86//Hs.9951:W56253
R-HEMBA1003976//ESTs//2.0e-29:232:84//Hs.133947:AI074525
R-HEMBA1003978//ESTs//3.2e-115:549:98//Hs.76798:AI050882
R-HEMBA1003985//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-91:448:97//Hs.117834:AA766771
R-HEMBA1003987//ESTs//8.1e-36:193:88//Hs.151844:N92756
R-HEMBA1003989//Human mRNA for KIAA0241 gene, partial cds//3.6e-43:360:81//Hs.150275:D87682
R-HEMBA1004000//EST//5.5e-62:308:97//Hs.50438:N74105
R-HEMBA1004011//ESTs//8.6e-85:431:96//Hs.36185:R99899
R-HEMBA1004012//ESTs//1.3e-40:309:83//Hs.140329:AA714011
R-HEMBA1004015//ESTs//5.1e-97:453:99//Hs.111446:AI333774
R-HEMBA1004024//ESTs//5.2e-19:159:79//Hs.138856:H47461
R-HEMBA1004038//ESTs//1.3e-41:346:79//Hs.146173:AA906191
R-HEMBA1004042//ESTs//0.0012:201:69//Hs.24248:AA528253
R-HEMBA1004045//ESTs, Weakly similar to putative p150 [H.sapiens]//1.5e-22:365:70//Hs.99692:AA811804
R-HEMBA1004048//ESTs//9.5e-104:497:98//Hs.77735:AI125469
R-HEMBA1004049//HEAT SHOCK 70 KD PROTEIN 1//6.3e-31:176:96//Hs.8997:M11717
R-HEMBA1004055//ESTs//1.7e-115:577:96//Hs.59503:W63754
R-HEMBA1004056//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.2e-78:577:82//Hs.113283:AF018080
R-HEMBA1004074//EST//1.0:152:61//Hs.149093:AI243988
R-HEMBA1004086//ESTs//4.0e-53:266:98//Hs.34658:N98652
R-HEMBA1004097//ESTs//4.4e-46:279:91//Hs.110533:H16251
R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds//3.0e-43:534:69//Hs.90998:D50918
R-HEMBA1004132//ESTs//4.6e-47:316:86//Hs.141602:N63562
R-HEMBA1004133
R-HEMBA1004138//EST//1.7e-08:211:64//Hs.129189:AA988736
R-HEMBA1004143//ESTs//4.0e-25:137:97//Hs.21307:AA203320
R-HEMBA1004146//Small inducible cytokine A5 (RANTES)//4.1e-27:191:86//Hs.155464:AF088219
R-HEMBA1004150//GRANCALCIN//0.99:357:59//Hs.79381:M81637
R-HEMBA1004164//Human mRNA for KIAA0118 gene, partial cds//9.5e-47:313:84//Hs.154326:D42087
R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//7.7e-112:563:96//Hs.59988:AF067855
R-HEMBA1004199
R-HEMBA1004200//EST//3.1e-89:441:97//Hs.141173:R97701
R-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays]//1.7e-107:552:94//Hs.10092:AI189282
R-HEMBA1004203//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.5e-96:275:98//Hs.15832:AB014518
R-HEMBA1004207//Leptin receptor//1.1e-117:573:97//Hs.54515:U50748
R-HEMBA1004225//EST//9.7e-34:186:95//Hs.137567:R20617
R-HEMBA1004227//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//4.0e-16:117:91//Hs.92033:AA255832

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R-HEMBA1004238//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:338:83//Hs.153014:AB002353
R-HEMBA1004241//ESTs//1.3e-10:93:87//Hs.137511:AA456389
R-HEMBA1004246//Homo sapiens LIM protein mRNA, complete cds//2.7e-43:511:72//Hs.154103:AF061258
R-HEMBA1004248//ESTs, Highly similar to INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 [Rattus norvegicus]//2.1e-61:221:86//Hs.7089:W37284
R-HEMBA1004264//ESTs//1.5e-80:425:95//Hs.107206:AA234962
R-HEMBA1004267//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//1.4e-89:465:95//Hs.113660:D20018
R-HEMBA1004272//ESTs//4.5e-111:577:94//Hs.115696:N57931
R-nnnnnnnnnnnn//Homo sapiens clone 617 unknown mRNA, complete sequence//1.4e-111:553:96//Hs.93677:AF091081
R-HEMBA1004276//ESTs, Highly similar to BETA-ADAPTIN [Homo sapiens; Rattus norvegicus; Bos taurus]//4.4e-92:559:89//Hs.28298:AA203228
R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds//6.2e-108:538:97//Hs.101766:AF022795
R-HEMBA1004289//Sulfotransferase, dehydroepiandrosterone (DHEA) -preferring//1.7e-34:223:75//Hs.81884:U13061
R-HEMBA1004295//ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-orf7 protein [C.elegans]//3.6e-93:496:94//Hs.14337:AA534961
R-HEMBA1004306//ESTs//3.4e-26:363:68//Hs.70279:AA757426
R-HEMBA1004312//ESTs//4.8e-64:351:94//Hs.138611:H82679
R-HEMBA1004321//Zinc finger protein 44 (KOX 7)//2.6e-37:415:64//Hs.51199:X16281
R-HEMBA1004323//ESTs//2.1e-40:280:70//Hs.153300:AA928904
R-HEMBA1004327//ESTs//3.8e-72:343:99//Hs.151708:AA554714
R-HEMBA1004330//ESTs//4.0e-52:270:97//Hs.24654:AA456561
R-HEMBA1004334//ESTs//1.6e-46:234:98//Hs.47159:AI310231
R-HEMBA1004335//ESTs//1.9e-25:250:76//Hs.155880:AA703336
R-HEMBA1004341//ESTs//3.7e-101:480:98//Hs.69321:AA633240
R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds//1.3e-75:444:90//Hs.80686:D89667
R-HEMBA1004354//Human mRNA for KIAA0355 gene, complete cds//5.9e-39:286:83//Hs.153014:AB002353
R-HEMBA1004356//SINGLE-STRANDED DNA-BINDING PROTEIN MSSP-1//1.3e-107:576:93//Hs.55458:X77494
R-HEMBA1004366//ESTs//2.3e-94:524:91//Hs.111496:AA652869
R-HEMBA1004372//EST//0.27:198:60//Hs.162665:AA605057
R-HEMBA1004389//ESTs//4.1e-102:490:98//Hs.153708:AA687264
R-HEMBA1004394//ESTs//1.5e-94:471:96//Hs.151647:AA002084
R-HEMBA1004396//Small inducible cytokine A5 (RANTES)//6.2e-41:285:83//Hs.155464:AF088219
R-HEMBA1004405//ESTs//2.0e-44:329:83//Hs.136839:H93717
R-HEMBA1004408//ESTs, Weakly similar to homologous to mouse Rsu-1 [H.sapiens]//6.1e-89:420:99//Hs.88365:AA648933
R-HEMBA1004429//ESTs, Weakly similar to homeotic protein protein zhx-1 [M.musculus]//3.0e-112:552:96//Hs.12940:AI123518
R-HEMBA1004433//Human Line-1 repeat mRNA with 2 open reading frames//2.9e-32:463:68//Hs.23094:M19503
R-HEMBA1004460//ESTs//2.0e-104:574:93//Hs.46848:AA195829
R-HEMBA1004461//ESTs//2.9e-102:503:98//Hs.16370:AA017033
R-HEMBA1004479//ELK1, member of ETS oncogene family//1.1e-45:310:75//Hs.116549:AL009172
R-HEMBA1004482//ESTs//9.1e-05:322:62//Hs.34489:AA759306
R-HEMBA1004502//ESTs//6.9e-112:566:96//Hs.93985:N50034
R-HEMBA1004506//EST//5.3e-59:456:80//Hs.72412:AA160941
R-HEMBA1004507
R-HEMBA1004509//ESTs, Moderately similar to HYPOTHETICAL 52.2 KD PROTEIN IN MPR1-GCN20 INTERGENIC REGION [Saccharomyces cerevisiae]//2.9e-82:262:99//Hs.12820:AA004271
R-HEMBA1004534//ESTs, Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]//1.1e-43:281:89//Hs.58414:AA196947
R-HEMBA1004538//EST//3.3e-15:270:71//Hs.136667:AA707972
R-HEMBA1004554
R-HEMBA1004560//ESTs//8.2e-25:179:88//Hs.96560:W22924

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R-HEMBA1004573//ESTs, Moderately similar to ALR [H.sapiens]//1.0:305:60//Hs.30272:AA134913
R-HEMBA1004577//ESTs//7.9e-50:319:89//Hs.22660:AA582243
R-HEMBA1004586//ESTs//2.6e-73:384:96//Hs.9582:R39769
R-nnnnnnnnnnnn//ESTs//6.0e-22:190:82//Hs.42530:N41661
R-HEMBA1004610//ESTs//1.2e-91:438:98//Hs.47823:AA780767
R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//4.6e-52:327:85//Hs.159897:AB007970
R-HEMBA1004629//ESTs//2.3e-19:215:76//Hs.111995:AI375915
R-HEMBA1004631//ESTs//3.6e-99:470:98//Hs.49303:AA810785
R-HEMBA1004632//ESTs//1.0:128:66//Hs.159182:AA831152
R-HEMBA1004637//ESTs, Highly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III [Caenorhabditis elegans]//4.8e-111:532:98//Hs.12263:AA282393
R-HEMBA1004638//ESTs//1.2e-66:341:95//Hs.122687:AI278454
R-HEMBA1004666//ESTs//2.1e-65:333:96//Hs.98873:AA625442
R-HEMBA1004669//ESTs//0.00039:116:74//Hs.138725:N76348
R-HEMBA1004670//ESTs//1.7e-16:116:89//Hs.56825:AI057560
R-HEMBA1004672//EST//6.7-e-76:315:97//Hs.20821:R19368
R-HEMBA1004693//ESTs//6.4e-68:327:99//Hs.159066:AI093252
R-HEMBA1004697//ESTs//9.3e-98:467:98//Hs.62637:AA043562
R-HEMBA1004705//EST//0.0034:271:58//Hs.112503:AA599042
R-HEMBA1004709//EST//1.3e-55:392:85//Hs.149580:AI281881
R-HEMBA1004711//Small inducible cytokine A5 (RANTES)//1.9e-47:449:76//Hs.155464:AF088219
R-HEMBA1004725//EST//1.8e-71:424:88//Hs.155712:AI309235
R-HEMBA1004730//Homo sapiens clone 23892 mRNA sequence//2.1e-44:467:73//Hs.91916:AF035317
R-HEMBA1004733//EST//0.99:84:65//Hs.161372:AI423151
R-HEMBA1004734//ESTs//1.8e-82:421:96//Hs.21275:N73275
R-HEMBA1004736//Ataxia telangiectasia mutated (includes complementation groups A, C and D)//9.5e-39:296:82//Hs.51187:U82828
R-HEMBA1004748//ESTs//1.7e-43:166:86//Hs.37573:H59651
R-HEMBA1004751//ESTs//8.0e-23:155:88//Hs.149464:AI279428
R-HEMBA1004752//Thromboxane A2 receptor//2.7e-45:281:89//Hs.89887:D38081
R-HEMBA1004753//40S RIBOSOMAL PROTEIN S20//8.3e-67:475:84//Hs.8102:L06498
R-HEMBA1004756//ESTs//2.0e-81:384:99//Hs.129545:N68679
R-HEMBA1004758//EST//2.0e-43:367:80//Hs.133006:AI049504
R-HEMBA1004763//ESTs//2.0e-108:567:94//Hs.3757:W87380
R-HEMBA1004768//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//1.4e-47:379:81//Hs.141273:H66705
R-HEMBA1004770//ESTs//0.0014:246:61//Hs.124857:AA687092
R-HEMBA1004771//ESTs//1.1e-12:323:63//Hs.124146:AA699633
R-HEMBA1004776//ESTs//2.5e-112:567:95//Hs.12680:W74476
R-HEMBA1004778//ESTs//1.4e-33:272:75//Hs.141123:AA848167
R-nnnnnnnnnnnn
R-HEMBA1004803//ESTs//1.0e-48:319:86//Hs.139231:W87732
R-HEMBA1004806
R-HEMBA1004807//ESTs//6.2e-77:362:100//Hs.140945:N47676
R-HEMBA1004816//EST//4.3e-18:246:72//Hs.150552:AI053784
R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds//5.0e-14:141:85//Hs.80510:M74002
R-HEMBA1004847
R-HEMBA1004850//ESTs//1.2e-83:395:99//Hs.30925:AA577120
R-HEMBA1004863//ESTs//7.5e-21:204:79//Hs.35036:H95267
R-HEMBA1004864
R-HEMBA1004865//EST//6.7e-18:191:75//Hs.129944:AA429362
R-HEMBA1004880//EST//4.4e-70:346:98//Hs.145094:AA452409
R-HEMBA1004889//ESTs//4.8e-117:496:97//Hs.15641:W63676
R-HEMBA1004900//ESTs//1.2e-15:283:68//Hs.157606:AI357470
R-HEMBA1004909//ESTs//7.3e-44:366:79//Hs.140329:AA714011
R-HEMBA1004918//Human mRNA for KIAA0392 gene, partial cds//4.6e-50:313:89//Hs.40100:AB002390

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R-HEMBA1004923//ESTs//0.013:162:64//Hs.143655:AI128388
R-HEMBA1004929//EST//2.3e-48:250:97//Hs.131589:AI025053
R-HEMBA1004930//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.2e-70:547:80//Hs.1361:M55053
R-HEMBA1004933//ESTs, Weakly similar to R06C7.6 [C.elegans]//5.3e-110:530:98//Hs.18029:AI422883
R-HEMBA1004934//ESTs//1.3e-103:522:96//Hs.40415:AA037215
R-HEMBA1004944//ESTs//6.0e-21:97:84//Hs.141973:N21434
R-HEMBA1004954//ESTs//7.9e-112:596:93//Hs.6226:W61007
R-HEMBA1004956//ESTs//3.1e-58:280:100//Hs.120750:AA741074
R-HEMBA1004960//ESTs//6.9e-89:476:93//Hs.163738:AA601040
R-HEMBA1004972//ESTs//3.0e-72:381:95//Hs.55014:AA934035
R-HEMBA1004973//ESTs//2.7e-91:441:98//Hs.28144:AI292065
R-HEMBA1004977//ESTs//2.0e-95:446:99//Hs.29690:AI168404
R-HEMBA1004978//Homo sapiens natual killer cell group 2-F (NKG2-F) mRNA, complete cds//0.43:187:67//Hs.129734:AJ001683
R-HEMBA1004980//Human mRNA for KIAA0331 gene, complete cds//6.4e-53:305:91//Hs.146395:AB002329
R-HEMBA1004983//ESTs//0.16:482:57//Hs.131929:AI021894
R-HEMBA1004995
R-HEMBA1005008//EST, Weakly similar to mariner transposase [H.sapiens]//6.9e-51:482:78//Hs.141601:N63520
R-HEMBA1005009//ESTs, Highly similar to ACTIN I [Naegleria fowleri]//3.8e-109:551:96//Hs.103180:AI365212
R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//2.0e-105:542:94//Hs.31921:AB014548
R-HEMBA1005029//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.4e-95:491:94//Hs.16085:AI261382
R-HEMBA1005035//Human mRNA for KIAA0033 gene, partial cds//2.3e-64:312:85//Hs.22271:D26067
R-HEMBA1005039//ESTs, Weakly similar to zinc finger protein [H.sapiens]//2.6e-48:443:78//Hs.139019:N99348
R-HEMBA1005047//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-5A [Canis familiaris]//1.2e-87:542:87//Hs.16258:AI376436
R-HEMBA1005050//ESTs//6.3e-46:311:86//Hs.159510:AA297145
R-HEMBA1005062//ESTs//1.1e-14:216:68//Hs.129935:AA994451
R-HEMBA1005066//Human clone 23574 mRNA sequence//2.2e-24:303:73//Hs.79385:U90905
R-HEMBA1005075//EST//0.65:214:62//Hs.133991:AI075789
R-HEMBA1005079//Human BENE mRNA, partial cds//1.9e-44:304:83//Hs.85889:U17077
R-HEMBA1005083//ESTs//2.8e-74:356:98//Hs.132272:AI393958
R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//1.7e-111:545:96//Hs.11170:AF080561
R-HEMBA1005113//ESTs//1.1e-101:512:95//Hs.7972:AI052739
R-HEMBA1005123//Ley I-L//3.6e-58:519:77//Hs.37062:AC005952
R-HEMBA1005133//H.sapiens mRNA for MACH-alpha-2 protein//8.3e-46:309:85//Hs.19949:X98173
R-HEMBA1005149//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//4.7e-36:394:75//Hs.67619:AB007957
R-HEMBA1005152//Homo sapiens antigen NY-CO-16 mRNA, complete cds//3.6e-32:362:77//Hs.132206:AF039694
R-HEMBA1005159//EST//7.4e-47:252:94//Hs.134930:AI093397
R-HEMBA1005185//ESTs//5.2e-48:305:89//Hs.14920:AA910914
R-HEMBA1005201//ESTs//4.7e-58:293:97//Hs.23752:C05766
R-HEMBA1005202//ESTs//1.0:169:59//Hs.153423:AI198239
R-HEMBA1005219//Homo sapiens putative tumor suppressor protein (123F2) mRNA, complete cds//0.84:191:61//Hs.26931:AF061836
R-HEMBA1005223//ESTs//0.75:90:70//Hs.127446:AA167284
R-HEMBA1005232//EST//0.056:162:67//Hs.65649:F13687
R-HEMBA1005241//ESTs//3.6e-113:564:96//Hs.12770:W84331
R-HEMBA1005244//ESTs//6.4e-22:118:100//Hs.21396:AA114834
R-HEMBA1005251//ESTs//8.5e-36:213:92//Hs.161554:AA393896
R-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//6.1e-49:277:93//Hs.72660:AB011157
R-HEMBA1005274//ESTs//3.7e-65:322:98//Hs.105166:AA668862
R-HEMBA1005275//ESTs//2.1e-29:298:73//Hs.33393:R83391
R-HEMBA1005293//ESTs//3.5e-93:448:98//Hs.12066:AI208611

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R-HEMBA1005296//ESTs//4.3e-33:168:100//Hs.13916:AI025750
R-HEMBA1005304//Small inducible cytokine A5 (RANTES)//2.8e-50:315:82//Hs.155464:AF088219
R-HEMBA1005311//Homo sapiens 4F5S mRNA, complete cds//1.3e-44:318:83//Hs.32567:AF073519
R-HEMBA1005314//ESTs//3.0e-103:491:98//Hs.41606:AI095046
R-HEMBA1005315//EST//1.9e-29:370:72//Hs.161483:N59169
R-HEMBA1005318//ESTs//3.9e-110:535:97//Hs.26771:AA126472
R-HEMBA1005331//Intercellular adhesion molecule 2//7.6e-39:256:87//Hs.83733:X15606
R-HEMBA1005353//ESTs//1.7e-81:406:96//Hs.155374:AI341467
R-HEMBA1005359//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//4.7e-46:294:81//Hs.129735:AF010144
R-HEMBA1005367//Alcohol dehydrogenase 2 (class I), beta polypeptide//1.0:210:62//Hs.4:X03350
R-HEMBA1005372//ESTs//6.2e-95:451:99//Hs.135219:AI091653
R-HEMBA1005374//ESTs//1.5e-107:502:99//Hs.118208:AA947305
R-HEMBA1005389//Fc fragment of IgA, receptor for//1.0e-39:311:80//Hs.54486:X54150
R-HEMBA1005394//ESTs, Weakly similar to coded for by C. elegans cDNA yk30b3.5 [C.elegans]//4.0e-88:489:92//Hs.43864:AA131568
R-HEMBA1005403//EST//0.0011:78:75//Hs.127061:AA863278
R-HEMBA1005408//ESTs//3.2e-29:395:71//Hs.117532:AA676725
R-HEMBA1005410//ESTs//1.5e-18:271:70//Hs.144604:AI052059
R-HEMBA1005411//ESTs//1.1e-35:335:77//Hs.141181:R98757
R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//1.8e-118:453:99//Hs.4854:AF041248
R-HEMBA1005426//Chromosome 1 specific transcript KIAA0491//0.25:264:61//Hs.136309:AB007960
R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment//1.7e-47:305:87//Hs.6445:L40391
R-HEMBA1005447//ESTs//5.7e-83:529:86//Hs.114253:AA745961
R-HEMBA1005468//ESTs//7.3e-23:249:73//Hs.61199:AA024494
R-HEMBA1005469//Human mRNA for KIAA0355 gene, complete cds//4.5e-45:320:85//Hs.153014:AB002353
R-HEMBA1005472//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//8.4e-73:464:87//Hs.103948:K00627
R-HEMBA1005475//ESTs//0.32:192:59//Hs.62694:AA100445
R-HEMBA1005497
R-HEMBA1005500//ESTs//2.2e-43:307:85//Hs.146811:AA410788
R-HEMBA1005506//75 kda infertility-related sperm protein [human, testis, mRNA Partial, 2427 nt]//0.11:295:60//Hs.62608:S58544
R-HEMBA1005508//ESTs//2.8e-55:319:93//Hs.50150:N90870
R-HEMBA1005511//ESTs, Weakly similar to similar to mouse MMR1 [C.elegans]//2.6e-82:387:99//Hs.67466:AI219740
R-HEMBA1005517//ESTs//4.6e-77:469:90//Hs.126787:AA203322
R-HEMBA1005518//ESTs//1.5e-108:561:94//Hs.123167:AA601045
R-HEMBA1005520//Putative mismatch repair/binding protein hMSH3//7.5e-44:179:84//Hs.42674:U61981
R-HEMBA1005526//ESTs//8.7e-46:308:86//Hs.146811:AA410788
R-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//8.6e-115:578:95//Hs.17035:AI080471
R-HEMBA1005530//ESTs//1.5e-110:551:96//Hs.107294:W72350
R-HEMBA1005548//ESTs//1.7e-100:510:96//Hs.9115:N90926
R-HEMBA1005552//Interleukin 10//2.4e-38:306:80//Hs.2180:M57627
R-HEMBA1005558//ESTs, Weakly similar to unknown [S.cerevisiae]//5.3e-77:439:91//Hs.22897:R43193
R-HEMBA1005568//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.4e-31:182:76//Hs.133526:N21103
R-HEMBA1005570//ESTs//3.3e-67:411:88//Hs.142245:AA489709
R-HEMBA1005576//EST//0.91:52:73//Hs.149518:AI280497
R-HEMBA1005577
R-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//3.1e-28:561:64//Hs.57929:AB011538
R-HEMBA1005582//ESTs//6.0e-73:371:97//Hs.103758:C06392
R-HEMBA1005583//ESTs//8.3e-79:413:95//Hs.62348:AA419539
R-HEMBA1005588//Human c-yes-1 mRNA//2.6e-52:403:83//Hs.75680:M15990
R-HEMBA1005593//ESTs//3.3e-30:139:80//Hs.142273:W37905
R-HEMBA1005595//ESTs//1.1e-97:454:100//Hs.27497:AI274820

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R-HEMBA1005606//EST//1.0e-12:313:64//Hs.162402:AA573125
R-HEMBA1005609//ESTs//0.49:278:58//Hs.76235:W56390
R-HEMBA1005616//EST//1.3e-98:470:99//Hs.122230:AA781422
R-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]//2.8e-95:539:92//Hs.19400:AA662845
R-HEMBA1005627//Human mRNa for adipogenesis inhibitory factor//5.5e-38:317:78//Hs.1721:X58377
R-HEMBA1005631//Human mRNA for KIAA0393 gene, complete cds//2.3e-11:279:65//Hs.15245:AF041081
R-HEMBA1005632//EST//1.5e-10:181:70//Hs.120259:AA731522
R-HEMBA1005634//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.4e-25:234:80//Hs.10458:AF088219
R-HEMBA1005666//ESTs//2.3e-103:534:95//Hs.14512:AA205973
R-HEMBA1005670//ESTs//2.6e-39:166:81//Hs.139414:AI279477
R-HEMBA1005679//Esterase D/formylglutathione hydrolase//1.3e-50:322:88//Hs.82193:M13450
R-HEMBA1005680//Homo sapiens LIM protein mRNA, complete cds//3.3e-43:343:81//Hs.154103:AF061258
R-HEMBA1005685//Human homeodomain protein (Prox 1) mRNA, complete cds//0.0050:235:64//Hs.159437:U44060
R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//1.7e-47:376:84//Hs.26988:U66406
R-HEMBA1005705//ESTs//3.0e-53:259:99//Hs.55314:AA772055
R-HEMBA1005717//EST//2.5e-59:287:99//Hs.146870:AI159943
R-HEMBA1005732//Homo sapiens mRNA for cartilage-associated protein (CASP)//1.2e-45:398:79//Hs.155481:AJ006470
R-HEMBA1005737//ESTs//2.5e-57:416:83//Hs.23245:AA053815
R-nnnnnnnnnnnn//EST//0.098:125:68//Hs.136945:AA765672
R-HEMBA1005755//EST//2.2e-22:180:84//Hs.141488:N47096
R-HEMBA1005765//Human peptide transporter (HPEPT1) mRNA, complete cds//3.9e-47:404:80//Hs.2217:U21936
R-HEMBA1005780//ESTs//1.3e-106:512:97//Hs.11901:AA173974
R-HEMBA1005813//Homo sapiens mRNA for chemokine LEC precursor, complete cds//2.0e-33:195:84//Hs.10458:AF088219
R-HEMBA1005815//ESTs//7.6e-19:290:71//Hs.112218:AI038601
R-HEMBA1005822//ESTs//5.4e-49:246:98//Hs.34804:AA514960
R-HEMBA1005829//ESTs//2.7e-72:344:99//Hs.54548:AI039201
R-HEMBA1005834//ESTs//1.6e-44:317:82//Hs.157029:AI080618
R-HEMBA1005852//ESTs//1.6e-102:544:93//Hs.9911:AA098911
R-HEMBA1005853//ESTs//1.8e-78:398:95//Hs.140248:AA757917
R-HEMBA1005884//EST//2.6e-18:275:67//Hs.139357:AA420970
R-HEMBA1005891//ESTs//2.1e-89:427:98//Hs.67317:AI022252
R-HEMBA1005894
R-HEMBA1005909//ESTs//2.6e-91:436:99//Hs.147492:AI215686
R-HEMBA1005911//ESTs//1.1e-85:446:95//Hs.134494:AI076363
R-HEMBA1005921//ESTs//1.4e-84:428:95//Hs.127993:AA970632
R-HEMBA1005931//Homo sapiens mRNA for KIAA0526 protein, complete cds//9.5e-45:446:75//Hs.59403:AB011098
R-HEMBA1005934//ESTs//0.20:142:65//Hs.97079:AA370867
R-HEMBA1005962//ESTs//1.8e-87:409:100//Hs.161292:AI199418
R-HEMBA1005963
R-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//2.2e-113:580:95//Hs.26285:AF082516
R-HEMBA1005991//Human antisecretory factor-1 mRNA, complete cds//2.0e-45:551:70//Hs.148495:AF050199
R-HEMBA1005999//ESTs//7.5e-24:201:69//Hs.157029:AI080618
R-HEMBA1006002//ESTs//3.1e-112:573:95//Hs.61233:AI379875
R-HEMBA1006005//EST//1.0:105:63//Hs.145273:AI249436
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0725 protein, partial cds//2.4e-28:444:67//Hs.26450:AB018268
R-HEMBA1006035//ESTs//4.5e-94:465:97//Hs.44625:N49951
R-HEMBA1006036//ESTs//6.1e-90:420:100//Hs.126771:AA916508
R-HEMBA1006042//EST//1.5e-88:424:98//Hs.132551:AA948490
R-nnnnnnnnnnnn

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R-HEMBA1006081//ESTs//7.8e-68:356:95//Hs.27410:N25612
R-HEMBA1006090//EST//5.1e-66:320:99//Hs.99551:AA461517
R-HEMBA1006091//ESTs//2.0e-84:441:94//Hs.9658:AA506313
R-HEMBA1006100//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//3.4e-43:328:82//Hs.73614:U83460
R-HEMBA1006108//ESTs//1.5e-44:228:98//Hs.26368:AA789297
R-HEMBA1006121//ESTs//1.6e-116:547:99//Hs.34151:AI279293
R-HEMBA1006124//EST//1.6e-20:286:64//Hs.148457:AI198931
R-HEMBA1006130//ESTs//8.8e-47:231:99//Hs.16470:AA121635
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0792 protein, complete cds//8.7e-27:296:73//Hs.119387:AB007958
R-HEMBA1006142//ESTs//1.5e-27:255:70//Hs.139507:T77542
R-HEMBA1006155//ESTs//4.9e-64:353:94//Hs.84560:R41212
R-HEMBA1006158//Deoxyuridine triphosphatase//0.99:162:62//Hs.82113:U31930
R-HEMBA1006173//ESTs//7.5e-85:462:92//Hs.79092:H29627
R-HEMBA1006182//ESTs//5.5e-29:218:72//Hs.141466:H96906
R-HEMBA1006198//ESTs//2.1e-34:282:82//Hs.142068:AA176125
R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//6.9e-112:545:97//Hs.109268:AF070557
R-HEMBA1006248//ESTs, Highly similar to ZINC FINGER PROTEIN MFG1 [Mus musculus]//3.3e-114:581:95//Hs.23617:AA928683
R-HEMBA1006252//Human mRNA for KIAA0080 gene, partial cds//7.0e-48:284:76//Hs.74554:D38522
R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds//5.7e-30:179:91//Hs.15836:AF083384
R-HEMBA1006259//Homo sapiens KIAA0421 mRNA, partial cds//1.5e-45:326:84//Hs.41742:AB007881
R-HEMBA1006268//ESTs, Highly similar to c-Jun leucine zipper interactive [M.musculus]//1.2e-97:529:93//Hs.10552:AA524401
R-HEMBA1006272//ESTs, Moderately similar to RETROVIRUS-RELATED PROTEASE [H.sapiens]//2.7e-88:484:92//Hs.104129:AA923278
R-nnnnnnnnnnnn//H.sapiens PAP mRNA//5.2e-56:585:71//Hs.49007:X76770
R-HEMBA1006283//ESTs, Weakly similar to NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2 [S.cerevisiae]//1.6e-66:377:91//Hs.108674:W25821
R-HEMBA1006284//ESTs//3.7e-110:544:96//Hs.55296:AI084735
R-HEMBA1006291//ESTs//2.2e-91:457:96//Hs.114611:N37019
R-HEMBA1006293//ESTs//5.4e-78:370:99//Hs.155111:AI202037
R-HEMBA1006309//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//3.7e-40:167:86//Hs.74478:U33931
R-HEMBA1006310//ESTs, Weakly similar to reverse transcriptase [M.musculus]//5.6e-76:417:94//Hs.111754:AI204587
R-HEMBA1006328//Small inducible cytokine A5 (RANTES)//2.8e-60:397:78//Hs.155464:AF088219
R-HEMBA1006334//Human occludin mRNA, complete cds//0.72:369:59//Hs.93518:U49184
R-HEMBA1006344//Human plectin (PLEC1) mRNA, complete cds//0.016:217:64//Hs.79706:U53204
R-HEMBA1006347//ESTs, Highly similar to HYPOTHETICAL 97.6 KD PROTEIN IN SHP1-SEC17 INTERGENIC REGION [Saccharomyces cerevisiae]//3.6e-119:582:97//Hs.42343:AI417075
R-HEMBA1006349//ESTs//5.2e-57:305:94//Hs.6338:AA411382
R-HEMBA1006359//ESTs//8.2e-90:426:99//Hs.100873:AA678008
R-HEMBA1006364//ESTs//2.2e-98:582:91//Hs.23837:AA541787
R-HEMBA1006377//EST//0.0097:145:621//Hs.133027:AI049830
R-HEMBA1006380//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.0e-41:349:79//Hs.154872:AB011166
R-HEMBA1006381//ESTs//5.1e-46:320:85//Hs.37573:H59651
R-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-87:5 82:84//Hs.23094:M19503
R-HEMBA1006416//ESTs//1.5e-17:251:73//Hs.33950:AI218923
R-HEMBA1006419//EST//8.5e-65:353:94//Hs.141309:H72778
R-HEMBA1006421//Oxytocin receptor//1.2e-12:249:68//Hs.2820:X64878
R-HEMBA1006424//ESTs, Weakly similar to pot. ORF II [H.sapiens]//6.3e-13:263:66//Hs.43127:AA258004
R-HEMBA1006426//ESTs//6.5e-84:401:99//Hs.37303:C16964
R-HEMBA1006438//EST//0.87:266:57//Hs.99456:AA457380
R-HEMBA1006445//ESTs//2.0e-81:414:96//Hs.58153:W72033

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R-HEMBA1006446//Homo sapiens mRNA for cadherin-6, complete cds//1.6e-05:487:58//Hs.32963:D31784
R-HEMBA1006461//ESTs//5.1e-78:393:97//Hs.142677:R95895
R-HEMBA1006467//ESTs, Weakly similar to putative p150 [H.sapiens]//3.0e-17:342:63//Hs.111730:AA604403
R-HEMBA1006471//ESTs//3.8e-66:370:92//Hs.14063:T77441
R-HEMBA1006474
R-HEMBA1006483//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.2e-40:365:78//Hs.46468:U45984
R-HEMBA1006485//H.sapiens mRNA for aminopeptidase//2.5e-92:517:91//Hs.132243:Y07701
R-HEMBA1006486//EST//7.0e-47:240:76//Hs.161917:AA483223
R-HEMBA1006489//ESTs//2.1e-93:440:99//Hs.125264:AA873350
R-HEMBA1006492//ESTs//0.00034:52:90//Hs.163219:AA810720
R-HEMBA1006494//EST//1.8e-06:192:67//Hs.141401:H93387
R-HEMBA1006497//ESTs//6.2e-45:232:97//Hs.118015:N33117
R-HEMBA1006502//Complement component 5 receptor 1 (C5a ligand)//8.7e-16:135:72//Hs.2161:M62505
R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//3.9e-117:570:96//Hs.153858:AB014566
R-HEMBA1006521//ESTs//9.9e-99:496:96//Hs.64906:AA677300
R-HEMBA1006530//ESTs//0.18:260:60//Hs.24970:AI057628
R-HEMBA1006535//GS1 PROTEIN//0.52:267:62//Hs.78991:M86934
R-HEMBA1006540//EST//0.016:143:66//Hs.148189:AA897331
R-HEMBA1006546//Homo sapiens mRNA for KIAA0582 protein, partial cds//2.2e-48:287:91//Hs.79507:AB011154
R-HEMBA10065597//ESTs, Moderately similar to neurodegeneration-associated protein 1 [R.norvegicus]//1.8e-109:547:96//Hs.21122:AA191594
R-HEMBA1006562//EST//1.1e-13:327:63//Hs.149641:AI283064
R-HEMBA1006566//ESTs//2.6e-59:311:97//Hs.146014:R51876
R-HEMBA1006569//ESTs//4.7e-89:458:96//Hs.42861:W74725
R-HEMBA1006579//ESTs//2.9e-19:110:99//Hs.126191:AA873876
R-HEMBA1006583//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.5e-29:276:76//Hs.144563:AF057280
R-HEMBA1006595//ESTs//1.3e-96:487:96//Hs.43228:N67390
R-HEMBA1006597//Small inducible cytokine A5 (RANTES)//9.8e-44:291:85//Hs.155464:AF088219
R-HEMBA1006612
R-nnnnnnnnnnnn//ESTs//1.2e-25:225:80//Hs.138852:AA284247
R-HEMBA1006624//ESTs//1.9e-93:454:98//Hs.72531:AA773630
R-HEMBA1006631//Human mRNA for KIAA0033 gene, partial cds//7.5e-60:286:90//Hs.22271:D26067
R-HEMBA1006635//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//2.7e-91:426:100//Hs.139469:AI299889
R-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]//3.4e-37:186:100//Hs.109818:AA411185
R-HEMBA1006643//ESTs//1.8e-35:189:97//Hs.139640:AA846777
R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//8.1e-108:567:94//Hs.6196:U40282
R-HEMBA1006652//ESTs//7.6e-100:536:93//Hs.142613:AA129427
R-HEMBA1006653//ESTs//2.0e-33:181:87//Hs.153599:AI282511
R-HEMBA1006665//EST//1.2e-13:141:72//Hs.145596:AI263102
R-HEMBA1006674//ESTs//3.1e-32:212:83//Hs.95115:AA206594
R-HEMBA1006676//ESTs//2.6e-95:510:93//Hs.39140:AI041842
R-HEMBA1006682//EST//1.4e-05:277:62//Hs.145762:AI269435
R-HEMBA1006695//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-32:261:79//Hs.77579:AF013263
R-HEMBA1006696//ESTs//4.5e-95:448:99//Hs.155694:AI032695
R-HEMBA1006708//ESTs, Weakly similar to Miller-Dieker lissencephaly gene [H.sapiens]//1.1e-92:483:94//Hs.6525:AI205313
R-HEMBA1006709//ESTs//3.4e-25:207:80//Hs.88617:AA872062
R-HEMBA1006717
R-HEMBA1006737//EST//5.9e-30:317:75//Hs.140568:AA826002
R-HEMBA1006744//Interleukin 10//3.7e-41:419:74//Hs.2180:M57627
R-HEMBA1006754//ESTs//1.2e-46:276:83//Hs.141254:AI334099

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R-HEMBA1006758//ESTs//0.00043:48:100//Hs.157265:AA489646
R-HEMBA1006767//EST//0.094:120:65//Hs.159873:R92763
R-HEMBA1006779//EST//9.3e-45:298:85//Hs.149580:AI281881
R-HEMBA1006780//ESTs//1.6e-46:423:77//Hs.141602:N63562
R-HEMBA1006789//ESTs//7.6e-55:245:95//Hs.6459:AI092936
R-HEMBA1006795//ESTs//8.6e-47:315:78//Hs.140491:W52705
R-HEMBA1006796//ESTs//0.26:175:65//Hs.103280:AI334978
R-HEMBA1006807//Homo sapiens DEC-205 mRNA, complete cds//5.7e-47:461:75//Hs.153563:AF011333
R-HEMBA1006821//ESTs//3.5e-12:222:68//Hs.150439:AI016305
R-HEMBA1006824//Homo sapiens mRNA, clone:RES4-16//6.7e-51:298:90//Hs.121493:D25272
R-HEMBA1006832//ESTs//0.0050:108:70//Hs.12853:T65556
R-HEMBA1006849//Human mRNA for KIAA0118 gene, partial cds//2.1e-49:367:83//Hs.154326:D42087
R-HEMBA1006865//ESTs//0.85:112:63//Hs.116430:AA644665
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0772 protein, complete cds//1.8e-67:611:74//Hs.15519:AB018315
R-HEMBA1006885//ESTs//2.4e-66:347:96//Hs.100624:N95453
R-HEMBA1006900//ESTs//2.7e-91:466:96//Hs.32984:R89739
R-HEMBA1006921//ESTs//2.2e-33:170:100//Hs.152277:AA593117
R-HEMBA1006926//ESTs, Weakly similar to ZK1053.6 [C.elegans]//2.9e-28:213:84//Hs.9096:AA029400
R-HEMBA1006929//ESTs//4.0e-13:210:66//Hs.100895:AA479308
R-HEMBA1006936//ESTs//3.9e-05:60:93//Hs.8737:W22712
R-HEMBA1006938//EST//0.0021:244:62//Hs.144237:W52382
R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//6.5e-77:371:98//Hs.42644:AJ010841
R-HEMBA1006949//ESTs//1.2e-67:335:98//Hs.25780:R51321
R-HEMBA1006973//ESTs//0.029:242:61//Hs.146074:N34457
R-HEMBA1006976//EST//0.70:206:61//Hs.147092:AI189827
R-HEMBA1006993//Human mRNA for KIAA0327 protein, complete cds//2.6e-47:368:80//Hs.149323:AB002325
R-HEMBA1006996//ESTs//0.027:326:58//Hs.105008:AA451679
R-HEMBA1007002//ESTs//0.13:116:66//Hs.26928:Z41440
R-HEMBA1007017//ESTs//4.3e-47:208:87//Hs.155243:N70293
R-HEMBA1007018//ESTs, Moderately similar to LIC-2 [R.norvegicus]//2.8e-112:558:96//Hs.107905:AI248363
R-HEMBA1007045
R-HEMBA1007051//ESTs//2.5e-39:321:80//Hs.146811:AA410788
R-HEMBA1007052//EST//3.4e-41:377:74//Hs.44634:N34839
R-HEMBA1007062//ESTs//1.2e-92:439:99//Hs.162882:AA807140
R-HEMBA1007066//ESTs//0.85:204:61//Hs.22795:AI208272
R-HEMBA1007073//ESTs//6.6e-52:362:85//Hs.30821:AI096866
R-HEMBA1007078//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//7.2e-40:163:83//Hs.152369:AA504818
R-HEMBA1007085//ESTs//8.1e-103:519:96//Hs.90638:AI348087
R-HEMBA1007087//ESTs//3.1e-51:354:86//Hs.6449:W95025
R-HEMBA1007112//EST//0.090:328:59//Hs.136623:AA633597
R-HEMBA1007113//Homo sapiens mRNA, clone:RES4-16//1.1e-47:427:76//Hs.121493:D25272
R-HEMBA1007129//ESTs//6.1e-13:314:65//Hs.137538:AA769438
R-HEMBA1007147
R-HEMBA1007149//ESTs//9.7e-103:540:94//Hs.127240:AA149818
R-HEMBA1007151//ESTs//8.2e-102:505:96//Hs.24948:AA977674
R-nnnnnnnnnnnn//Homo sapiens epsin 2b mRNA, complete cds//1.6e-104:529:94//Hs.22396:AF062085
R-HEMBA1007178//ESTs//2.2e-57:366:90//Hs.21648:AI302954
R-HEMBA1007194//ESTs//9.0e-68:336:98//Hs.49760:AA741051
R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.7e-62:332:95//Hs.3363:D86987
R-HEMBA1007206//Human c-yes-1 mRNA//4.5e-49:390:80//Hs.75680:M15990
R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//7.4e-98:471:97//Hs.27197:AB018340
R-HEMBA1007251//ESTs//1.6e-78:377:99//Hs.98912:AA436864
R-HEMBA1007256//ESTs//3.5e-20:127:79//Hs.137352:AA024934
R-HEMBA1007267//Homo sapiens KIAA0395 mRNA, partial cds//8.8e-48:343:83//Hs.43681:AL022394

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R-HEMBA1007273//ESTs//1.0e-98:472:98//Hs.122610:AA807062
R-HEMBA1007279//ESTs//3.3e-107:558:94//Hs.126480:AI221207
R-HEMBA1007281//EST//0.074:244:63//Hs.29304:R73543
R-HEMBA1007288//EST//9.4e-43:344:81//Hs.162112:AA524804
R-HEMBA1007300//ESTs//0.096:371:57//Hs.102680:N52990
R-HEMBA1007301
R-HEMBA1007319//ESTs//7.7e-113:570:96//Hs.29263:AI337917
R-HEMBA1007320//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//5.5e-15:311:64//Hs.142764:AA205569
R-HEMBA1007322//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//5.7e-49:383:83//Hs.139107:K00629
R-HEMBA1007327//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.9e-42:371:79//Hs.154069:U06452
R-HEMBA1007341//EST//3.0e-17:291:68//Hs.150788:AI301848
R-HEMBA1007342//EST//2.7e-11:263:67//Hs.145259:AI218684
R-HEMBA1007347//Homo sapiens DEC-205 mRNA, complete cds//9.7e-47:368:82//Hs.153563:AF011333
R-HEMBB1000005//ESTs, Weakly similar to putative p150 [H.sapiens]//3.3e-44:341:71//Hs.111730:AA604403
R-HEMBB1000008//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//3.2e-40:292:83//Hs.129708:AF064090
R-HEMBB1000018//H.sapiens mRNA for urea transporter//5.0e-49:311:87//Hs.66710:X96969
R-HEMBB1000024//ESTs//7.5e-21:234:76//Hs.157049:AI345418
R-HEMBB1000025//ESTs//2.2e-36:371:78//Hs.56562:AA056332
R-HEMBB1000030//ESTs//3.2e-76:373:97//Hs.140190:AA701449
R-HEMBB1000036//ESTs, Highly similar to HYPOTHETICAL 43.2 KD PROTEIN C34E10.1 IN CHROMOSOME III [Caenorhabditis elegans]//6.0e-92:477:95//Hs.4877:AA418465
R-HEMBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//2.5e-92:467:97//Hs.20815:AF084928
R-HEMBB1000039//ESTs//1.8e-43:361:71//Hs.108206:N64702
R-HEMBB1000044//EST//7.6e-70:367:95//Hs.140860:R42954
R-HEMBB1000048//EST//1.5e-45:262:91//Hs.157627:AI357802
R-HEMBB1000050//ESTs//0.039:91:74//Hs.163189:AA236903
R-HEMBB1000054//ESTs//3.0e-104:550:94//Hs.152395:AA533107
R-HEMBB1000055//ESTs, Moderately similar to UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX SUBUNIT VI REQUIRING PROTEIN [H.sapiens]//1.1e-72:350:99//Hs.116490:AA659584
R-HEMBB1000059//ESTs//1.7e-10:200:70//Hs.163954:N57939
R-HEMBB1000083//Homo sapiens mRNA for GCP170, complete cds//6.0e-41:337:80//Hs.4953:D63997
R-HEMBB1000089//Human mRNA for KIAA0355 gene, complete cds//3.5e-39:487:70//Hs.153014:AB002353
R-HEMBB1000099//ESTs//5.7e-37:353:75//Hs.22910:W18193
R-HEMBB1000103//Homo sapiens mRNA for KIAA0640 protein, partial cds//6.5e-18:298:69//Hs.153026:AB014540
R-HEMBB1000113//EST//8.2e-94:437:100//Hs.136893:AA805239
R-HEMBB1000119//Homo sapiens ASMTL gene//1.2e-84:428:95//Hs.6315:Y15521
R-HEMBB1000136//ESTs//0.043:262:59//Hs.61304:AA025692
R-HEMBB1000141//ESTs//5.0e-38:254:79//Hs.141658:N77915
R-HEMBB1000144//ESTs//9.6e-05:235:60//Hs.61700:AA033951
R-HEMBB1000173//EST//9.6e-44:258:76//Hs.161917:AA483223
R-HEMBB1000175//ESTs//4.8e-98:475:97//Hs.149740:AI199558
R-HEMBB1000198//ESTs//1.0:123:62//Hs.116602:AA665965
R-HEMBB1000215//Human mRNA for KIAA0355 gene, complete cds//2.2e-46:302:86//Hs.153014:AB002353
R-HEMBB1000217//ESTs//2.2e-105:496:99//Hs.65973:AI339364
R-HEMBB1000218//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//1.1e-48:292:79//Hs.133089:AF064019
R-HEMBB10002267/ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II [C.elegans]//5.1e-73:449:89//Hs.16803:AA843214
R-HEMBB1000240//ESTs//1.1e-109:536:97//Hs.13528:AA523106
R-HEMBB1000244//Small inducible cytokine A5 (RANTES)//9.5e-42:323:83//Hs.155464:AF088219
R-HEMBB1000250//EST//8.8e-12:284:64//Hs.145960:AI276783
R-HEMBB1000258//EST//4.5e-14:315:66//Hs.162551:AA584782

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R-HEMBB1000264
R-HEMBB1000266//ESTs, Weakly similar to similar to the beta transducin family [C.elegans]//2.7e-102:556:93//Hs.16079:AA083522
R-HEMBB1000272//ESTs//4.3e-91:480:94//Hs.107467:H11385
R-HEMBB1000274//Homo sapiens mRNA for KIAA0557 protein, partial cds//7.9e-24:198:72//Hs.101414:AB011129
R-HEMBB1000284//ESTs//4.8e-64:389:91//Hs.118043:N50458
R-HEMBB1000307//Human mRNA for KIAA0355 gene, complete cds//3.6e-43:288:87//Hs.153014:AB002353
R-HEMBB1000312//ESTs//6.0e-23:272:73//Hs.121354:AA758601
R-HEMBB1000317//ESTs//7.5e-90:424:99//Hs.150042:AI298034
R-HEMBB1000318//Small inducible cytokine A5 (RANTES)//3.3e-41:318:80//Hs.155464:AF088219
R-HEMBB1000335//ESTs//3.7e-15:324:65//Hs.85077:AA968576
R-HEMBB1000336//ESTs//6.4e-76:402:95//Hs.17207:H92480
R-HEMBB-1000337//ESTs//2.1e-80:391:97//Hs.118990:AI378084
R-HEMBB1000338//Small inducible cytokine A5 (RANTES)//4.0e-39:274:85//Hs.155464:AF088219
R-HEMBB1000339//EST//5.8e-41:336:79//Hs.151873:AA205736
R-HEMBB1000341//ESTs//3.8e-19:310:68//Hs.37573:H59651
R-HEMBB1000343//EST//1.1e-77:396:95//Hs.162664:AA605020
R-HEMBB1000354//Human mRNA for KIAA0186 gene, complete cds//1.7e-15:293:65//Hs.36232:D80008
R-HEMBB1000369//ESTs//1.6e-21:234:73//Hs.111583:AA463590
R-HEMBB1000374//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.3e-56:335:77//Hs.92381:AB007956
R-HEMBB1000376//H.sapiens mRNA for urea transporter//2.7e-50:525:74//Hs.66710:X96969
R-HEMBB1000391//ESTs//6.6e-50:316:88//Hs.142259:AA828840
R-HEMBB1000399//Homo sapiens mRNA for cell cycle checkpoint protein//3.8e-109:531:97//Hs.16184:AJ001642
R-HEMBB1000402//H.sapiens mRNA for MACH-alpha-2 protein//2.7e-35:369:72//Hs.19949:X98173
R-HEMBB1000404//ESTs//0.088:298:59//Hs.61607:AA032026
R-HEMBB1000420//EST//2.2e-78:376:98//Hs.160787:AI336591
R-HEMBB1000434//Human mRNA for KIAA0118 gene, partial cds//3.9e-50:302:89//Hs.154326:D42087
R-HEMBB1000438//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//0.30:214:63//Hs.142209:AA873303
R-HEMBB1000441//Human c-yes-1 mRNA//2.2e-46:280:90//Hs.75680:M15990
R-HEMBB1000449//ESTs//7.8e-59:332:92//Hs.87013:AA130221
R-HEMBB1000455//EST//4.8e-14:421:65//Hs.68832:AA088438
R-HEMBB1000472//ESTs//1.1e-104:505:98//Hs.132824:AI033396
R-HEMBB1000480//Human mRNA for KIAA0392 gene, partial cds//2.5e-49:295:90//Hs.40100:AB002390
R-HEMBB1000487//EST//0.78:87:68//Hs.134601:AI081506
R-HEMBB1000490//Small inducible cytokine A5 (RANTES)//4.0e-39:320:80//Hs.155464:AF088219
R-HEMBB1000491//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.7e-50:312:76//Hs.113283:AF018080
R-HEMBB1000493//ESTs//7.1e-18:150:82//Hs.142068:AA176125
R-HEMBB1000510//EST//1.4e-45:139:97//Hs.152260:AA489703
R-HEMBB1000518//Human mRNA for KIAA0118 gene, partial cds//4.8e-50:415:78//Hs.154326:D42087
R-HEMBB1000523//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.7e-57:497:78//Hs.113283:AF018080
R-HEMBB1000530//ESTs//2.7e-73:425:90//Hs.141254:AI334099
R-HEMBB1000550//EST//2.9e-11:113:79//Hs.161503:N68662
R-HEMBB1000554//Human huntingtin interacting protein (HIP1) mRNA, complete cds//8.2e-13:92:81//Hs.97206:AF052288
R-HEMBB1000556//ESTs//1.1e-94:529:92//Hs.33476:N36986
R-HEMBB1000564//ESTs//1.3e-19:128:91//Hs.142058:N34258
R-HEMBB1000573//ESTs//1.6e-86:494:90//Hs.120979:AI160709
R-HEMBB1000575//ESTs//1.6e-45:232:74//Hs.141019:AA287618
R-HEMBB1000586//ESTs//5.1e-42:281:83//Hs.138852:AA284247
R-HEMBB1000589//ESTs//1.0e-10:184:71//Hs.142677:R95895
R-HEMBB1000591//ESTs//3.2e-40:406:75//Hs.138787:H73704
R-HEMBB1000592//ESTs//1.8e-97:455:99//Hs.94229:W65391
R-HEMBB1000598//Human anti secretory factor-1 mRNA, complete cds//1.8e-46:305:85//Hs.148495:AF050199
R-HEMBB1000623//ESTs//8.3e-47:277:92//Hs.6045:W67125
R-HEMBB1000630//ESTs//5.1e-106:538:96//Hs.13422:AI082249

BNSDOCID: <EP___1074617A2_I_>

R-HEMBB1000631//ESTs//5.1e-100:508:96//Hs.110379:N58152
R-HEMBB1000632//ESTs//6.2e-44:371:80//Hs.132722:AA618531
R-HEMBB1000637//Human mRNA for KIAA0080 gene, partial cds//6.4e-49:254:86//Hs.74554:D38522
R-HEMBB1000638//EST//2.2e-38:371:76//Hs.162236:AA551582
R-HEMBB1000643//ESTs//0.0049:191:62//Hs.55445:W31963
R-HEMBB1000649//ESTs, Moderately similar to hTAFII68 [H.sapiens]//4.0e-76:399:95//Hs.124106:AA948100
R-HEMBB1000652//ESTs//1.5e-14:271:64//Hs.163954:N57939
R-HEMBB1000665//ESTs//4.2e-12:109:87//Hs.41407:W94988
R-HEMBB1000671//ESTs//2.8e-68:439:87//Hs.140491:W52705
R-HEMBB1000673//EST//0.58:46:82//Hs.142286:AA338293
R-HEMBB1000684//ESTs//8.5e-20:307:72//Hs.122825:AA765454
R-nnnnnnnnnnnn//Homo sapiens neuroan1 mRNA, complete cds//6.5e-52:287:93//Hs.158300:AF040723
R-HEMBB1000705//Small inducible cytokine A5 (RANTES)//4.6e-24:165:78//Hs.155464:AF088219
R-HEMBB1000706//EST//1.2e-10:211:65//Hs.105524:AA521412
R-HEMBB1000709//ESTs, Weakly similar to putative p150 [H.sapiens]//3.9e-50:245:99//Hs.111730:AA604403
R-HEMBB1000725//Human mRNA for KIAA0308 gene, partial cds//0.11:350:59//Hs.10351:AB002306
R-HEMBB1000726//EST//5.3e-49:303:88//Hs.149580:AI281881
R-HEMBB100073 8//Homo sapiens mRNA, clone:RES4-16//2.5e-49:302:89//Hs.121493:D25272
R-HEMBB1000749//ESTs//1.6e-49:331:86//Hs.152788:AA630925
R-HEMBB1000763//ESTs//9.7e-104:474:95//Hs.77480:AA100522
R-HEMBB1000770//EST//1.0e-75:359:99//Hs.136564:AA642445
R-HEMBB1000781//ESTs//5.3e-66:317:99//Hs.28827:AI125541
R-HEMBB1000789//ESTs//5.9e-83:394:99//Hs.120842:AA435771
R-HEMBB1000790//PLATELET GLYCOPROTEIN V PRECURSORY//1.3e-37:193:75//Hs.73734:Z23091
R-HEMBB1000794//ESTs//7.1e-98:490:96//Hs.105743:AA532718
R-HEMBB1000807//ESTs//2.6e-22:145:92//Hs.53913:AA908961
R-HEMBB1000810//Small inducible cytokine A5 (RANTES)//1.8e-34:206:79//Hs.155464:AF088219
R-HEMBB1000821//ESTs//2.4e-90:425:99//Hs.118659:AI052447
R-HEMBB1000822//ESTs//1.7e-45:288:89//Hs.24130:R27124
R-HEMBB1000826//Small inducible cytokine A5 (RANTES)//2.9e-51:245:82//Hs.155464:AF088219
R-HEMBB1000827//EST//2.8e-40:295:84//Hs.149580:AI281881
R-HEMBB1000831//ESTs//4.0e-59:291:98//Hs.62675:AA044176
R-HEMBB1000835//ESTs//7.3e-21:124:82//Hs.102671:N52545
R-HEMBB1000840//ATPase, Na^+/K^+ transporting, beta 2 polypeptide//1.3e-43:163:84//Hs.78854:AF007876
R-HEMBB1000848//Homo sapiens mRNA for KIAA0565 protein, complete cds//9.5e-41:367:78//Hs.129740:AB011137
R-HEMBB1000852//EST//1.2e-09:188:70//Hs.127869:AA968599
R-HEMBB1000870//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1.0e-41:483:73//Hs.2379:U23942
R-HEMBB1000876//EST//0.0022:211:63//Hs.125552:AA884141
R-HEMBB1000883//ESTs//1.4e-65:343:95//Hs.98269:H27247
R-HEMBB1000887//ESTs//4.0e-22:212:79//Hs.138965:AI004740
R-HEMBB1000888//EST//8.2e-07:196:64//Hs.118276:W15258
R-HEMBB1000890//ISLET AMYLOID POLYPEPTIDE PRECURSORY//1.1e-46:327:83//Hs.51048:X68830
R-HEMBB1000893//EST//4.7e-34:242:85//Hs.149580:AI281881
R-HEMBB1000908//EST//0.95:27:100//Hs.142568:AA285066
R-HEMBB1000910//ESTs//1.9e-36:318:78//Hs.141140:AA715983
R-HEMBB1000913//Human mRNA for KIAA0327 protein, complete cds//2.5e-33:367:73//Hs.149323:AB002325
R-HEMBB1000915//ESTs//0.00018:188:61//Hs.44847:AI222742
R-HEMBB1000917//Homo sapiens KIAA0414 mRNA, partial cds//3.7e-41:228:84//Hs.127649:AB007874
R-HEMBB1000927//ESTs//2.2e-62:307:98//Hs.97044:AA365784
R-HEMBB1000947//ESTs, Weakly similar to F26E4.13 [C.elegans]//3.3e-60:350:91//Hs.49163:AA532881
R-HEMBB1000959//Human Line-1 repeat mRNA with 2 open reading frames//8.1e-84:546:86//Hs.23094:MI9503
R-HEMBB1000973//ESTs//6.8e-95:445:99//Hs.105859:AI419354
R-HEMBB1000975//ESTs//1.2e-39:197:100//Hs.26176:AI032007
R-HEMBB1000981//EST//7.7e-58:284:98//Hs.60179:AA007242
R-HEMBB1000985//ESTs//1.2e-103:524:95//Hs.43102:AA131369
R-HEMBB1000991//EST//0.99:58:72//Hs.100246:T23625
R-HEMBB1000996//Homo sapiens LIM protein mRNA, complete cds//1.3e-41:482:70//Hs.154103:AF061258

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R-HEMBB1001004//ESTs//5.7e-70:362:95//Hs.6434:W27112
R-HEMBB1001008//ESTs, Weakly similar to hypothetical L1 protein [H.sapiens]//2.3e-25:339:71//Hs.129992:H58762
R-HEMBB1001011//ESTs//4.0e-53:325:92//Hs.33268:AI191214
R-HEMBB1001014//ESTs//1.3e-46:323:83//Hs.163980:AA715814
R-HEMBB1001020//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.0e-46:305:76//Hs.113283:AF018080
R-HEMBB1001024//ESTs//8.5e-47:374:80//Hs.141602:N63562
R-HEMBB1001037//ESTs//2.6e-47:282:91//Hs.155384:Z78385
R-HEMBB1001047//EST//6.2e-33:232:74//Hs.160146:AI049975
R-HEMBB1001051//ESTs//3.7e-79:385:98//Hs.95290:AA046107
R-HEMBB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.1e-87:497:91//Hs.15832:AB014518
R-HEMBB1001058//Homo sapiens mRNA for KIAA0475 protein, complete cds//2.2e-26:125:81//Hs.5737:AB007944
R-HEMBB1001060//ESTs//1.9e-37:541:69//Hs.141534:N64785
R-HEMBB1001063//ESTs//4.7e-42:269:88//Hs.55855:AA621381
R-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.1e-107:512:97//Hs.12953:AF034803
R-HEMBB1001096//Human HsLIM15 mRNA for HsLim15, complete cds//1.2e-20:233:70//Hs.37181:D64108
R-HEMBB1001102//Human mRNA for KIAA0355 gene, complete cds//9.1e-40:299:82//Hs.153014:AB002353
R-HEMBB1001105//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.8e-46:296:87//Hs.113283:AF018080
R-HEMBB1001114//ESTs//6.2e-44:293:86//Hs.70279:AA757426
R-HEMBB1001117//ESTs//1.1e-80:471:90//Hs.61935:T75092
R-HEMBB1001119//ESTs//4.0e-38:213:84//Hs.109140:AI289942
R-HEMBB1001126
R-HEMBB1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subunit mRNA, complete cds//1.6e-24:285:73//Hs.554:M25077
R-HEMBB1001137//ESTs//4.6e-10:66:100//Hs.74924:AI332962
R-HEMBB1001142//EST//6.4e-48:315:85//Hs.149580:AI281881
R-HEMBB1001151
R-HEMBB1001153//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.3e-65:331:96//Hs.154179:AA579197
R-HEMBB1001169//Oxytocin receptor//1.5e-25:165:73//Hs.2820:X64878
R-nnnnnnnnnnnn//ESTs//3.5e-41:233:93//Hs.129218:AA991162
R-HEMBB1001177
R-HEMBB1001182//ESTs//1.9e-86:455:95//Hs.6937:AA524349
R-HEMBB1001199
R-HEMBB1001208//ESTs//3.3e-43:216:99//Hs.121806:N71183
R-HEMBB1001209//ESTs//6.7e-80:409:96//Hs.141185:R99549
R-HEMBB1001210//ESTs//2.2e-46:290:88//Hs.103329:D11573
R-HEMBB1001218//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//3.1e-44:298:87//Hs.103458:X53795
R-HEMBB1001221//ESTs//9.4e-75:353:100//Hs.151504:AA550817
R-HEMBB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Gallus gallus]//3.8e-80:400:96//Hs.71873:AA148213
R-HEMBB1001242//ESTs//1.6e-63:404:87//Hs.25534:AA149560
R-HEMBB1001249//ESTs//3.8e-34:360:70//Hs.150727:AI292236
R-HEMBB1001253//EST//0.0011:84:77//Hs.124579:AA853987
R-HEMBB1001254//ESTs//4.5e-95:444:99//Hs.161059:AI431268
R-HEMBB1001267//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.3e-50:524:73//Hs.159897:AB007970
R-HEMBB1001271//Human mRNA for KIAA0118 gene, partial cds//4.0e-45:323:84//Hs.154326:D42087
R-HEMBB1001282//EST//2.9e-78:401:96//Hs.72871:AA169412
R-HEMBB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III [Caenorhabditis elegans]//2.6e-104:515:97//Hs.16606:W81021
R-HEMBB1001289//ESTs//7.8e-45:440:75//Hs.44702:AI148840
R-HEMBB1001294//ESTs//1.9e-100:476:99//Hs.109017:AI057112
R-HEMBB1001302
R-HEMBB1001304//ESTs//4.0e-92:431:99//Hs.113750:AI091154

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R-HEMBB1001314//Interleukin 10//6.3e-41:334:79//Hs.2180:M57627
R-HEMBB1001315//Interleukin 10//1.9e-43:285:87//Hs.2180:M57627
R-HEMBB1001317//Human cytochrome P450-IIB (hIIB3) mRNA, complete cds//8.4e-45:357:81//Hs.110194:M29873
R-HEMBB1001326//ESTs//0.85:174:62//Hs.133487:AI393754
R-HEMBB1001331//ESTs, Weakly similar to DFS70 [H.sapiens]//6.5e-61:313:96//Hs.43071:AA206222
R-HEMBB1001335//EST//5.2e-80:381:99//Hs.116769:AA630365
R-HEMBB1001337//ESTs//2.7e-84:404:99//Hs.148966:AI242639
R-HEMBB1001339//ESTs//2.1e-97:485:96//Hs.88357:AA262470
R-HEMBB1001346
R-HEMBB1001348//ESTs//1.1e-43:295:85//Hs.163604:R94354
R-HEMBB1001356//EST//6.0e-11:89:88//Hs.152366:AA486721
R-HEMBB1001364//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-12:129:79//Hs.9792:AA027055
R-HEMBB1001366//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:550:72//Hs.154326:D42087
R-HEMBB1001367//ESTs//1.2e-19:165:82//Hs.146314:R99617
R-HEMBB1001369//Small inducible cytokine A5 (RANTES)//1.9e-25:217:80//Hs.155464:AF088219
R-HEMBB1001380//ESTs//4.0e-08:216:63//Hs.143763:AI174205
R-HEMBB1001384//ESTs//6.6e-110:547:96//Hs.6671:AI341699
R-HEMBB1001387//ESTs//1.1e-104:497:98//Hs.87654:AA853970
R-HEMBB1001394//ESTs//6.4e-73:428:89//Hs.139922:AA281350
R-HEMBB1001410//Alcohol dehydrogenase 7 sigma subunit (class IV)//0.88:365:58//Hs.389:X76342
R-HEMBB1001424//ESTs//1.3e-88:466:94//Hs.42174:AA194644
R-HEMBB1001426//ESTs//2.2e-45:337:82//Hs.37573:H59651
R-HEMBB1001429//EST//3.8e-59:543:76//Hs.158803:AI376846
R-HEMBB1001436//ESTs//3.7e-69:332:99//Hs.156518:AA724317
R-HEMBB1001443//ESTs//4.8e-54:270:98//Hs.21898:AI088201
R-HEMBB1001449//ESTs//3.2e-43:170:84//Hs.150727:AI292236
R-HEMBB1001454//ESTs//9.1e-46:304:86//Hs.139190:N55515
R-HEMBB1001458//ESTs//3.2e-98:478:97//Hs.50144:N67293
R-HEMBB1001463//Homo sapiens KIAA0421 mRNA, partial cds//4.3e-50:440:78//Hs.41742:AB007881
R-HEMBB1001464//ESTs, Weakly similar to K01H12.1 [C.elegans]//0.25:222:61//Hs.13275:AI341468
R-HEMBB1001482//ESTs, Moderately similar to zinc finger protein [R.norvegicus]//0.80:53:83//Hs.26799:W74481
R-HEMBB1001500//EST//1.4e-13:310:67//Hs.162663:AA604515
R-HEMBB1001521//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.5e-29:186:92//Hs.17630:AB018280
R-HEMBB1001527//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//4.7e-51:404:81//Hs.141429:AA631915
R-HEMBB1001531//ESTs//3.3e-13:250:67//Hs.139158:AA226159
R-HEMBB1001535//H.sapiens mRNA for sigma 3B protein//1.9e-39:291:82//Hs.154782:X99459
R-HEMBB1001536//Human mRNA for KIAA0355 gene, complete cds//5.0e-44:318:83//Hs.153014:AB002353
R-HEMBB1001537//Homo sapiens KIAA0409 mRNA, pardal cds//3.2e-47:318:80//Hs.5158:AB007869
R-HEMBB1001555//ESTs//2.6e-13:182:71//Hs.112671:AI377274
R-HEMBB1001562//ESTs//1.7e-43:316:83//Hs.151365:AA643962
R-HEMBB1001564//EST//1.3e-35:141:81//Hs.162197:AA53521
R-HEMBB1001565//Human mRNA for KIAA0331 gene, complete cds//5.1e-18:152:85//Hs.146395:AB002329
R-HEMBB1001585//ESTs//1.1e-32:190:84//Hs.33354:AA179944
R-HEMBB1001586//ESTs//4.9e-94:447:99//Hs.124084:AA843219
R-HEMBB1001588//EST//8.3e-27:363:69//Hs.141603:N66015
R-HEMBB1001603//ESTs//1.2e-101:482:99//Hs.12403:AI090184
R-HEMBB1001618//ESTs//5.8e-35:437:70//Hs.136868:AA805044
R-HEMBB1001619//EST//1.7e-38:476:70//Hs.139093:AA166888
R-HEMBB1001630//Homo sapiens mRNA, clone:RES4-16//5.7e-41:193:90//Hs.121493:D25272
R-HEMBB1001635//ESTs//9.5e-34:304:82//Hs.140444:AI002082
R-HEMBB1001637//ESTs//1.0e-42:443:74//Hs.21978:AA009633
R-HEMBB1001641//EST//2.4e-06:67:86//Hs.162398:AA572813
R-HEMBB1001653//ESTs//4.8e-80:381:99//Hs.140502:AA806438
R-HEMBB1001665//ESTs//2.3e-44:372:79//Hs.132818:AI038577

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R-HEMBB1001668//ESTs//0.73:212:62//Hs.8928:N32572
R-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//5.9e-117:573:97//Hs.24439:AB014546
R-HEMBB1001684//ESTs, Moderately similar to Tbcl [M.musculus]//5.4e-106:523:97//Hs.26939:AA804534
R-HEMBB1001685//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.9e-43:292:86//Hs.96337:AA225358
R-HEMBB1001695//ESTs//3.7e-101:539:94//Hs.78289:R60867
R-HEMBB1001704//EST//0.96:248:57//Hs.163025:AA703038
R-HEMBB1001706//ESTs//1.3e-39:308:81//Hs.141318:N71080
R-HEMBB1001707//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.9e-32:277:73//Hs.142764:AA205569
R-HEMBB1001717//ESTs//1.6e-34:225:87//Hs.57883:AA218645
R-HEMBB1001735//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.6e-11:158:71//Hs.141263:H64113
R-HEMBB1001736//ESTs//0.0035:223:60//Hs.21354:AA203403
R-HEMBB1001747//EST//9.9e-55:293:81//Hs.112866:AA620488
R-HEMBB1001749//ESTs//2.5e-13:95:91//Hs.139888:N25287
R-HEMBB1001753//ESTs//2.6e-07:141:70//Hs.144604:AI052059
R-HEMBB1001756//EST//2.6e-06:165:64//Hs.121195:AA757211
R-HEMBB1001760//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//1.3e-24:264:74//Hs.70008:L00352
R-HEMBB1001762//ESTs//2.1e-81:447:93//Hs.152766:AA211369
R-HEMBB1001785//ESTs//0.040:390:58//Hs.116651:AA993406
R-HEMBB1001797//ESTs//2.1e-90:428:99//Hs.8958:AA169253
R-HEMBB1001802//Desmin//9.9e-95:497:93//Hs.119104:M63391
R-HEMBB1001812//ESTs//1.2e-12:91:78//Hs.138852:AA284247
R-HEMBB1001816//Human Line-1 repeat mRNA with 2 open reading frames//5.9e-13:143:76//Hs.23094:M19503
R-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds//5.5e-106:498:98//Hs.159396:AF056209
R-HEMBB1001836//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//9.6e-39:288:73//Hs.67619:AB007957
R-HEMBB1001839
R-HEMBB1001850//EST//0.020:119:68//Hs.32767:H38125
R-HEMBB1001863//ESTs//4.5e-17:226:72//Hs.157253:AI357539
R-HEMBB1001867//ESTs//2.3e-16:254:68//Hs.123664:AA806106
R-HEMBB1001868//EST//9.8e-30:155:100//Hs.160572:AA888397
R-HEMBB1001869//ESTs//2.8e-42:376:78//Hs.141973:N21434
R-HEMBB1001872//EST//0.85:156:64//Hs.119501:AA487980
R-HEMBB1001874//EST//0.64:107:70//Hs.147482:AI215572
R-HEMBB1001875//EST//0.079:199:59//Hs.121810:AA775240
R-HEMBB1001880//Thromboxane A2 receptor//9.0e-47:297:88//Hs.89887:D38081
R-HEMBB1001899//ESTs//6.3e-68:323:100//Hs.121538:AA609310
R-HEMBB1001905//ESTs//4.4e-19:227:73//Hs.146173:AA906191
R-HEMBB1001906//ESTs//1.6e-90:463:95//Hs.28266:H46725
R-HEMBB1001908//Homo sapiens EVI5 homolog mRNA, complete cds//3.7e-27:557:64//Hs.26929:AF008915
R-HEMBB1001910//EST//6.0e-37:308:78//Hs.162197:AA535216
R-HEMBB1001911//Homo sapiens tapasin (NGS-17) mRNA, complete cds//8.0e-58:367:79//Hs.5247:AF029750
R-HEMBB1001915//ESTs//3.1e-73:395:93//Hs.17054:AI139897
R-HEMBB1001921//Human mRNA for KIAA0392 gene, partial cds//2.7e-50:323:88//Hs.40100:AB002390
R-HEMBB1001922//H.sapiens mRNA for novel member of serine-arginine domain protein, SRrp129//7.4e-38:531:70//Hs.153086:Y11251
R-HEMBB1001925//Human mRNA for KIAA0327 protein, complete cds//9.5e-19:199:77//Hs.149323:AB002325
R-HEMBB1001930//EST//1.9e-18:136:78//Hs.132635:AI032875
R-HEMBB1001944//EST//0.034:228:57//Hs.93664:N23366
R-HEMBB1001945//ESTs//1.8e-83:439:95//Hs.7341:N57875
R-HEMBB1001947//ESTs//5.6e-109:533:97//Hs.48855:AA134589
R-HEMBB1001950//ESTs//1.5e-107:583:93//Hs.8033:N94998
R-HEMBB1001952//ESTs//3.1e-40:283:85//Hs.146811:AA410788

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R-HEMBB1001953//Human mRNA for KIAA0080 gene, partial cds//6.2e-50:284:83//Hs.74554:D38522
R-HEMBB1001957//EST//4.8e-50:382:81//Hs.149580:AI281881
R-HEMBB1001962//ESTs//1.5e-20:143:88//Hs.11924:W26972
R-HEMBB1001967//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.3e-61:296:88//Hs.153468:AB011147
R-HEMBB1001973//ESTs//1.4e-48:303:88//Hs.132722:AA618531
R-HEMBB1001983//ESTs//2.6e-72:374:95//Hs.141022:H06475
R-HEMBB1001988//ESTs//2.0e-31:204:88//Hs.142531:N91572
R-HEMBB1001990//ESTs//9.4e-115:574:96//Hs.44426:AA173223
R-HEMBB1001996
R-HEMBB1001997//ESTs//7.6e-78:380:98//Hs.32682:H37798
R-HEMBB1002002//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//3.0e-18:222:71//Hs.103948:K00627
R-HEMBB1002005//EST//2.2e-41:339:80//Hs.160833:AI345334
R-HEMBB1002009//EST//2.9e-44:245:94//Hs.28788:R66896
R-HEMBB1002015//EST//0.0027:198:63//Hs.160868:AI359052
R-HEMBB1002042//ESTs//1.1e-75:529:84//Hs.106919:AA523900
R-HEMBB1002043//ESTs//7.9e-40:292:83//Hs.70279:AA757426
R-HEMBB1002044//ESTs//2.1e-92:460:94//Hs.115897:AA156638
R-HEMBB1002045//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-75:301:85//Hs.113283:AF018080
R-HEMBB1002049//ESTs//3.8e-77:409:94//Hs.122624:R82638
R-HEMBB1002050//ESTs//8.7e-45:330:82//Hs.44702:AI148840
R-HEMBB1002068//ESTs//8.3e-70:333:99//Hs.134807:AI090671
R-HEMBB1002069//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.5e-75:486:81//Hs.129735:AF010144
R-HEMBB1002092//ESTs//6.5e-46:331:83//Hs.22910:W18193
R-HEMBB1002094//EST//3.6e-45:280:88//Hs.149580:AI281881
R-HEMBB1002115
R-HEMBB1002139//ESTs//4.2e-45:318:85//Hs.107657:AA126814
R-HEMBB1002142//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//1.4e-45:281:88//Hs.125231:AF068006
R-HEMBB1002152//EST//4.3e-39:250:89//Hs.156552:AA833553
R-HEMBB1002189//H.sapiens mRNA for translin associated protein X//1.4e-47:328:85//Hs.96247:X95073
R-HEMBB1002190//ESTs//8.3e-05:122:70//Hs.41974:AF039185
R-HEMBB1002193//Human sky mRNA for Sky, complete cds//8.9e-24:398:69//Hs.301:U18934
R-HEMBB1002217//EST//6.6e-50:303:89//Hs.149580:AI281881
R-HEMBB1002218//ESTs//2.3e-19:150:86//Hs.136031:W95841
R-HEMBB1002232//ESTs//8.9e-47:445:77//Hs.163971:N27584
R-HEMBB1002247//EST//6.6e-09:236:65//Hs.130578:AI004631
R-HEMBB1002249//ESTs//5.2e-16:325:64//Hs.156253:AI334807
R-HEMBB1002254//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-99:590:88//Hs.23094:M19503
R-HEMBB1002255//Human mRNA for KIAA0365 gene, partial cds//5.6e-45:342:83//Hs.84123:AB002363
R-HEMBB1002266//ESTs//4.4e-98:472:98//Hs.65366:AI189112
R-HEMBB1002280//EST//2.9e-41:247:90//Hs.161917:AA483223
R-HEMBB1002300//ESTs//8.4e-19:229:75//Hs.138463:N72305
R-HEMBB1002306//Homo sapiens KIAA0432 mRNA, complete cds//0.0021:138:67//Hs.155174:AB007892
R-HEMBB1002327//EST//0.042:249:61//Hs.121097:AA714637
R-HEMBB1002329//ESTs//1.7e-94:453:99//Hs.7114:R24312
R-HEMBB1002340//ESTs//5.8e-15:163:77//Hs.26378:H10228
R-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein//0.85:46:84//Hs.42644:AJ010841
R-HEMBB1002358//ESTs//2.0e-52:319:81//Hs.140255:AA708322
R-HEMBB1002359//ESTs//2.7e-106:517:97//Hs.13634:AI051613
R-HEMBB1002364//Human mRNA for KIAA0080 gene, partial cds//5.3e-37:360:65//Hs.74554:D38522
R-HEMBB1002371//Catalase//3.3e-22:235:77//Hs.76359:X04085
R-HEMBB1002381//Homo sapiens (JH8) mRNA, partial cds//1.0e-08:120:78//Hs.142296:AF072467
R-HEMBB1002383//ESTs//3.5e-108:520:98//Hs.45140:D80055
R-HEMBB1002387
R-HEMBB1002415//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.3e-23:

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168:77//Hs.133526:N21103
R-HEMBB1002425//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.2e-57:304:90//Hs.144563:AF057280
R-HEMBB1002442//ESTs//2.7e-48:289:87//Hs.155243:N70293
R-HEMBB1002453//Human mRNA for KIAA0355 gene, complete cds//6.2e-45:292:87//Hs.153014:AB002353
R-HEMBB1002457//Human mRNA for KIAA0118 gene, partial cds//2.7e-46:546:71//Hs.154326:D42087
R-HEMBB1002458//EST//1.8e-72:343:100//Hs.162006:AA508089
R-HEMBB1002477//ESTs//1.6e-38:215:93//Hs.18240:AA460083
R-HEMBB1002489//ESTs//1.2e-101:534:94//Hs.7981:H15176
R-HEMBB1002492//ESTs//5.0e-14:350:62//Hs.99205:AA204969
R-HEMBB1002495//ESTs//2.1e-19:147:86//Hs.163747:AA174017
R-HEMBB1002502//ESTs, Weakly similar to p40 [H.sapiens]//1.2e-68:336:98//Hs.141515:T41142
R-HEMBB1002509//ESTs//2.7e-97:459:99//Hs.127638:AI014615
R-HEMBB1002510//ESTs, Weakly similar to located at OATL1 [H.sapiens]//2.2e-48:265:95//Hs.48827:AA873278
R-HEMBB1002520//EST//7.2e-40:198:84//Hs.140493:AA804538
R-HEMBB1002522//Human putative transmembrane receptor IL-1Rrp mRNA, complete cds//0.50:142:69//Hs.159301:U43672
R-HEMBB1002531//EST//0.024:147:61//Hs.148305:AA909605
R-HEMBB1002534//EST//3.1e-22:168:84//Hs.146794:AI149478
R-HEMBB1002545//ESTs//9.2e-90:421:99//Hs.118317:AI033259
R-HEMBB1002550//ESTs, Weakly similar to similar to S. cerevisiae LAG1 [C.elegans]//5.1e-22:210:81//Hs.11896:T68813
R-HEMBB1002556//ISLET AMYLOID POLYPEPTIDE PRECURSORY//1.9e-45:344:82//Hs.51048:X68830
R-HEMBB1002579//ESTs//4.6e-47:326:85//Hs.155184:AA573189
R-HEMBB1002582//ESTs//0.00036:91:76//Hs.140039:AA047045
R-HEMBB1002590//ESTs//1.0e-37:210:84//Hs.36658:N91138
R-HEMBB1002596//Human mRNA for KIAA0118 gene, partial cds//2.2e-46:297:87//Hs.154326:D42087
R-HEMBB1002600//EST//2.5e-17:147:84//Hs.121918:AA777424
R-HEMBB1002601//ESTs//7.8e-68:358:95//Hs.101489:R66923
R-HEMBB1002603//EST//1.1e-47:281:90//Hs.149580:AI281881
R-HEMBB1002607//ESTs//5.4e-75:379:97//Hs.29438:H42896
R-HEMBB1002610//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.2e-07:140:70//Hs.155456:AA707265
R-HEMBB1002613//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//8.5e-47:278:83//Hs.159187:AB007977
R-HEMBB1002614//ESTs//3.4e-81:383:99//Hs.13012:AI094150
R-HEMBB1002617//Homo sapiens protease-activated receptor 4 mRNA, complete cds//7.4e-19:151:80//Hs.137574:AF055917
R-HEMBB1002623//ESTs//1.6e-45:288:87//Hs.138852:AA284247
R-HEMBB1002635//Small inducible cytokine A5 (RANTES)//5.5e-39:278:81//Hs.155464:AF088219
R-HEMBB1002664//EST//8.9e-49:315:87//Hs.149580:AI281881
R-HEMBB1002677//ESTs//0.65:159:62//Hs.163517:AI419775
R-HEMBB1002683//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase//8.6e-54:543:75//Hs.2638:Z28339
R-HEMBB1002684//ESTs//3.0e-18:148:87//Hs.158270:AA776646
R-HEMBB1002686//ESTs//6.1e-80:419:96//Hs.103002:W02753
R-HEMBB1002692//ESTs//3.3e-58:451:82//Hs.141254:AI334099
R-HEMBB1002697//ESTs//6.2e-86:423:98//Hs.129812:AA769487
R-HEMBB1002699//EST//5.6e-46:322:84//Hs.140231:AI054398
R-HEMBB1002702//ESTs//5.6e-36:412:72//Hs.154993:AA142842
R-HEMBB1002705//POLYPOSIS LOCUS PROTEIN 1//0.024:412:58//Hs.74648:M73547
R-HEMBB1002712//ESTs//9.0e-96:451:99//Hs.136806:AA805682
R-MAMMA1000009//ESTs//3.0e-78:392:96//Hs.163947:AA678701
R-MAMMA1000019//Small inducible cytokine A5 (RANTES)//1.5e-47:247:87//Hs.155464:AF088219
R-MAMMA1000020//Zinc finger protein 2 (A1-5)//4.9e-49:384:80//Hs.155533:X60152
R-MAMMA1000025//Homo sapiens KIAA0441 mRNA, complete cds//4.7e-11:154:71//Hs.32511:AB007901
R-MAMMA1000043//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.0e-58:277:84//Hs.93121:AB018304

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R-MAMMA1000045//ESTs//1.0e-38:225:92//Hs.142567:AA287165
R-MAMMA1000055//EST//0.14:91:67//Hs.144061:AA996350
R-MAMMA1000057//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//3.8e-77:545:83//Hs.69747:M35531
R-MAMMA1000069//ESTs//8.0e-108:546:96//Hs.44856:N37065
R-MAMMA1000084//Homo sapiens clone 23632 mRNA sequence//7.3e-43:313:83//Hs.46918:AF052099
R-MAMMA1000085//ESTs, Highly similar to PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C [Schizosaccharomyces pombe]//7.7e-104:546:94//Hs.7779:AA045241
R-MAMMA1000092//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.2e-22:287:71//Hs.136063:U51713
R-MAMMA1000103//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//8.4e-49:334:86//Hs.70008:L00352
R-MAMMA1000117//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.1e-08:96:80//Hs.115088:AA230172
R-MAMMA1000129//EST//2.8e-64:310:99//Hs.136394:AA523577
R-MAMMA1000133
R-MAMMA1000134//ESTs//1.1e-21:152:87//Hs.163747:AA174017
R-MAMMA1000139//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.3e-40:288:78//Hs.159897:AB007970
R-MAMMA1000143//EST//5.0e-52:314:89//Hs.149580:AI281881
R-MAMMA1000155//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.5e-59:562:75//Hs.77579:AF013263
R-MAMMA1000163//ESTs//2.8e-92:457:96//Hs.114413:AA884787
R-MAMMA1000171//Homo sapiens mRNA for putative lipoic acid synthetase, partial//2.5e-39:173:83//Hs.53531:AJ224162
R-MAMMA1000173//ESTs, Highly similar to SRC SUBSTRATE P80/85 PROTEINS [Gallus gallus]//2.4e-07:63:90//Hs.90367:AI357069
R-MAMMA1000175//EST//0.66:217:58//Hs.146444:AI127611
R-MAMMA1000183//ESTs//6.7e-30:341:73//Hs.125254:AA872054
R-MAMMA1000198//EST//2.8e-45:185:88//Hs.149580:AI281881
R-MAMMA1000221//ESTs, Weakly similar to circadian clock protein [M.musculus]//1.4e-41:272:90//Hs.68398:AA421103
R-MAMMA1000227//EST//2.4e-39:388:76//Hs.144175:H70425
R-MAMMA1000241//EST//0.0027:263:61//Hs.37532:H57946
R-MAMMA1000251//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.3e-47:322:86//Hs.15519:AB018315
R-MAMMA1000254//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//2.2e-43:315:83//Hs.129708:AF064090
R-MAMMA1000257//EST//1.6e-62:330:93//Hs.141728:W73041
R-MAMMA1000264//Von Hippel-Lindau syndrome//2.3e-31:141:81//Hs.78160:AF010238
R-MAMMA1000266//ESTs//3.4e-34:150:81//Hs.163980:AA715814
R-MAMMA1000270//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//2.7e-57:304:78//Hs.159187:AB007977
R-MAMMA1000277//Thiopurine S-methyltransferase//3.7e-27:380:71//Hs.51124:AF019369
R-MAMMA1000278//ESTs//5.2e-99:504:95//Hs.8494:W72694
R-MAMMA1000279//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//3.1e-58:295:83//Hs.92381:AB007956
R-MAMMA1000284//EST//4.1e-10:151:73//Hs.60742:AA017066
R-MAMMA1000287
R-MAMMA1000302//Homo sapiens KIAA0432 mRNA, complete cds//1.0:50:84//Hs.155174:AB007892
R-MAMMA1000307//Human mRNA for KIAA0033 gene, partial cds//1.8e-48:468:76//Hs.22271:D26067
R-MAMMA1000309//ESTs//1.7e-94:491:94//Hs.135106:AI335251
R-MAMMA1000312//ESTs//8.9e-74:377:96//Hs.133163:AI051434
R-MAMMA1000313//EST//8.3e-19:294:62//Hs.127400:AA954491
R-MAMMA1000331//ESTs, Moderately similar to envelope protein [H.sapiens]//8.6e-54:278:97//Hs.139170:AA662998
R-MAMMA1000339//EST//6.8e-44:169:89//Hs.149580:AI281881
R-MAMMA1000340//Homo sapiens mRNA for KIAA0625 protein, partial cds//0.82:204:61//Hs.154919:AB014525

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R-MAMMA1000348//ESTs//3.3e-34:320:75//Hs.139158:AA226159
R-MAMMA1000356//ESTs, Highly similar to URIDYLATE KINASE [Saccharomyces cerevisiae]//0.42:172:61//Hs.11463:AA535912
R-MAMMA1000360//Human mRNA for KIAA0118 gene, partial cds//3.8e-43:212:82//Hs.154326:D42087
R-MAMMA1000361//ESTs//3.1e-17:188:68//Hs.164036:AA845659
R-MAMMA1000372//ESTs//1.0e-46:307:85//Hs.145032:AA343523
R-MAMMA1000385//ESTs//8.2e-97:467:98//Hs.152282:AA412065
R-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//8.6e-14:106:92//Hs.32170:AB015132
R-MAMMA1000395//ESTs//1.9e-57:292:96//Hs.11365:AB01060
R-MAMMA1000402//ESTs, Moderately similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//9.1e-47:316:81//Hs.138698:N38973
R-MAMMA1000410//Archain//1.8e-40:443:74//Hs.33642:X81198
R-MAMMA1000413//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.3e-27:304:72//Hs.119387:AB007958
R-MAMMA1000414//ESTs//2.9e-27:181:87//Hs.141254:AI334099
R-MAMMA1000416//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//1.5e-58:282:82//Hs.97203:U83171
R-MAMMA1000421//Thromboxane A2 receptor//4.9e-48:372:80//Hs.89887:D38081
R-MAMMA1000422//ESTs//0.077:240:62//Hs.123136:AA631067
R-MAMMA1000423//Human mRNA for KIAA0392 gene, partial cds//1.3e-48:375:81//Hs.40100:AB002390
R-MAMMA1000424//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.4e-44:418:75//Hs.154069:U06452
R-MAMMA1000429//ESTs//3.9e-113:565:96//Hs.5076:N53461
R-MAMMA1000431//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//8.6e-68:302:85//Hs.97203:U83171
R-MAMMA1000444//Calcium modulating ligand//5.5e-44:344:81//Hs.13572:AF068179
R-MAMMA1000446//ESTs//1.0:236:60//Hs.126958:AI147447
R-MAMMA1000458
R-MAMMA1000468//ESTs//4.4e-51:271:96//Hs.6839:AA055176
R-MAMMA1000472//ESTs//5.4e-39:146:86//Hs.141581:AA315361
R-MAMMA1000478//ESTs//2.3e-74:365:98//Hs.140591:AA828959
R-MAMMA1000483//ESTs//9.9e-23:235:75//Hs.163592:AA280886
R-MAMMA1000490//EST//2.1e-80:500:87//Hs.142137:AA213759
R-MAMMA1000500//Small inducible cytokine A5 (RANTES)//4.7e-43:283:86//Hs.155464:AF088219
R-MAMMA1000501//ESTs//4.2e-37:250:86//Hs.141323:N80390
R-MAMMA1000516//Human mRNA for KIAA0392 gene, partial cds//5.1e-46:459:75//Hs.40100:AB002390
R-MAMMA1000522//ESTs//9.5e-16:226:70//Hs.116673:AA669267
R-MAMMA1000559//ESTs//5.2e-34:244:84//Hs.150727:AI292236
R-MAMMA1000565//EST//2.7e-38:386:76//Hs.162404:AA573131
R-MAMMA1000567//EST//0.33:49:79//Hs.147754:AI220561
R-MAMMA1000576//ESTs//4.9e-57:348:89//Hs.108921:N31211
R-MAMMA1000583//Homo sapiens KIAA0412 mRNA, partial cds//1.3e-52:373:77//Hs.6200:AB007872
R-MAMMA1000585//ESTs//5.1e-40:337:78//Hs.130815:AA936548
R-MAMMA1000594//Small inducible cytokine A5 (RANTES)//3.0e-45:225:80//Hs.155464:AF088219
R-MAMMA1000597//ESTs//2.0e-98:461:99//Hs.43212:AA993042
R-MAMMA1000605//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.5e-50:500:73//Hs.116007:S79267
R-MAMMA1000612//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.6e-108:559:94//Hs.29203:AI344105
R-MAMMA1000616//EST//0.071:169:60//Hs.144096:AI032180
R-MAMMA1000621//ESTs//1.0e-90:477:94//Hs.26073:R96361
R-MAMMA1000623
R-MAMMA1000625//ESTs//3.4e-98:556:91//Hs.119482:AI361002
R-MAMMA1000643//EST//4.9e-74:379:96//Hs.137447:AA342203
R-MAMMA1000664//Homo sapiens mRNA for putative lipoic acid synthetase, partial//3.2e-43:400:76//Hs.53531:AJ224162
R-MAMMA1000669//EST//6.9e-53:368:84//Hs.149580:AI281881

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R-MAMMA1000670//ESTs, Highly similar to HYPOTHETICAL PROTEIN IN TONB 3'REGION [Klebsiella pneumoniae]//8.4e-98:464:98//Hs.31431:AI022065
R-MAMMA1000672//ESTs//2.0e-80:382:99//Hs.106747:AI080476
R-MAMMA1000684//ESTs//6.2e-72:357:98//Hs.67896:AA865212
R-MAMMA1000696//Human mRNA for KIAA0345 gene, complete cds//3.3e-52:216:75//Hs.98938:AB002343
R-MAMMA1000707//EST//7.0e-11:195:68//Hs.147002:AI184644
R-MAMMA1000713//Homo sapiens DEC-205 mRNA, complete cds//1.5e-45:485:74//Hs.153563:AF011333
R-MAMMA1000714//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//1.2e-29:158:79//Hs.142764:AA205569
R-MAMMA1000718//ESTs//3.1e-45:264:88//Hs.152413:AA780515
R-MAMMA1000720//ESTs//7.4e-44:244:87//Hs.111742:R39329
R-MAMMA1000723//Homo sapiens mRNA for alpha(l,2)fucosyltransferase, complete cds//5.6e-52:350:82//Hs.46328:D87942
R-MAMMA1000731//ESTs//1.1e-19:420:66//Hs.35036:H95267
R-MAMMA1000732//EST//2.9e-20:229:74//Hs.135400:AI056893
R-MAMMA1000733//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.2e-35:371:74//Hs.141429:AA631915
R-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.1e-58:253:98//Hs.31575:AF100141
R-MAMMA1000738//ESTs, Weakly similar to similar to Achlya ambisexualis antheridiol steroid receptor [C.elegans]//2.3e-116:557:98//Hs.71472:AA632288
R-MAMMA1000744//ESTs//0.015:143:67//Hs.135382:AI224205
R-MAMMA1000746//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-90:568:86//Hs.23094:M19503
R-MAMMA1000752//Interleukin 10//2.8e-43:339:80//Hs.2180:M57627
R-MAMMA1000760//EST//5.0e-44:306:86//Hs.162404:AA573131
R-MAMMA1000761//EST//5.0e-41:187:85//Hs.162335:AA564256
R-MAMMA1000775//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:465:76//Hs.153014:AB002353
R-MAMMA1000776//ESTs//1.9e-43:429:73//Hs.141742:W22204
R-MAMMA1000778//ESTs//1.8e-31:445:70//Hs.111723:H57439
R-MAMMA1000782//EST//0.0019:102:68//Hs.120686:AA747150
R-MAMMA1000798//ESTs//1.4e-13:267:69//Hs.140156:AA704163
R-MAMMA1000802//Clathrin, light polypeptide (Lcb)//1.5e-45:358:76//Hs.73919:X81637
R-MAMMA1000831//ESTs//1.3e-1,04:510:97//Hs.17494:AA572675
R-MAMMA1000839//EST//2.9e-51:307:89//Hs.149580:AI281881
R-MAMMA1000841//ESTs//1.3e-34:412:72//Hs.121256:AA757902
R-MAMMA1000842//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//9.4e-44:363:79//Hs.96337:AA225358
R-MAMMA1000843//ESTs//2.2e-106:525:97//Hs.152016:AA603097
R-MAMMA1000845//ESTs//1.6e-66:327:98//Hs.156900:AA468955
R-MAMMA1000851//ESTs//3.7e-14.115:86//Hs.140590:R76251
R-MAMMA1000855//Human mRNA for KIAA0392 gene, partial cds//5.7e-47:281:91//Hs.40100:AB002390
R-MAMMA1000856//EST//1.8e-16:150:79//Hs.136811:AA789212
R-MAMMA1000862//EST//3.2e-05:93:73//Hs.161205:AI419311
R-MAMMA1000863//ESTs//1.0e-46:446:73//Hs.153432:AA098922
R-MAMMA1000865//Homo sapiens clone 23632 mRNA sequence//3.0e-39:324:80//Hs.46918:AF052099
R-MAMMA1000867//ESTs//9.8e-16:193:76//Hs.152340:AA521399
R-MAMMA1000875//EST//3.1e-24:301:72//Hs.132635:AI032875
R-MAMMA1000876//ESTs//9.9e-48:246:97//Hs.112165:AA621243
R-MAMMA1000877//ESTs//1.4e-38:324:79//Hs.141024:H07128
R-MAMMA1000880//Homo sapiens mRNA for KIAA0594 protein, partial cds//3.2e-40:542:68//Hs.154872:AB011166
R-MAMMA1000883//ESTs//1.0:207:60//Hs.47199:N51107
R-MAMMA1000897//ESTs//2.6e-78:383:97//Hs.41067:AI310215
R-MAMMA1000905//Human mRNA for KIAA0331 gene, complete cds//9.7e-53:307:91//Hs.146395:AB002329
R-MAMMA1000906//ESTs//8.0e-25:206:83//Hs.141825:AA017093
R-MAMMA1000908//ESTs//4.4e-32:176:96//Hs.38559:AA701634
R-MAMMA1000914//ESTs//0.032:150:63//Hs.119162:AA399989
R-MAMMA1000921//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//7.7e-38:269:74//Hs.108966:U48696

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R-MAMMA1000931//ESTs//1.2e-80:457:91//Hs.122319:AA782335
R-MAMMA1000940//ESTs//3.3e-43:329:82//Hs.35254:AI133727
R-MAMMA1000941//ESTs//7.5e-55:306:84//Hs.163936:AA632281
R-MAMMA1000942//ESTs//2.5e-83:405:98//Hs.116491:AA650428
R-MAMMA1000943//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//9.3e-79:567:80//Hs.1361:M55053
R-MAMMA1000956//EST//5.7e-53:256:100//Hs.162209:AA536178
R-MAMMA1000957//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//7.5e-49:340:85//Hs.103458:X53795
R-MAMMA1000962//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.0e-48:216:85//Hs.153468:AB011147
R-MAMMA1000968//EST//6.2e-46:302:86//Hs.149580:AI281881
R-MAMMA1000975//ESTs//1.4e-85:428:96//Hs.141742:W22204
R-MAMMA1000979//Homo sapiens mRNA for KIAA0761 protein, partial cds//8.0e-39:338:79//Hs.93121:AB018304
R-MAMMA1000987//EST//2.8e-41:249:90//Hs.149580:AI281881
R-MAMMA1000998//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//3.9e-50:445:77//Hs.77579:AF013263
R-MAMMA1001003//Sialophorin (gpL115, leukosialin, CD43)//4.1e-51:282:82//Hs.80738:X52075
R-MAMMA1001008//ESTs, Weakly similar to renin [H.sapiens]//1.9e-82:405:97//Hs.25863:AA630313
R-MAMMA1001021//Homo sapiens DEC-205 mRNA, complete cds//3.0e-44:309:86//Hs.153563:AF011333
R-MAMMA1001024//ESTs//6.8e-35:333:78//Hs.107657:AA126814
R-MAMMA1001030//ESTs//1.6e-110:552:96//Hs.59483:AA524536
R-MAMMA1001035//ESTs//1.0e-45:273:85//Hs.138856:H47461
R-MAMMA1001038//Human mRNA for KIAA0392 gene, partial cds//3.0e-50:298:91//Hs.40100:AB002390
R-nnnnnnnnnnnn//ESTs//3.6e-86:445:95//Hs.122625:R68650
R-MAMMA1001050//EST//2.2e-54:387:85//Hs.149580:AI281881
R-MAMMA1001059//ESTs, Moderately similar to RNA helicase [M.musculus]//1.7e-13:273:65//Hs.98738:AI015487
R-MAMMA1001067//ESTs//1.3e-38:324:78//Hs.20190:AA525532
R-MAMMA1001073//ESTs//5.2e-106:554:94//Hs.12336:W63748
R-MAMMA1001074//Human mRNA for KIAA0355 gene, complete cds//1.2e-38:544:68//Hs.153014:AB002353
R-MAMMA1001075//ESTs//2.0e-98:463:99//Hs.18341:N38944
R-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-84:556:85//Hs.23094:M19503
R-MAMMA1001082//ESTs//2.4e-71:356:97//Hs.152302:T90222
R-MAMMA1001091//ESTs//4.7e-83:429:95//Hs.154412:AA310926
R-MAMMA1001092//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//6.4e-34:262:82//Hs.129727:AF035587
R-MAMMA1001105//Human putative RNA binding protein RNPL mRNA, complete cds//4.2e-27:232:76//Hs.61840:U28686
R-MAMMA1001110//ESTs//1.6e-17:128:87//Hs.161314:AI421576
R-MAMMA1001126//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//8.8e-53:462:78//Hs.116007:S79267
R-MAMMA1001133//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.8e-59:460:81//Hs.5247:AF029750
R-MAMMA1001139//ESTs//1.3e-62:341:94//Hs.18819:R01029
R-MAMMA1001143//ESTs//3.0e-48:383:80//Hs.152340:AA521399
R-MAMMA1001145//Calcium modulating ligand//5.1e-48:403:79//Hs.13572:AF068179
R-MAMMA1001154//EST//6.8e-35:313:75//Hs.162404:AA573131
R-MAMMA1001161//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.1e-58:409:84//Hs.5247:AF029750
R-MAMMA1001162//ESTs, Highly similar to t-BOP [M.musculus]//2.1e-91:430:99//Hs.129982:AI420970
R-MAMMA1001181//ESTs//5.0e-112:557:96//Hs.118181:W02251
R-MAMMA1001186//ESTs//3.8e-85:410:99//Hs.163811:W44959
R-MAMMA1001191//ESTs//0.018:57:87//Hs.141253:AA226519
R-MAMMA1001198//ESTs, Weakly similar to involved in signaling by the epidermal growth factor receptor [M.musculus]//2.6e-80:358:96//Hs.163827:AA074202
R-MAMMA1001202//ESTs//7.0e-43:230:95//Hs.79788:AA527348
R-MAMMA1001203//Clathrin, light polypeptide (Lcb)//2.8e-65:348:79//Hs.73919:X81637
R-MAMMA1001206//EST//0.098:84:72//Hs.162941:AA635148

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R-MAMMA1001215//ESTs//1.3e-43:156:86//Hs.155243:N70293
R-MAMMA1001220//ESTs//8.9e-17:276:68//Hs.116518:AA653202
R-MAMMA1001222//ESTs//0.49:112:66//Hs.24668:AA897315
R-MAMMA1001243//EST//0.99:143:62//Hs.68522:C20701
R-MAMMA1001244//ESTs//2.2e-06:79:83//Hs.123163:AA809619
R-MAMMA1001249//ESTs//4.2e-68:343:97//Hs.147139:AI191307
R-MAMMA1001256//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.7e-31:221:77//Hs.142764:AA205569
R-MAMMA1001259//ESTs//1.3e-43:266:90//Hs.6193:AA045149
R-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.0e-21:226:75//Hs.65238:AB014561
R-MAMMA1001268//H.sapiens HCG II mRNA//2.4e-53:181:85//Hs.146333:X81001
R-MAMMA1001271//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK [Mus musculus]//1.1e-108:546:95//Hs.18999:N30643
R-MAMMA1001274//Homo sapiens mRNA for KIAA0572 protein, partial cds//4.4e-32:188:94//Hs.14409:AB011144
R-MAMMA1001280//EST//0.0015:170:62//Hs.116770:AA630371
R-MAMMA1001292//ESTs//5.6e-102:481:99//Hs.94810:AA811876
R-MAMMA1001296//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.2e-27:348:70//Hs.15731:AB011135
R-MAMMA1001298//ESTs//1.4e-44:375:79//Hs.70279:AA757426
R-MAMMA1001305//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.0e-43:300:85//Hs.46468:U45984
R-MAMMA1001322//Homo sapiens stress-activated protein kinase 4 mRNA, complete cds//8.8e-12:188:70//Hs.55771:AF004709
R-MAMMA1001324//ESTs//5.3e-68:297:88//Hs.121228:AA709471
R-MAMMA1001330//ESTs//1.6e-57:429:83//Hs.70279:AA757426
R-MAMMA1001341//Homo sapiens 4F5S mRNA, complete cds//4.8e-27:285:75//Hs.32567:AF073519
R-MAMMA1001343//ESTs//8.1e-51:273:93//Hs.162208:AA536127
R-MAMMA1001346//ESTs//1.0:122:65//Hs.33028:AA482478
R-MAMMA1001383//ESTs//1.4e-45:377:80//Hs.114671:N39322
R-MAMMA1001388//EST//7.7e-47:361:80//Hs.162197:AA535216
R-MAMMA1001397//EST//8.7e-48:337:83//Hs.149580:AI281881
R-MAMMA1001408//EST//1.2e-38:251:87//Hs.162677:AA604831
R-MAMMA1001411//ESTs//4.3e-93:435:99//Hs.105460:AA780275
R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, complete cds//1.6e-19:117:96//Hs.19122:AF038957
R-MAMMA1001420//ESTs//7.3e-96:507:95//Hs.55299:AI335267
R-MAMMA1001435//ESTs//5.0e-97:459:99//Hs.144843:AI222168
R-MAMMA1001442//ESTs//7.1e-28:167:83//Hs.141019:AA287618
R-MAMMA1001446//Homo sapiens KIAA0432 mRNA, complete cds//6.2e-19:328:67//Hs.155174:AB007892
R-MAMMA1001452//EST//5.6e-44:487:75//Hs.161476:N57542
R-MAMMA1001465
R-MAMMA1001476//Homo sapiens yolk sac permease-like molecule 3 (YSPL3) mRNA, complete cds//0.79:182:66//Hs.136529:AF058317
R-MAMMA1001487//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-35:328:78//Hs.43681:AL022394
R-MAMMA1001501//ESTs//4.6e-100:472:98//Hs.123660:AA813065
R-MAMMA1001502//Human mRNA for KIAA0080 gene, partial cds//5.6e-15:220:69//Hs.74554:D38522
R-MAMMA1001510
R-MAMMA1001522//ESTs//3.2e-16:214:75//Hs.152816:AA634242
R-MAMMA1001547//H.sapiens mRNA for urea transporter//2.3e-45:282:89//Hs.66710:X96969
R-MAMMA1001551//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.9e-56:489:76//Hs.108966:U48696
R-MAMMA1001575//ESTs//4.3e-92:440:98//Hs.162882:AA807140
R-MAMMA1001576//ESTs, Highly similar to TUBULIN GAMMA CHAIN [Homo sapiens]//1.9e-111:549:96//Hs.21635:AI417305
R-MAMMA1001590//ESTs//1.1e-63:324:96//Hs.142217:AA278441
R-MAMMA1001600//ESTs//5.6e-15:159:78//Hs.138633:H98792

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R-MAMMA1001604
R-MAMMA1001606//ESTs, Weakly similar to finger protein kox1 [H.sapiens]//1.9e-97:488:96//Hs.143263:AI057616
R-MAMMA1001620//Homo sapiens mRNA, clone:RES4-16//5.4e-43:408:76//Hs.121493:D25272
R-MAMMA1001627//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.0e-49:472:76//Hs.15519:AB018315
R-MAMMA1001630//ESTs, Weakly similar to putative p150 [H.sapiens]//6.8e-15:168:73//Hs.115216:AA291074
R-MAMMA1001633//EST//5.1e-14:228:68//Hs.141456:N36377
R-MAMMA1001635//ESTs//3.4e-37:368:75//Hs.164033:AA769606
R-MAMMA1001649
R-MAMMA1001663//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.7e-54:272:81//Hs.129735:AF010144
R-MAMMA1001670//Small inducible cytokine A5 (RANTES)//5.7e-50:304:89//Hs.155464:AF088219
R-MAMMA1001671//EST//1.9e-14:312:65//Hs.137153:R46248
R-MAMMA1001679//H.sapiens mRNA for rho GDP-dissociation Inhibitor 1//0.066:196:62//Hs.159161:X69550
R-MAMMA1001683//ESTs//4.9e-94:447:98//Hs.134464:AI151081
R-MAMMA1001686//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-17:246:73//Hs.67619:AB007957
R-MAMMA1001692//Human mRNA for KIAA0063 gene, complete cds//2.1e-47:294:89//Hs.3094:D31884
R-MAMMA1001711//ESTs//2.4e-86:439:96//Hs.18498:N52088
R-MAMMA1001715//ESTs//1.2e-73:399:9311Hs.124620:AI082338
R-MAMMA1001730//ESTs//1.1e-85:403:99//Hs.125464:AI084596
R-MAMMA1001735//ESTs, Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]//3.7e-110:552:96//Hs.6923:AI161158
R-MAMMA1001740//ESTs//4.6e-45:342:82//Hs.37573:H59651
R-MAMMA1001743//EST//2.7e-58:412:85//Hs.149742:AI285666
R-MAMMA1001744
R-MAMMA1001745//EST//5.6e-54:374:84//Hs.137041:AA877817
R-MAMMA1001751//EST//3.5e-36:375:73//Hs.139715:N25041
R-MAMMA1001754//EST//0.18:144:66//Hs.71957:AA151413
R-MAMMA1001757//ESTs//1.0e-9.8:488:96//Hs.45184:C14904
R-MAMMA1001760//ESTs//8.7e-29:206:86//Hs.143310:AI142276
R-MAMMA1001764//ESTs//0.00012:434:58//Hs.120051:AA707847
R-MAMMA1001768//Human mRNA for KIAA0327 protein, complete cds//2.3e-41:299:85//Hs.149323:AB002325
R-MAMMA1001769//EST//1.7e-15:139:81//Hs.162399:AA572825
R-MAMMA1001771//ESTS, Moderately similar to semaphorin B [M.musculus]//7.6e-43:257:91//Hs.7634:AA481246
R-MAMMA1001783//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.6e-42:272:86//Hs.73614:U83460
R-MAMMA1001785//ESTs//1.5e-87:431:98//Hs.131065:AA972238
R-MAMMA1001788//EST//0.95:108:62//Hs.145881:AI274644
R-MAMMA1001790//ESTs//4.0e-41:340:80//Hs.158045:AA425744
R-MAMMA1001806//EST//1.4e-40:297:84//Hs.141240:H60313
R-MAMMA1001812//ESTs//2.4e-93:446:98//Hs.129034:AA776892
R-MAMMA1001815//EST//0.00053:371:59//Hs.133255:AI052659
R-MAMMA1001817//Human mRNA for KIAA0226 gene, complete cds//2.1e-46:325:87//Hs.44106:D86979
R-MAMMA1001818
R-MAMMA1001820//EST//1.9e-49:303:89//Hs.149580:AI281881
R-MAMMA1001824//Homo sapiens 4F5S mRNA, complete cds//4.3e-48:438:75//Hs.32567:AF073519
R-MAMMA1001836//ESTs//3.8e-06:128:71//Hs.143611:M78140
R-MAMMA1001837//Homo sapiens KIAA0395 mRNA, partial cds//3.8e-47:339:83//Hs.43681:AL022394
R-MAMMA1001848//ESTs//2.1e-16:125:85//Hs.161662:AA836811
R-MAMMA1001851//ESTs//4.5e-48:344:84//Hs.138856:H47461
R-MAMMA1001854//Small inducible cytokine A5 (RANTES)//2.6e-38:280:83//Hs.155464:AF088219
R-MAMMA1001858//ESTs//1.1e-44:331:83//Hs.44702:AI148840
R-MAMMA1001864//Homo sapiens mRNA for KIAA0475 protein, complete cds//7.8e-31:262:77//Hs.5737:AB007944
R-nnnnnnnnnnnn//Homo sapiens antigen NY-CO-16 mRNA, complete cds//9.2e-06:450:58//Hs.132206:

BNSDOCID: <EP___1074617A2_I_>

AF039694
R-MAMMA1001874//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.9e-46:332:83//Hs.73614:U83460
R-MAMMA1001878//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1.2e-46:429:78//Hs.2379:U23942
R-MAMMA1001880//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//7.6e-26:230:79//Hs.106008:AA147606
R-MAMMA1001890//ESTs//1.1e-39:338:79//Hs.146811:AA410788
R-MAMMA1001907//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//6.7e-47:283:89//Hs.103458:X53795
R-nnnnnnnnnnnn//ESTs//0.043:134:65//Hs.145333:AI251374
R-MAMMA1001931//ESTs//1.8e-75:361:99//Hs.148125:AA693801
R-MAMMA1001956//Homo sapiens mRNA for KIAA0706 protein, complete cds//1.4e-18:174:77//Hs.139648:AB014606
R-MAMMA1001963//ESTs//6.7e-28:206:84//Hs.163254:AA828790
R-MAMMA1001969//ESTs, Weakly similar to hypothetical protein [H.sapiens]//6.7e-24:331:71//Hs.140506:AA308018
R-MAMMA1001970//ESTs//8.9e-61:286:84//Hs.141575:AA211734
R-MAMMA1001992//ESTs//4.4e-43:339:82//Hs.155498:W27084
R-MAMMA1002009//Small inducible cytokine A5 (RANTES)//4.6e-24:330:70//Hs.155464:AF088219
R-MAMMA1002011//ESTs//9.5e-72:360:97//Hs.13525:R39054
R-MAMMA1002032//Human melanoma antigen recognized by T-cells (MART-1) mRNA//3.7e-45:370:80//Hs.154069:U06452
R-MAMMA1002033//EST//4.6e-23:264:74//Hs.161917:AA483223
R-MAMMA1002041//ESTs//3.8e-100:465:100//Hs.141361:AI206412
R-MAMMA1002042//Homo sapiens 4F5S mRNA, complete cds//1.1e-43:407:76//Hs.32567:AF073519
R-MAMMA1002047//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.9e-37:316:74//Hs.10458:AF088219
R-MAMMA1002056//EST//1.3e-51:310:90//Hs.149580:AI281881
R-MAMMA1002058//ESTs//5.9e-16:135:84//Hs.95807:AA146979
R-MAMMA1002068//ESTs, Weakly similar to HYPOTHETICAL 43.3 KD PROTEIN IN QOXD-VPR INTERGENIC REGION [Bacillus subtilis]//4.0e-45:404:7811Hs/138596:N38806
R-MAMMA1002078//EST//2.2e-15:207:71//Hs.132635:AI032875
R-MAMMA1002082//Homo sapiens mRNA for TSC403 protein, complete cds//1.7e-42:314:83//Hs.10887:AB013924
R-MAMMA1002084//Human mRNA for KIAA0392 gene, partial cds//3.7e-46:308:87//Hs.40100:AB002390
R-MAMMA1002093//EST//0.89:213:60//Hs.151201:AI125907
R-MAMMA1002108//ESTs//1.0e-95:515:93//Hs.29002:H11347
R-MAMMA1002118
R-MAMMA1002125//Thromboxane A2 receptor//7.2e-43:335:83//Hs.89887:D38081
R-MAMMA1002132//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.4e-58:396:78//Hs.129735:AF010144
R-MAMMA1002140//Homo sapiens nephrin (NPHS1) mRNA, complete cds//1.4e-37:422:75//Hs.128834:AF035835
R-MAMMA1002143//ESTs//0.050:123:69//Hs.8231:AA152276
R-MAMMA1002145//Homo sapiens KIAA0426 mRNA, complete cds//5.0e-21:371:69//Hs.97476:AB007886
R-MAMMA1002153//ESTs//2.0e-31:159:77//Hs.130815:AA936548
R-MAMMA1002155//Human Line-1 repeat mRNA with 2 open reading frames//8.7e-39:506:69//Hs.23094:M19503
R-MAMMA1002156//Homo sapiens mRNA for putative lipoic acid synthetase, partial//2.9e-44:336:82//Hs.53531:AJ224162
R-MAMMA1002158//ESTs//3-0e-40:313:83//Hs.118273:AA626040
R-MAMMA1002170//Homo sapiens mRNA for TRAF5, complete cds//7.7e-37:370:77//Hs.29736:AB000509
R-MAMMA1002174//ESTs//2.5e-16:186:75//Hs.141203:H52638
R-MAMMA1002198//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//6.2e-51:318:82//Hs.92381:AB007956
R-MAMMA1002209//ESTs//9.2e-34:111:88//Hs.141575:AA211734
R-MAMMA1002215//ESTs//3.6e-101:530:94//Hs.26780:N50038
R-MAMMA1002219//Homo sapiens mRNA for KIAA0640 protein, partial cds//5.2e-45:283:88//Hs.153026:AB014540

BNSDOCID: <EP___1074617A2_I_>

R-MAMMA1002230//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//9.1e-50:330:77//Hs.108966:U48696
R-MAMMA1002236
R-MAMMA1002243
R-MAMMA1002250//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.2e-44:299:87//Hs.113283:AF018080
R-MAMMA1002267//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.6e-54:207:81//Hs.92381:AB007956
R-MAMMA1002268//ESTs//2.9e-94:439:100//Hs.68061:AI042283
R-MAMMA1002269//ESTs//7.4e-05:170:65//Hs.140466:AA766772
R-MAMMA1002282//ESTs//7.8e-09:69:78//Hs.159502:AA225141
R-MAMMA1002292//ESTs//5.3e-64:334:94//Hs.113606:AI138751
R-MAMMA1002293//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//1.7e-39:203:81//Hs.154257:AI275982
R-MAMMA1002294//EST//8.1e-43:326:82//Hs.149580:AI281881
R-MAMMA1002297//ESTs//6.5e-45:323:83//Hs.155475:AA761454
R-MAMMA1002298//ESTs//1.7e-68:355:96//Hs.52683:H87153
R-MAMMA1002299//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//2.3e-58:346:91//Hs.140385:AA773359
R-MAMMA1002308
R-MAMMA1002310//Human melanoma antigen recognized by T-cells (MART-1) mRNA//2.2e-44:280:87//Hs.154069:U06452
R-MAMMA1002311//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-70:503:81//Hs.23094:M19503
R-MAMMA1002312//EST//1.7e-31:144:80//Hs.135936:N36094
R-MAMMA1002317//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//4.3e-49:457:76//Hs.144563:AF057280
R-MAMMA1002319//ESTs//3.9e-38:297:70//Hs.140326:AA827183
R-MAMMA1002322//ESTs//1.1e-46:301:86//Hs.155498:W27084
R-MAMMA1002329//EST//2.6e-09:146:72//Hs.132366:AI026658
R-MAMMA1002332//Homo sapiens clone 23892 mRNA sequence//2.6e-45:387:70//Hs.91916:AF035317
R-MAMMA1002333//EST//1.8e-09:139:74//Hs.137800:AA886897
R-MAMMA1002339//ESTs//4.2e-47:310:76//Hs.138865:W57618
R-MAMMA1002347//ESTS//1.5e-44:326:83//Hs.111723:H57439
R-MAMMA1002351//ESTs//3.0e-112:545:97//Hs.26209:AI143127
R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2//1.5e-58:259:92//Hs.43628:Y15228
R-MAMMA1002353//Human mRNA for KIAA0392 gene, partial cds//4.5e-40:360:77//Hs.40100:AB002390
R-MAMMA1002355//ESTs//1.4e-29:307:75//Hs.3769:AI085367
R-MAMMA1002356//Clathrin, light polypeptide (Lcb)//4.9e-31:217:88//Hs.73919:X81637
R-MAMMA1002359//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-70:483:84//Hs.113283:AF018080
R-MAMMA1002360//ESTs//3.5e-19:301:69//Hs.124701:AA701475
R-MAMMA1002361//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//2.6e-30:244:81//Hs.129727:AF035587
R-MAMMA1002362//ESTs//2.3e-43:241:88//Hs.150727:AI292236
R-MAMMA1002380//ESTs//5.1e-36:322:79//Hs.136994:AA843542
R-MAMMA1002384//Small inducible cytokine A5 (RANTES)//1.8e-42:298:84//Hs.155464:AF088219
R-MAMMA1002385//ESTs//0.57:203:63//Hs.146303:AA579061
R-MAMMA1002392//Human mRNA for platelet-activating factor acetylhydrolase 2, complete cds//5.8e-41:305:83//Hs.86188:D87845
R-MAMMA1002411//ESTs//4.4e-68:385:92//Hs.53478:N92294
R-MAMMA1002413//Homo sapiens mRNA for small GTP-binding protein, complete cds//3.3e-14:138:75//Hs.115325:D84488
R-MAMMA1002417//ESTs//1.6e-98:475:98//Hs.96345:N22588
R-MAMMA1002427//ESTs//3.1e-39:274:79//Hs.141130:H28477
R-MAMMA1002428//ESTs//8.4e-11:215:66//Hs.141022:H06475
R-MAMMA1002434//ESTS, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//2.5e-106:521:98//Hs.112152:AA487348
R-MAMMA1002446//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//4.7e-37:374:68//Hs.157142:U85996
R-MAMMA1002454//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0485//2.0e-60:323:81//Hs.

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89121:AB007954
R-MAMMA1002461//ESTs//4.7e-111:548:97//Hs.104281:AA147076
R-MAMMA1002470//ESTs, Highly similar to HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.5e-104:544:93//Hs.94570:AI192106
R-MAMMA1002475//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.4e-31:263:79//Hs.38687:AA744496
R-MAMMA10024807/ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-34:159:79//Hs.133526:N21103
R-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//8.9e-116:560:97//Hs.155223:AF055460
R-MAMMA1002494//ESTs//3.2e-47:303:88//Hs.155243:N70293
R-MAMMA1002498//Human novel homeobox mRNA for a DNA binding protein//0.0043:331:58//Hs.37035:U07664
R-MAMMA1002524//ESTs//0.0039:354:61//Hs.125797:AA806277
R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//3.9e-103:529:95//Hs.18858:AF065214
R-MAMMA1002545//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.5e-50:317:88//Hs.153468:AB011147
R-MAMMA1002554//ESTs//2.3e-85:445:95//Hs.139140:AA218851
R-MAMMA1002556//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-12:280:65//Hs.12725:T65058
R-MAMMA1002566//ESTs//2.3e-88:421:99//Hs.17602:AA705681
R-MAMMA1002571//ESTs//5.1e-97:456:99//Hs.152834:AA595693
R-MAMMA1002573//ESTs//3.1e-38:258:87//Hs.163989:R74433
R-MAMMA1002585//ESTs//7.8e-96:533:91//Hs.26009:H49371
R-MAMMA1002590//ESTs//0.61:202:62//Hs.161190:AI419258
R-MAMMA1002597//Cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6//2.9e-21:177:75//Hs.1360:M29874
R-MAMMA1002598//ESTs//3.4e-113:544:97//Hs.20263:AA573737
R-MAMMA1002603//Thiopurine S-methyltransferase//7.6e-35:225:80//Hs.51124:AF019369
R-MAMMA1002612//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//4.2e-46:424:75//Hs.1361:M55053
R-MAMMA1002617//ESTs//1.1e-38:229:92//Hs.96987:W27389
R-MAMMA1002618//Landsteiner-Wiener blood group glycoprotein//1.3e-27:185:73//Hs.108287:L27670
R-MAMMA1002619//ESTs//1.7e-95:480:96//Hs.54873:AA526306
R-MAMMA1002622//Thromboxane A2 receptor//3.2e-46:298:87//Hs.89887:D38081
R-MAMMA1002623//EST//4.3e-49:336:85//Hs.149580:AI281881
R-MAMMA1002625//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//2.3e-35:308:79//Hs.93332:AA811920
R-MAMMA1002629//Homo sapiens mRNA for small GTP-binding protein, complete cds//9.7e-57:283:86//Hs.115325:D84488
R-MAMMA1002636//Human mRNA for KIAA0392 gene, partial cds//1.2e-49:303:89//Hs.40100:AB002390
R-MAMMA1002637//ESTs//1.3e-55:391:85//Hs.95074:AI144421
R-MAMMA1002646//ESTs//7.4e-36:182:80//Hs.163937:N69915
R-MAMMA1002650//ESTs//1.6e-102:547:94//Hs.57841:W63776
R-MAMMA1002655
R-MAMMA1002662//Homo sapiens KIAA0426 mRNA, complete cds//2.2e-46:462:75//Hs.97476:AB007886
R-MAMMA1002665//Human mRNA for KIAA0118 gene, partial cds//9.1e-51:376:82//Hs.154326:D42087
R-MAMMA1002671//ESTs, Weakly similar to coded for by C. elegans cDNA yk52e10.5 [C.elegans]//5.3e-108:544:96//Hs.16464:W19606
R-MAMMA1002673//EST//3.3e-35:169:79//Hs.140046:AA668213
R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//4.6e-109:544:96//Hs.3363:D86987
R-MAMMA1002685//EST//1.9e-31:223:86//Hs.112540:AA601385
R-MAMMA1002698//ESTs//5.9e-43:292:85//Hs.144660:AA652675
R-MAMMA1002699//ESTs//3.2e-25:134:100//Hs.126049:F22510
R-MAMMA1002701//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.9e-70:353:96//Hs.138404:R70986

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R-MAMMA1002708//ESTs//2.1e-76:413:94//Hs.57932:W69234
R-MAMMA1002711//ESTs//1.9e-44:236:96//Hs.138575:H67858
R-MAMMA1002721//Homo sapiens DEC-205 mRNA, complete cds//2.7e-43:273:89//Hs.153563:AF011333
R-MAMMA1002727//ESTs//2.9e-84:395:10011Hs.162826:AA679571
R-MAMMA1002728//Small inducible cytokine A5 (RANTES)//3.4e-42:266:88//Hs.155464:AF088219
R-MAMMA1002744//ESTs//4.2e-18:473:63//Hs.42826:AA846757
R-MAMMA1002746//ESTs//1.8e-100:473:99//Hs.117558:AA779907
R-MAMMA1002748//Human melanoma antigen recognized by T-cells (MART-1) mRNA//5.8e-40:330:80//Hs.154069:U06452
R-MAMMA1002754//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-40:369:77//Hs.105292:AA504776
R-MAMMA1002758
R-MAMMA1002764//ESTs//4.2e-103:486:99//Hs.159909:AI393281
R-MAMMA1002765//ESTs//1.6e-37:338:76//Hs.37573:H59651
R-MAMMA1002769//ESTs//0.72:409:57//Hs.141376:AI301272
R-MAMMA1002780//ESTs//1.6e-52:292:92//Hs.135985:AA342750
R-MAMMA1002782//ESTs//1.0e-31:157:80//Hs.159510:AA297145
R-MAMMA1002796//ESTs//3.8e-49:284:92//Hs.156479:AA513812
R-MAMMA1002807//Archain//1.4e-39:315:80//Hs.33642:X81198
R-MAMMA1002820//ESTs//5.0e-14:192:74//Hs.134635:AA226260
R-MAMMA1002830//EST//4.0e-50:255:97//Hs.160674:AI248319
R-MAMMA1002833//EST//1.2e-48:306:88//Hs.149580:AI281881
R-MAMMA1002835
R-MAMMA1002838//EST//2.7e-12:161:76//Hs.163252:AA828723
R-MAMMA1002842//ESTs//1.7e-41:366:78//Hs.141899:N22395
R-MAMMA1002843//Von Hippel-Lindau syndrome//8.8e-38:258:79//Hs.78160:AF010238
R-MAMMA1002844//ESTs//3.5e-51:250:99//Hs.151445:AA351081
R-MAMMA1002858//H.sapiens ERF-1 mRNA 3' end//9.0e-101:361:91//Hs.85155:X79067
R-MAMMA1002868//ESTs//2.1e-38:301:80//Hs.132717:AA171941
R-MAMMA1002871//EST//6.0e-88:413:99//Hs.149057:AI243592
R-MAMMA1002880//ESTs//6.5e-100:506:96//Hs.163533:N52194
R-MAMMA1002881//EST//1.1e-40:335:80//Hs.160895:AI365871
R-MAMMA1002886//Small inducible cytokine A5 (RANTES)//3.4e-36:228:88//Hs.155464:AF088219
R-MAMMA1002887//ESTs//4.7e-87:409:99//Hs.152155:AA424811
R-MAMMA1002890//ESTs, Weakly similar to coded for by C. elegans cDNA CEESB82F [C.elegans]//4.2e-92:438:99//Hs.155871:AA533783
R-MAMMA1002892//Homo sapiens EVI5 homolog mRNA, complete cds//4.9e-62:322:80//Hs.26929:AF008915
R-MAMMA1002895//ESTs//2.7e-32:330:76//Hs.139132:AA211087
R-MAMMA1002908//Calcium modulating ligand//4.6e-48:313:86//Hs.13572:AF068179
R-MAMMA1002909//Human mRNA for KIAA0180 gene, partial cds//3.4e-09:132:76//Hs.90981:D80002
R-MAMMA1002930//EST//4.9e-44:260:91//Hs.149580:AI281881
R-MAMMA1002938
R-MAMMA1002941//Human Line-1 repeat mRNA with 2 open reading frames//1.1e-83:556:85//Hs.23094:M19503
R-MAMMA1002947//ESTs//7.0e-22:222:80//Hs.103395:T79243
R-MAMMA1002964//Human mRNA for KIAA0355 gene, complete cds//1.6e-44:427:77//Hs.153014:AB002353
R-MAMMA1002970//Thromboxane A2 receptor//7.9e-48:300:84//Hs.89887:D38081
R-MAMMA1002972//ESTs, Weakly similar to KIAA0371 [H.sapiens]//9.6e-104:525:95//Hs.94396:AA399630
R-MAMMA1002973//ESTs//4.4e-40:257:87//Hs.163580:H15835
R-MAMMA1002982//ESTs//2.5e-28:115:87//Hs.141694:W15279
R-MAMMA1002987//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//2.1e-41:402:67//Hs.133089:AF064019
R-MAMMA1003003//Calcium modulating ligand//1.9e-45:380:79//Hs.13572:AF068179
R-MAMMA1003004//ESTs//3.0e-07:378:60//Hs.61885:AI127857
R-MAMMA1003007//ESTs//2.0e-47:404:80//Hs.146314:R99617
R-MAMMA1003011//ESTs, Highly similar to HISTONE MACRO-H2A.1 [Rattus norvegicus]//1.4e-53:320:90//Hs.92023:AI022248
R-MAMMA1003015//ESTs//1.5e-42:363:79//Hs.155184:AA573189
R-MAMMA1003019//ESTs//4.8e-10:232:66//Hs.111341:AA251268

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R-MAMMA1003026//ESTs//2.3e-83:394:99//Hs.24668:AA897315
R-MAMMA1003031//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.5e-27:257:77//Hs.96337:AA225358
R-MAMMA1003035//ESTs//1.3e-94:481:94//Hs.92411:AA603321
R-MAMMA1003039//EST//0.56:210:61//Hs.162248:AA552160
R-MAMMA1003040//ESTs//2.1e-17:261:70//Hs.46980:W55940
R-MAMMA1003044//EST//2.4e-18:124:91//Hs.130321:AI002941
R-MAMMA1003047//ESTs//1.0e-20:209:78//Hs.15916:H12862
R-MAMMA1003049//14-3-3 PROTEIN SIGMA//0.94:184:60//Hs.2510:X57348
R-MAMMA1003055//EST//1.0e-49:281:92//Hs.149580:AI281881
R-MAMMA1003056//ESTs//0.99:107:66//Hs.30348:AI038559
R-MAMMA1003057//ESTs, Highly similar to hypothetical protein MD6 [M.musculus]//1.1e-102:545:93//Hs.13755:AA878911
R-MAMMA1003066//H.sapiens mRNA for urea transporter//8.1e-45:322:83//Hs.66710:X96969
R-MAMMA1003089//ESTS, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.4e-34:421:70//Hs.161959:AA493652
R-MAMMA1003099//ESTs//1.1e-43:379:79//Hs.37573:H59651
R-MAMMA1003104//ESTs//2.1e-97:498:96//Hs.9299:T51283
R-MAMMA1003113//EST//3.7e-29:457:70//Hs.123616:AA815366
R-MAMMA1003127//ESTs//2.6e-41:283:86//Hs.146811:AA410788
R-MAMMA1003135//ESTs//7.2e-101:504:97//Hs.87729:AA863125
R-MAMMA1003140//ESTs//4.3e-44:200:89//Hs.152093:AI149537
R-MAMMA1003146//Wingless-type MMTV integration site 5A, human homolog//0.020:413:61//Hs.152213:L20861
R-nnnnnnnnnnnn
R-MAMMA1003166//ESTs, Moderately similar to PEANUT PROTEIN [Drosophila melanogaster]//2.0e-87:524:89//Hs.6884:W30736
R-NT2RM2002580//Homo sapiens clone 24781 mRNA sequence//1.6e-111:587:94//Hs.108112:AF070640
R-NT2RM4000024//ESTs//2.9e-98:523:94//Hs.26641:R59312
R-NT2RM4000027
R-NT2RM4000030//ESTs//1.6e-96:482:96//Hs.90625:T03663
R-NT2RM4000046//ESTs//1.6e-91:461:97//Hs.151237:AI86169
R-NT2RM4000061//ESTs//4.3e-31:167:97//Hs.110821:Z78379
R-NT2RM4000085//Homo sapiens clone 24700 unknown mRNA, partial cds/4.0e-113:549:97//Hs.95665:AF070639
R-NT2RM4000086//EST//2.7e-17:212:76//Hs.137041:AA877817
R-NT2RM4000104//ESTs//3.0e-85:452:94//Hs.101750:H19708
R-NT2RM4000139//EST//3.3e-05:156:66//Hs.133228:AI052312
R-NT2RM4000155//ESTs, Moderately similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [H.sapiens]//1.9e-99:536:92//Hs.127810:AI246301
R-NT2RM4000156//EST//0.89:169:62//Hs.162967:AA676397
R-nnnnnnnnnnnn//ESTs//1.0:214:61//Hs.119370:W52962
R-NT2RM4000169//ESTs//5.4e-82:440:93//Hs.159379:AI382160
R-NT2RM4000191//ESTs, Weakly similar to P68 PROTEIN [H.sapiens]//4.1e-99:542:93//Hs.6366:AA614113
R-NT2RM4000197//ESTs//5.4e-113:567:96//Hs.22975:AA156723
R-NT2RM400019911ESTsI10.020:95:6511Hs.146203:AI254528
R-NT2RM4000200//ESTs//1.4e-100:488:97//Hs.126538:AA931876
R-NT2RM4000202//Small inducible cytokine A5 (RANTES)//4.3e-37:330:77//Hs.155464:AF088219
R-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.7e-103:546:94//Hs.111138:AB018255
R-NT2RM4000215
R-nnnnnnnnnn//ESTs//7.1e-92:457:97//Hs.162074:AA477760
R-NT2RM4000233//Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)//0.00020:174:66//Hs.235:X51602
R-NT2RM4000244//ESTs//6.6e-61:320:95//Hs.108646:AA613031
R-NT2RM4000251//Homo sapiens mRNA for TRIP6 (thyroid receptor interacting protein)//0.63:219:62//Hs.119498:AF000974
R-NT2RM4000265//ESTs//8.8e-105:489:99//Hs.131001:AI378742

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R-NT2RM4000290//ESTs//4.0e-87:435:96//Hs.162592:AA594128
R-NT2RM4000324//ESTs//2.2e-80:413:96//Hs.12313:R43673
R-NT2RM4000327//Small inducible cytokine A5 (RANTES)//3.2e-45:286:87//Hs.155464:AF088219
R-NT2RM4000344//Clathrin, light polypeptide (Lcb)//8.6e-60:452:84//Hs.73919:X81637
R-NT2RM4000349//ESTs, Weakly similar to KIAA0005 [H.sapiens]//2.5e-. 117:579:96//Hs.5216:AA534881
R-NT2RM4000354//ESTs//2.1e-85:406:99//Hs.126774:AI224479
R-NT2RM4000356//ESTs//7.9e-109:548:96//Hs.44278:AA418063
R-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds//2.8e-113:577:95//Hs.8152:AB014542
R-NT2RM4000368//ESTs//2.2e-61:310:97//Hs.143611:M78140
R-NT2RM4000386//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//1.0e-93:521:92//Hs.41793:AA775879
R-NT2RM4000395//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//1.9e-99:524:94//Hs.5249:U55977
R-NT2RM4000414//EST//2.7e-06:196:64//Hs.136648:AA688285
R-NT2RM4000421//ESTs, Weakly similar to No definition line found [C.elegans]//5.4e-75:470:90//Hs.69235:AA192359
R-NT2RM4000425//H.sapiens mRNA for MACH-alpha-2 protein//0.17:112:69//Hs.19949:X98173
R-NT2RM4000433//ESTs//2.7e-100:479:98//Hs.24553:AI150687
R-NT2RM4000457//ESTs//5.1e-107:535:95//Hs.7579:AA775865
R-NT2RM4000471//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//6.0e-99:492:96//Hs.21090:AA418587
R-NT2RM4000486//ESTs, Moderately similar to unnamed protein product [H.sapiens]//2.2e-102:493:97//Hs.111279:W84558
R-NT2RM4000496
R-NT2RM4000511//EST//5.1e-43:326:81//Hs.157658:AI358465
R-NT2RM4000514//ESTS//1.7e-112:552:96//Hs.6686:AA205496
R-nnnnnnnnnnnn//ESTs, Weakly similar to HYPOTHETICAL 85.0 KD PROTEIN IN CPA2-ATP2 INTERGENIC REGION [Saccharomyces cerevisiae]//1.4e-60:343:93//Hs.16014:AA074879
R-NT2RM4000520//ESTs//2.7e-55:266:100//Hs.99838:AA204731
R-NT2RM4000531//ESTs//2.0e-88:502:91//Hs.13110:T67461
R-NT2RM4000532//ESTs//0.47:290:58//Hs.148753:T91777
R-NT2RM4000534//EST//0.00025:303:60//Hs.162809:AA632198
R-NT2RM4000585//EST//0.28:63:77//Hs.150024:AI291981
R-NT2RM4000590//ESTs//5.8e-65:320:98//Hs.116017:AA613437
R-NT2RM4000595//Homo sapiens KIAA0431 mRNA, partial cds//0.99:189:64//Hs.16349:AB007891
R-NT2RM4000603//ESTs//4.6e-68:356:96//Hs.48855:AA134589
R-nnnnnnnnnnnn//ESTs//1.5e-89:431:97//Hs.26117:W16697
R-NT2RM4000616//ESTs, Highly similar to ACETYL-COENZYME A SYNTHETASE [Escherichia coli]//1.4e-102:519:96//Hs.14779:N64822
R-NT2RM4000674//ESTs//5.1e-78:398:97//Hs.8268:N70144
R-NT2RM4000689//ESTs, Weakly similar to T01G9.4 [C.elegans]//2.9e-115:550:98//Hs.11820:AA205531
R-NT2RM4000698//ESTs//2.0e-17:130:87//Hs.86420:AA927510
R-nnnnnnnnnnnn
R-NT2RM4000712//EST//0.99:103:65//Hs.114039:AA701128
R-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//2.2e-103:519:95//Hs.6823:W18181
R-NT2RM4000733//ESTs//8.7e-88:429:98//Hs.72185:AA465311
R-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//3.6e-105:536:95//Hs.137168:AB018303
R-NT2RM40007.41//ESTs//0.99:266:58//Hs.142718:AA034046
R-NT2RM4000751//ESTs//1.6e-20:351:66//Hs.43145:AA776988
R-NT2RM4000764
R-NT2RM4000778//EST//0.066:254:61//Hs.148232:AA904174
R-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//9.3e-106:546:94//Hs.18586:AB007920
R-NT2RM4000787//Human melanoma antigen recognized by T-cells (MART-1) mRNA//6.5e-40:424:73//Hs.154069:U06452
R-NT2RM4000790//EST//9.0e-48:259:94//Hs.159694:AI417008

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R-NT2RM4000795//Human mRNA for KIAA0067 gene, complete cds//1.0:203:63//Hs.20991:D31891
R-NT2RM4000796//ESTs//7.0e-106:506:98//Hs.43559:AI003520
R-NT2RM4000798//Human polymorphic epithelial mucin core protein mRNA, 3' end//2.5e-28:158:96//Hs.118249:M21868
R-NT2RM4000813
R-NT2RM4000820//ESTs, Weakly similar to hypothetical protein [H.sapiens]//1.3e-109:539:97//Hs.99636:AI219667
R-NT2RM4000833//ESTs, Moderately similar to ZK863.3 [C.elegans]//4.0e-112:448:99//Hs.20223:AA482031
R-NT2RM4000848//ESTs//8.1e-97:476:97//Hs.16036:AA883864
R-NT2RM4000852//ESTs//6.4e-94:467:97//Hs.11556:AI309597
R-NT2RM4000855//ESTs//2.9e-95:544:90//Hs.106525:AI283343
R-nnnnnnnnnnnn
R-NT2RM4000895//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//9.3e-96:450:99//Hs.142076:AA604514
R-NT2RM4000950//ESTs//2.6e-91:438:98//Hs.43827:AA455262
R-NT2RM4000971//EST//2.9e-96:461:99//Hs.139709:AA227887
R-NT2RM4000979//EST//1.6e-67:329:98//Hs.96927:AA349647
R-NT2RM4000996//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//1.7e-82:414:96//Hs.115342:AA650126
R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//3.8e-114:545:97//Hs.19542:AB018272
R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//2.5e-114:556:97//Hs.15711:AB014539
R-NT2RM4001032//ESTs//7.8e-17:132:84//Hs.138720:N53352
R-NT2RM4001047//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//0.42:133:67//Hs.32170:AB015132
R-NT2RM4001054//ESTs//1.7e-84:404:99//Hs.116407:AA815300
R-nnnnnnnnnn//ESTs//3.4e-91:439:99//Hs.103177:W72798
R-NT2RM4001092//ESTs//1.4e-86:517:8911Hs.132969:Z78324
R-NT2RM4001116//EST//5.2e-57:275:100//Hs.131115:AI016962
R-NT2RM4001140//ESTs//5.5e-96:461:98//Hs.86965:AA252276
R-NT2RM4001151//ESTs//0.40:263:58//Hs.113189:R08311
R-NT2RM4001155//ESTs//8.3e-105:544:94//Hs.29647:W60848
R-NT2RM4001160//EST//7.6e-25:380:68//Hs.147405:AI209085
R-NT2RM4001187//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//9.2e-43:273:91//Hs.109005:N31174
R-NT2RM4001191//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//3.1e-32:274:70//Hs.2379:U23942
R-NT2RM4001200//ESTs//4.5e-102:494:97//Hs.31844:N32849
R-NT2RM4001203
R-NT2RM4001204//ESTs//9.8e-88:468:93//Hs.4990:T65307
R-NT2RM4001217//ESTs//1.2e-75:396:94//Hs.25042:R72410
R-NT2RM4001256//ESTs//1.0:157:62//Hs.65377:AA994677
R-NT2RM4001258//ESTs//9.6e-41:260:88//Hs.27633:N76184
R-NT2RM4001309
R-NT2RM4001313//EST//0.0022:150:66//Hs.161573:W84857
R-NT2RM4001316//ESTs//3.5e-26:139:99//Hs.23100:AI128899
R-NT2RM4001320//ESTs//1.6e-97:308:99//Hs.112024:AI042352
R-NT2RM4001340//ESTs, Highly similar to UTR4 PROTEIN [Saccharomyces cerevisiae]//1.9e-105:522:97//Hs.18442:AI129307
R-NT2RM4001344//EST//1.1e-90:436:99//Hs.95900:AA160339
R-NT2RM4001347//EST//0.17:186:61//Hs.16751:T90476
R-NT2RM4001371//EST//0.0069:270:62//Hs.99239:AA450211
R-NT2RM4001382
R-NT2RM4001384//ESTs//9.6e-91:445:98//Hs.55000:AA805507
R-NT2RM4001410//EST//0.13:50:82//Hs.157675:AI358790
R-NT2RM4001411//ESTs, Weakly similar to lymphocyte specific adaptor protein Lnk [M.musculus]//4.0e-102:539:94//Hs.15744:AI055859
R-NT2RM4001412

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R-NT2RM4001414//ESTs//6.5e-35:226:88//Hs.121727:AA775895
R-NT2RM4001437//EST//0.017:169:67//Hs.13207:F10054
R-NT2RM4001444//ESTs, Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [S.cerevisiae]//7.4e-108:544:94//Hs.7558:AA526812
R-NT2RM4001454//ESTs//4.7e-108:517:98//Hs.32295:N32277
R-NT2RM4001455//EST//9.6e-81:395:97//Hs.127978:AA969739
R-NT2RM4001483//Human mRNA for KIAA0033 gene, partial cds//1.8e-58:324:85//Hs.22271:D26067
R-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//7.0e-104:547:93//Hs.153121:AB014585
R-NT2RM4001519//Histatin 1//0.53:340:59//Hs.119101:M26664
R-NT2RM40015227/Small inducible cytokine A5 (RANTES)//8.4e-55:306:80//Hs.155464:AF088219
R-NT2RM40015577/ESTs, Weakly similar to F11A10.4 [C.elegans]//6.1e-21:165:83//Hs.29134:H43072
R-NT2RM4001565//ESTs//2.0e-103:483:99//Hs.121273:AA758027
R-NT2RM4001566//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//2.7e-43:446:72//Hs.4943:Z98046
R-NT2RM4001569//ESTs//3.6e-37:186:100//Hs.86959:AA888009
R-NT2RM4001582//ESTs//1.2e-96:459:98//Hs.114432:N52946
R-nnnnnnnnnnnn
R-NT2RM4001594//ESTs//1.6e-83:404:98//Hs.134740:AA282171
R-NT2RM4001597//ESTs//6.9e-111:558:96//Hs.11408:AI358871
R-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//2.1e-112:565:95//Hs.23255:AB018334
R-NT2RM4001611//EST//5.9e-74:353:99//Hs.125318:AA837079
R-NT2RM4001629//ESTs//6.1e-95:453:99//Hs.115765:AA485957
R-NT2RM4001650
R-NT2RM4001662
R-NT2RM4001666//Homo sapiens mRNA for KIAA0469 protein, complete cds//3.6e-36:230:70//Hs.7764:AB007938
R-NT2RM4001682//EST//4.3e-68:393:90//Hs.157362:AI367496
R-NT2RM4001710//ESTs//4.3e-48:235:99//Hs.7299:AA203440
R-NT2RM4001714//ESTs//0.0014:568:58//Hs.50458:AA868686
R-nnnnnnnnnnn//ESTs//6.5e-104:487:99//Hs.153581:AA630465
R-NT2RM4001731//ESTs, Weakly similar to No definition line found [C.elegans]//3.1e-108:563:94//Hs.18510:AA522887
R-NT2RM4001741//T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2930 nt]//0.083:124:68//Hs.120980:S83390
R-NT2RM4001746//ESTs//6.1e-90:420:100//Hs.139003:AA948200
R-NT2RM4001754//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//5.4e-59:504:78//Hs.139107:K00629
R-NT2RM4001758//ESTs//8.9e-27:140:100//Hs.149973:AI290740
R-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//6.4e-24:236:80//Hs.39871:AB018270
R-NT2RM4001783//ESTs//9.9e-30:156:99//Hs.115260:AA314956
R-NT2RM4001810//ESTs//1.3e-65;346:95//Hs.131915:W22567
R-NT2RM4001813//ESTs//5.7e-102:473:100//Hs.87574:AI089920
R-NT2RM4001823//ESTs//3.8e-62:324:95//Hs.124109:AA888839
R-NT2RM4001828//ESTs//1.3e-119:563:98//Hs.102397:AA706551
R-NT2RM4001836//ESTs//5.5e-16:92:100//Hs.26996:AA551070
R-NT2RM4001841//ESTs//1.3e-99:540:94//Hs.42322:AA082619
R-NT2RM4001842//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//4.1e-10:274:62//Hs.161959:AA493652
R-NT2RM4001856//ESTs, Weakly similar to contains similarity to ATP/GTP-binding site motif [C.elegans]//3.0e-43:292:86//Hs.14202:N46000
R-nnnnnnnnnnnn//ESTs//6.2e-104:495:98//Hs.118686:AA682280
R-NT2RM40018657/Homo sapiens mRNA for atopy related autoantigen CALC//1.6e-120:592:97//Hs.61628:Y17711
R-NT2RM4001876//ESTs//2.9e-98:532:92//Hs.100734:AA158252
R-NT2RM4001880//ESTs//2.5e-29:224:86//Hs.6193:AA045149

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R-NT2RM4001905//ESTs//5.6e-109:565:95//Hs.9536:AA114178
R-NT2RM4001922//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-105:535:95//Hs.30991:AA994438
R-NT2RM4001930//ESTs//4.1-84:425:96//Hs.80042:N63143
R-NT2RM4001938//EST//0.00040:241:60//Hs.147235:AI205893
R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//2.0e-110:556:95//Hs.118631:AF098162
R-NT2RM4001953//ESTs//5.3e-65:338:96//Hs.33718:AA453268
R-NT2RM4001965//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//5.7e-62:326:95//Hs.3385:N25917
R-nnnnnnnnnnnn//ESTs, Weakly similar to IP63 protein [R.norvegicus]//1.9e-21:121:98//Hs.8772:AA521097
R-NT2RM4001979//ESTs//1.4e-96:465:98//Hs.157103:W60265
R-NT2RM4001984
R-NT2RM4001987
R-NT2RM4002013//EST//2.2e-14:110:90//Hs.160835:AI345528
R-NT2RM4002018
R-NT2RM4002034//Human mRNA for KIAA0118 gene, partial cds//9.4e-46:293:87//Hs.154326:D42087
R-NT2RM4002044//ESTs//2.8e-107:537:96//Hs.24078:W44435
R-NT2RM4002054//ESTs//3.7e-88:482:94//Hs.4243:T78226
R-NT2RM4002062//ESTs//1.4e-55:377:85//Hs.152592:AA587887
R-NT2RM4002063//Calcium modulating ligand//1.8e-43:385:78//Hs.13572:AF068179
R-nnnnnnnnnnnn//Homo sapiens OPA-containing protein mRNA, complete cds//5.5e-42:554:68//Hs.85313:AF071309
R-NT2RM4002067//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//2.3e-43:468:73//Hs.139107:K00629
R-NT2RM4002073//ESTs, Weakly similar to very-long-chain acyl-CoA synthetase [H.sapiens]//6.8e-57:290:96//Hs.109274:AA193416
R-NT2RM4002075//ESTs//0.078:267:61//Hs.163563:AA641655
R-NT2RM4002093//ESTs//1.2e-64:316:99//Hs.34956:AI052528
R-nnnnnnnnnnnn//ESTs//1.0:95:69//Hs.25897:W65409
R-NT2RM4002128//Homo sapiens mRNA for BCL9 gene//0.51:258:60//Hs.122607:Y13620
R-NT2RM4002140//ESTs//5.5e-46:187:94//Hs.8737:W22712
R-NT2RM4002145//ESTs//4.6e-70:374:94//Hs.141082:H18987
R-NT2RM4002146//ESTs//1.9e-93:43 9:99//Hs.119295:AA442090
R-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.5e-111:560:96//Hs.22464:AF084535
R-NT2RM4002174//Homo sapiens LIM protein mRNA, complete cds//3.2e-46:552:72//Hs.154103:AF061258
R-NT2RM4002189//ESTs//9.6e-75:352:100//Hs.98350:H15400
R-NT2RM4002194//EST//0.22:68:72//Hs.149104:AI244343
R-NT2RM4002205//EST//0.00028:103:72//Hs.130032:AA897678
R-NT2RM4002213//ESTs//3.3e-15:160:78//Hs.63304:W22079
R-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]//5.1e-112:569:95//Hs.23900:U82984
R-NT2RM4002251//ESTs, Weakly similar to similar to alpha-1,3-mannosyl-glycoprotein beta-1, 2-N-acetylglucosaminyltransferase [C.elegans]//1.1e-100:544:93//Hs.27567:W72190
R-NT2RM4002256//Small inducible cytokine A5 (RANTES)//1.0e-44:341:81//Hs.155464:AF088219
R-NT2RM4002266//ESTs//2.6e-100:539:93//Hs.57976:AA535864
R-NT2RM4002278//ESTs//1.8e-112:569:95//Hs.87281:AA128263
R-NT2RM4002281//ESTs//4.9e-20:187:80//Hs.141203:H52638
R-NT2RM4002287//ESTs//7.9e-84:388:94//Hs.33977:N52461
R-NT2RM4002294
R-NT2RM4002301//ESTs//4.5e-111:556:96//Hs.85916:AA194164
R-NT2RM4002323//ESTs//4.5e-102:498:97//Hs.85782:AA191498
R-nnnnnnnnnnnn//ESTs//5.0e-59:283:100//Hs.125048:AA682913
R-NT2RM4002344//V-akt murine thymoma viral oncogene homolog 2//0.29:153:66//Hs.155129:M77198
R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//2.8e-122:593:97//Hs.26163:AB014549
R-NT2RM4002374//ESTs//3.3e-40:505:70//Hs.95115:AA206594
R-NT2RM4002383//ESTs//2.7e-93:455:97//Hs.134278:AA648884
R-NT2RM4002390//ESTs//3.3e-93:481:95//Hs.48764:AA613328
R-NT2RM4002409//ESTs, Weakly similar to coded for by C. elegans cDNA yk52e10.5 [C.elegans]//1.3e-97:473:

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98//Hs.16464:W19606
R-NT2RM4002438//ESTs//0.74:162:61//Hs.65377:AA994677
R-NT2RM4002446
R-NT2RM4002452//EST//1.0:164:60//Hs.1166I9:AA668142
R-NT2RM4002457
R-NT2RM4002460//ESTs//3.0e-74:385:96//Hs.6933:R07890
R-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.6e-103:507:97//Hs.8765:AF083255
R-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//2.3e-32:172:98//Hs.94781:AB014591
R-NT2RM4002493//ESTs//6.4e-73:366:97//Hs.157114:T58884
R-NT2RM4002499//ESTs//3.5e-61:307:97//Hs.117737:AI088029
R-NT2RM4002504//ESTs//2.1e-55:306:94//Hs.10949:AA464464
R-nnnnnnnnnnnn//ESTs, Weakly similar to peroxisome targeting signal 2 receptor [H.sapiens]//1.4e-73:360:91//Hs.31030:H50467
R-NT2RM4002532//ESTs//1.3e-21:191:78//Hs.146811:AA410788
R-NT2RM4002534//ESTs//1.8e-99:512:95//Hs.13526:AI417057
R-NT2RM4002567//ESTs//7.6e-41:272:87//Hs.7114:R24312
R-NT2RM4002571//ESTs, Highly similar to POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE [Bos taurus]//2.3e-89:435:97//Hs.15830:AA165698
R-NT2RM4002593//ESTs//2.3e-109:552:96//Hs.17424:AA190569
R-NT2RM4002623//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]//9.6e-28:194:87//Hs.59346:AI126802
R-NT2RP2000001//ESTs//2.6e-80:386:99//Hs.105061:N45096
R-NT2RP2000006//Thromboxane A2 receptor//7.2e-37:253:84//Hs.89887:D38081
R-NT2RP2000008//Zinc finger protein 37a (KOX 21)//5.2e-25:366:67//Hs.54488:X69115
R-NT2RP2000027//ESTs//9.5e-74:377:96//Hs.96557:AA286713
R-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//2.7e-42:223:96//Hs.8309:AB018290
R-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//4.3e-64:309:98//Hs.6216:AF061749
R-NT2RP2000054//EST//1.2e-71:375:96//Hs.98835:AA435798
R-NT2RP2000056//EST//2.8e-28:342:69//Hs.135526:AI094910
R-NT2RP2000067//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//2.3e-35:199:94//Hs.41793:AA775879
R-NT2RP2000070//ESTs, Weakly similar to proto-cadherin 3 [R.norvegicus]//1.4e-78:383:98//Hs.58254:W72881
R-NT2RP2000076//EST//0.0014:227:63//Hs.136761:AA738097
R-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//1.1e-78:379:97//Hs.54877:AF050078
R-NT2RP2000079//Homo sapiens RET finger protein-like 1 antisense transcript, partial//2.9e-21:232:75//Hs.102576:AJ010230
R-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.8e-75:378:96//Hs.22926:AB018338
R-NT2RP2000091//Carcinoembryonic antigen gene family member 6//0.030:236:63//Hs.41:D90064
R-NT2RP2000097//ESTs//4.2e-15:92:97//Hs.7432:AA281757
R-NT2RP2000098//ESTs//9.0e-53:279:94//Hs.87807:AA813827
R-NT2RP2000108//EST//1.5e-75:378:96//Hs.162105:AA524419
R-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//5.8e-76:386:95//Hs.17706:AB018356
R-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [C.elegans]//1.9e-19:153:86//Hs.5268:W22670
R-nnnnnnnnnn//ESTs//1.0e-55:293:95//Hs.14570:AI422099
R-nnnnnnnnnnnn//ESTs//0.24:354:59//Hs.157564:AI356513
R-NT2RP2000147//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [Mus musculus]//3.0e-89:457:95//Hs.3832:AI208601
R-NT2RP2000153//EST//0.0039:93:68//Hs.140386:AA773548
R-NT2RP2000157//ESTs//1.1e-53:322:91//Hs.6877:AA040820
R-NT2RP2000161//EST5//1.6e-99:492:97//Hs.21738:AI188190
R-NT2RP2000175//ESTs//1.4e-98:489:96//Hs.4849:AI143741
R-NT2RP2000183//ESTs//9.0e-72:358:96//Hs.4856:N51373
R-NT2RP2000195//ESTs//3.9e-92:439:98//Hs.145091:AA814510

BNSDOCID: <EP___1074617A2_I_>

R-NT2RP2000205//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.4e-80:415:95//Hs.11807:T86897
R-NT2RP2000224//RNA polymerase II, polypeptide C (33kD)//1.1e-57:306:94//Hs.79402:AC004382
R-NT2RP2000232
R-NT2RP2000233//ESTs//1.1e-08:63:96//Hs.124861:AI090683
R-NT2RP2000239//ESTs//5.3e-87:427:96//Hs.86211:AA604379
R-NT2RP2000248//ESTs, Weakly similar to O-linked GlcNAc transferase [H.sapiens]//1.3e-95:454:99//Hs.102057:AA649005
R-NT2RP2000257//ESTs//5.1e-58:282:99//Hs.122565:AI126840
R-NT2RP2000258//EST//1.0:67:68//Hs.61812:AA035649
R-NT2RP2000270//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.4e-59:298:96//Hs.16085:AI261382
R-NT2RP2000274//ESTs//7.5e-61:296:98//Hs.86081:AA196635
R-NT2RP2000288//ESTs//1.8e-56:305:93//Hs.7579:AA775865
R-NT2RP2000289
R-NT2RP2000297//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//9.8e-106:494:99//Hs.102951:AA574249
R-NT2RP2000298//ESTs//2.1e-62:256:90//Hs.8737:W22712
R-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds//2.8e-39:222:93//Hs.58218:U82381
R-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two unknown genes. Contains ESTs and GSSs//2.9e-71:342:98//Hs.87684:AL022398
R-NT2RP2000329//ESTs, Highly similar to GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL [Bos taurus]//3.4e-69:371:94//Hs.43436:N32441
R-NT2RP2000337//ESTs//5.2e-79:411:95//Hs.101799:AI276062
R-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds//1.1e-47:262:94//Hs.76556:U83981
R-NT2RP2000369//ESTs//4.3e-102:531:94//Hs.15855:H98103
R-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//8.4e-09:93:83//Hs.808:L28010
R-NT2RP2000420//ESTs//8.2e-24:142:94//Hs.144893:AI222324
R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.2e-20:140:90//Hs.5819:AF102265
R-NT2RP2000438//ESTs, Weakly similar to misato [D.melanogaster]//1.3e-65:362:93//Hs.22197:AI151425
R-NT2RP2000448//ESTs, Highly similar to HYPOTHETICAL 51.6 KD PROTEIN IN PAP1-MRPL13 INTERGENIC REGION [Saccharomyces cerevisiae]//3.6e-75:435:92//Hs.21938:W81045
R-NT2RP2000459//ESTs//2.8e-95:527:93//Hs.103422:AI352013
R-NT2RP2000498//ESTs//2.3e-17:119:79//Hs.161714:AA229078
R-NT2RP2000503//ESTs//5.2e-91:438:98//Hs.152335:AI290215
R-NT2RP2000510//Homo sapiens KIAA0436 mRNA, partial cds//0.13:455:58//Hs.110:AB007896
R-nnnnnnnnnn//ESTs//9.9e-63:376:89//Hs.47546:AA181348
R-NT2RP2000523
R-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.5e-30:167:97//Hs.14409:AB011144
R-NT2RP2000617//ESTs//9.5e-103:493:98//Hs.9412:W72446
R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//8.1e-66:335:96//Hs.7314:AB014514
R-NT2RP2000644//ESTs//1.1e-18:372:63//Hs.82419:AA789222
R-NT2RP2000656//ESTs//1.0e-10:128:80//Hs.23977:AA115275
R-NT2RP2000658//ESTs//0.31:278:59//Hs.15661:W02396
R-NT2RP2000668//ESTs//8.2e-40:255:88//Hs.113310:R16767
R-NT2RP2000678//ESTs//2.6e-53:271:9611Hs.23790:N99347
R-NT2RP2000710//ESTs//0.49:190:63//Hs.145521:AI261368
R-NT2RP2000715//EST//1.2e-87:418:9911Hs.139425:AA429279
R-NT2RP2000731//EST//5.3e-65:322:97//Hs.136754:AA713965
R-NT2RP2000758//ESTS//1.0:187:61//Hs.10545:N62642
R-NT2RP2000764//ESTs//5.8e-84:485:91//Hs.121816:AA775419
R-NT2RP2000809
R-NT2RP2000812//ESTs//1.2e-45:231:97//Hs.121028:AA902745

BNSDOCID: <EP___1074617A2_I_>

R-nnnnnnnnnnnn//ESTs//6.3e-87:433:97//Hs.145479:AA969404
R-NT2RP2000816//ESTS//0.45:100:69//Hs.147529:AA458918
R-NT2RP2000819
R-NT2RP2000841//ESTs//1.9e-73:351:99//Hs.116385:AI224511
R-NT2RP2000842//TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR//4.6e-10:247:66//Hs.29352:M31165
R-NT2RP2000845//ESTs//2.8e-91:443:97//Hs.66810:AI206552
R-NT2RP2000863//ESTs//4.3e-49:310:88//Hs.104336:W07345
R-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//2.8e-43:277:89//Hs.3615: AB018284
R-NT2RP2000892//ESTs//2.8e-50:25 8:96//Hs.119238:AA476267
R-NT2RP2000931//MATRIN 3//7.2e-57:290:96//Hs.78825:AB018266
R-NT2RP2000938//ESTs, Highly similar to HYPOTHETICAL 6.3 KD PROTEIN ZK652.2 IN CHROMOSOME III [Caenorhabditis elegans]//3.9e-37:199:95//Hs.112318:AA186477
R-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//9.8e-98:494:96//Hs.19822: AB018298
R-NT2RP2000965//EST//0.22:223:60//Hs.105703:AA487021
R-NT2RP2000970//EST//8-7e-06:255:62//Hs.149202:AI246481
R-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION [S.cerevisiae]//7.8e-92:468:95//Hs.12124:AA522537
R-NT2RP2000987//ESTs//4.5e-78:419:93//Hs.21968:H97521
R-NT2RP2001036//EST//2.0e-33:148:82//Hs.163196:AA767643
R-NT2RP2001044//ESTs//5.6e-95:493:95//Hs.21958:AA453660
R-NT2RP2001065//ESTs//3.6e-28:153:96//Hs.119314:AA432108
R-NT2RP2001070//EST//0.30:94:67//Hs.94289:N73665
R-NT2RP2001094//EST//0.75:101:69//Hs.161040:H82068
R-NT2RP2001119
R-NT2RP2001127//Homa sapiens mRNA for HRIHFB2060, partial cds//1.5e-56:304:94//Hs.146282:AB015348
R-NT2RP2001137
R-NT2RP2001149//ESTs//5.1e-66:324:9711Hs.27475:AA704512
R-NT2RP2001168//ESTs//2.0e-98:539:92//Hs.77870:AI188145
R-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//1.5e-96:490:96//Hs.26247: AB007949
R-NT2RP2001174//ESTs//2.2e-63:354:93//Hs.24266:R28287
R-NT2RP2001196//ESTs//1.4e-83:463:93//Hs.124304:AA825510
R-NT2RP2001218//ESTs//1.4e-100:506:96//Hs.93391:AI188402
R-NT2RP2001226//EST//0.0074:154:63//Hs.128612:AA909358
R-NT2RP2001233/TESTs, Highly similar to ZINC FINGER PROTEIN ZFP-36 [Homo sapiens]//3.7e-65:538:80// Hs.44014:AA632298
R-NT2RP2001245//ESTs//5.2e-90:447:97//Hs.14559:H92996
R-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//1.5e-112:544:97//Hs.7531:AB018353
R-NT2RP2001277//ESTs//2.0e-81:387:99//Hs.13751:AA908229
R-NT2RP2001290//ESTs//2.4e-91:501:92//Hs.12600:AA044775
R-NT2RP2001295//ESTs//1.4e-70:337:99//Hs.123854:AA412665
R-NT2RP2001312//ESTs//4.6e-53:276:95//Hs.7961:AA401205
R-NT2RP2001327//ESTs, Moderately similar to tumor necrosis factor-alpha-induced protein B12 [H.sapiens]// 2.3e-43:238:93//Hs.106632:N25679
R-NT2RP2001328//ESTs//5.1e-99:499:96//Hs.34868:AI341138
R-NT2RP2001347//ESTs//6.7e-05:100:77//Hs.9536:AA114178
R-NT2RP2001378//ESTs//4.2e-83:456:93//Hs.10554:N50028
R-NT2RP2001381//ESTs//1.1e-26:148:96//Hs.161859:AA444038
R-NT2RP2001392//ESTs, Weakly similar to MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H. sapiens]//3.9e-74:411:93//Hs.47305:AA195153
R-NT2RP2001394//ESTs//9.5e-54:305:93//Hs.70256:R07875
R-NT2RP2001397//ESTs, Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus]//5.2e-97: 469:97//Hs.20483:AA522505
R-NT2RP2001420//ESTs//1.6e-49:228:88//Hs.163602:N32030
R-NT2RP2001423//ESTs//2.0e-37:190:99//Hs.101565:R35431

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R-NT2RP2001427//EST//1.7e-1 1:107:84//Hs.148584:AI201728
R-NT2RP2001436//ESTs, Weakly similar to F02D8.3 [C.elegans]//2.9e-114:558:97//Hs.7627:AI341556
R-NT2RP2001440//EST//0.17:192:58//Hs.133442:AI061394
R-NT2RP2001445//ESTs//1.1e-43:215:100//Hs.145497:AA501453
R-NT2RP2001449//ESTs//4.1e-08:234:61//Hs.134067:AI076765
R-NT2RP2001450//ESTs//9.5e-65:356:94//Hs.61829:AI079539
R-NT2RP2001467//Small inducible cytokine A5 (RANTES)//1.2e-34:255:83//Hs.155464:AF088219
R-NT2RP2001506//ESTs//2.9e-23:170:88//Hs.7147:T23513
R-NT2RP2001511//ESTs//2.0e-08:59:100//Hs.57660:AA251146
R-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1//6.7e-106:545:95//Hs.4277:Y14494
R-NT2RP2001526//ESTs//3.7e-23:295:72//Hs.8514:AF039240
R-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//1.9e-15:99:95//Hs.99742:AF035586
R-NT2RP2001560//ESTs//2.2e-58:310:94//Hs.87454:AA732816
R-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//2.0e-76:387:96//Hs.67619:AB007957
R-NT2RP2001576//Human mRNA for KIAA0105 gene, complete cds//0.17:193:60//Hs.119:D14661
R-NT2RP2001581//ESTs//5.1e-08:107:78//Hs.157114:T58884
R-NT2RP2001597//EST//5.2e-22:151:88//Hs.158613:AI369995
R-NT2RP2001601//ESTs//1.5e-78:373:99//Hs.137558:AI393767
R-NT2RP2001613
R-NT2RP2001628//EST//0.99:195:60//Hs.144238:W52294
R-NT2RP2001663//ESTs//4.0e-37:282:84//Hs.12319:W56090
R-NT2RP2001677//ESTs//1.4e-44:232:96//Hs.159387:AI370845
R-NT2RP2001678//ESTs//0.91:124:60//Hs.10593:AI201336
R-NT2RP2001699//EST//0.0033:230:61//Hs.146544:AI125323
R-NT2RP2001720//ESTs//1.8e-52:255:99//Hs.101064:AA290579
R-NT2RP2001721//ESTs//7.0e-101:479:99//Hs.129750:AA987538
R-NT2RP2001740//ESTs//3.3e-76:379:96//Hs.144704:AI147100
R-NT2RP2001748//ESTs//1.4e-44:352:81//Hs.142259:AA828840
R-NT2RP2001762//Homo sapiens exonuclease 1a (EXO1a) mRNA, complete cds//2.1e-105:519:96//Hs.47504:AF091754
R-NT2RP2001813//ESTs//6.3e-78:406:95//Hs.21902:R44037
R-NT2RP2001861
R-NT2RP2001869//EST//2.8e-21:173:82//Hs.130321:AI002941
R-NT2RP2001876//ESTs//6.1e-102:526:95//Hs.4944:AA533088
R-NT2RP2001883//ESTs, Weakly similar to No definition line found [C.elegans]//6.9e-110:556:95//Hs.23159:AA113849
R-NT2RP2001900//ESTs//6.9e-85:442:95//Hs.154220:AA171724
R-NT2RP2001907//ESTs//2.1e-82:432:94//Hs.142257:AA188423
R-NT2RP2001926//EST//2.3e-24:299:71//Hs.135085:AI097268
R-NT2RP2001936//ESTs//1.1e-45:265:92//Hs.112482:T66087
R-NT2RP2001943//EST//1.4e-05:246:61//Hs.144096:AI032180
R-NT2RP2001946//ESTs//3.6e-87:410:99//Hs.20242:W72594
R-NT2RP2001947//ESTs//1.9e-55:338:88//Hs.58582:T72588
R-NT2RP2001969
R-NT2RP2001976//ESTs//1.2e-98:499:95//Hs.121028:AA902745
R-NT2RP2001985//ESTs, Weakly similar to GTPASE-ACTIVATING PROTEIN SPA-1 [M.musculus]//8.3e-15:118:89//Hs.18760:AA166678
R-NT2RP2002025//ESTs//2.1e-82:393:98//Hs.159488:AI378233
R-NT2RP2002032//ESTs//4.4e-98:531:91//Hs.93836:AA813332
R-NT2RP2002033//ESTs//3.5e-43:229:96//Hs.30563:AA102627
R-NT2RP2002041
R-NT2RP2002046//ESTs//1.6e-101:476:99//Hs.101107:AA825938
R-NT2RP2002047//ESTs//9.1e-85:431:95//Hs.116750:AA629895
R-NT2RP2002058//ESTs//1.3e-31:163:99//Hs.33085:AA258068
R-NT2RP2002066//ESTS//1.9e-87:459:93//Hs.118871:AA846091

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R-NT2RP2002070//ESTs//4.1e-63:332:96//Hs.156446:T92265
R-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//1.7e-26:178:87//Hs.11039:AF052183
R-NT2RP2002079//ESTs//1.2e-79:389:97//Hs.135214:AI350524
R-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein//1.5e-60:376:89//Hs.155218:AJ007509
R-NT2RP2002105//ESTs//8.4e-54:313:90//Hs.98702:AI123000
R-NT2RP2002124//ESTs//6.6e-81:431:93//Hs.127326:AA525134
R-NT2RP2002137//Deoxycytidine kinase//0.29:183:62//Hs.709:M60527
R-NT2RP2002154//ESTs//9.6e-97:539:91//Hs.18624:AA523268
R-NT2RP2002172//EST//0.69:53:75//Hs.156238:AI334495
R-NT2RP2002185//ESTs, Weakly similar to F15C11.2 [C.elegans]//1.4e-54:269:98//Hs.107201:W52859
R-NT2RP2002192//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.9e-15:245:71//Hs.87578:AI125363
R-NT2RP2002193//ESTs//3.5e-79:45 3:90//Hs.76578:AI290672
R-NT2RP2002208//ESTs//2.0e-72:347:99//Hs.164028:AI003946
R-NT2RP2002219//EST//0.039:229:63//Hs.149830:AI287499
R-NT2RP2002231//ESTs//3.3e-64:337:94//Hs.79828:AA642341
R-nnnnnnnnnnnn//ESTs, Highly similar to co-repressor protein [M.musculus]//5.4e-48:238:99//Hs.22583:AA188168
R-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds//1.6e-15:131:83//Hs.150595:AF005418
R-NT2RP2002259//Human L-myc protein gene, complete cds//5.3e-99:548:91//Hs.92137:M19720
R-NT2RP2002270//ESTs, Weakly similar to AF-9 PROTEIN [H.sapiens]//4.8e-100:550:91//Hs.4029:Z78373
R-NT2RP2002292//ESTs, Weakly similar to F13B12.1 [C.elegans]//3.2e-92:482:93//Hs.5570:AI377863
R-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//4.1e-103:527:94//Hs.24812:AF069532
R-NT2RP2002316//ESTs//4.2e-91:425:100//Hs.3350:AI368015
R-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds//1.2e-112:567:95//Hs.31034:AB015594
R-NT2RP2002333//ESTs//1.9e-86:483:91//Hs.155198:AA767372
R-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds//1.2e-103:600:89//Hs.109051:AF038958
R-NT2RP2002394//ESTS//0.11:158:65//Hs.28792:AI343467
R-NT2RP2002408//ESTs//1.5e-51:278:93//Hs.6044:W22815
R-NT2RP2002426//Homo sapiens mRNA for KIAA0563 protein, complete cds//1.7e-33:285:80//Hs.15731:AB011135
R-NT2RP2002439//ESTS//3.2e-12:134:76//Hs.32246:AA464020
R-NT2RP2002457//ESTs//4.7e-52:282:94//Hs.21968:H97521
R-NT2RP2002464//ESTs//5.3e-27:148:98//Hs.115660:AI362230
R-NT2RP2002475//ESTs//3.9e-85:439:94//Hs.9873:W27233
R-nnnnnnnnnnnn//Homo sapiens mRNA for ABC transporter 7 protein, complete cds//9.9e-115:605:92//Hs.125856:AB005289
R-NT2RP2002498//ESTs//6.3e-37:227:93//Hs.108779:N73180
R-NT2RP2002503//ESTs//1.9e-54:358:86//Hs.57800:W60838
R-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//8.5e-107:583:91//Hs.23255:AB018334
R-NT2RP2002520//ESTs//4.2e-99:509:94//Hs.32368:AA205305
R-NT2RP2002537//ESTs//4.2e-105:552:93//Hs.154363:AA533090
R-NT2RP2002546//Homo sapiens clone TUA8 Cri-du-chat region mRNA//2.6e-109:570:93//Hs.49476:AF009314
R-NT2RP2002549//DNA polymerase gamma//1.1e-35:189:86//Hs.80961:U60325
R-NT2RP2002591//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//7.5e-118:564:97//Hs.94549:AA149547
R-NT2RP2002595//EST//1.4e-15:101:95//Hs.129528:AA994783
R-NT2RP2002606//ESTs//4.5e-99:475:98//Hs.45046:N40170
R-NT2RP2002609//ESTs//1.9e-104:568:92//Hs.9175:AI184220
R-NT2RP2002618//ESTs//0.014:493:57//Hs.96322:AA541615
R-NT2RP2002621//EST//4.4e-36:252:84//Hs.149580:AI281881
R-NT2RP2002643//ESTs//6.9e-32:247:74//Hs.33354:AA179944

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R-NT2RP2002672
R-NT2RP2002701//N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB//0.99:184:63//Hs.50727:U43572
R-NT2RP2002706//EST//2.8e-41:148:86//Hs.161917:AA483223
R-NT2RP2002710//EST//0.34:105:71//Hs.136747:AA749210
R-NT2RP2002727//ESTs//8.7e-68:368:94//Hs.14366:T78626
R-NT2RP2002736//ESTs//9.7e-98:457:99//Hs.74899:AA993300
R-NT2RP2002740//Homo sapiens mRNA for KIAA0536 protein, partial cds//0.66:360:59//Hs.119139:AB011108
R-NT2RP2002741//ESTs//3.1e-102:489:98//Hs.112024:AI042352
R-NT2RP2002750//EST//3.6e-43:166:86//Hs.162404:AA573131
R-NT2RP2002752//ESTs//5.0e-56:355:89//Hs.95867:M62042
R-NT2RP2002753//ESTs//1.7e-49:262:96//Hs.49005:W89124
R-NT2RP2002769//ESTs//1.3e-59:376:88//Hs.4046:H03587
R-NT2RP2002778//Homo sapiens clone 24606 mRNA sequence//4.0e-65:341:94//Hs.17481:AF070537
R-NT2RP2002800//ESTs//6.5e-08:79:84//Hs.153262:AA551124
R-NT2RP2002839//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.6e-100:501:97//Hs.136202:AA206578
R-NT2RP2002857//ESTs//4.3e-94:463:97//Hs.134292:AA603031
R-NT2RP2002862//ESTs//2.3e-42:302:82//Hs.117969:H94870
R-NT2RP2002880
R-NT2RP2002891
R-NT2RP2002925//ESTs//1.3e-103:564:92//Hs.142079:AA182894
R-NT2RP2002928//ESTs//3.9e-108:502:99//Hs.29105:AA574143
R-NT2RP2002929//ESTs//4.1e-106:499:99//Hs.44743:AA837096
R-NT2RP2002954//ESTs//2.6e-88:417:99//Hs.100824:AI308771
R-NT2RP2002959//ESTs//7.5e-101:489:97//Hs.32690:N57480
R-NT2RP2002979//ESTs//5.4e-06:197:65//Hs.146726:AI147060
R-NT2RP2002980//ESTs//1.0e-110:562:96//Hs.28444:AA083213
R-NT2RP2002986//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//3.1e-119:578:97//Hs.106290:AI125291
R-NT2RP2002987//Human mRNA for KIAA0331 gene, complete cds//1.0:78:74//Hs.146395:AB002329
R-NT2RP2002993//ESTS, Weakly similar to DNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE [H.sapiens]//2.4e-98:467:98//Hs.86337:AA149311
R-NT2RP2003000//ESTs//0.0070:400:61//Hs.138506:U85642
R-NT2RP2003034//ESTs//9.3e-87:408:96//Hs.164042:H12594
R-NT2RP2003073//Human transporter protein (g17) mRNA, complete cds//0.95:259:61//Hs.76460:U49082
R-NT2RP2003099//Thromboxane A2 receptor//2.6e-42:328:81//Hs.89887:D38081
R-NT2RP2003108//ESTs//2.3e-82:398:98//Hs.5105:AA115512
R-NT2RP2003117//Human mRNA for KIAA0347 gene, complete cds//2.4e-49:336:86//Hs.101996:AB002345
R-NT2RP2003121//ESTs//2.0e-75:380:96//Hs.133127:AA133355
R-NT2RP2003125
R-NT2RP2003129//EST//0.68:115:69//Hs.122196:AA780986
R-NT2RP2003137//ESTs//2.1e-37:259:85//Hs.63169:N78506
R-NT2RP2003161//ESTs//2.5e-88:451:96//Hs.29041:W37379
R-NT2RP2003164//ESTs//4.3e-113:543:97//Hs.8980:AA629067
R-NT2RP2003165//ESTs//6.9e-83:486:89//Hs.138632:H97952
R-NT2RP2003177//ESTs//0.47:38:100//Hs.61790:AA421156
R-NT2RP2003194//ESTs//4.7e-118:582:96//Hs.27266:AA053816
R-NT2RP2003206//ESTs//0.032:388:58//Hs.122148:AA442074
R-NT2RP2003230//ESTs//8.8e-103:478:99//Hs.40140:AI079253
R-NT2RP2003237//ESTs//2.7e-76:392:96//Hs.106278:R37661
R-NT2RP2003243//ESTs//3.6e-53:300:92//Rs.18793:AA192438
R-NT2RP2003265//ESTs, Highly similar to protein NGD5 [M.musculus]//3.3e-110:557:96//Hs.24994:AA236937
R-NT2RP2003272//ESTs, Weakly similar to F15C11.2 [C.elegans]//1.2e-34:228:89//Hs.107201:W52859
R-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//1.4e-111:565:95//Hs.154919:AB014525
R-NT2RP2003280//ESTs//2.6e-101:541:94//Hs.6982:AA622427
R-NT2RP2003286//ESTs//1.2e-104:497:98//Hs.113052:AI222106
R-NT2RP2003293//Human mRNA for KIAA0118 gene, partial cds//9.1e-44:458:74//Hs.154326:D42087

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R-NT2RP2003295//Protein serine/threonine kinase stk2//0.31:321:57//Hs.1087:L20321
R-NT2RP2003297//ESTs//3.0e-15:118:87//Hs.16621:AA098874
R-NT2RP2003308//ESTs, Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]//4.8e-109:553:96//Hs.26089:AA195126
R-NT2RP2003329//ESTs//0.99:208:62//Hs.143607:AI424948
R-NT2RP2003339//ESTs//1.3e-85:441:96//Rs.24115:N32618
R-NT2RP2003347//ESTs//1.5e-70:365:96//Hs.155773:AI312825
R-NT2RP2003367//EST//5.8e-80:376:100//Hs.112500:AA599014
R-NT2RP2003391//ESTs//2.8e-98:484:97//Hs.5842:AA534476
R-NT2RP2003393//ESTs//2.0e-96:510:93//Hs.75844:AA115502
R-NT2RP2003394//EST//5.2e-06:264:63//Hs.144234:W52249
R-NT2RP2003401//ESTs//6.1e-25:161:90//Hs.155360:AA984683
R-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.2e-106:508:98//Hs.131840:AI016073
R-NT2RP2003445//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.6e-21:161:70//Hs.43153:N22360
R-NT2RP2003446//ESTs, Weakly similar to C27H6.4 [C.elegans]//6.0e-105:529:96//Hs.8055:W60903
R-NT2RP2003456//ESTs//7.5e-96:449:99//Hs.25362:AI277332
R-NT2RP2003480//ESTs//1.6e-116:583:96//Hs.59757:AA176121
R-NT2RP2003499//ESTs, Weakly similar to elastin like protein [D.melanogaster]//7.0e-71:365:95//Hs.101056:R52777
R-NT2RP2003506//ESTs, Weakly similar to ORF YPL207w [S.cerevisiae]//2.3e-115:577:96//Hs.16277:N36831
R-NT2RP2003511//ESTs//1.6e-22:182:85//Hs.28249:AA203733
R-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//1.3e-108:566:94//Hs.78482:Y16270
R-NT2RP2003517//Platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)//4.9e-62:518:79//Hs.1976:M12783
R-NT2RP2003522//ESTs//2.0e-97:462:99//Hs.24512:D60170
R-NT2RP2003533//ESTs//4.4e-45:273:78//Hs.140225:AA704101
R-NT2RP2003543//EST//1.0:80:68//Hs.65646:F13684
R-NT2RP2003559//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.8e-58:316:94//Hs.28891:W72439
R-NT2RP2003564//ESTs//3.2e-112:528:99//Hs.53940:N46696
R-NT2RP2003581//ESTs//1.3e-88:506:93//Hs.16157:AA203719
R-NT2RP2003596//ESTs, Weakly similar to No definition line found [C.elegans]//4.7e-101:495:98//Hs.34627:AA126463
R-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.7e-103:501:97//Hs.58488:U97067
R-NT2RP2003629//EST//0.032:440:59//Hs.135297:AI038981
R-NT2RP2003643//ESTs, Weakly similar to HYPOTHETICAL 14.1 KD PROTEIN IN MURZ-RPON INTERGENIC REGION [E.coli]//9.1e-62:359:92//Hs.12492:AA203188
R-NT2RP2003668//EST//9.4e-110:535:97//Hs.116279:AA628951
R-NT2RP2003687//EST//5.9e-05:196:65//Hs.139064:AA135523
R-NT2RP2003691//ESTs, Weakly similar to F59C6.9 [C.elegans]//1.0:202:62//Hs.65539:AI148540
R-NT2RP2003702//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//4.3e-99:492:96//Hs.93332:AA811920
R-NT2RP2003704//ESTs//1.0:155:63//Hs.104166:AA740246
R-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.4e-47:265:93//Hs.78494:AB011097
R-NT2RP2003713//EST//0.81:210:59//Hs.14551:T79401
R-NT2RP2003714//ESTs//1.7e-99:495:96//Hs.158101:AI365003
R-nnnnnnnnnnnnn//Human 19.8 kDa protein mRNA, complete cds//0.84:221:60//Hs.2384:U18914
R-NT2RP2003737//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD [Caenorhabditis elegans]//2.4e-50:302:90//Hs.19196:W74577
R-NT2RP2003751
R-NT2RP2003760//ESTs//2.6e-101:548:93//Hs.115987:AA483808
R-NT2RP2003764//ESTs//8.2e-25:134:98//Hs.64036:AA127709
R-NT2RP2003769//ESTs//1.7e-108:545:95//Hs.56847:AA541606
R-NT2RP2003770//Homo sapiens sperm acrosomal protein mRNA, complete cds//6.0e-106:531:96//Hs.90436:AF047437

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R-NT2RP2003777//ESTs//2.6e-59:323:94//Hs.10101:AI381811
R-NT2RP2003781//ESTs//2.0e-25:269:75//Hs.144951:N34836
R-NT2RP2003793//ESTs//8.7e-94:466:97//Hs.93949:AA782955
R-NT2RP2003840//ESTs//3.4e-97:533:93//Hs.16130:AA195077
R-NT2RP2003857//H.sapiens mRNA for G9a//2.8e-23:351:65//Hs.75196:X69838
R-NT2RP2003859//ESTs//3.0e-07:96:81//Hs.153262:AA551124
R-NT2RP2003871//ESTs//1.9e-102:509:97//Hs.25726:AA430167
R-NT2RP2003885//ESTs//1.0e-102:502:97//Hs.36353:AA702341
R-NT2RP2003912//EST//1.2e-38:336:76//Hs.134975:AI094611
R-NT2RP2003952//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//0.90:190:60//Hs.75875:U49278
R-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//7.6e-116:568:97//Hs.35086:AB014458
R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//3.6e-109:540:97//Hs.7302:AB007916
R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//2.5e-115:568:96//Hs.7316:AB018347
R-NT2RP2003984
R-NT2RP2003986//ESTs//4.9e-36:272:82//Hs.158268:AA738087
R-NT2RP2003988//ESTs, Weakly similar to reverse transcriptase [H.sapiens]//3.2e-110:519:99//Hs.36093:AI149968
R-NT2RP2004014//ESTs//8.4e-102:483:99//Hs.22867:AI417478
R-NT2RP2004041
R-NT2RP2004042//ESTs//1.5e-105:466:97//Hs.7296:N29706
R-nnnnnnnnnnn//ESTs//1.4e-110:559:96//Hs.71916:AA219699
R-NT2RP2004081//ESTs//3.7e-105:503:98//Hs.27542:AA977204
R-NT2RP2004098//EST//7.3e-26:203:87//Hs.21897:R41461
R-NT2RP2004124//ESTs//1.1e-83:435:95//Hs.43299:N23036
R-NT2RP2004142//EST//1.3e-06:165:65//Hs.146742:AI147500
R-NT2RP2004152//ESTs//7.0e-98:455:100//Hs.17731:AI342241
R-NT2RP2004165//ESTs, Highly similar to DYNEIN BETA CHAIN, CILIARY [Anthocidaris crassispina]//1.0e-118:583:97//Hs.16520:AI224533
R-NT2RP2004170//ESTs//6.7e-66:407:88//Hs.157138:AI348544
R-NT2RP2004172//ESTs//1.5e-109:567:95//Hs.159091:AA033974
R-NT2RP2004187//ESTs//3.6e-92:488:93//Hs.22954:W26589
R-NT2RP2004194//ESTs//6.2e-114:585:95//Hs.18778:AA203167
R-NT2RP2004196
R-NT2RP2004207//ESTs//6.3e-102:488:98//Hs.22678:AA604756
R-NT2RP2004226//ESTs//8.8e-18:252:71//Hs.11924:W26972
R-NT2RP2004232//ESTs, Highly similar to protein kinase C mu [H.sapiens]//5.2e-105:499:98//Hs.143460:AA483305
R-NT2RP2004239//ESTs//1.2e-16:171:80//Hs.16134:AA203116
R-NT2RP2004240//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cds//3.4e-103:530:93//Hs.54900:AF039687
R-NT2RP2004242//ESTs//1.3e-85:460:93//Hs.104535:AA211483
R-NT2RP2004245//ESTs//6.4e-117:575:97//Hs.23744:AA035744
R-NT2RP2004270//ESTs//1.0:95:69//Hs.141371:H92187
R-NT2RP2004300//ESTs//4.4e-80:379:99//Hs.130874:AA905056
R-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds//4.7e-110:544:96//Hs.61152:AF000416
R-NT2RP2004321//ESTs//2.1e-18:104:99//Hs.107207:AA044788
R-NT2RP2004339//EST//1.4e-47:309:86//Hs.161917:AA483223
R-NT2RP2004347
R-NT2RP2004364//ESTs//1.1e-113:566:96//Hs.25880:AI268173
R-NT2RP2004365//ESTs//0.022:271:62//Hs.38897:AI129310
R-NT2RP2004366//ESTs//9.5e-71:335:100//Hs.91867:AI218624
R-NT2RP2004373//ESTs//4.2e-25:172:87//Hs.83243:N32192
R-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.4e-11:108:82//Hs.30490:AA146916

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R-NT2RP2004392//ESTs//3.4e-81:427:94//Hs.5827:AA581646
R-NT2RP2004396//EST//5.6e-06:100:77//Hs.138623:H92473
R-NT2RP2004399//EST//0.98:337:59//Hs.118446:N67900
R-NT2RP2004400//ESTs//2.1e-90:422:100//Hs.152460:AA602921
R-NT2RP2004412//ESTS//1.4e-105:503:98//Hs.15929:AA403121
R-NT2RP2004425//EST//0.00017:225:60//Hs.146935:AI168124
R-NT2RP2004476//ESTs//1.4e-88:477:94//Hs.4859:N29695
R-NT2RP2004490//Homo sapiens 3-phosphoinositide dependent protein kinase-1 (PDK1) mRNA, complete cds//8.6e-34:143:98//Hs.154729:AF017995
R-NT2RP2004512//ESTs//2.6e-91:426:100//Hs.94133:AI270700
R-NT2RP2004523//ESTs//1.6e-74:377:97//Hs.14217:R61320
R-NT2RP2004538//Thromboxane A2 receptor//1.4e-45:279:89//Hs.89887:D38081
R-NT2RP2004551//ESTs//0.47:147:66//Hs.131519:AI024347
R-NT2RP2004568//ESTs//1.3e-107:567:94//Hs.65234:AA195470
R-NT2RP2004580//ESTs//5.9e-29:156:98//Hs.147801:AI221661
R-NT2RP2004587//ESTs//1.0e-102:495:97//Hs.91662:AA781126
R-NT2RP2004594//ESTs//4.1e-56:298:95//Hs.24641:AA954666
R-NT2RP2004600//ESTs//4.8e-67:374:93//Hs.49762:N69862
R-NT2RP2004602//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-07:149:76//Hs.12845:N28835
R-NT2RP2004614//ESTs//1.0e-111:557:96//Hs.37892:N53497
R-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//2.4e-118:587:96//Hs.5198:AJ006291
R-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds//5.9e-107:520:96//Hs.29956:AB007929
R-NT2RP2004675//ESTs//2.7e-82:407:97//Hs.116113:F18930
R-NT2RP2004681//NUCLEOLIN//0.34:387:58//Hs.79110:M60858
R-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds//5.0e-120:600:96//Hs.154919:AB014525
R-NT2RP2004709//ESTs//1.1e-106:511:98//Hs.38034:AI149793
R-NT2RP2004710//ESTs//9.9e-87:477:93//Hs.6834:AA203433
R-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds//1.3e-118:594:96//Hs.4236:AB007947
R-NT2RP2004743//ESTs//2.1e-48:327:88//Hs.43635:AA447015
R-NT2RP2004767//EST//4.0e-57:328:81//Hs.142796:N51423
R-NT2RP2004775//ESTs//9.4e-60:326:94//Hs.115339:AA136774
R-NT2RP2004791//ESTs//3.2e-82:367:96//Hs.141911:N64013
R-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//8.0e-116:564:96//Hs.40820:AF058953
R-NT2RP2004802//ESTs//6.5e-111:586:94//Hs.90375:W74579
R-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//8.7e-120:584:97//Hs.67052:AF054179
R-NT2RP2004841//EST//3.8e-31:323:74//Hs.147714:AI219906
R-NT2RP2004861//EST//0.92:147:63//Hs.23064:R20803
R-NT2RP2004897//ESTs//1.7e-46:390:80//Hs.139225:H96567
R-NT2RP2004936//EST//0.97:176:63//Hs.137436:AA280529
R-nnnnnnnnnnn//ESTs//0.059:137:64//Hs.144109:AI345543
R-NT2RP2004961//ESTs//1.8e-87:409:100//Hs.138297:AA781941
R-NT2RP2004962//ESTs//0.0021:292:59//Hs.145917:AI275458
R-NT2RP2004967//Human mRNA for KIAA0118 gene, partial cds//7.4e-51:506:75//Hs.154326:D42087
R-NT2RP2004978//ESTs//0.95:138:63//Hs.13619:W93496
R-NT2RP2004982//ESTs//7.8e-95:468:97//Hs.22545:R43910
R-NT2RP2004985
R-NT2RP2004999//ESTs//2.9e-94:450:98//Hs.128766:AI419902
R-NT2RP2005000
R-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//9.6e-113:577:95//Hs.155972:AB014515
R-NT2RP2005003//EST//1.3e-75:387:96//Hs.140843:R42235
R-nnnnnnnnnnn//Homo sapiens SEC63 (SEC63) mRNA, complete cds//3.1e-116:568:97//Hs.31575:AF100141

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R-NT2RP2005018//ESTs//7.5e-46:280:90//Hs.126857:AA932161
R-NT2RP2005020//ESTs//1.6e-105:554:94//Hs.14846:AA148507
R-NT2RP2005031//EST//3.1e-79:379:99//Hs.139709:AA227887
R-NT2RP2005037//ESTs//5.3e-102:551:93//Hs.26516:AA195220
R-NT2RP2005038//ESTs//5.8e-101:566:92//Hs.46964:N49757
R-NT2RP2005108
R-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//2.7e-105:518:97//Hs.22616:AB014564
R-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//4.6e-69:464:85//Hs.100555:X98743
R-NT2RP2005139//ESTs//1.0e-108:545:95//Hs.21006:AA523383
R-NT2RP2005140//ESTs//4.3e-90:422:99//Hs.62180AI341261
R-NT2RP2005144//ESTs//0.91:162:62//Hs.52399:AI075744
R-NT2RP2005147//ESTs//4.6e-100:502:96//Hs.27931:AA633438
R-NT2RP2005159//ESTs//7.5e-105:533:95//Hs.109819:AI357582
R-NT2RP2005162//ESTs//6.6e-83:419:96//Hs.113998:H50648
R-NT2RP2005168//Homo sapiens mRNA for EIB-55kDa-associated protein//2.4e-101:513:95//Hs.155218:AJ007509
R-NT2RP2005204//ESTs, Weakly similar to UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG [H.sapiens]//1.9e-115:577:96//Hs.7600:H98166
R-NT2RP2005227//Homo sapiens UM protein mRNA, complete cds//1.0e-45:359:82//Hs.154103:AF061258
R-NT2RP2005239//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//1.0e-47:245:97//Hs.21090:AA418587
R-NT2RP2005254//ESTs//3.3e-111:581:94//Hs.22549:AA524503
R-NT2RP2005270//ESTs, Highly similar to HYPOTHETICAL 67.6 KD PROTEIN ZK637.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.1e-79:412:95//Hs.23047:N66596
R-NT2RP2005276//ESTs//4.6e-85:426:96//Hs.24550:AA316272
R-NT2RP2005287//ESTs//1.7e-109:565:94//Hs.61976:AI279001
R-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.4e-125:594:98//Hs.27007:AF060219
R-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//4.9e-112:545:96//Hs.44766:AJ007590
R-NT2RP2005293//ESTs//5.1e-116:538:99//Hs.62180:AI341261
R-NT2RP2005315//ESTs//1.4e-82:415:97//Hs.155829:AA018338
R-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds//2.5e-45:272:91//Hs.1569:U11701
R-NT2RP2005336//ESTs//1.9e-93:444:99//Hs.110966:AA151699
R-NT2RP2005 344//Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA, complete cds//0.011:463:58//Hs.150926:AF017445
R-NT2RP2005354//ESTs//7.2e-22:148:91//Hs.153783:H14544
R-NT2RP2005360//ESTs//0.048:225:60//Hs.7602:AA099247
R-NT2RP2005393//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.9e-41:248:82//Hs.93121:AB018304
R-NT2RP2005407//ESTs, Weakly similar to OSH1 PROTEIN [Saccharomyces cerevisiae]//2.5e-75:461:88//Hs.70849:AA121697
R-NT2RP2005436//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II [C.elegans]//8.1e-96:491:95//Hs.7194:AI185631
R-NT2RP2005441//ESTs//1.1e-110:548:96//Hs.5209:AA780068
R-NT2RP2005453//ESTs//0.94:352:58//Hs.25870:H14423
R-NT2RP2005457//ESTs//2.1e-46:236:97//Hs.19522:AA975096
R-NT2RP2005464//ESTS//1.8e-72:349:99//Hs.44045:N51307
R-NT2RP2005465//ESTs//0.0058:322:58//Hs.127009:AI378936
R-NT2RP2005472//ESTs//0.47:309:60//Hs.144838:AI222019
R-NT2RP2005476//ESTS//5.1 e-40:205:9811Hs.101577:AI168526
R-NT2RP2005490//ESTs//L3e-70:364:96//Hs.134382:AA083573
R-NT2RP2005491//EST//0.012:220:60//Hs.144448:AA812455
R-NT2RP2005495//ESTs//1.2e-86:501:91//Hs.99445:R93540
R-NT2RP2005496//ESTs//3.2e-34:263:81//Hs.70279:AA757426
R-NT2RP2005498//ESTS, Highly similar to PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, NEURONAL ISOFORM [Oryctolagus cuniculus]//2.3e-45:284:88//Hs.85752:AI138993

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R-NT2RP2005501//ESTs//2.5e-84:404:98//Hs.143812:AI141755
R-NT2RP2005509//ESTs, Highly similar to HYPOTHETICAL 37.2 KD PROTEIN C12C2.09C IN CHROMOSOME I [Schizosaccharomyces pombe]//8.2e-36:215:92//Hs.5298:AA725071
R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//3.2e-110:570:9411Hs.119023:AF092563
R-NT2RP2005525//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.3e-84:433:95//Hs.36942:AA524535
R-NT2RP2005531//EST//0.98:64:70//Hs.146573:AI139856
R-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.8e-108:560:94//Hs.159597:AJ012449
R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.7e-115:583:96//Hs.62515:AB007963
R-NT2RP2005549//EST//0.61:111:62//Hs.147482:AI215572
R-NT2RP2005555//ESTs//6.6e-108:507:99//Hs.68613:AI357567
R-NT2RP2005557//ESTs//3.1e-105:495:99//Hs.105985:AA885169
R-NT2RP2005581//ESTs//1.7e-79:445:92//Hs.138152:H03240
R-NT2RP2005600//ESTs//1.3e-38:192:100//Hs.48329:W92733
R-NT2RP2005605//ESTs//7.6e-87:409:99//Hs.45005:AA975060
R-NT2RP2005620//ESTs//2.9e-96:463:97//Hs.7407:AI376788
R-NT2RP2005622//ESTs//1.8e-104:497:98//Hs.22595:AA394229
R-NT2RP2005637//EST//2.5e-20:163:71//Hs.161164:AI418211
R-NT2RP2005640//ESTs//5.0e-99:473:98//Hs.23467:AA708740
R-NT2RP2005645//ESTs//9.5e-23:231:77//Hs.5534:AA195173
R-NT2RP2005651//ESTS, Highly similar to XFIN PROTEIN [Xenopus laevis]//2.9e-103:525:96//Hs.70589:AA868470
R-NT2RP2005654//Insulin-like growth factor binding protein 2//0.94:223:60//Hs.162:X16302
R-NT2RP2005669//Homo sapiens nitrilase 1 (VIII) mRNA, complete cds//2.7e-14:87:100//Hs.146406:AF069987
R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//5.8e-91:434:98//Hs.25664:AF089814
R-NT2RP2005683//ESTs//1.5e-98:494:96//Hs.22595:AA394229
R-NT2RP2005690//ESTs//4.8e-43:286:86//Hs.150727:AI292236
R-NT2RP2005694//EST//3.1e-82:386:100//Hs.149391:AI273643
R-NT2RP2005701//ESTs, Highly similar to BUTYROPHILIN PRECURSOR [Bos tauros]//2.8e-68:376:93//Hs.9095:AA532630
R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//1.3e-105:503:98//Hs.61638:AB018342
R-NT2RP2005719//ESTs, Weakly similar to GPI-anchored protein p137 precursor [H.sapiens]//5.4e-105:500:98//Hs.14298:AI417523
R-NT2RP2005722//EST//6.5e-76:395:94//Hs.142150:AA223982
R-NT2RP2005723//ESTs//1.5e-84:452:93//Hs.91753:R44455
R-NT2RP2005726//ESTs//3.5e-64:500:82//Hs.100526:AI223153
R-NT2RP2005741//ESTs//4.7e-60:333:93//Hs.107242:R40258
R-NT2RP2005748//ESTs//3.4e-102:498:97//Hs.82660:N78064
R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//4.3e-42:223:96//Hs.159651:AF068868
R-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//1.2e-104:494:98//Hs.26285:AF082516
R-NT2RP2005763//ESTs//1.1e-97:456:99//Hs.65412:AI362163
R-NT2RP2005767//ESTs//8.0e-38:204:96//Hs.18460:AA193463
R-NT2RP2005773//ESTs, Highly similar to PYRROLINE-5-CARBOXYLATE REDUCTASE [Homo sapiens]//5.4e-112:559:96//Hs.14214:AI189379
R-NT2RP2005775//ESTs, Highly similar to NEUROLYSIN PRECURSOR [Sus scrofa]//3.0e-108:544:96//Hs.22151:AI214321
R-NT2RP2005781//ESTs//1.7e-43:217:99//Hs.144391:AA365664
R-NT2RP2005784//EST//0.0071:217:60//Hs.117332:AA699724
R-NT2RP2005804//ESTs//8.8e-107:512:98//Hs.15496:W44398
R-NT2RP2005812//ESTs//9.0e-76:359:99//Hs.113937:AI298746
R-NT2RP2005815//ESTs//5.5e-76:363:99//Hs.136230:AA594981

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R-NT2RP2005835//ESTs//1.5e-100:541:94//Hs.86813:N25122
R-NT2RP2005841//ESTs//2.8e-105:556:92//Hs.69993:AA628403
R-NT2RP2005853//EST//2.0e-13:219:70//Hs.134016:AI076062
R-NT2RP2005857//ESTS//1.0e-115:576:96//Hs.30663:AI338462
R-NT2RP2005859//ESTs//7.3e-116:571:97//Hs.85986:AA195105
R-NT2RP2005868//EST//0.00023:320:61//Hs.149689:AI284133
R-NT2RP2005890//ESTs//1.0e-96:466:98//Hs.122579:AA766315
R-NT2RP2005901//ESTs//8.3e-116:548:98//Hs.66296:AI125268
R-NT2RP2005908//ESTs, Weakly similar to weakly similar to gastrula zinc finger protein [C.elegans]//2.4e-73:397:94//Hs.16667:T92427
R-NT2RP2005933//ESTs, Highly similar to nucleoporin p54 [R.norvegicus]//2.8e-114:560:97//Hs.9082:AA873170
R-NT2RP2005942//ESTs//5.6e-117:582:96//Hs.146123:AI338419
R-NT2RP2005980//ESTs//6.9e-101:478:98//Hs.43145:AA776988
R-NT2RP2006023//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.5e-51:398:80//Hs.113283:AF018080
R-NT2RP2006038//ESTs//0.025:284:59//Hs.97852:AA404347
R-NT2RP2006043//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II [C.elegans]//1.2e-50:278:94//Hs.7194:AI185631
R-NT2RP2006052//ESTs//5.0e-52:272:95//Hs.99545:AA461492
R-NT2RP2006069//ESTs//1.8e-90:495:93//Hs.43654:AA522714
R-NT2RP2006071//ESTs//1.5e-38:218:94//Hs.107882:W72093
R-NT2RP2006098//ESTs//2.9e-105:540:95//Hs.26860:N56918
R-NT2RP2006100//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.031:254:62//Hs.46440:U21943
R-NT2RP2006103//ESTs//1.5e-86:416:98//Hs.152114:AA401365
R-NT2RP2006141//ESTs//5.3e-88:432:98//Hs.77480:AA100522
R-NT2RP2006166//Homo sapiens LIM protein mRNA, complete cds//2.8e-17:255:72//Hs.154103:AF061258
R-NT2RP2006184//ESTs//8.4e-101:487:98//Hs.58009:W69435
R-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//6.1e-110:553:95//Hs.109299:AB014554
R-NT2RP2006196//Human clone 23960 mRNA sequence//0.0037:48:100//Hs.151293:U79276
R-NT2RP2006200//ESTs//6.5e-77:398:96//Hs.163953:R01398
R-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//1.2e-94:532:90//Hs.153910:X96484
R-NT2RP2006237//ESTs//1.2e-57:305:95//Hs.86149:AI341312
R-NT2RP2006238//ESTs, Highly similar to rA8 [R.norvegicus]//1.5e-29:183:91//Hs.4048:AA404253
R-NT2RP2006258//ESTs//3.2e-87:462:94//Hs.141556:N49928
R-NT2RP2006261//ESTs//3.4e-57:3 26:92//Hs.22523:W02999
R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//4.7e-96:481:97//Hs.3404:AF035262
R-NT2RP2006320//EST//3.4e-21:335:65//Hs.141603:N66015
R-NT2RP2006321//ESTs, Moderately similar to karyopherin beta 3 [H.sapiens]//1.9e-89:460:96//Hs.21889:N78664
R-NT2RP2006323//ESTs//3.5e-91:439:98//Hs.61697:AI081771
R-NT2RP2006333//ESTs//4.9e-38:301:82//Hs.155999:AA196412
R-NT2RP2006334//EST//3.1e-45:264:91//Hs.149599:AI282321
R-NT2RP2006365//ESTs//2.9e-81:417:95//Hs.11814:W44411
R-NT2RP2006393//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//3.9e-48:403:77//Hs.1361:M55053
R-NT2RP2006436//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.4e-27:155:76//Hs.115325:D84488
R-NT2RP2006441//ESTs//6.0e-108:529:97//Hs.101282:N45092
R-NT2RP2006454//ESTs//9.2e-20:110:99//Hs.144687:AI341146
R-NT2RP2006456//ESTs//7.1e-91:508:92//Hs.12488:W63595
R-NT2RP2006464//Homo sapiens mRNA for AND-1 protein//2.1e-109:524:97//Hs.72160:AJ006266
R-NT2RP2006467//EST//0.99:140:61//Hs.146958:AI174478
R-NT2RP2006472//ESTs//3.3e-92:473:95//Hs.29216:AA916679
R-NT2RP2006534//ESTs//1.2e-83:394:99//Hs.162116:AA524947
R-NT2RP2006554//ESTs//1.0e-87:460:95//Hs.47095:AA181474
R-NT2RP2006565//ESTs//3.2e-24:129:100//Hs.13499:AI299886
R-NT2RP2006571//ESTs//2.6e-56:306:94//Hs.98370:AA316622

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R-nnnnnnnnnnn//ESTs//2.0e-112:533:98//Hs.18685:AI393829
R-NT2RP2006598//ESTs, Weakly similar to retinoid X receptor interacting protein [M.musculus]//4.1e-109:542:97//Hs.7889:AI337112
R-NT2RP3000002//ESTs//1.3e-08:399:59//Hs.126044:AI301598
R-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//1.9e-116:560:97//Hs.6764:AJ011972
R-NT2RP3000046//Small inducible cytokine A5 (RANTES)//1.9e-57:312:85//Hs.155464:AF088219
R-NT2RP3000047//EST//0.91:130:66//Hs.140208:AA702213
R-NT2RP3000050//ESTs, Weakly similar to putative p150 [H.sapiens]//3.1e-41:249:90//Hs.156155:AI222202
R-NT2RP3000055//EST//2.4e-19:146:86//Hs.160497:AI255095
R-NT2RP3000072//ESTs//2.2e-82:424:96//Hs.21542:N49574
R-NT2RP3000080//ESTs//2.1e-29:186:89//Hs.153372:AA424029
R-NT2RP3000085//ESTs//4.5e-101:482:98//Hs.47649:AA838715
R-NT2RP3000109//ESTs//9.5e-97:455:99//Hs.17731:AI342241
R-NT2RP3000134//EST//4.7e-106:497:99//Hs.125531:AA884000
R-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.2e-116:578:96//Hs.13273:AB011164
R-NT2RP3000149//ESTs//7.7e-62:361:90//Hs.6649:N93418
R-NT2RP3000186
R-NT2RP3000197//ESTs//1.5e-75:436:91//Hs.140931:R51882
R-NT2RP3000207//ESTs//1.3e-98:468:98//Hs.126908:AA933091
R-NT2RP3000220//ESTs//2.2e-27:144:99//Hs.106861:R61306
R-NT2RP3000233//EST//7.8e-77:368:99//Hs.49075:N64817
R-NT2RP3000235//ESTs//0.43:82:74//Hs.132828:AI032819
R-NT2RP3000247//EST//2.2e-97:459:99//Hs.127928:AA969239
R-NT2RP3000251
R-NT2RP3000252//ESTs, Weakly similar to Lpg15p [S.cerevisiae]//2.0e-108:532:97//Hs.111086:AI379177
R-NT2RP3000255//EST//0.67:93:67//Hs.120579:AA743073
R-NT2RP3000267//ESTs//8.5e-108:542:95//Hs.24984:AA534446
R-NT2RP3000299//ESTs, Weakly similar to enhancer of filmentation 1 [H.sapiens]//3.6e-103:516:96//Hs.4894:AI191323
R-NT2RP3000312//ESTs//1.3e-100:493:97//Hs.29379:AI094117
R-NT2RP3000320//ESTs//3.2e-95:538:91//Hs.118793:AA192438
R-NT2RP3000324
R-NT2RP3000333//ESTs//6.0e-39:194:100//Hs.119238:AA476267
R-NT2RP3000341//ESTS//0.51:251:61//Hs.94090:AA777689
R-NT2RP3000348//EST//1.8e-80:389:98//Hs.145944:AI276225
R-NT2RP3000350//ESTs, Weakly similar to Lpg15p [S.cerevisiae]//3.1e-110:556:96//Hs.111086:AI379177
R-NT2RP3000359//EST//4.9e-61:340:92//Hs.126495:AA913741
R-NT2RP3000361//ESTs, Weakly similar to PRE-MRNA SPLICING FACTOR PRP6 [S.cerevisiae]//4.8e-91:439:97//Hs.31334:AI144423
R-NT2RP3000366//EST//0.20:392:57//Hs.149652:AI283303
R-NT2RP3000397//EST//8.7e-26:150:94//Hs.124617:AA855106
R-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds//4.2e-111:529:98//Hs.28307:AF071185
R-NT2RP3000418//EST//3.3e-09:202:67//Hs.117189:AA682947
R-NT2RP3000433
R-NT2RP3000439//ESTs//3.1e-79:426:92//Hs.26548:W26340
R-NT2RP3000441//ESTs//6.3e-84:420:97//Hs.137482:AA421254
R-NT2RP3000449//ESTs//4.9e-93:435:99//Hs.54617:AI379102
R-NT2RP3000451//ESTs//2.3e-89:439:97//Hs.9196:AA748492
R-NT2RP3000456//Homo Sapiens (clone B3B3E13) chromosome 4p16.3 DNA fragment//1.8e-23:347:70//Hs.114963:L34408
R-NT2RP3000484//Heparin cofactor II//0.98:166:62//Hs.1478:M58600
R-NT2RP3000487//ESTs//0.012:384:60//Hs.88684:AA885141
R-NT2RP3000512//Homeo box B3//2.0e-69:377:93//Hs.49931:X16667
R-NT2RP3000526//ESTS//1.6e-91:432:99//Hs.38042:AA187151
R-NT2RP3000527//ESTs//1.2e-100:518:94//Hs.104557:AI078161

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R-NT2RP3000531//ESTs, Weakly similar to TH1 protein [D.melanogaster]//0.95:85:71//Hs.5184:AA709151
R-NT2RP3000542//ESTs//2.6e-53:375:84//Hs.44158:N30180
R-NT2RP3000561//EST//1.1e-13:170:75//Hs.148421:AI198036
R-NT2RP3000562//Human mRNA for KIAA0233 gene, complete cds//0.97:141:68//Hs.79077:D87071
R-NT2RP3000578//ESTs//2.6e-68:324:100//Hs.5445:AA779447
R-NT2RP3000582//ESTS//2.1 e-25:131:80//Hs.152465:AA563785
R-NT2RP3000584//ESTs//1.8e-97:460:99//Hs.120698:AI241511
R-NT2RP3000590//ESTs//2.0e-97:453:100//Hs.105355:AA953817
R-NT2RP3000592//ESTs//2.8e-91:432:99//Hs.144304:AI190916
R-nnnnnnnnnnnn//Human mRNA for KIAA0314 gene, partial cds//1.5e-09:447:58//Hs.155045:AB002312
R-NT2RP3000599//ESTs//3.8e-93:437:99//Hs.23971:AA829880
R-NT2RP3000605//ESTs//4.2e-111:554:96//Hs.40780:AA422049
R-NT2RP3000622//ESTs//2.0e-100:473:99//Hs.11387:AI127394
R-NT2RP3000624//ESTs, Weakly similar to KIAA0256 [H.sapiens]//5.4e-115:545:98//Hs.4857:AI090739
R-NT2RP3000628//Homo sapiens mRNA for KIAA0772 protein, complete cds//4.3e-49:397:80//Hs.15519:AB018315
R-NT2RP3000632//ESTs, Moderately similar to cyclin-selective ubiquitin carrier protein [H.sapiens]//6.3e-92:434:99//Hs.152517:AA719022
R-NT2RP3000644//ESTs//1.0e-44:306:84//Hs.155498:W27084
R-NT2RP3000661//ESTs//3.1e-95:470:97//Hs.126069:W76185
R-NT2RP3000665//ESTs//3.3e-95:503:94//Hs.34313:W81185
R-NT2RP3000685//ESTs//2.7e-99:515:94//Hs.9711:R60873
R-NT2RP3000690//ESTs//3.3e-88:414:99//Hs.1465 89:AI085578
R-NT2RP3000736
R-NT2RP3000742//ESTs, Highly similar to 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 [Rattus norvegicus]//1.8e-07:114:75//Hs.136065:W21960
R-NT2RP3000753//ESTs//3.1e-99:461:100//Hs.150901:AI310447
R-NT2RP3000759//ESTs//2.0e-74:384:95//Hs.104222:AA207243
R-NT2RP3000815//ESTs//8.5e-97:455:99//Hs.158897:AI378583
R-NT2RP3000825//EST//0.0089:343:59//Hs.42897:N20810
R-NT2RP3000826//EST//3.4e-33:342:74//Hs.162236:AA551582
R-NT2RP3000836//ESTs//6.8e-24:181:84//Hs.134464:AI151081
R-NT2RP3000841//ESTs//4.5e-93:491:93//Hs.23618:H98082
R-NT2RP3000845//ESTs//2.4e-88:473:93//Hs.8312:AA813022
R-NT2RP3000847//ESTs//9.3e-89:460:95//Hs.154106:AI051657
R-NT2RP3000850
R-NT2RP3000852//Fibrillin 2//0.55:237:63//Hs.79432:U03272
R-NT2RP3000859//ESTs//1.4e-96:509:94//Hs.7187:AA576895
R-NT2RP3000865//EST//4.8e-23:461:66//Hs.162088:AA505741
R-NT2RP3000868//ESTs//5.4e-78:430:93//Hs.102796:N70837
R-NT2RP3000869//ESTs//8.5e-77:397:94//Hs.84484:AI014673
R-NT2RP3000875//Mevalonate kinase//3.8e-78:531:84//Hs.75138:M88468
R-NT2RP3000901//ESTs//2.1e-95:466:97//Hs.10647:AA428217
R-NT2RP3000904//ESTs//1.6e-79:380:99//Hs.100850:AA479385
R-NT2RP3000917//ESTs, Highly similar to mouse Dhml protein [M.musculus]//9.5e-113:566:96//Hs.5900:AA035728
R-NT2RP3000919
R-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A/1.5e-25:375:71//Hs.2953:X84407
R-NT2RP3000980//ESTs//3.3e-72:364:96//Hs.9536:AA114178
R-NT2RP3000994//ESTs//3.5e 111:537:97//Hs.21146:AA683542
R-NT2RP3001004//ESTs//9.6e-91:456:96//Hs.58974:W87405
R-NT2RP3001007//ESTs//6.7e-99:482:97//Hs.117737:AI088029
R-NT2RP3001055//ESTs//0.0012:294:60//Hs.66479:AA863044
R-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN HF.12 [Homo sapiens]//5.6e-102:486:99//Hs.145956:AA007349
R-NT2RP3001081//Retinal pigment epithelium-specific protein (65kD)//0.0012:447:58//Hs.2133:U18991
R-NT2RP3001084//ESTs//4.3e-102:528:96//Hs.25277:W87874
R-NT2RP3001096//ESTS//1.1e-110:540:96//Hs.42824:AA873182

BNSDOCID: <EP___1074617A2_I_>

R-NT2RP3001107//ESTs//7.6e-100:478:98//Hs.99669:AA287832
R-nnnnnnnnnnnn//DNA polymerase gamma//0.0014:50:100//Hs.80961:U60325
R-NT2RP3001111//ESTs, Weakly similar to Trf-proximal protein [D.melanogaster]//3.2e-104:543:95//Hs.93796:C06063
R-NT2RP3001113//ESTs//3.3e-100:467:99//Hs.97757:AA401575
R-NT2RP3001115//0xytocin receptor//7.9e-30:505:67//Hs.2820:X64878
R-NT2RP3001116//ESTs//4.6e-41:229:96//Hs.58412:W74779
R-NT2RP3001119//ESTs//6.9e-88:478:92//Hs.19469:AA203180
R-NT2RP3001120//ESTs//3.1e-82:430:93//Hs.110956:AI190166
R-NT2RP3001126//ESTs//4.4e-52:264:96//Hs.25264:R78188
R-NT2RP3001133//ESTs//4.7e-105:541:94//Hs.73239:AA573761
R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//2.6e-115:549:97//Hs.5378:AB018305
R-NT2RP3001147//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]//9.6e-113:552:97//Hs.23900:U82984
R-NT2RP3001150//ESTs//2.9e-90:444:97//Hs.99601:AA760717
R-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//9.4e-118:563:98//Hs.72160:AJ006266
R-NT2RP3001176//ESTs//1.8e-110:534:98//Hs.58650:AI074460
R-NT2RP3001214//ESTs//1.7e-109:545:96//Hs.24481:AA573139
R-NT2RP3001216//EST//0.00098:128:66//Hs.160493:AI254963
R-NT2RP3001221//EST//0.010:106:66//Hs.147774:AI221196
R-NT2RP3001232//ESTs//1.5e-101:518:94//Hs.21630:AA778399
R-NT2RP3001236//ESTs, Highly similar to KIAA0377 [H.sapiens]//2.8e-89:462:95//Hs.116793:AA779588
R-NT2RP3001239//ESTs, Moderately similar to NEURAXIN [Rattus norvegicus]//5.2e-82:466:91//Hs.66048:AA524416
R-NT2RP3001245//EST//0.53:237:62//Hs.161131:AI417631
R-NT2RP3001253//ESTs//1.7e-105:535:96//Hs.42315:AI222997
R-NT2RP3001260//EST//0.16:144:62//Hs.126856:AA932135
R-NT2RP3001268//Human Aac11(aac11) mRNA, complete cds//0.12:494:59//Hs.151031:U83857
R-NT2RP3001272//ESTs//1.4e-92:436:99//Hs.149831:AI383965
R-NT2RP3001274//ESTs//3.9e-81:424:95//Hs.1113184:N25651
R-NT2RP3001281//EST//3.1e-60:298:98//Hs.149230:AI247332
R-NT2RP3001307//EST//0.42:215:62//Hs.126165:AA868691
R-NT2RP3001318//ESTs//4.1e-74:363:97//Hs.130832:H92571
R-NT2RP3001325//ESTs//1.7e-106:534:96//Hs.21214:H98989
R-NT2RP3001338//Human protein tyrosine phosphatase sigma mRNA, complete cds//0.22:199:63//Hs.159534:U35234
R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//3.9e-114:566:96//Hs.18586:AB007920
R-NT2RP3001340//ESTs//1.1e-72:411:92//Hs.21135:W81653
R-NT2RP3001355//ESTs//9.0e-103:521:95//Hs.99486:AA776798
R-NT2RP3001374//ESTs//2.7e-82:395:98//Hs.117102:AA993090
R-NT2RP3001383//ESTs//3.6e-10:118:78//Hs.111055:AA169778
R-NT2RP3001384//ESTs, Weakly similar to A-kinase anchor protein 95, AKAP95 [R.norvegicus]//5.7e-92:522:90//Hs.96200:AA218942
R-NT2RP3001392//ESTs//5.9e-62:296:100//Hs.125034:AA907375
R-NT2RP3001396//ESTS//3.7e-111:528:98//Hs.22612:AA152232
R-NT2RP3001398//ESTs//2.6e-94:449:99//Hs.146332:AI276628
R-NT2RP3001399//ESTs//2.6e-82:401:97//Hs.7932:AI041186
R-NT2RP3001407//ESTs//2.2e-101:488:97//Hs.71573:AA496898
R-NT2RP3001420//EST//7.4e-44:394:79//Hs.137041:AA877817
R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequence//3.6e-106:550:94//Hs.6957:AF052158
R-NT2RP3001427//ESTs//1.3e-87:374:97//Hs.5457:H05692
R-nnnnnnnnnnnn//Neurotrophic tyrosine kinase, receptor, type 1//4.7e-96:533:91//Hs.85844:X66397
R-NT2RP3001432//ESTs//1.9e-102:523:95//Hs.132978:AI041374
R-NT2RP3001447//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.1e-101:482:98//Hs.124135:AA910560
R-NT2RP3001449//ESTs//2.2e-99:502:96//Hs.7834:N45994
R-NT2RP3001453//Small inducible cytokine A5 (RANTES)//8.1e-45:295:85//Hs.155464:AF088219

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R-NT2RP3001457//ESTS//1.5e-52:256:99//Hs.117982:AA644658
R-NT2RP3001459//ESTs//3.4e-62:299:99//Hs.146098:AA167280
R-NT2RP3001472//ESTs//4.8e-108:540:96//Hs.69594:N37009
R-NT2RP3001490//ESTs//3.5e-91:549:88//Hs.6606:AA211783
R-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds//1.4e-61:338:93//Hs.519:U13395
R-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds//6.8e-112:549:9711Hs.28285:AF064801
R-NT2RP3001527//ESTs//4.4e-105:543:95//Hs.158761:AA631047
R-NT2RP3001529//Homo sapiens tapasin (NGS-17) mRNA, complete cds//7.9e-59:427:83//Hs.5247:AF029750
R-NT2RP3001538//ESTs//1.6e-94:521:92//Hs.6846:AA209463
R-NT2RP3001554//ESTs, Moderately similar to NEURAXIN [Rattus norvegicus]//2.8e-76:392:95//Hs.66048:AA524416
R-NT2RP3001580//ESTs//3.7e-82:398:98//Hs.23490:N49477
R-NT2RP3001587//Homa sapiens mRNA for HRIHFB2115, partial cds//1.8e-09:86:88//Hs.4311:AB015337
R-NT2RP3001589//ESTs//0.0029:243:62//Hs.158924:AA605194
R-NT2RP3001607//EST//0.00096:76:78//Hs.140319:AA748328
R-NT2RP3001608//ESTs//3.8e-105:525:96//Hs.144655:AI279798
R-NT2RP3001621//ESTs//3.3e-108:535:97//Hs.47378:AI193598
R-NT2RP3001629
R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//2.7e-109:541:96//Hs.9899:AF099149
R-NT2RP3001642//ESTs//6.0e-105:525:96//Hs.3376:AA915989
R-NT2RP3001646//ESTs//4.8e-95:523:92//Hs.64036:AA127709
R-NT2RP3001671//ESTs//0.0013:367:60//Hs.106090:AA457030
R-NT2RP3001672//ESTs//3.4e-37:191:98//Hs.57475:AI382189
R-NT2RP3001676//ESTs//1.5e-81:408:97//Hs.142547:N67648
R-NT2RP3001678//ESTs//4.3e-85:405:99//Hs.121915:AI268225
R-NT2RP3001679//ESTs//3.4e-100:545:93//Hs.5943:AI222558
R-NT2RP3001688//Human mRNA for KIAA0392 gene, partial cds//8.6e-46:301:87//Hs.40100:AB002390
R-NT2RP3001690//ESTs//3.3e-111:542:97//Hs.86149:AI341312
R-NT2RP3001708//ESTs//1.4e-96:349:95//Hs.17975:AA868618
R-NT2RP3001712//ESTs//9.3e-14:102:92//Hs.78041:N29669
R-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//4.1e-80:444:91//Hs.6823:W18181
R-NT2RP3001724//ESTs//1.8e-109:547:96//Hs.14570:AI422099
R-NT2RP3001730//ESTs//4.1e-98:528:92//Hs.155115:AA669923
R-NT2RP3001739//ESTs//4.4e-87:444:94//Hs.27239:W27810
R-NT2RP3001752//ESTS//6.1e-93:490:94//Hs.4210:AA740440
R-NT2RP3001753//ESTs//2.5e-82:395:99//Hs.126435:AA912968
R-NT2RP3001764//ESTs, Weakly similar to protein-tyrosine phosphatase [H.sapiens]//1.2e-87:450:96//Hs.20281:N92517
R-NT2RP3001777//ESTs//1.1e-86:360:97//Hs.100530:H06725
R-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//4.2e-113:549:97//Hs.28169:AB007928
R-NT2RP3001792//ESTs, Weakly similar to F35C12.2 [C.elegans]//1.1e-21:119:99//Hs.44268:AA455900
R-NT2RP3001799//OX40L RECEPTOR PRECURSOR//2.8e-45:374:79//Hs.129780:X75962
R-NT2RP3001819//ESTs//2.6e-87:432:96//Hs.10414:AI291292
R-NT2RP3001844//ESTs//0.024:128:67//Hs.25131:N50117
R-NT2RP3001854//ESTs//1.4e-92:490:92//Hs.15165:N52900
R-NT2RP3001855//ESTs//1.9e-66:361:93//Hs.10043:D81792
R-NT2RP3001896//ESTs//1.4e-96:343:97//Hs.24809:N73642
R-NT2RP3001898//ESTs//4.1e-90:515:91//Hs.4867:AA521180
R-NT2RP3001915//ESTs//4.4e-32:175:95//Hs.24641:AA954666
R-NT2RP3001926//ESTs, Highly similar to NUCLEOLYSIN TIA-1 [Homo sapiens]//1.0e-40:202:100//Hs.24709:AI123300
R-NT2RP3001929//ESTs//6.6e-84:449:94//Hs.26962:AA682781
R-NT2RP3001931//ESTs//1.0e-41:214:99//Hs.32360:AA534737
R-NT2RP3001938//ESTs, Highly similar to SPORULATION-SPECIFIC PROTEIN 1 [Saccharomyces cerevisiae]//1.3e-95:483:96//Hs.5771:W74591

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R-NT2RP3001943//ESTs//1.2e-23:169:88//Hs.103930:AA160990
R-NT2RP3001944//ESTs//2.0e-90:439:97//Hs.103380:AI291325
R-NT2RP3001969//ESTs//0.95:133:65//Hs.131669:AI025889
R-NT2RP3001989//ESTS, Weakly similar to C01A2.4 [C.elegans]//8.9e-64:310:99//Hs.11449:AI201540
R-NT2RP3002002//ESTs//2.1e-95:562:89//Hs.5997:AA897088
R-NT2RP3002004//H.sapiens mRNA for FAST kinase//1.6e-42:335:82//Hs.75087:X86779
R-NT2RP3002007//ESTs//0.12:184:66//Hs.94030:AA846729
R-NT2RP3002014//Small inducible cytokine A5 (RANTES)//6.8e-47:291:89//Hs.155464:AF088219
R-NT2RP3002033
R-NT2RP3002045//ESTs//1.0e-92:555:88//Hs.106411:W29081
R-NT2RP3002054//EST//0.45:155:63//Hs.5656:D20426
R-NT2RP3002056//ESTs//1.4e.95:504:93//Hs.17428:AI365221
R-NT2RP3002057//Human mRNA for KIAA0152 gene, complete cds//0.69:127:66//Hs.90438:D63486
R-NT2RP3002062
R-nnnnnnnnnnnn//ESTs//2.1e-113:552:97//Hs.9591:AA069657
R-NT2RP3002081//ESTs//5.5e-43:212:100//Hs.124852:AA969139
R-NT2RP3002097//EST//2.3e-10:80:91//Hs.102717:N59148
R-NT2RP3002102
R-NT2RP3002108
R-NT2RP3002146//ESTs//5.5e-58:296:97//Hs.65328:AA625385
R-NT2RP3002147//EST//2.5e-53:387:81//Hs.147928:M249703
R-NT2RP3002151//ESTs, Highly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [Homo sapiens]//6.2e-107:534:96//Hs.59523:AA602837
R-NT2RP3002163//ESTs//2.7c-106:520:97//Hs.21258:AA412293
R-NT2RP3002165//ESTs//7.4e-93:479:95//Hs.27299:AI074024
R-NT2RP3002166//ESTs//1.0:261:59//Hs.132817:AA593713
R-NT2RP3002173//ESTs//2.7e-93:512:92//Hs.23648:H07120
R-NT2RP3002181//ESTs//1.0e-84:435:96//Hs.47378:AI193598
R-NT2RP3002244//ESTs//2.7e-11:97:89//Hs.9412:W72446
R-NT2RP3002248//ESTs//4.3e-90:459:95//Hs.9848:AA130588
R-NT2RP3002255//ESTs//1.3e-45:289:88//Hs.9100:AA431672
R-NT2RP3002273//ESTs//2.3e-100:489:97//Hs.8258:AA744743
R-NT2RP3002276//ESTs//1.2e-50:306:91//Hs.16160:AA778171
R-NT2RP3002303//ESTs//1.1e-67:323:99//Hs.129761:AA836898
R-NT2RP3002304//ESTs//2.8e-86:405:99//Hs.29643:AA418500
R-NT2RP3002330//ESTs, Weakly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [H.sapiens]//1.8e-19:136:87//Hs.106928:AI041737
R-NT2RP3002343//ESTs//1.0e-42:260:93//Hs.7797:W25667
R-NT2RP3002351//Homo sapiens 9G8 splicing factor mRNA, complete cds//0.0048:221:64//Hs.556:L41887
R-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene//5.8e-105:516:94//Hs.6483:Y16355
R-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//1.5e-103:524:95//Hs.12707:AB014578
R-NT2RP3002484//Human APRT gene for adenine phosphoribosyltransferase//0.54:108:71//Hs.28914:Y00486
R-NT2RP3002501//ESTs//2.7e-96:489:95//Hs.27335:N74185
R-NT2RP3002512//ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III [C.elegans]//3.2e-90:526:90//Hs.8083:AA521436
R-NT2RP3002529//ESTs, Highly similar to PUTATIVE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN C2G11.03C [Schizosaccharomyces pombe]//3.8e-101:497:96//Hs.6650:AA843246
R-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.1e-83:438:94//Hs.19542:AB018272
R-NT2RP3002549//ESTs//3.8e-98:493:96//Hs.7358:AA191673
R-NT2RP3002566//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.14:184:63//Hs.89230:AF031815
R-NT2RP3002587//Homo sapiens KIAA0420 mRNA, complete cds//2.0e-18:138:78//Hs.129883:AB007880
R-NT2RP3002590//ESTs//2.9e-51:290:93//Hs.162942:AI243850
R-NT2RP3002602//Homo sapiens stannin mRNA, complete cds//5.5e-06:58:100//Hs.76691:AF070673
R-NT2RP3002603
R-NT2RP3002631//ESTs//4.8e-54:367:85//Hs.13109:AA192514

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R-NT2RP3002659//ESTs//5.3e-30:229:85//Hs.152114:AA401365
R-NT2RP3002660//ESTs//1.9e-88:452:95//Hs.120146:AA708573
R-NT2RP3002663//EST//3.2e-89:469:95//Hs.105767:AA525172
R-NT2RP3002671//ESTs, Highly similar to ELONGATION FACTOR 2 [Drosophila melanogaster]//5.9e-109:537:97//Hs.19348:AA151678
R-NT2RP3002682//ESTs//2.3e-98:541:91//Hs.75844:AA115502
R-NT2RP3002687//ESTs//5.5e-103:498:97//Hs.72782:AA910871
R-NT2RP3002688//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.0e-101:524:95//Hs.32580:AI123601
R-NT2RP3002701//EST//0.87:131:63//Hs.161916:AA483169
R-NT2RP3002713//ESTs//4.7e-106:542:95//Hs.14479:AA160945
R-NT2RP3002763//ESTs//1.3e-54:290:94//Hs.142031:AA809159
R-NT2RP3002770//ESTs//0.047:275:61//Hs.122984:AA526973
R-NT2RP3002785//ESTs//2.4e-52:255:99//Hs.132959:AI376958
R-NT2RP3002799//EST//8.2e-61:321:94//Hs.140992:R71377
R-NT2RP3002810//EST//0.19:116:68//Hs.121810:AA775240
R-NT2RP3002818//ESTs//1.3e-109:531:98//Hs.58924:AI348080
R-NT2RP3002861//ESTs//2.5e-84:429:95//Hs.23920:AA909678
R-NT2RP3002869//EST//0.00011:116:71//Hs.161606:AA019641
R-NT2RP3002876//ESTs//0.0024:182:63//Hs.117306:AA687262
R-NT2RP3002877//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//8.1e-14:146:72//Hs.129727:AF035587
R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.5e-110:570:95//Hs.6162:AB018314
R-NT2RP3002911//ESTs//3.6e-92:436:99//Hs.143917:AI206286
R-NT2RP3002948//EST//1.0:102:65//Hs.144730:AI191975
R-NT2RP3002953//ESTs//1.8e-107:513:98//Hs.119693:AI201698
R-NT2RP3002955//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.23:563:56//Hs.127338:AB007961
R-NT2RP3002969//ESTS, Weakly similar to LONG-CHAIN-FATTY-ACID--COA LIGASE 1 [Saccharomyces cerevisiae]112.0e-56:387:86//Hs.144597:W20143
R-NT2RP3002972//ESTs//1.7e-97:502:96//Hs.7274:AA476850
R-NT2RP3002978//ESTs//8.6e-104:498:98//Hs.118923:AA252116
R-NT2RP3002988//EST//1.2e-59:315:94//Hs.157743:AI360553
R-NT2RP3003008//ESTs//1.4e-97:515:94//Hs.6544:AA524423
R-NT2RP3003032//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//3.0e-100:528:94//Hs.90353:N98551
R-NT2RP3003059//ESTs//1.7e-76:398:95//Hs.102971:W05355
R-NT2RP3003061//ESTs//4.9e-82:414:96//Hs.99603:AI141912
R-NT2RP3003068//ESTs, Weakly similar to M18.3 [C.elegans]//5.9e-83:392:99//Hs.101364:AA534439
R-NT2RP3003071//ESTs//6.3e-85:399:99//Hs.109755:AA180809
R-NT2RP3003078//ESTs//1.0e-98:471:99//Hs.7995:AI359466
R-NT2RP3003101//EST//0.032:235:60//Hs.147920:AI202441
R-NT2RP3003121//ESTs//3.0e-47:238:97//Hs.43559:AI003520
R-NT2RP3003133//EST//1.5e-77:395:96//Hs.142150:AA223982
R-NT2RP3003138//ESTs, Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus musculus]//3.3e-107:535:96//Hs.27437:AA004208
R-NT2RP3003139//ESTs//2.5e-106:504:98//Hs.106795:AI271632
R-NT2RP3003150//ESTs//1.6e.99:539:91//Hs.46500:AA129774
R-NT2RP3003157//ESTs//1.5e-114:563:97//Hs.58608:AA081007
R-NT2RP3003185//ESTs//3.9e-93:443:98//Hs.9741:AI131226
R-NT2RP3003193//ESTs//2.0e-37:428:71//Hs.33354:AA179944
R-NT2RP3003197//ESTs//5.8e-56:312:94//Hs.7016:AA215796
R-NT2RP3003203//EST//0.0073:212:63//Hs.161355:AI422634
R-NT2RP3003204//ESTs//7.4e-52:253:99//Hs.120146:AA708573
R-NT2RP3003212//ESTs//1.8e-76:401:95//Hs.29067:N26107
R-NT2RP3003230//ESTs, Highly similar to CORONIN [Dictyostelium discoideum]//2.0e-40:229:93//Hs.17377:AI078151
R-NT2RP3003242//ESTs//8.3e-97:458:99//Hs.23057:AI290343

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R-NT2RP3003251//ESTs//1.5e-60:320:95//Hs.36495:AA151628
R-NT2RP3003264//ESTs//2.1e-103:521:95//Hs.4094:AA173960
R-NT2RP3003278//ESTs//8.2e-109:536:96//Hs.23788:AA524061
R-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//2.4e-102:550:93//Hs.11702:L36983
R-NT2RP3003290//EST//4.3e-27:372:70//Hs.159131:AI384035
R-NT2RP3003301//ESTs//4.4e-56:285:97//Hs.95370:AA601055
R-NT2RP3003302//EST//7.2e-10:395:63//Hs.162554:AA584818
R-NT2RP3003311//ESTs//4.2e-110:538:97//Hs.62180:AI341261
R-NT2RP3003313//ESTs//2.1e-106:531:96//Hs.22630:C05931
R-NT2RP3003327//ESTs//4.3e-102:518:95//Hs.120355:AA625445
R-NT2RP3003330//ESTs//8.6e-104:497:97//Hs.72071:AI125289
R-NT2RP3003344//ESTs//2.5e-105:494:99//Hs112188:AA872993
R-NT2RP3003346//ESTs//1.0:123:69//Hs.116029:AA813102
R-NT2RP3003353//EST//0.0014:162:68//Hs.149191:AI246155
R-NT2RP3003377//EST//4.5e-15:119:85//Hs.148129:AA885567
R-NT2RP3003384//EST//0.0057:86:74//Hs.127735:AA962272
R-NT2RP3003385//ESTs//0.64:347:59//Hs.5646:W72721
R-NT2RP3003403//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//2.2e-24:418:67//Hs.139488:AI124095
R-NT2RP3003409//ESTs//5.3e-98:479:97//Hs.155198:AA767372
R-NT2RP3003411//ESTs//4.8e-86:416:97//Hs.129059:AA126041
R-NT2RP3003427//ESTs//7.4e-103:510:96//Hs.25303:AA641023
R-NT2RP3003433//ESTs//3.5e-85:405:99//Hs.63131:AA664156
R-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//3.6e-97:479:96//Hs.14934:AF004828
R-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//4.1e-102:527:93//Hs.26450:AB018268
R-NT2RP3003491//ESTs, Weakly similar to No definition line found [C.elegans]//4.0e-106:549:94//Hs.7886:AI057529
R-NT2RP3003500//Human RP3 mRNA, complete cds//0.66:401:60//Hs.75307:U02556
R-NT2RP3003543//Human clone A9A2BRB7 (CAC)n/(GTG)n repeat-containing mRNA//4.1e-33:217:88//Hs.8068:U00952
R-NT2RP3003552//ESTs//3.1e-106:546:94//Hs.101754:AI123430
R-NT2RP3003555//ESTs//3.4e-106:537:95//Hs.85550:AA187681
R-NT2RP3003564
R-NT2RP3003572//ESTs//1.2e-20:122:88//Hs.8253:N48721
R-NT2RP3003576//ESTs//2.7e-71:394:94//Hs.151136:R99944
R-NT2RP3003589//EST//0.58:242:59//Hs.130804:AA894759
R-NT2RP3003625//ESTs//7.6e-41:349:80//Hs.140608:N53448
R-NT2RP3003656//Human LIM protein (LPP) rnRNA, partial cds//0.26:222:60//Hs.17217:U49957
R-NT2RP3003659//ESTs//2.0e-113:547:97//Hs.23389:AA769310
R-NT2RP3003665//ESTs//1.6e-80:415:95//Hs.141084:H11714
R-NT2RP3003672
R-NT2RP3003686//ESTs//6.8e-114:552:97//Hs.43299:N23036
R-NT2RP3003701//ESTs//2.1e-16:282:66//Hs.115512:AI208768
R-NT2RP3003716//ESTs//2.1e-45:195:91//Hs.41296:N71923
R-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//5.6e-103:492:97//Hs.48513:AB018300
R-NT2RP3003746//ESTs//1.9e-85:411:98//Hs.54835:AI050863
R-NT2RP3003795//EST//6.2e-97:459:99//Hs.134769:AI089747
R-NT2RP3003799//ESTs//2.8e-62:337:94//Hs.124023:H18913
R-NT2RP3003800//PROTO-ONCOGENE TYRO SINE-PROTEIN KINASE SRC//8.9e-108:551:95//Hs.115742:AF077754
R-NT2RP3003805//ESTs//2.2e-103:490:99//Hs.9412:W72446
R-NT2RP3003809//ESTs, Highly similar to SAV PROTEIN [Sulfolobus acidocaldarius]//3.4e-89:456:95//Hs.5555:AI285198
R-NT2RP3003819//Interieukin 10//3.3e-43:173:89//Hs.2180:M57627
R-NT2RP3003825//ESTs//1.6e-66:485:80//Hs.7405:W27761

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R-NT2RP3003828//ESTs, Weakly similar to unknown.[H.sapiens]//9.6e-98:511:95//Hs.26955:AI333224
R-NT2RP3003831//ESTs//2.2e-38:317:79//Hs.142173:AA757743
R-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//5.2e-110:541:97//Hs.25300:AF070611
R-NT2RP3003842//EST//9.9e-44:506:70//Hs.139093:AA166888
R-NT2RP3003846//ESTs//4.6e-10:66:100//Hs.74924:AI332962
R-NT2RP3003870//ESTs//3.4e-82:449:92//Hs.122691:AA152298
R-NT2RP3003876//ESTs//1.9e-89:449:96//Hs.45046:N40170
R-NT2RP3003914//ESTs//1.3e-99:470:98//Hs.118966:AA926726
R-NT2RP3003918//ESTs//1.3e-79:417:94//Hs.5005:W25933
R-NT2RP3003932//ESTs//6.0e-83:427:94//Hs.93581:H50221
R-NT2RP3003989//ESTs//4.8e-76:403:93//Hs.127243:W80409
R-NT2RP3003992//ESTs//2.4e-88:508:90//Hs.134200:D19593
R-NT2RP3 004013//ESTs//3.7e-111:551:97//Hs.105108:AA781142
R-NT2RP3004016//ESTs//1.7e-81:394:98//Hs.63368:AA613714
R-NT2RP3004041
R-NT2RP3004051//ESTs//3.5e-69:386:93//Hs.51347:T72820
R-NT2RP3004070//ESTs//5.5e-108:552:9511Hs.23392:AI310139
R-NT2RP3004078//ESTs//3.3e-82:443:93//Hs.26407:W4537
R-NT2RP3004093//ESTs//4.4e-83:426:94//Hs,140932:AI262104
R-NT2RP3004095//ESTs//0.00013:93:78//Hs.36567:AA262045
R-NT2RP3004110//ESTs, Weakly similar to similar to oxysterol-binding proteins: partial CDS [C.elegans]//3.5e-76:402:95//Hs.55847:W31092
R-NT2RP3004125//ESTs//9.3e-74:363:97//Hs.32988:C01696
R-NT2RP3004145//ESTs//2.6e-96:451:99//Hs.59584:AA587334
R-NT2RP3004148//ESTs//1.3e-10:77:92//Hs.135890:AI183425
R-NT2RP3004155//ESTS//1.7e-110:558:96//Hs.27003:AI279093
R-NT2RP3004206//ESTs, Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]//1.8e-40:200:100//Hs.26089:AA195126
R-NT2RP3004207//ESTs, Weakly similar to gene SEZ-6 [M.musculus]//1.1e-41:266:89//Hs.6314:AA522619
R-NT2RP3004209//ESTs, Highly similar to PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C [Schizosaccharomyces pombe]//3.7e-112:547:97//Hs.99819:AI346680
R-NT2RP3004215//ESTs//1.1e-103:541:95//Hs.124918:N64794
R-NT2RP3004242//ESTs//4.5e-105:524:96//Hs.29724:N46252
R-NT2RP3004246//EST//1.9e-07:67:91//Hs.125687:AA884827
R-NT2RP3004253//EST//2.9e-88:454:94//Hs.127713:AA961628
R-NT2RP3004258//ESTs, Weakly similar to PRE-MRNA SPLICING FACTOR SRP75 [Homo sapiens]//1.6e-89:468:95//Hs.5117:AA831530
R-NT2RP3004262//ESTs//4.1e-86:443:96//Hs.101393:T87623
R-NT2RP3004334//EST//0.00057:206:63//Hs.149388:AI273630
R-NT2RP3004341//EST//0.00042:151:68//Hs.148498:AI200264
R-NT2RP3004348//Homo sapiens LIM protein mRNA, complete cds//5.9e-61:299:85//Hs.154103:AF061258
R-NT2RP3004349//EST//3.6e-42:175:88//Hs.161917:AA483223
R-NT2RP3004378//ESTs//0.27:294:60//Hs.66479:AA863044
R-NT2RP3004399//ESTs//5.8e-99:479:98//Hs.120234:AA732224
R-NT2RP3004424//EST, Highly similar to F21G4.6 [C.elegans]//0.30:253:58//Hs.97184:AA385934
R-NT2RP3004428//ESTs//2.8e-48:279:91//Hs.106826:W25985
R-NT2RP3004451//ESTs//4.8e-101:509:96//Hs.29725:W74621
R-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//9.3e-108:526:98//Hs.27349:AB007917
R-NT2RP3004466//ESTs//0.25:51:90//Hs.7778:AA195616
R-NT2RP3004470//EST//0.032:70:71//Hs.147925:AI249332
R-NT2RP3004472//ESTs//0.0069:430:59//Hs.116651:AA993406
R-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//5.0e-107:521:97//Hs.5003:AB007925
R-NT2RP3004480
R-NT2RP3004490//ESTs//4.7e-68:354:95//Hs.163721:H42504
R-NT2RP3004498//ESTs, Moderately similar to ORF2: function unknown [H.sapiens]//3.4e-100:508:95//Hs.47393:AA218858

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R-NT2RP3004503//ESTs//4.6e-90:478:93//Hs.133998:AA994735
R-NT2RP3004504//ESTs, Highly similar to cytoplasmic polyadenylation element-binding protein [M.musculus]//1.8e-83:465:92//Hs.137064:AA318257
R-NT2RP3004507//ESTs//1.5e-98:495:96//Hs.128905:AI051971
R-NT2RP3004527//EST//1.6e-109:535:97//Hs.149481:AI279865
R-nnnnnnnnnnn
R-NT2RP3004544//EST//0.035:226:60//Hs.99195:AA449232
R-NT2RP3004566//ESTs//4.1e-86:455:95//Hs.13110:T67461
R-NT2RP3004569//ESTs//2.9e-94:493:94//Hs.24948:AA977674
R-NT2RP3004572//ESTs//1.1e-92:437:99//Hs.24846:AI420493
R-NT2RP3004578//ESTs//0.98:166:64//Hs.124593:AA854456
R-NT2RP3004594//EST//5.8e-89:426:98//Hs.134213:AI080213
R-NT2RP3004617//ESTs//1.4e-40:226:85//Hs.15921:R71157
R-NT2RP3004618//ESTs//1.8e-38:229:90//Hs.125153:AA453723
R-NT2RP3004670//Homo sapiens GN6ST mRNA for long form of N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete cds//7.2e-57:291:95//Hs.8786:AB014680
R-NT2RP4000008//ESTs//8.9e-119:561:98//Hs.25035:AI123335
R-NT2RP4000023//EST//1.2e-34:271:80//Hs.98300:AA418560
R-NT2RP4000035//Small inducible cytokine A5 (RANTES)//2.1e-68:320:82//Hs.155464:AF088219
R-NT2RP4000049//Homo sapiens TRAIL receptor 2 mRNA, complete cds//6.7e-60:289:82//Hs.51233:AF016266
R-NT2RP4000051//ESTs, Weakly similar to protein B [H.sapiens]//8.3e-98:462:99//Hs.10114:AI345945
R-NT2RP4000078//ESTs//0.00068:367:60//Hs.106090:AA457030
R-NT2RP4000102//ESTs//9.7e-50:256:97//Hs.24266:R28287
R-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.1e-107:536:96//Hs.57929:AB011538
R-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//3.5e-112:554:97//Hs.64691:AB007952
R-NT2RP4000147//ESTs//3.9e-11:122:80//Hs.25584:AA632014
R-NT2RP4000150//EST//4.4e-84:510:88//Hs.144238:W52294
R-NT2RP4000151//ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III [C.elegans]//5.7e-93:515:92//Hs.8083:AA521436
R-NT2RP4000159//ESTs//0.0019:209:65//Hs.161816:AA400295
R-NT2RP4000167//ESTs//2.1e-113:549:97//Hs.109441:N66569
R-NT2RP4000185//ESTs//0.65:232:59//Hs.144445:AA807257
R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.5e-100:505:96//Hs.13999:AB014600
R-NT2RP4000212//ESTs//8.5e-14:169:75//Hs.8520:AA081788
R-NT2RP4000214//Human mRNA for KIAA0392 gene, partial cds//6.2e-43:272:90//Hs.40100:AB002390
R-NT2RP4000218//ESTs//6.1e-10:335:64//Hs.105658:AA978185
R-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP)//2.9e-70:354:96//Hs.155481:AJ006470
R-NT2RP4000246//ESTs//7.1e-26:154:94//Hs.14838:AA502757
R-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.3e-79:379:99//Hs.43728:AF091092
R-NT2RP4000263
R-nnnnnnnnnnnn/ESTs, Weakly similar to similar to Achlya ambisexualis antheridiol steroid receptor [C.elegans]//4.7e-104:525:96//Hs.152069:AA548972
R-NT2RP4000312//ESTs//8.2e-66:319:99//Hs.35091:AI271631
R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequence//1.3e-109:513:99//Hs.13410:AF070524
R-NT2RP4000323//ESTs//7.7e-109:534:97//Hs.34790:AA192760
R-NT2RP4000355//ESTs//3.1e-44:320:83//Hs.141323:N80390
R-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//7.6e-111:520:99//Hs.107479:AB018281
R-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//2.8e-110:527:98//Hs.31323:AF044195
R-NT2RP4000370//ESTs//8.9e-32:166:98//Hs.70488:AI301130
R-NT2RP4000376//ESTs//6.8e-99:465:99//Hs.27182:AA604498
R-NT2RP4000381//ESTs//3.0e-50:280:93//Hs.8395:W27376
R-NT2RP4000415//ESTs, Weakly similar to coded for by C. elegans cDNA yk30b3.5 [C.elegans]//3.9e-87:499:

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91//Hs.26156:AA630975
R-NT2RP4000417//ESTs, Moderately similar to HYPOTHETICAL 91.2 KD PROTEIN IN RPS7A-SCH9 INTERGENIC REGION [Saccharomyces cerevisiae]//8.9e-95:468:96//Hs.93871:AI191318
R-NT2RP4000424//ESTs//3.7e-98:473:98//Hs.24945:AI189011
R-NT2RP4000448//ESTs//2.6e-79:446:91//Hs.25159:R60955
R-NT2RP4000449//ESTs//3.6e-98:468:98//Hs.31176:AI037953
R-NT2RP4000455//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//0.35:153:63//Hs.113286:U77783
R-nnnnnnnnnnnn//ESTs//4.5e-89:455:96//Hs.62638:AA127740
R-NT2RP4000480//ESTs//4.9e-92:431:99//Hs.121072:AI204167
R-nnnnnnnnnnnn
R-NT2RP4000500//ESTs, Weakly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III [C.elegans]//1.2e-40:125:97//Hs.56124:AI424792
R-NT2RP4000515//EST//6.7e-30:183:90//Hs.150710:AI122713
R-NT2RP4000517//Aldehyde dehydrogenase 7//7.5e-28:183:76//Hs.83155:U10868
R-NT2RP4000518//EST//0.091:178:58//Hs.133031:AI049874
R-NT2RP4000519
R-NT2RP4000524//ESTS, Highly similar to rsec8 [R.norvegicus]//3.4e-93:496:93//Hs.107394:H07126
R-NT2RP4000528//EST//0.84:130:66//Hs.140208:AA702213
R-NT2RP4000541//EST//5.2e-63:337:94//Hs.156337:AI337328
R-NT2RP4000556//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.norvegicus]//8.2e-92:448:98//Hs.25597:H93026
R-NT2RP4000588//ESTs//3.8e-94:445:98//Hs.44077:N28840
R-NT2RP4000614//ESTs//6.5e-18:159:83//Hs.24549:N57263
R-NT2RP4000638//ESTs//2.5e-46:296:87//Hs.132722:AA618531
R-NT2RP4000648//ESTs//2.6e-103:559:93//Hs.23794:W80393
R-NT2RP4000657//ESTs//1.0:189:60//Hs.87073:AA972704
R-NT2RP4000704//ESTs//2.8e-101:509:96//Hs.84824:AA935651
R-NT2RP4000724//ESTS//1.5e-83:442:94//Hs.142114:AA205615
R-NT2RP4000728//ESTs//0.84:61:75//Hs.145334:AI251399
R-NT2RP4000739//ESTs//8.8e-80:418:94//Hs.42959:N21211
R-NT2RP4000781//ESTs//1.4e-79:376:99//Hs.135458:AI081312
R-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//3.1e-106:550:94//Hs.25132:AB007939
R-NT2RP4000833//ESTs//5.8e-46:309:85//Hs.163979:AA828834
R-NT2RP4000837//ESTs//1.7e-112:539:97//Hs.97718:AI334028
R-NT2RP4000855//ESTs//1.1e-95:486:95//Hs.5345:AA988104
R-NT2RP4000865//EST//6.2e-68:412:89//Hs.142196:AA258356
R-NT2RP4000878//ESTs//1.9e-80:417:95//Hs.104716:AI023185
R-NT2RP4000879//ESTs//1.8e-42:211:99//Hs.89991:AI374617
R-nnnnnnnnnnn//ESTs//1.2e-89:453:97//Hs.100182:N92594
R-nnnnnnnnnnnn//EST//9.4e-06:197:63//Hs.145970:AI277106
R-NT2RP4000925//ESTs, Weakly similar to KIAA0405 [H.sapiens]//5.9e-17:134:85//Hs.14146:W92235
R-nnnnnnnnnnnn//ESTs//4.3e-14:84:100//Hs.155360:AA984683
R-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//8.2e-108:548:95//Hs.24812:AF069532
R-NT2RP4000929//ESTs//1.3e-119:567:98//Hs.62717:AA044905
R-NT2RP4000955//ESTs//3.5e-10:l 19:78//Hs.42946:N21111
R-NT2RP4000973//ESTs//2.8e-05:93:69//Hs.155126:AA563986
R-NT2RP4000975//ESTs//4.4e-58:324:95//Hs.126070:AA045179
R-NT2RP4000979//ESTs//3.5e-42:468:73//Hs.106210:AI193017
R-NT2RP4000984//Homo sapiens clone 23770 mRNA sequence//8.7e-120:570:98//Hs.12457:AF052123
R-NT2RP4000989//ESTs//1.3e-122:581:98//Hs.10499:AA528018
R-NT2RP4000996//ESTs//9.2e-113:579:94//Hs.23762:N26620
R-NT2RP4000997//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.1e-28:439:68//Hs.129735:AF010144
R-NT2RP4001004//ESTs//3.6e-78:389:98//Hs.156290:AI016769
R-NT2RP4001006//ESTS, Moderately similar to ORF2: function unknown [H.sapiens]//6.6e-124:574:99//Hs.

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47393:AA218858
R-NT2RP4001010//EST//2.8e-31:194:90//Hs.161186:AI418635
R-NT2RP4001029//ESTs//4.4e-111:523:99//Hs.28423:AI336292
R-NT2RP4001041//ESTs, Highly similar to LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC [Saccharomyces cerevisiae]//3.6e-114:569:96//Hs.6762:AA088424
R-NT2RP4001057//Homo sapiens KIAA0399 mRNA, partial cds//2.0e-51:282:94//Hs.100955:AB007859
R-NT2RP4001064//ESTs, Weakly similar to protein B [H.sapiens]//2.1e-103:485:99//Hs.10114:AD45945
R-NT2RP4001078
R-NT2RP4001079//Homo sapiens mRNA for putative Ca^{2+}-transporting ATPase, partial//1.7e-119:569:98//Hs.106778:AJ010953
R-NT2RP4001080//ESTs//7.6e-10:65:100//Hs.131694:AA927668
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0592 protein, partial cds//5.9e-121:548:95//Hs.13273:AB011164
R-NT2RP4001095//ESTs//1.5e-113:563:96//Hs.118732:AI344055
R-NT2RP4001100//ESTs//2.0e-46:413:79//Hs.146314:R99617
R-NT2RP4001117//EST//7.4e-51:294:92//Hs.7260:T23737
R-NT2RP4001122//ESTs//5.4e-109:509:99//Hs.16390:AI052357
R-NT2RP4001126//EST//0.97:169:61//Hs.148107:AA693476
R-NT2RP4001138//ESTs//3.0e-110:543:97//Hs.57655:AI056890
R-NT2RP4001143//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//5.4e-113:573:96//Hs.5249:U55977
R-NT2RP4001148//ESTs//3.1e-103:490:98//Hs.121282:AI091453
R-NT2RP4001149//EST//1.7e-50:281:93//Hs.101727:H16171
R-NT2RP4001150//ESTS//1.9e-90:422:100//Hs.125490:AI138884
R-NT2RP4001159
R-NT2RP4001174//ESTs//2.5e-110:526:98//Hs.116555:AA639278
R-nnnnnnnnnnnn//ESTs//1.1 e-25:140:97//Hs.83756:AI002822
R-NT2RP4001207//ESTs//4.4e-70:432:89//Hs.13109:AA192514
R-NT2RP4001210//ESTs//1.4e-108:509:99//Hs.27021:AI359495
R-NT2RP4001213//ESTs, Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]//4.4e-123:624:95//Hs.22744:AI379892
R-NT2RP4001219//ESTs//0.0043:142:65//Hs.6733:AI160750
R-NT2RP4001228//ESTs//4.9e-101:482:98//Hs.62684:AA806103
R-NT2RP4001235//ESTs//3.7e-105:571:93//Hs.37706:AA005120
R-NT2RP4001256//ESTs//1.1e-12:189:74//Hs.20621:W28255
R-NT2RP4001260//EST//6.9e-05:313:61//Hs.116438:AA648430
R-NT2RP4001274//EST//0.0020:246:63//Hs.149955:AI289933
R-nnnnnnnnnnnn//ESTs//2.9e-34:213:91//Hs.43100:AA186588
R-NT2RP4001313
R-NT2RP4001315//EST//6.1e-38:217:93//Hs.97832:AA400892
R-NT2RP4001339//ESTs//3.8e-91:430:99//Hs.34840:AI279612
R-NT2RP4001345//ESTs//5.3e-89:443:96//Hs.6770:AA972732
R-NT2RP4001351//ESTs//6.0e-78:394:97//Hs.102796:N70837
R-NT2RP4001353//ESTs//4.8e-06:90:82//Hs.7778:AA195616
R-NT2RP4001372
R-NT2RP4001373//ESTs, Weakly similar to HYPOTHETICAL 48.8 KD PROTEIN IN TRK2-MRS4 INTERGENIC REGION [Saccharomyces cerevisiae]//1.7e-108:546:96//Hs.32271:AA203680
R-NT2RP4001375//ESTs//2.4e-19:155:87//Hs.62119:AA043299
R-NT2RP4001379//EST//4.4e-29:288:72//Hs.157848:AI362501
R-NT2RP4001389//ESTs, Highly similar to HYPOTHETICAL 51.6 KD PROTEIN IN PAP1-MRPL13 INTERGENIC REGION [Saccharomyces cerevisiae]//3.8e-79:438:93//HS.21938:W81045
R-NT2RP4001407//ESTs//8.3e-112:541:97//Hs.22587:AA743132
R-NT2RP4001414//ESTs//8.6e-18:117:90//Hs.90789:W27649
R-NT2RP4001433//ESTs, Moderately similar to PROHIBITIN [H.sapiens]//1.6e-102:498:97//Hs.62386:AA512948
R-NT2RP4001442//ESTs//8.8e-104:489:99//Hs.101619:AI339433
R-NT2RP4001447
R-NT2RP4001474
R-NT2RP4001483//ESTs//2.1e-100:528:92//Hs.17860:AA706655
R-NT2RP4001498//ESTs//1.1e-97:470:98//Hs.95744:AI392846

BNSDOCID: <EP___1074617A2_I_>

R-NT2RP4001502//ESTs//6.7e-73:382:96//Hs.11874:N93511
R-NT2RP4001507//ESTs//2.6e-57:302:96//Hs.65328:AA625385
R-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [C.elegans]//2.9e-107:546:96//Hs.5570:AI377863
R-NT2RP4001529//ESTs//3.3e-112:524:99//Hs.28423:AI336292
R-NT2RP4001547//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Paramecium tetraurelia]//2.8e-120:566:98//Hs.108530:AA523928
R-nnnnnnnnnnnn//ESTs, Weakly similar to CELL DIVISION CONTROL PROTEIN 68 [S.cerevisiae]//1.4e-26:184:88//Hs.136189:AA133224
R-NT2RP4001555//ESTs//1.1e-95:445:100//Hs.134403:AA677552
R-NT2RP4001567//ESTs//2.8e-106:506:98//Hs.102708:AA292285
R-NT2RP4001568//ESTs//6.4e-55:300:94//Hs.57442:N63437
R-NT2RP4001571//ESTs//1.3e-114:556:97//Hs.30340:AA521251
R-NT2RP4001574//ESTs//0.0035:120:67//Hs.96339:AA225906
R-NT2RP4001575
R-NT2RP4001592//ESTs, Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL[S.cerevisiae]//8.7e-112:557:97//Hs.7558:AA526812
R-NT2RP4001610//ESTs//6.2e-77:382:96//Hs.21543:AA166776
R-NT2RP4001614//ESTs//2.8e-117:565:98//Hs.9591:AA069657
R-NT2RP4001634//ESTs//2.0e-39:213:96//Hs.32360:AA534737
R-NT2RP4001638//Homo sapiens clone 23967 unknown mRNA, partial cds//1.7e-116:559:97//Hs.5332:AF007151
R-NT2RP4001644//ESTs, Moderately similar to MNK1 [H.sapiens]//5.3e-36:192:97//Hs.5662:AA868361
R-NT2RP4001656//ESTs, Highly similar to HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II [Caenorhabditis elegans]//1.1e-104:525:96//Hs.20472:W28734
R-NT2RP4001677//ESTs//1.8e-106:522:97//Hs.106390:AA156805
R-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence//5.7e-118:583:96//Hs.15562:U96629
R-NT2RP4001725//ESTs//2.0e-11:141:74//Hs.117589:N25941
R-nnnnnnnnnnnn//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]//3.4e-73:362:97//Hs.152332:AI141922
R-NT2RP4001739//ESTs//6.6e-59:340:91//Hs.122293:AA843692
R-NT2RP4001753//Zinc finger protein 3 (A8-51)//5.6e-113:552:96//Hs.2481:X78926
R-NT2RP4001760//ESTs//2.5e-94:453:98//Hs.122579:AA766315
R-NT2RP4001790//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//2.0e-62:326:94//Hs.110839:W28098
R-NT2RP4001803
R-NT2RP4001822//ESTs//4.4e-98:526:92//Hs.96908:AI161133
R-NT2RP4001823//ESTs//1.7e-72:357:97//Hs.144900:AI218434
R-NT2RP4001828//ESTs//3.3e-101:536:92//Hs.18851:AA857826
R-NT2RP4001838//ESTs//4.2e-58:344:90//Hs.48723:N66663
R-NT2RP4001849//EST//0.24:105:71//Hs.136747:AA749210
R-NT2RP4001889//Human mRNA for KIAA0118 gene, partial cds//3.4e-34:212:88//Hs.154326:D42087
R-NT2RP4001893//ESTs//3.0e-58:321:95//Hs.158787:W79602
R-NT2RP4001896//EST//3.8e-15:108:92//Hs.160835:AI345528
R-NT2RP4001901//ESTs//1.2e-110:536:97//Hs.31443:AI018606
R-NT2RP4001927//ESTs//2.1e-105:546:93//Hs.73291:AI417099
R-NT2RP4001938//ESTs//2.8e-40:235:78//Hs.163641:R61848
R-NT2RP4001946//ESTs//1.3e-29:175:93//Hs.43703:AA088436
R-NT2RP4001950//ESTs//4.6e-95:458:98//Hs.150890:AI341793
R-NT2RP4001953//Clathrin, light polypeptide (Lcb)//2.3e-62:310:82//Hs.73919:X81637
R-NT2RP4001966//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//8.3e-87:457:94//Hs.41793:AA775879
R-NT2RP4001975//ESTs//1.9e-52:281:94//Hs.7704:W58252
R-NT2RP4002018
R-NT2RP4002047//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]//4.7e-09:90:86//Hs.41127:AA555184
R-NT2RP4002052//ESTs//0.054:353:60//Hs.117510:AA903738
R-NT2RP4002058//EST//7.8e-26:151:94//Hs.124617:AA855106

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R-NT2RP4002071//ESTs//6.9e-99:475:98//Hs.29216:AA916679
R-NT2RP4002075//ESTs//0.67:121:65//Hs.153939:AI284198
R-NT2RP4002078//ESTs, Highly similar to ZINC FINGER PROTEIN 35 [Homo sapiens]//1.6e-61:464:82//Hs.144228:N99507
R-nnnnnnnnnnnn//ESTs, Weakly similar to HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN CHROMOSOME II [C.elegans]//2.3e-56:271:100//Hs.6185:AA428565
R-NT2RP4002083//ESTs//2.0e-108:548:96//Hs.6120:W80407
R-NT2RP4002408//ESTs//2.6e-77:391:96//Hs.14014:AA745592
R-NT2RP4002791//ESTs//7.9e-101:527:93//Hs.22394:N32555
R-NT2RP4002888//ESTs, Highly similar to ENV POLYPROTEIN [Avian spleen necrosis virus]//1.9e-65:373:92//Hs.31532:H18272
R-NT2RP4002905//ESTs//1.5e-107:517:98//Hs.40460:N36090
R-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//2.8e-115:605:94//Hs.108258:AB007934
R-OVARC1000004
R-OVARC1000006//ESTs//1.5e-19:139:89//Hs.143034:AI126929
R-OVARC1000013//ESTs//5.9e-98:531:93//Hs.16470:AA121635
R-OVARC1000014//ESTs//0.24:243:60//Hs.19569:AA464273
R-OVARC1000017
R-OVARC1000035//ESTs//0.035:252:63//Hs.134123:AI078286
R-OVARC1000058//H.sapiens mRNA for translin associated protein X//3.8e-46:331:83//Hs.96247:X95073
R-OVARC1000060//EST//2.8e-28:348:71//Hs.141728:W73041
R-OVARC1000068//ESTs//3.0e-83:491:90//Hs.29397:N51367
R-OVARC1000071//ESTs//2.5e-60:321:96//Us.25010:R6787
R-OVARC1000085//Proteasome component C5//8.6e-67:366:92//Hs.75748:AL031259
R-nnnnnnnnnnnn//ESTs//1.0e-111:526:98//Hs.129020:AI380703
R-OVARC1000091//ESTS, Weakly similar to HOST CELL FACTOR CI [H.sapiens]//3.9e-112:596:94//Hs.20597:W58370
R-OVARC1000092//ESTs//5.1e-18:144:82//Hs.109140:AI289942
R-OVARC1000106
R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//8.3e-102:495:97//Hs.3688:AF069250
R-OVARC1000114//H.sapiens mRNA for phosphoinositide 3-kinase//1.7e-45:489:74//Hs.101238:Y11312
R-OVARC1000133//EST//0.00028:284:61//Hs.30547:H05482
R-OVARC1000145//EST//3.9e-40:201:99//Hs.156148:AI333214
R-OVARC1000148//EST//0.79:150:62//Hs.100078:T05090
R-OVARC1000151
R-OVARC1000168//EST//1.7e-19:142:90//Hs.38441:H66023
R-OVARC1000191//EST//0.0072:292:63//Hs.132492:AA922629
R-OVARC1000198//Homo sapiens LIM protein mRNA, complete cds//6.1e-44:339:81//Hs.154103:AF061258
R-OVARC1000209//ESTs, Moderately similar to ZINC FINGER PROTEIN 93 [H.sapiens]//1.1e-32:196:92//Hs.64322:AA142864
R-OVARC1000212//EST//0.20:178:61//Hs.133031:AI049874
R-OVARC1000240//ESTs//9.0e-64:314:98//Hs.42300:AA204958
R-OVARC1000241//EST//0.00018:115:68//Hs.150728:AI123130
R-OVARC1000288//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROTEIN IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]//3.3e-74:403:93//Hs.108117:AI097079
R-OVARC1000302//EST//4.0e-14:102:90//Hs.136617:AA630476
R-OVARC1000304//ESTs, Highly similar to PUTATIVE GTP-BINDING PROTEIN MOV10 [Mus musculus]//2.9e-37:191:98//Hs.20725:AI027777
R-OVARC1000309//ESTs//3.6e-66:348:94//Hs.9547:AA532449
R-OVARC1000321//ESTs//3.6e-87:454:95//Hs.110445:AA044743
R-OVARC1000326//ESTs, Moderately similar to lamina associated polypeptide 1C [R.norvegicus]//1.3e-98:488:96//Hs.125749:AI377682
R-OVARC1000335//ESTs//3.0e-115:565:97//Hs.54835:AI050863
R-OVARC1000347//EST//0.0018:145:65//Hs.136945:AA765672
R-OVARC1000384//ESTs//2.8e-38:253:89//Hs.15093:AA203423
R-OVARC1000408//ESTs//2.6e-98:515:94//Hs.119808:C05928

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R-OVARC1000411//ESTs//3.2e-82:395:98//Hs.104747:AA406219
R-OVARC1000414//Landsteiner-Wiener blood group glycoprotein//1.5e-27:211:79//Hs.108287:L27670
R-OVARC1000420//EST//2.8e-38:255:74//Hs.138525:R99237
R-OVARC1000427//EST//2.6e-58:302:96//Hs.122914:AA767034
R-OVARC1000431//ESTs//4.9e-108:551:96//Hs.11668:AI123426
R-OVARC1000437
R-OVARC1000440//ESTs//2.9e-91:456:96//Hs.93701:AI018671
R-OVARC1000442//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.3e-45:320:84//Hs.73614:U83460
R-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.6e-79:418:94//Hs.12334:AB014583
R-OVARC1000461//ESTs//3.1e-62:342:93//Hs.23241:R46582
R-OVARC1000465//ESTs//1.7e-67:349:95//Hs.127238:AA477576
R-OVARC1000466//ESTs//1.9e-66:337:95//Hs.5212:AI421211
R-OVARC1000473//ESTs//5.4e-89:320:99//Hs.29173:AA134926
R-OVARC1000479//ESTs, Highly similar to TIP120 [R.norvegicus]//1.1e-102:514:96//Hs.11833:AI299947
R-OVARC1000486//ESTs//3.9e-78:405:95//Hs.98312:AA424983
R-OVARC1000496
R-OVARC1000520//ESTs//1.2e-20:145:88//Hs.87456:AA434484
R-OVARC1000526//Small inducible cytokine A5 (RANTES)//8.9e-47:217:87//Hs.155464:AF088219
R-OVARC1000533//ESTs, Moderately similar to integrase [H.sapiens]//8.5e-48:264:92//Hs.49860:AA702248
R-OVARC1000543//ESTs//5.7e-74:410:94//Hs.62817:AA047021
R-OVARC1000556//H.sapiens mRNA for ribosomal S6 kinase//9.5e-27:202:85//Hs.90859:X85106
R-OVARC1000557//EST//2.8e-18:169:79//Hs.149101:AI244285
R-OVARC1000564//EST//2.3e-34:199:92//Hs.146637:AI141587
R-OVARC1000573//Interleukin 10//4.7e-42:300:83//Hs.2180:M57627
R-OVARC1000578//Small inducible cytokine A5 (RANTES)//5.2e-58:392:84//Hs.155464:AF088219
R-OVARC1000588//EST//1.8e-41:174:85//Hs.163333:AA879053
R-OVARC1000605
R-OVARC1000622//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.4e-47:417:77//Hs.159897:AB007970
R-OVARC1000640//H.sapiens mRNA for translin associated protein X//1.9e-28:366:72//Hs.96247:X95073
R-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//5.1e-31:162:100//Hs.111862:AB011162
R-OVARC1000678//EST//0.92:199:60//Hs.122025:AA778480
R-nnnnnnnnnnnn//ESTs//0.94:416:59//Hs.130754:AA279522
R-OVARC1000681//EST//9.2e-21:179:80//Hs.132635:AI032875
R-OVARC1000689//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.053:160:64//Hs.108447:AJ000517
R-OVARC1000700//Homo sapiens KIAA0441 mRNA, complete cds//7.1e-09:141:73//Hs.32511:AB007901
R-OVARC1000703//ESTs//1.7e-46:298:87//Hs.138856:H47461
R-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//1.7e-17:137:86//Hs.7049:AI141736
R-OVARC1000746//ESTs//0.16:366:60//Hs.136969:AA830918
R-OVARC1000769//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D.melanogaster]//4.6e-28:430:69//Hs.42457:AA523306
R-OVARC1000771//ESTs//1.3e-87:461:94//Hs.22399:AA531016
R-OVARC1000781//ESTs//8.3e-119:572:97//Hs.41972:AA626793
R-OVARC1000787//ESTs//7.4e-18:115:93//Hs.164036:AA845659
R-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR//4.9e-19:119:95//Hs.3069:L11066
R-OVARC1000802//ESTs//2.2e-41:383:78//Hs.161228:AI419764
R-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC//1.2e-106:536:95//Hs.61628:Y17711
R-OVARC1000846//Clathrin, light polypeptide (Lcb)//1.6e-66:282:87//Hs.73919:X81637
R-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//1.2e-115:579:96//Hs.18910:AF045584
R-OVARC1000862//EST//4.3e-14:129:81//Hs.150663:AA923096
R-OVARC1000876//ESTs//1.0e-115:573:96//Hs.87287:AI150674
R-OVARC1000883//ESTs//3.5e-109:523:98//Hs.28423:AI336292
R-OVARC1000885//ESTs, Highly similar to HYPOTHETICAL OXIDOREDUCTASE IN ROCC-PTA INTERGENIC

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REGION [Bacillus subtilis]//7.9e-98:525:93//Hs.10366:W21953
R-OVARC1000886//ESTs//8.2e-79:417:94//Hs.7729:AA830777
R-OVARC1000891//ESTs//6.8e-75:401:94//Hs.5833:H15401
R-OVARC1000897//ESTs//3.5e-91:440:98//Hs.125264:AA873350
R-OVARC1000912
R-OVARC1000915//ESTs//1.0e-45:328:82//Hs.163980:AA715814
R-OVARC1000924//ESTs//1.0e-100:501:96//Hs.30204:AA497127
R-OVARC1000936//EST//3.0e-74:367:98//Hs.145098:AA421696
R-OVARC1000937//EST//1.1e-53:290:95//Hs.162846:AA631215
R-OVARC1000945//ESTs//4.9e-51:301:89//Hs.20100:W25794
R-OVARC1000948//ESTs//3.7e-67:332:98//Hs.112570:AA621971
R-OVARC1000959//Small inducible cytokine A5 (RANTES)//7.2e-44:283:86//Hs.155464:AF088219
R-OVARC1000960//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-41:348:80//Hs.43681:AL022394
R-OVARC1000971//EST//6.2e-05:126:70//Hs.160491:AI254909
R-OVARC1000984//ESTS, Weakly similar to No definition line found [C.elegans]//3.5e-68:346:96//Hs.25544:AA532784
R-OVARC1000996//EST//0.12:92:71//Hs.117141:AA678811
R-OVARC1000999//Homo sapiens KIAA0414 mRNA, partial cds//1.5e-44:513:73//Hs.127649:AB007874
R-OVARC1001000//ESTs//1.8e-22:198:80//Hs.140608:N53448
R-OVARC1001004//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//1.7e-28:181:77//Hs.139107:K00629
R-OVARC1001010//EST//2.1e-09:92:85//Hs.147893:AI223270
R-OVARC1001011//EST//2.4e-14:200:75//Hs.149290:AI248117
R-OVARC1001032//EST//2.7e-29:304:73//Hs.141733:W80630
R-OVARC1001034//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//2.1e-09:137:74//Hs.77579:AF013263
R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//4.1e-101:501:96//Hs.9899:AF099149
R-OVARC1001040//ESTs//2.9e-87:415:99//Hs.132812:AI032046
R-OVARC1001044//ESTs//1.1e-83:432:96//Hs.55043:N94384
R-OVARC1001051//60S RIBOSOMAL PROTEIN L41//1.2e-16:124:88//Hs.108124:Z12962
R-OVARC1001055//ESTs//2.4e-23:238:76//Hs.141421:H99231
R-OVARC1001062//ESTs//3.4e-92:469:96//Hs.34658:N98652
R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds//7.3e-97:463:98//Hs.3426:AF082657
R-OVARC1001072//ESTs//1.3e-34:227:89//Hs.126704:W95844
R-OVARC1001074
R-OVARC1001085//Human T-cell leukemia virus enhancer factor//1.0:94:69//Hs.103126:U57029
R-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))//1.4e-96:325:98//Hs.21753:AJ005897
R-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds//3.3e-75:386:95//Hs.26584:AF051782
R-OVARC1001117//Human G protein-coupled receptor (STRL22) mRNA, complete cds//3.9e-37:283:84//Hs.46468:U45984
R-OVARC1001118//ESTs//5.3e-99:485:97//Hs.130815:AA936548
R-OVARC1001129//ESTs//9.8e-66:351:95//Hs.18616:T99312
R-OVARC1001161//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//2.2e-66:346:95//Hs.53263:AA173226
R-OVARC1001162//EST//1.5e-44:376:80//Hs.161917:AA483223
R-OVARC1001167//ESTs//4.7e-110:548:96//Hs.35254:AI133727
R-OVARC1001169//ESTs//0.22:152:68//Hs.149424:AI274200
R-OVARC1001170//Small inducible cytokine A5 (RANTES)//1.8e-42:305:84//Hs.155464:AF088219
R-OVARC1001173//EST//2.5e-35:182:84//Hs.161917:AA483223
R-OVARC1001180//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//6.6e-64:247:80//Hs.97203:U83171
R-OVARC1001188//ESTs//4.1e-18:296:69//Hs.139197:AA228343
R-OVARC1001200//ESTs//2.0e-28:207:85//Hs.35121:AA877826
R-OVARC1001232//ESTs//3.2e-61:358:91//Hs.6449:W95025
R-OVARC1001240//ESTs//6.7e-45:316:85//Hs.121675:AA629668
R-OVARC1001243//ESTs//2.3e-86:409:99//Hs.163091:AA742361

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R-OVARC1001261//ESTs//0.63:125:64//Hs.155743:AI344166
R-OVARC1001268//ESTs//8.1e-20:113:98//Hs.109477:AA477929
R-OVARC1001270//ESTs//1.5e-107:530:97//Hs.62905:AA460708
R-OVARC1001271//ESTs//4.5e-36:401:72//Hs.20190:AA525532
R-OVARC1001282//EST//4.0e-91:428:99//Hs.145599:AI263113
R-OVARC1001296//ESTs//2.6e-63:301:100//Hs.125753:AA740885
R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0518 protein, partial cds//3.8e-70:334:100//Hs.23763: AB011090
R-OVARC1001329//Clathrin, light polypeptide (Lcb)//1.3e-68:304:83//Hs.73919:X81637
R-OVARC1001330//Proline arginine-rich end leucine-rich repeat protein//1.0:147:63//Hs.76494:U41344
R-OVARC1001339//Small inducible cytokine A5 (RANTES)//5.0e-48:452:76//Hs.155464:AF088219
R-OVARC1001341//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//6.9e-85:464:93//Hs.23651:AA650356
R-OVARC1001342//40S RIBOSOMAL PROTEIN S8//4.9e-110:568:95//Hs.118690:X67247
R-OVARC1001344//EST//3.6e-44:341:81//Hs.162197:AA535216
R-OVARC1001357//TUMOR-ASSOCIATED ANTIGEN L6//9.8e-44:250:93//Hs.3337:M90657
R-OVARC1001360//ESTs//5.2e-110:534:98//Hs.24743:AA843844
R-OVARC1001369//ESTs//1.7e-98:478:97//Hs.7729:AA830777
R-OVARC1001372//ESTs//2.6e-97:456:99//Hs.153648:AI341415
R-OVARC1001376//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.1e-53:344:72//Hs.153468: AB011147
R-OVARC1001381//ESTs//5.1e-19:200:66//Hs.114031:AA700958
R-OVARC1001391
R-nnnnnnnnnnnn//ESTs//0.003 9:48:95//Hs.117964:N20913
R-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//3.2e-111:561:95//Hs.21586:AB006651
R-OVARC1001419
R-OVARC1001425//EST//5.7e-20:395:66//Hs.159707:AI393136
R-OVARC1001436//ESTs//9.6e-90:427:99//Hs.6982:AA622427
R-OVARC1001442//ESTs//1.1e-66:317:100//Hs.18437:AI206345
R-OVARC1001453//ESTs//2.0e-20:163:84//Hs.133503:AA628592
R-OVARC1001476//EST//0.23:125:66//Hs.71444:AA131700
R-OVARC1001480//ESTs//3.1e-56:181:97//Hs.40109:AA928694
R-OVARC1001489//ESTs//1.0:297:58//Hs.86723:AA393089
R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds//3.0e-117:585:96//Hs.6534: AF016507
R-OVARC1001506//Small inducible cytokine A5 (RANTES)//1.8e-48:283:90//Hs.155464:AF088219
R-OVARC1001525//EST//0.80:170:60//Hs.157398:AI364539
R-OVARC1001542//Homo sapiens hJTB mRNA, complete cds//1.6e-111:566:95//Hs.6396:AB016492
R-OVARC1001547//ESTs//5.7e-105:564:93//Hs.68835:AA088388
R-OVARC1001577//Homo sapiens SRp46 splicing factor retropseudogene mRNA7/4.4e-20:150:89//Hs.155160: AF031166
R-OVARC1001600//Human mRNA for KIAA0118 gene, partial cds//8.6e-21:282:72//Hs.154326:D42087
R-OVARC1001610//ESTs//4.6e-108:555:95//Hs.44295:N32019
R-OVARC1001611//ESTs//0.0021:117:71//Hs.135568:AA972965
R-OVARC1001615//Homo sapiens KIAA0409 mRNA, partial cds//9.2e-19:114:78//Hs.5158:AB007869
R-OVARC1001668//ESTs//1.0:127:69//Hs.153290:AI022659
R-OVARC1001702//ESTs//4.8e-44:225:97//Hs.96855:AA346854
R-OVARC1001703//ESTs//2.3e-89:426:99//Hs.27099:W60080
R-OVARC1001711//ESTs//1.9e-57:251:99//Hs.9732:AA527784
R-OVARC1001726//ESTs, Highly similar to APICAL PROTEIN [Xenopus laevis]//1.2e-27:236:81//Hs.15485: AA046954
R-OVARC1001731//Tropomyosin4(fibroblast)//7.9e-74:422:90//Hs.102824:X05276
R-OVARC1001745//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//1.7e-62:300:83//Hs.144563: AF057280
R-nnnnnnnnnnnnn//ESTs, Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [S.cerevisiae]//6.8e-100: 540:92//Hs.117741:AA903456
R-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds// 1.1e-109:567:94//Hs.155377:U97670

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R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0675 protein, complete cds//2.0e-109:529:97//Hs.15869:AB014575
R-OVARC1001768//ESTs//3.5e-59:327:94//Hs.107923:H66127
R-OVARC1001791//ESTs//1.3e-111:565:96//Hs.6107:AA160604
R-OVARC1001795//ESTs//2.8e-97:526:93//Hs.72158:AA156978
R-OVARC1001802//Homo sapiens DEC-205 mRNA, complete cds//4.8e-36:276:81//Hs.153563:AF011333
R-OVARC1001805//ESTs//4.1e-78:375:98//Hs.126902:AI374688
R-OVARC1001812//EST//4.8e-45:349:80//Hs.162677:AA604831
R-OVARC1001813//Homo sapiens mRNA for KIAA0538 protein, partial cds//2.1e-15:519:63//Hs.25639:AB011110
R-OVARC1001820//ESTs//9.5e-50:314:80//Hs.140491:W52705
R-OVARC1001828//ESTs//0.11:186:63//Hs.29055:AI374621
R-OVARC1001846//ESTs//0.34:134:66//Hs.152992:AI242160
R-OVARC1001861//ESTs//2.3e-19:120:92//Hs.42225:N31809
R-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence/1.9e-105:571:91//Hs.25300:AF070611
R-OVARC1001879//EST//1.3e-24:185:85//Hs.136617:AA630476
R-OVARC1001880//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.2e-49:302:90//Hs.153468:AB011147
R-OVARC1001883//ESTs//1.0e-51:295:93//Hs.164059:AA447310
R-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//1.6e-87:346:90//Hs.6216:AF061749
R-OVARC1001901//ESTs//6.8e-24:132:98//Hs.130797:AA904435
R-OVARC1001911//ESTs//1.1e-88:491:92//Hs.32343:W73855
R-OVARC1001916//ESTs//7.9e-97:491:95//Hs.24989:H97842
R-OVARC1001928
R-OVARC1001942//ESTs, Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [S.cerevisiae]//2.5e-39:253:88//Hs.117741:AA903456
R-OVARC1001943//ESTs//9.3e-13:78:100//Hs.143680:W38637
R-OVARC1001949//ESTs, Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]//8.3e-96:498:94//Hs.22744:AI379892
R-OVARC1001950//EST//1.3e-35:236:81//Hs.132635:AI032875
R-OVARC1001987//ESTs//5.6e-94:514:92//Hs.21148:AI183729
R-OVARC1001989//ESTs//9.7e-46:228:99//Hs.127046:AA935887
R-OVARC1002044//ESTS//3.4e-45:303:85//Hs.132722:AA618531
R-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.4e-109:542:96//Hs.108258:AB007934
R-OVARC1002066//ESTs//8.5e-97:455:99//Hs.135477:AI088556
R-OVARC1002082//Homo sapiens mRNA for KIAA0772 protein, complete cds//8.1e-47:340:82//Hs.15519:AB018315
R-OVARC1002107//ESTs//5.9e-103:498:98//Hs.157207:AA629860
R-OVARC1002127//ESTs//3.0e-87:419:98//Hs.127833:AI347130
R-OVARC1002138//ESTs, Weakly similar to HYPOTHETICAL 54.7 KD PROTEIN C07A9.1 IN CHROMOSOME III [Caenorhabditis elegans]//1.7e-102:485:98//Hs.137516:AA805691
R-OVARC1002143//ESTs//1.3e-79:428:92//Hs.158126:W26825
R-OVARC1002156//ESTs//1.6e-38:198:98//Hs.22957:AA478923
R-OVARC1002158//ESTs//7.3e-81:412:96//Hs.12211:AA908631
R-OVARC1002165//ESTs//1.8e-09:154:72//Hs.49354:AA424160
R-OVARC1002182//ESTs//4.3e-80:465:91//Hs.77067:AA040478
R-PLACE1000004//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//7.5e-32:164:99//Hs.144194:AA706337
R-PLACE1000005//EST//0.37:212:60//Hs.127020:AA934920
R-PLACE1000007//Homo sapiens clone 24422 mRNA sequence//3.8e-16:100:97//Hs.109268:AF070557
R-PLACE1000014//EST//9.6e-44:344:77//Hs.161917:AA483223
R-PLACE1000031//ESTs//2.2e-32:374:70//Hs.117969:H94870
R-PLACE1000040//ESTs//0.00017:316:59//Hs.23342:AI310440
R-PLACE1000048//Human Line-1 repeat mRNA with 2 open reading frames//4.8e-79:519:86//Hs.23094:M19503
R-PLACE100005011ESTs//9.7e-90:453:96//Hs.27410:N25612
R-PLACE1000061//Ribosomal protein L37a//5.5e-22:126:97//Hs.1946:L06499

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R-PLACE1000066//ESTs, Weakly similar to coded for by C. elegans cDNA yk10c10.3 [C.elegans]//1.4e-61:331:94//Hs.30026:AI356771
R-PLACE1000078//ESTs//2.6e-30:212:85//Hs.89312:AA167659
R-PLACE1000081
R-PLACE1000094
R-PLACE1000133//ESTs//4.4e-87:448:94//Hs.93748:AA884505
R-PLACE1000142//ESTs, Weakly similar to enoyl-CoA hydratase [H.sapiens]//5.5e-103:538:94//Hs.9670:AA632135
R-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds//4.1e-114:594:94//Hs.151017:AF058291
R-PLACE1000185//ESTs, Weakly similar to No definition line found [C.elegans]//2.0e-19:114:95//Hs.7036:W22072
R-PLACE1000213//ESTs//9.4e-99:494:96//Hs.24398:AI262946
R-PLACE1000214//ESTs//5.3e-98:466:98//Hs.28661:AA805916
R-PLACE1000236//Human BENE mRNA, partial cds//1.7e-19:162:84//Hs.85889:U17077
R-PLACE1000246//EST//0.026:134:66//Hs.135611:Z21545
R-PLACE1000292//ESTs//2.5e-80:418:96//Hs.138233:N57912
R-PLACE1000332//EST//1.7e-82:422:96//Hs.118637:T61940
R-PLACE1000347//ESTs//8.5e-36:180:100//Hs.6377:AA632424
R-PLACE1000374//ESTs//2.8e-90:434:98//Hs.161785:AI423126
R-PLACE1000380//ESTs//1.0e-81:399:97//Hs.47105:AI334994
R-PLACE1000383//ESTs//3.7e-75:405:94//Hs.23200:AA203708
R-PLACE1000401//ESTs//1.4e-16:212:72//Hs.151665:AA020959
R-PLACE1000406//ESTs//2.1e-51:259:97//Hs.129651:N53089
R-PLACE1000420//ESTs//7.7e-92:471:95//Hs.144407:AA737799
R-PLACE1000421//ESTs//2.9e-14:282:67//Hs.142068:AA176125
R-PLACE1000424//EST//2.9e-35:453:70//Hs.162404:AA573131
R-PLACE1000435//Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete cds//1.6e-47:472:77//Hs.113259:AF023456
R-PLACE1000444//ESTs, Moderately similar to platelet glycoprotein IIb precursor [H.sapiens]//2.0e-58:410:81//Hs.97579:AA398118
R-PLACE1000453//ESTs//2.3e-85:442:95//Hs.9725:AA039793
R-PLACE1000481//ESTS, Weakly similar to Ndr protein kinase [H.sapiens]//3.2e-109:549:95//Hs.19074:U69566
R-PLACE1000492//ESTs, Highly similar to vacuolar protein sorting homolog r-vps33b [R.norvegicus]//3.5e-83:435:94//Hs.26510:AA700425
R-PLACE1000540//ESTs//3.2e-58:281:99//Hs.118270:AA844729
R-PLACE1000547//Homo sapiens mRNA for KIAA0640 protein, partial cds//2.2e-32:208:88//Hs.153026:AB014540
R-PLACE1000562//ESTs, Weakly similar to HYPOTHETICAL 23.0 KD PROTEIN IN IXR1-TFA1 INTERGENIC REGION [Saccharomyces cerevisiae]//1.9e-26:220:81//Hs.163791:W25348
R-PLACE1000564//ESTs//1.1e-54:302:92//Hs.158520:AI380485
R-PLACE1000583//Human mRNA for KIAA0355 gene, complete cds//5.5e-43:404:75//Hs.153014:AB002353
R-nnnnnnnnnnnn//Guanylate binding protein 1, interferon-inducible, 67kD//6.1e-79:542:82//Hs.62661:M55542
R-PLACE1000596//ESTs//0.0028:364:59//Hs.106090:AA457030
R-PLACE1000599//Human mRNA for KIAA0118 gene, partial cds//4.3e-49:295:90//Hs.154326:D42087
R-PLACE1000610//ESTs//0.0010:104:74//Hs.17413:N45301
R-PLACE1000636//ESTs//1.8e-64:340:95//Hs.100895:AA479308
R-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//5.3e-101:506:96//Hs.5819:AF102265
R-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin))//1.4e-102:559:92//Hs.29595:AJ005896
R-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds//2.8e-10:281:64//Hs.128763:AF009353
R-PLACE1000712//ESTs//7.8e-60:317:95//Hs.8245:AA115485
R-PLACE1000716
R-PLACE1000748//ESTs//8.9e-87:466:93//Hs.25245:AA176701
R-PLACE1000749//EST//0.019:186:61//Hs.135443:AI077396
R-PLACE1000755//ESTs, Weakly similar to HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III [C.el-

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egans]//3.9e-40:224:94//Hs.87889:AA262008
R-PLACE1000769//Homo sapiens clone 24566 mRNA sequence//6.5e-27:531:66//Hs.133342:AF070536
R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds//8.5e-103:513:96//Hs.31921:AB014548
R-PLACE1000786//ESTs//5.2e-93:449:97//Hs.58389:W74482
R-nnnnnnnnnnnn//H.sapiens mRNA for chemokine HCC-1//0.88:201:60//Hs.20144:AF088219
R-PLACE1000798//ESTs//1.1e-97:508:94//Hs.139119:N32189
R-PLACE1000841//ESTs, Highly similar to guanine nucleotide regulatory protein [H.sapiens]//7.7e-31:220:86//Hs.117576:R33135
R-nnnnnnnnnnnn//ESTs//1.8e-87:459:94//Hs.43100:AA186588
R-PLACE1000856//ESTs//0.0084:224:59//Hs.145906:AI275039
R-PLACE1000863//ESTs, Highly similar to PUTATIVE 40S RIBOSOMAL PROTEIN YHR148W [Saccharomyces cerevisiae]//2.2e-92:467:95//Hs.6118.-AI141558
R-PLACE1000909//ESTs//4.7e-89:435:97//Hs.95744:AI392846
R-PLACE1000931//EST//1.9e-28:261:73//Hs.135545:AI097091
R-PLACE1000948//ESTs//0.034:329:58//Hs.114851:AA608697
R-PLACE1000972//EST//3.3e-24:264:74//Hs.130321:AI002941
R-PLACE1000977//EST//0.085:153:65//Hs.131646:AI025689
R-PLACE1000979
R-PLACE1001000//ESTs//4.7e-56:284:96//Hs.117978:AA810725
R-PLACE1001007//ESTs, Moderately similar to MNK1 [H.sapiens]//5.2e-63:343:93//Hs.5662:AA868361
R-PLACE1001010//EST//0.96:53:71//Hs.96973:AA351146
R-PLACE1001015//Oxytocin receptor//2.8e-25:308:71//Hs.2820:X64878
R-PLACE1001024//ESTs//5.0e-12:79:96//Hs.97910:AA404736
R-PLACE1001036//ESTs//4.0e-15:301:65//Hs.137947:AI025762
R-PLACE1001062//ESTs//5.2e-15:199:73//Hs.138982:AA056120
R-PLACE1001076//ESTs//3.9e-84:406:98//Hs.115455:AA678124
R-PLACE1001088//ESTs//3.0e-106:518:97//Hs.158964:AA639580
R-PLACE1001092//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.035:259:59//Hs.31575:AF100141
R-PLACE1001104//ESTs//6.1e-115:582:95//Hs.10972:AA164268
R-PLACE1001118//ESTs//6.9e-81:440:93//Hs.5383:AA913610
R-PLACE1001136//ESTs//7.4e-41:168:83//Hs.95115:AA206594
R-PLACE1001168//ESTs//3.9e-21:116:99//Hs.5897:AA148834
R-PLACE1001171//ESTs, Highly similar to CYTOCHROME B-245 LIGHT CHAIN [H.sapiens]//0.91:77:71//Hs.115211:AA287527
R-PLACE1001185//ESTs//1.5e-65:330:96//Hs.26368:AA789297
R-PLACE1001238//ESTs, Moderately similar to RNA polymerase I associated factor [M.musculus]//1.9e-99:512:94//Hs.24884:AA176812
R-PLACE1001241//ESTs//1.1e-81:446:93//Hs.42278:AI073464
R-PLACE1001257//EST//6.4e-46:298:87//Hs.162404:AA573131
R-PLACE1001272//ESTs//0.31:158:61//Hs.42960:N95371
R-PLACE1001279//ESTs//1.8e-77:376:97//Hs.29276:AA427780
R-PLACE1001280//ESTs//1.1e-30:134:89//Hs.163492:AI334460
R-PLACE1001294//ESTs, Moderately similar to GAMETOGENESIS EXPRESSED PROTEIN GEG-154 [M.musculus]//2.7e-22:181:84//Hs.48320:AA149548
R-PLACE1001304//ESTs, Weakly similar to ZINC FINGER PROTEIN 135 [H.sapiens]//4.2e-34:195:92//Hs.86276:W27601
R-PLACE1001311//ESTs//9.1e-91:438:97//Hs.41055:AI339056
R-PLACE1001323//Human transmembrane 4 superfamily protein (SAS) mRNA, complete cds//5.5e-44:215:86//Hs.50984:U01160
R-PLACE1001351//ESTs//2.4e-101:494:97//Hs.23944:AI097077
R-PLACE1001366//Small inducible cytokine A5 (RANTES)//8.7e-43:284:85//Hs.155464:AF088219
R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//2.3e-81:431:93//Hs.152005:AF009615
R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence/1.0e-36:192:97//Hs.12342:AF055030
R-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//1.0e-86:456:94//Hs.21301:AF093419
R-PLACE1001387//ESTs//6.0e-74:383:94//Hs.55016:AI298280

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R-PLACE1001395//ESTs//2.3e-94:473:95//Hs.22394:N32555
R-PLACE1001399//ESTs//2.6e-41:204:100//Hs.24462:N36348
R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//2.6e-45:242:95//Hs.110404:AF091087
R-PLACE1001414//ESTs//0.0013:77:75//Hs.144614:AA291800
R-PLACE1001440
R-PLACE1001456//EST//0.76:120:62//Hs.34011:H48115.
R-PLACE1001468//ESTs//4.0e-80:403:96//Hs.131832:AI017547
R-PLACE1001484//ESTs//3.0e-16:201:72//Hs.153413:AI248625
R-PLACE1001502//ESTs//8.1e-31:161:99//Hs.126264:AA455617
R-PLACE1001503//ESTs//2.4e-37:176:81//Hs.141581:AA315361
R-PLACE1001517//Homo sapiens hGAAI mRNA, complete cds//2.1e-57:339:90//Hs.4742:AB006969
R-PLACE1001534//ESTs//3.6e-61:304:97//Hs.45207:AI042153
R-PLACE1001545/TESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.6e-22:170:85//Hs.155456:AA707265
R-PLACE1001551//ESTs//1.5e-39:202:98//Hs.139269:AA894431
R-PLACE1001570//EST//1.1e-70:495:82//Hs.144234:W52249
R-PLACE1001602//EST//0.33:297:57//Hs.149839:AI287601
R-PLACE1001603//ESTs//2.0e-17:181:76//Hs.155334:AA827904
R-PLACE1001610//EST//1.1e-86:442:95//Hs.112580:AA608683
R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds//1.1e-42:217:97//Hs.75258:AF054174
R-PLACE1001632//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//1.5e-78:458:91//Hs.114547:AA167095
R-PLACE1001634//ESTs//0.0035:40:97//Hs.101577:AI168526
R-PLACE1001640//ESTs//0.0028:377:57//Hs.131044:D61640
R-PLACE10016727/ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.98:141:62//Hs.153060:AA195804
R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//4.7e-113:545:97//Hs.3688:AF069250
R-PLACE1001692//EST//3.0e-43:430:75//Hs.162975:AA679124
R-PLACE1001705//ESTs//3.0e-81:418:94//Hs.22646:AI374903
R-PLACE1001716//EST//0.76:150:62//Hs.128906:AA983667
R-PLACE1001720//ESTs//2.4e-64:385:90//Hs.60455:AA010993
R-PLACE1001729//ESTs//2.9e-84:418:96//Hs.134740:AA282171
R-PLACE1001739//ESTs, Weakly similar to P68 PROTEIN [H.sapiens]//9.1e-32:206:89//Hs.6366:AA614113
R-PLACE1001740//EST//6.5e-05:113:68//Hs.139949:AA644266
R-PLACE1001745//ESTs//3.3e-92:473:95//Hs.104270:AA236479
R-PLACE1001746//ESTs//8.8e-93:443:98//Hs.112198:AI423937
R-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//4.1e-93:540:89//Hs.4812:AF061243
R-PLACE1001756//ESTs//0.17:157:66//Hs.141565:N64662
R-PLACE1001761
R-PLACE1001771//ESTs//0.92:165:62//Hs.473 87:N51980
R-PLACE1001781//ESTs//5.7e-84:437:95//Hs.23363:AA081236
R-PLACE1001799//EST//0.00039:126:65//Hs.123267:AA807352
R-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA; partial cds//1.3e-93:463:95//Hs.40820:AF058953
R-PLACE1001821//Small inducible cytokine A5 (RANTES)//2.7e-35:328:75//Hs.155464:AF088219
R-PLACE1001845
R-PLACE1001869//EST//1.0:207:62//Hs.137298:W32868
R-PLACE1001897//ESTs//2.4e-23:219:80//Hs.7503:H50009
R-PLACE1001912//ESTs//1.5e-32:162:78//Hs.136810:AA789098
R-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//3.9e-74:363:97//Hs.17839:AF099936
R-PLACE1001928//Homo sapiens mRNA for KIAA0623 protein, complete cds//0.85:130:66//Hs.151406:AB014523
R-PLACE1001983//ESTs//2.8e-66:334:96//Hs.110155:AA007313

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R-PLACE1001989//ESTs//1.3e-88:453:95//Hs.132717:AA171941
R-PLACE1002046
R-PLACE1002052//ESTs//1.7e-79:428:94//Hs.6737:N32595
R-PLACE1002066//ESTs//2.8e-82:427:94//Hs.132972:AA543094
R-PLACE1002072//ESTs//0.27:108:66//Hs.123163:AA809619
R-PLACE1002073//EST//5.5e-70:369:95//Hs.132339:AI028552
R-PLACE1002090//ESTs//6.3e-73:361:96//Hs.134469:AA731632
R-PLACE1002115//ESTs//4.6e-34:233:88//Hs.163443:R23311
R-PLACE1002119//ESTs//1.2e-88:444:96//Hs.15725:AA521293
R-PLACE1002140//ESTs//6.6e-22:118:100//Hs.22793:W91937
R-PLACE1002150//ESTs//4.0e-96:465:98//Hs.7312:AI167614
R-PLACE1002157//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG[H.sapiens]//3.6e-39:400:76//Hs.162172:AA534189
R-PLACE1002163//ESTs//3.2e-83:428:95//Hs.137011:AI185965
R-PLACE1002171//ESTs//5.3e-68:392:90//Hs.62273:AA143745
R-PLACE1002205//ESTS//1.5e-39:211:95//Hs.28338:N48793
R-PLACE1002213//ESTs//5.1e-38:290:83//Hs.146811:AA410788
R-PLACE1002227//EST//1.3e-14:214:72//Hs.46979:N49892
R-PLACE1002256//ESTs//2.4e-100:484:98//Hs.9343:AI004257
R-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//5.8e-67:501:81//Hs.23094:M19503
R-PLACE1002319//ESTs//1.4e-28:17 8:92//Hs.7353:AA209308
R-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds//1.6e-95:501:93//Hs.18277:AB018271
R-PLACE1002395//ESTs//3.6e-25:248:77//Hs.3853:AA034291
R-PLACE1002399//ESTs//1.5e-27:238:78//Hs.13014:W26381
R-PLACE1002433//ESTs//4.3e-108:511:98//Hs.98324:AA621959
R-PLACE1002437//EST//1.2e-06:158:61//Hs.159833:T24110
R-PLACE1002438//Sjogren syndrome antigen B (autoantigen La)//0.93:176:60//Hs.83715:X69804
R-PLACE1002450//ESTs//1.5e-89:432:98//Hs.47371:AA136333
R-PLACE1002465//ESTS//1.6e-92:488:93//Hs.78110:AA741320
R-PLACE1002474//Human matrilin-2 precursor mRNA, partial cds//4.9e-23:166:85//Hs.19368:U69263
R-PLACE1002477//ESTs//2.5e-62:305:98//Hs.88605:AA421132
R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds//3.6e-55:307:91//Hs.17200:AF042273
R-PLACE1002499//ESTs//7.4e-72:373:96//Hs.128221:AA972429
R-PLACE1002500//Homo sapiens KIAA0409 mRNA, partial cds//1.2e-40:296:83//Hs.5158:AB007869
R-PLACE1002514//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.sapiens]//6.4e-14:217:69//Hs.152230:AI140609
R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//5.1e-88:582:85//Hs.88756:AB018256
R-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//2.7e-19:116:93//Hs.99348:AC004774
R-PLACE1002537//ESTs//4.8e-93:440:99//Hs.164005:AA766491
R-PLACE1002571//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]//1.3e-108:555:95//Hs.23259:AA532437
R-PLACE1002578//EST//1.9e-40:337:81//Hs.162404:AA573131
R-PLACE1002583//EST//1.2e-07:264:65//Hs.156414:AI339738
R-PLACE1002591//ESTs//2.3e-67:372:94//Hs.143046:N73778
R-PLACE1002598//ESTs, Highly similar to PROTEIN HI1715 [Haemophilus influenzae]//1.2e-44:228:97//Hs.7527:AA843208
R-PLACE1002604//ESTs//3.3e-106:532:96//Hs.86828:AA632147
R-PLACE1002625//EST//3.8e-13:173:74//Hs.138597:H77749
R-PLACE1002665//Small inducible cytokine A4 (homologous to mouse Mip-1b)//1.0:189:58//Hs.75703:J04130
R-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//3.8e-79:390:97//Hs.124903:AF068180
R-PLACE1002714//ESTs//8.2e-63:340:93//Hs.7973:H19830
R-PLACE1002722//ESTs, Weakly similar to putative G-protein-coupled receptor [H.sapiens]//6.8e-75:445:90//Hs.29202:R71586
R-PLACE1002768//ESTs//1.2e-70:359:95//Hs.132600:H12865
R-PLACE1002772//ESTs//8.1e-49:362:82//Hs.141254:AI334099
R-PLACE1002782//ESTs//2.4e-58:284:98//Hs.143545:AI149014

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R-PLACE1002794//ESTs//5.4e-21:114:100//Hs.77365:W93593
R-PLACE1002811//ESTs//6.7e-68:329:98//Hs.78026:AA456955
R-PLACE1002815//ESTs//6.8e-103:537:93//Hs.5459:AI304392
R-PLACE1002816//ESTs//3.9e-05:118:68//Hs.98641:AA429916
R-PLACE1002834//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//2.1e-42:233:94//Hs.61518:AA167094
R-PLACE1002839//ESTs//1.7e-10:292:64//Hs.93012:R96142
R-PLACE1002851//ESTs//1.7e-73:381:95//Hs.135021:AI096756
R-PLACE1002853//ESTs//1.2e-89:453:96//Hs.23630:N57539
R-PLACE1002881//ESTs//1.1e-71:360:96//Hs.34392:AI066762
R-PLACE1002908//EST//2.7e-31:177:94//Hs.147925:AI249332
R-PLACE1002941//ESTs//4.0e-96:519:92//Hs.125139:AA523995
R-PLACE1002962
R-PLACE1002968//ESTs//4.7e-31:420:69//Hs.116518:AA653202
R-PLACE1002991//ESTs//9.0e-81:418:95//Hs.132717:AA171941
R-PLACE10029937/ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]//1.3e-86:502:89//Hs.32232:AA604268
R-PLACE1002996//ESTs//1.9e-44:218:100//Hs.63657:AI144268
R-PLACE1003025//ESTs//8.4e-104:517:96//Hs.10711:AI151499
R-PLACE1003027//Human mRNA for KIAA0238 gene, partial cds//0.97:156r60//Hs.82042:D87075
R-PLACE1003044//Human onconeural ventral antigen-1 (Nova-1) mRNA, complete cds//1.0:200:63//Hs.214:U04840
R-PLACE1003092//ESTs//0.0046:267:60//Hs.133095:AA927777
R-PLACE1003100//ESTs, Highly similar to NODULATION PROTEIN G [Rhizobium meliloti]//9.5e-94:491:93//Hs.6318:AI131178
R-PLACE1003108//ESTs//0.00065:184:66//Hs.154366:AA527359
R-PLACE1003136//Signal recognition particle 54 kD protein//0.057:317:59//Hs.49346:U51920
R-PLACE1003145//ESTs//1.9e-98:534:92//Hs.61929:AA044757
R-PLACE1003153//ESTs//5.8e-76:367:98//Hs.105196:AA483467
R-PLACE1003174//ESTs//1.7e-44:226:98//Hs.59688:AA453924
R-PLACE1003176
R-PLACE1003190//ESTs//1.6e-74:356:99//Hs.121282:AI091453
R-PLACE1003200//ESTs//4.6e-93:461:96//Hs.24321:AA971017
R-PLACE1003205//ESTs//0.037:171:61//Hs.157077:H44802
R-PLACE100323 8//ESTs, Weakly similar to KIAA0001 [H.sapiens]//2.5e-82:436:94//Hs.58561:W79123
R-PLACE1003249//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//7.9e-44:313:84//Hs.73614:U83460
R-PLACE1003256//EST//9.6e-46:284:88//Hs.162404:AA573131
R-PLACE1003258//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//8.3e-102:551:92//Hs.52431:AA625326
R-PLACE1003296//ESTs//1.9e-88:451:96//Hs.57749:W92986
R-PLACE1003302//ESTs, Highly similar to ZINC FINGER PROTEIN 43 [Homo sapiens]//8.2e-93:458:96//Hs.29147:AA883993
R-PLACE1003334//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//3.3e-94:463:97//Hs.155050:AA908765
R-PLACE1003342//ESTs//6.0e-88:447:96//Hs.107527:R66438
R-PLACE1003343//EST//0.0087:412:58/Hs.159963:AA977701
R-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds//1.1e-99:469:98//Hs.6564:U92715
R-PLACE1003361//ESTs//3.5e-64:332:95//Hs.163861:AI199636
R-PLACE1003366//ESTs//1.0e-87:492:92//Hs.72222:AA158234
R-PLACE1003369//ESTs, Weakly similar to ZK1058.4 [C.elegans]//3.5e-18:109:95//Hs.27670:AI051591
R-PLACE1003373//Homo sapiens mRNA for KIAA0472 protein, partial cds//2.6e-54:279:80//Hs.6874:AB007941
R-PLACE1003375//ESTs//1.7e-88:431:97//Hs.41327:AI039909
R-PLACE1003383//ESTs//0.00084:177:64//Hs.120695:AI377755
R-PLACE1003401//ESTs//1.1e-16:147:80//Hs.132187:AI039020
R-PLACE1003420//ESTs//1.4e-93:481:94//Hs.122565:AI126840
R-PLACE1003454//ESTs//4.0e-57:310:93//Hs.121688:AA743697

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R-PLACE1003478//EST//1.0:162:63//Hs.147003:AI184671
R-PLACE1003493//ESTs//1.2e-73:383:95//Hs.28852:R64270
R-PLACE1003516//ESTs//3.2e-23:206:80//Hs.138632:H97952
R-PLACE1003519//H.sapiens hnRNP-E1 mRNA//1.7e-22:236:79//Hs.2853:Z29505
R-PLACE1003521//ESTs//5.8e-74:371:96//Hs.30818:AA194980
R-PLACE1003528//ESTs//1.1e-40:219:82//Hs.138856:H47461
R-PLACE1003537//ESTs, Weakly similar to multispanning membrane protein [H.sapiens]//7.4e-69:338:98//Hs.110439:N93209
R-PLACE1003553//ESTs//2.2e-87:438:97//Hs.132022:AI040321
R-PLACE1003566//ESTs//1.2e-62:298:92//Hs.30799:AI052591
R-PLACE1003575//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.4e-22:145:80//Hs.92381:AB007956
R-PLACE1003583//ESTs, Weakly similar to hypothetical L1 protein [H.sapiens]//1.5e-14:264:65//Hs.158253:R86178
R-PLACE1003584
R-PLACE1003592//ESTs//1.3e-15:213:69//Hs.139507:T77542
R-PLACE1003593//ESTs, Highly similar to FRG1 gene product [H.sapiens]//5.8e-75:459:89//Hs.23884:AD77106
R-PLACE1003596//ESTs//0.011:273:61//Hs.71719:AA142875
R-PLACE1003602//Homo sapiens mRNA expressed in placenta//7.8e-97:576:88//Hs.56851:D83200
R-PLACE1003605//ESTs//3.7e-86:407:99//Hs.136057:AA988299
R-nnnnnnnnnnnn//ESTs//1.0:78:71//Hs.101248:T26446
R-PLACE1003618//ESTs//6.8e-30:281:79//Hs.114455:AA411943
R-PLACE1003625//ESTs//7.2e-78:377:98//Hs.102708:AA292285
R-PLACE1003638//ESTs//6.7e-38:274:82//Hs.138852:AA284247
R-PLACE1003669//ESTs//9.7e-83:418:95//Hs.4842:AI342607
R-PLACE1003704//ESTs//3.0e-13:99:89//Hs.81648:W26521
R-PLACE1003709//ESTs//0.019:178:60//Hs.32100:N59866
R-PLACE1003711//ESTs//0.99:126:63//Hs.47005:N98639
R-PLACE1003723//ESTS//1.7e-89:448:96//Hs.157222:AA766987
R-PLACE1003738//ESTs//2.5e-36:182:100//Hs.122162:AI057087
R-PLACE1003760//Human globin gene//L9e-98:538:91//Hs.100090:M69023
R-PLACE1003762//EST//2.9e-15:125:85//Hs.162083:AA487512
R-PLACE1003768//Human P042 gene, complete cds//3.1e-18:300:69//Hs.158302:U88965
R-PLACE1003771//ESTs//1.2e-09:64:100//Hs.23799:AI003798
R-PLACE1003783//ESTs, Weakly similar to D2085.5 [C.elegans]//3.8e-38:199:97//Hs.115197:AA215757
R-PLACE1003784//ESTs//3.7e-87:428:97//Hs.157985:AI366909
R-PLACE1003795//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.2e-36:236:88//Hs.153468:AB011147
R-PLACE1003833//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//8.5e-62:313:96//Hs.121020:AA526092
R-PLACE1003850//ESTs//4.0e-67:351:96//Hs.159303:T91059
R-PLACE1003858//ESTs//0.96:87:66//Hs.107112:AA679058
R-nnnnnnnnnnnn
R-PLACE1003870//EST//2.9e-34:281:79//Hs.160895:AI365871
R-nnnnnnnnnnnn
R-PLACE1003886//ESTs//6.7e-85:410:97//Hs.25129:W93595
R-PLACE1003888//ESTs//0.0085:165:64//Hs.96739:AA441915
R-PLACE1003900//EST//2.4e-05:129:69//Hs.127931:AA969259
R-PLACE1003903//ESTs, Highly similar to CTP SYNTHASE [Homo sapiens]//1.5e-54:282:96//Hs.58553:AA100804
R-PLACE1003915//EST//0.87:55:76//Hs.145930:AI275760
R-PLACE1003923//ESTs//1.7e-89:456:95//Hs.14125:AA156236
R-PLACE1003932//ESTs//3.0e-50:340:84//Hs.151208:AI126110
R-PLACE1003936//EST//1.8e-08:208:65//Hs.162656:AA603567
R-PLACE1003968//ESTs//7.4e-49:301:90//Hs.93850:AA115330
R-PLACE1004104//ESTs//1.9e-46:254:94//Hs.96802:AA443231
R-PLACE1004114//ESTs//1.2e-64:322:97//Hs.28928:AI052052
R-PLACE1004118//ESTs//1.0e-83:404:98//Hs.112764:AA609770

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R-PLACE1004128//ESTs//5.3e-80:415:95//Hs.11835:AA040244
R-PLACE1004149//ESTs//7.2e-25:331:72//Hs.141084:H11714
R-PLACE1004156//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.0e-56:491:76//Hs.113283:AF018080
R-PLACE1004161//ESTs//2.0e-59:355:88//Hs.13830:AA918601
R-PLACE1004183//Homo sapiens cytochrome c oxidase assembly protein COX11(COX11) mRNA, complete cds//4.7e-78:434:91//Hs.153504:AF044321
R-PLACE1004197
R-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds//1.5e-105:501:98//Hs.24640:AF069493
R-PLACE1004242//ESTs//1.0e-71:364:87//Hs.138632:H97952
R-PLACE1004256//EST//0.0011:347:61//Hs.131385:AI022630
R-PLACE1004257//EST//0.027:99:71//Hs.97587:AA398209
R-PLACE1004258//KERATIN, TYPE I CYTOSKELETAL 14//0.72:180:63//Hs.117729:100124
R-PLACE1004270//ESTS//0.011:264:59//Hs.110044:AA181800
R-PLACE1004274//Human retinoic acid receptor-beta associated open reading frame, complete sequence//0.28:121:66//Hs.1938:S82362
R-PLACE1004277//Homo sapiens two pore domain K^+ channel (TASK-2) mRNA, complete cds//1.4e-107:581:91//Hs.127007:AF084830
R-PLACE1004284//ESTs//5.0e-22:187:82//Hs.23141:W92114
R-PLACE1004289//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.9e-28:279:77//Hs.38687:AA744496
R-PLACE1004302//ESTs, Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]//8.2e-61:313:95//Hs.71435:AI253099
R-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//6.0e-115:590:94//Hs.11171:Y11588
R-PLACE1004336//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//6.7e-69:572:77//Hs.1361:M55053
R-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//7.7e-72:379:93//Hs.16232:AF100153
R-PLACE1004376//ESTs//0.49:362:59//Hs.138086:AI056309
R-PLACE1004384//EST//1.0:47:76//Hs.128546:AA905556
R-PLACE1004388//ESTs, Weakly similar to contains similarity to ATP/GTP-binding site motif [C.elegans]//1.3e-98:572:90//Hs.14202:N46000
R-PLACE1004405//ESTs//3.4e-99:507:95//Hs.28792:AI343467
R-PLACE1004425//ESTs//2.7e-85:442:95//Hs.12544:N53665
R-PLACE1004428//ESTs//1.0e-07:114:78//Hs.140225:AA704101
R-PLACE1004437//Human NAD^+-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds//9.4e-90:516:88//Hs.155410:U49283
R-PLACE1004451
R-PLACE1004460//ESTs//5.4e-14:338:64//Hs.97464:AA662980
R-PLACE1004467//ESTs//3.3e-85:467:92//Hs.9527:W52721
R-PLACE1004471//ESTs//3.0e-73:389:94//Hs.23240:R46578
R-PLACE1004473//ESTs, Weakly similar to F20D1.2 [C.elegans]//3.8e-101:510:95//Hs.16986:W89194
R-PLACE1004491//Human mitochondrial 1.25-dihydroxyvitamin D3 24-hydroxylase mRNA, complete cds//0.23:278:61//Hs.89663:L13286
R-PLACE1004506//ESTs//2.5e-98:559:90//Hs.19447:AI057117
R-PLACE1004510//ESTs//1.5e-91:436:98//Hs.24846:AI420493
R-PLACE1004516//EST//1.7e-66:344:96//Hs.99303:AA453164
R-PLACE1004518//ESTs//5.2e-79:410:94//Hs.27091:AA436553
R-PLACE1004548//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.8e-40:332:72//Hs.115325:084488
R-PLACE1004550
R-PLACE1004564//ESTs//5.5e-76:367:98//Hs.49683:AA564742
R-PLACE1004629//ESTs, Weakly similar to OS-9 precurosor [H.sapiens]//8.1e-40:272:87//Hs.7100:W07181
R-PLACE1004645//ESTs//6.3e-14:83:100//Hs.17270:AA701903
R-PLACE1004646//ESTs//3.7e-22:231:76//Hs.141250:N29734
R-PLACE1004658//ESTs//2.0e-12:109:84//Hs.23508:AA101113
R-nnnnnnnnnnn//Homo sapiens mRNA for KIAA0714 protein, partial cds//7.8e-23:129:99//Hs.123129:AB018257
R-PLACE1004672//ESTs//2.0e-50:256:98//Hs.136367:AI144254

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R-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//L8e-90:510:91//Hs.80019:AF035606
R-PLACE1004681//EST//2.1e-08:283:62//Hs.99543:AA461482
R-PLACE1004686
R-PLACE1004691//EST//7.3e-42:305:82//Hs.141833:AA021552
R-PLACE1004693//ESTs//0.014:135:64//Hs.145333:AI251374
R-PLACE1004716//ESTs, Weakly similar to No definition line found [C.elegans]//3.4e-80:413:94//Hs.23528:AI279571
R-PLACE1004722//EST//0.14:165:63//Hs.18213:T97997
R-PLACE1004736//ESTs//1.0e-72:385:94//Hs.10657:N6391
R-PLACE1004740//ESTs//1.0:267:58//Hs.101661:AA416619
R-nnnnnnnnnnnn//EST//0.45:94:69//Hs.147174:AI192195
R-PLACE1004751//EST//9.8e-32:174:83//Hs.147901:AI223374
R-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds//2.7e-89:437:96//Hs.104715:AF084367
R-PLACE1004777//ESTs//7.4e-68:351:94//Hs.23395:AA398548
R-PLACE1004793//ESTs//1.3e-53:290:78//Hs.142375:AA398619
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0606 protein, partial cds//1.9e-99:580:88//Hs.38176:AB011178
R-PLACE1004813//ESTs//7.6e-86:433:96//Hs.85640:AA535856
R-PLACE1004814//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//1.1e-108:358:99//Hs.3688:AF069250
R-PLACE1004815//EST//4.7e-50:333:84//Hs.142196:AA258356
R-PLACE1004824//Protein kinase, interferon-inducible double stranded RNA dependent//4.8e-46:450:76//Hs.73821:M35663
R-PLACE1004827//ESTs//2.3e-48:250:96//Hs.138766:AA342185
R-PLACE1004836//ESTs//2.7e-39:222:94//Hs.78661:AA195299
R-PLACE1004838//EST//0.056:198:60//Hs.129589:AA995901
R-PLACE1004840//ESTs, Highly similar to TRANSCRIPTIONAL ACTIVATOR GCN5 [Saccharomyces cerevisiae]//6.5e-71:381:93//Hs.8383:AA013272
R-PLACE1004868//ESTs//4.9e-70:367:94//Hs.100895:AA479308
R-PLACE1004885//Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete cds//1.8e-37:330:78//Hs.113259:AF023456
R-PLACE1004900//EST//1.2e-46:306:86//Hs.149580:AI211881
R-PLACE1004902//Sucrase-isomaltase//0.87:254:61//Hs.2996:X63597
R-nnnnnnnnnnnn//ESTs//4.5e-75:375:96//Hs.91115:AI221563
R-PLACE1004918//ESTs//2.6e-103:519:95//Hs.143607:AI424948
R-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//6.6e-102:532:93//Hs.17839:AF099936
R-PLACE1004934//EST//0.035:156:67//Hs.162071:AA478980
R-PLACE1004937//ESTs, Weakly similar to F55B12.3 [C.elegans]//6.4e-80:409:95//Hs.31945:AA702166
R-PLACE1004969//ESTs//9.8e-18:101:99//Hs.112837:N78013
R-PLACE1004972//ESTs//1.3e-65:337:95//Hs.75798:H29106
R-PLACE1004979//EST//1.2e-96:475:96//Hs.120158:AA708789
R-PLACE1004982//ESTs//1.0e-98:471:98//Hs.106496:AI291776
R-PLACE1004985//ESTs//2.1e-88:456:93//Hs.135050:AI420335
R-PLACE1005026
R-PLACE1005027//ESTs, Weakly similar to N-methyl-D-aspartate receptor glutamate-binding chain [R.norvegicus]//0.72:145:66//Hs.11215:N56719
R-PLACE1005046//Homo sapiens mRNA for KIAA0575 protein, complete cds//5.3e-66:297:88//Hs.153468:AB011147
R-PLACE1005052//ESTs, Weakly similar to weak similarity to rat cytosolic acyl coenzyme A thioester hydrolase [C.elegans]//1.2e-106:543:95//Hs.18625:AI074605
R-PLACE1005066//ESTs//3.9e-92:459:96//Hs.62684:AA806103
R-PLACE1005077//Human triadin mRNA, complete cds//1.8e-05:121:69//Hs.68731:U18985
R-PLACE1005085//Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.6e-49:314:74//Hs.113283:AF018080
R-PLACE1005086//ESTs//1.2e-73:379:94//Hs.110128:AA584364
R-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end ofcds//8.0e-99:531:92//Hs.75437:L40401
R-PLACE1005102//ESTs//7.2e-68:493:84//Hs.10593:AI201336
R-PLACE1005108//Human DNA fragmentation factor-45 mRNA, complete cds//9.2e-40:232:82//Hs.155344:

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U91985
R-PLACE1005111//EST//8.1e-10:189:68//Hs.136356:AA493225
R-PLACE1005128//ESTs//1.4e-78:501:87//Hs.15093:AA203423
R-PLACE1005146//ESTs//4.8e-93:460:97//Hs.37896:AA777349
R-PLACE1005162//ESTs//7.5e-51:277:95//Hs.28838:AI089013
R-nnnnnnnnnnn//ESTs//5.4e-75:366:97//Hs.48119:AA454227
R-PLACE1005181//EST//0.012:172:66//Hs.147107:AI190589
R-PLACE1005187//ESTs//5.6e-72:363:95//Hs.16577:AI022830
R-PLACE1005206//ESTs//5.3e-48:203:88//Hs.31792:H45211
R-PLACE1005232//ESTs//5.1e-41:287:84//Hs.138552:R99532
R-PLACE1005243//ESTs//1.1e-48:348:83//Hs.113310:R16767
R-PLACE1005261//ESTs//0.19:175:62//Hs.124337:AA829524
R-PLACE1005266//ESTs//1.9e-22:388:66//Hs.124146:AA699633
R-PLACE1005277//ESTs//1.5e-29:314:72//Hs.163710:AA024516
R-PLACE1005287//ESTs//3.6e-95:456:98//Hs.49282:AA970322
R-PLACE1005305//ESTs//9.9e-71:428:88//Hs.144855:AI197937
R-PLACE1005308//ESTs//3.8e-32:173:96//Hs.58239:AA215797
R-PLACE1005313//ESTs//5.2e-74:409:93//Hs.33368:AA206614
R-PLACE1005327//Chromosome 1 specific transcript KIAA0491//1.7e-104:537:94//Hs.136309:AB007960
R-PLACE1005331//ESTs//2.1e-91:487:93//Hs.9291:AI189343
R-PLACE1005335//ESTs, Weakly similar to F23B2.4 [C.elegans]//3.8e-90:442:97//Hs.70202:AA732975
R-PLACE1005373//ESTs//8.0e-93:526:91//Hs.98541:N38901
R-PLACE1005374//Homo sapiens KIAA0395 mRNA, partial cds//3.3e-44:344:80//Hs.43681:AL022394
R-PLACE1005409//EST//0.43:174:59//Hs.162077:AA479978
R-PLACE1005453//EST//7.9e-57:330:90//Hs.162306:AA555304
R-PLACE1005467//ESTs//2.2e-42:294:84//Hs.142257:AA188423
R-PLACE1005471//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-88:561:86//Hs.23094:M19503
R-PLACE1005477//Human methionine aminopeptidase mRNA, complete cds//6.9e-80:549:83//Hs.78935:U29607
R-PLACE1005480//EST//0.99:39:82//Hs.157275:AI364046
R-PLACE1005481//EST//1.5e-31:281:79//Hs.132635:AI032875
R-PLACE1005494//Homo sapiens mRNA for semaphorin E, complete cds//0.036:319:59//Hs.62705:AB000220
R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cds//5.4e-57:277:98//Hs.28307:AF071185
R-PLACE1005526//ESTs//2.5e-30:233:83//Hs.119304:AA443325
R-PLACE1005528//Homo sapiens mRNA for cartilage-associated protein (CASP)//8.9e-20:321:69//Hs.155481:AJ006470
R-PLACE1005530//ESTs//3.7e-81:438:92//Hs.103380:AI291325
R-PLACE1005550//ESTs, Highly similar to HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III [Caenorhabditis elegans]//5.2e-95:458:98//Hs.38114:N62927
R-PLACE1005554//ESTs//8.8e-36:267:86//Hs.98288:AA203555
R-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR [Saccharomyces cerevisiae]//2.2e-64:345:94//Hs.7736:W81261
R-PLACE1005574//ESTs//2.3e-27:231:83//Hs.117771:R99835
R-PLACE1005584//ESTs//1.6e-36:188:98//Hs.152050:AA724612
R-PLACE1005595//ESTs//1.6e-91:453:96//Hs.85079:AI276023
R-PLACE1005603//ESTs//8.2e-99:533:93//Hs.96357:AI026927
R-PLACE1005611//ESTs//5.2e-28:183:89//Hs.24941:AA261857
R-PLACE1005623//ESTs//1.4e-102:505:96//Hs.58382:AA808964
R-PLACE1005630
R-PLACE1005639//ESTs//1.4e-51:256:98//Hs.1975:W72452
R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.0e-111:585:93//Hs.8765:AF083255
R-PLACE1005656//ESTs//2.7e-88:469:92//Hs.164054:AA528169
R-PLACE1005666//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//3.3e-24:401:66//Hs.129727:AF035587
R-PLACE1005698//ESTs//0.00013:82:79//Hs.116331:AA629355
R-PLACE1005727//EST//0.15:206:63//Hs.105002:AA449332
R-PLACE1005730//EST//0.0014:129:70//Hs.127931:AA969259

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R-PLACE1005739//ESTs, Moderately similar to unknown intracellular protein [M.musculus]//1.3e-42:236:94//Hs.23889:AI341137
R-PLACE1005755//ESTs//2.8e-32:308:80//Hs.159821:AA524070
R-PLACE1005763//Human mRNA for KIAA0118 gene, partial cds//3.3e-47:268:87//Hs.154326:D42087
R-PLACE1005799//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]//7.7e-15:88:98//Hs.109857:AA088385
R-PLACE1005802//ESTs//2.8e-19:208:76//Hs.9271:W30941
R-PLACE1005803//ESTs//2.6e-75:417:92//Hs.71414:AA131327
R-PLACE1005804//EST//6.5e-20:182:70//Hs.149844:AI287693
R-PLACE1005828//ESTs//3.0e-15:194:77//Hs.106236:N50058
R-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)//0.040:435:58//Hs.75770:L41870
R-PLACE1005845//EST//5.0e-61:294:99//Hs.133202:AI050965
R-PLACE1005850//ESTs//3.4e-82:425:96//Hs.7966:AI203471
R-PLACE1005851//ESTs//2.9e-21:165:84//Hs.23607:N98305
R-PLACE1005876//ESTs//0.48:296:57//Hs.39140:AI041842
R-PLACE1005884//ESTs//0.0027:177:66//Hs.150295:AA570558
R-PLACE1005898//ESTs//1.7e-98:467:98//Hs.159475:AI339981
R-PLACE1005921//ESTs//5.8e-96:480:95//Hs.30822:AA885501
R-PLACE1005923//ESTs//1.8e-66:333:96//Hs.150890:AI341793
R-PLACE1005925//Human Line-1 repeat mRNA with 2 open reading frames//2.8e-27:382:70//Hs.23094:M19503
R-PLACE1005932//ESTs, Moderately similar to MNK1 [H.sapiens]//1.1e-70:377:93//Hs.5662:AA868361
R-PLACE1005934//ESTs//1.0e-42:251:91//Hs.25092:AA922142
R-PLACE1005936//ESTs//1.2e-88:461:94//Hs.94125:N62913
R-PLACE1005951//ESTs//1.4e-83:533:86//Hs.21148:AI183729
R-PLACE1005953
R-PLACE1005955//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROTEIN-IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]//2.2e-83:494:88//Hs.108117:AI097079
R-PLACE1005966//ESTs//1.1e-95:465:97//Hs.98510:AI016239
R-PLACE1005968//EST//0.26:103:66//Hs.161300:AI420897
R-PLACE1005990
R-PLACE1006002//Human mRNA for KIAA0355 gene, complete cds//2.0e-45:481:74//Hs.153014:AB002353
R-PLACE1006003//ESTs, Highly similar to HYPOTHETICAL 30.3 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION [Saccharomyces cerevisiae]//3.1e-112:593:93//Hs.111449:AI192946
R-PLACE1006011//ESTs, Moderately similar to NAD(+) ADP-RIBOSYLTRANSFERASE [D.melanogaster]//5.7e-100:596:88//Hs.24284:AA595596
R-PLACE1006017//ESTs//4.2e-18:296:68//Hs.133350:AI056276
R-PLACE1006037//ESTs, Weakly similar to T23D8.3 [C.elegans]//4.1e-102:491:98//Hs.61164:AI096332
R-PLACE1006040//ESTs//1.2e-92:443:98//Hs.111680:N93765
R-PLACE1006076//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//2.0e-26:213:77//Hs.139007:H74314
R-PLACE1006119//ESTs//0.14:257:61//Hs.113149:AA908904
R-PLACE1006129//ESTs//3.8e-54:285:97//Hs.18827:W68002
R-PLACE1006139//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//2.6e-99:560:91//Hs.5249:U55977
R-PLACE1006143//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)//0.038:463:59//Hs.904:U84010
R-PLACE1006157//ESTs//0.014:341:58//Hs.121773:AI357886
R-PLACE1006159//EST//0.00036:247:61//Hs.140054:AA668925
R-PLACE1006164//ESTs//2.6e-31:362:73//Hs.141024:H07128
R-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//5.8e-54:286:94//Hs.152894:AC005239
R-nnnnnnnnnnnn//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicus]//2.7e-79:393:96//Hs.19121:AI125280
R-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//5.1e-118:597:95//Hs.30464:AF091433
R-PLACE1006195//ESTS, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.8e-94:532:91//Hs.105216:AI361807
R-PLACE1006196//ESTs//3.2e-66:382:90//Hs.18665:T99507
R-PLACE1005205//EST//1.7e-89:448:96//Hs.116665:AA669114
R-PLACE1006223//Human RNaseP protein p38 (RPP38) mRNA, complete cds//0.90:304:58//Hs.94986:U77664

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R-PLACE1006225//ESTs//7.2e-96:474:97//Hs.91165:AI079555
R-PLACE1006236//ESTs//8.8e-105:535:95//Hs.7919:AI341472
R-nnnnnnnnnnnn//Homo sapiens BAC clone RG118D07 from 7q31//3.2e-99:497:95//Hs.3781:AC004142
R-PLACE1006246//ESTs, Weakly similar to CMP-sialic acid transporter [M.musculus]//1.3e-104:532:95//Hs.41151:AI301961
R-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//3.0e-97:499:95//Hs.31921:AB014548
R-PLACE1006262//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//1.6e-07:321:62//Hs.53057:W67839
R-PLACE1006288//Voltage-dependent anion channel 1//3.8e-100:605:88//Hs.2060:L06132
R-PLACE1006318//ESTs//2.4e-102:536:94//Hs.8109:AA005265
R-PLACE1006325//ESTs//5.2e-105:518:96//Hs.102319:AI246503
R-PLACE1006335//ESTs//5.1e-45:254:93//Hs.153585:R70900
R-PLACE1006357//EST//6.5e-09:309:62//Hs.132493:AA923168
R-PLACE1006360//Human mRNA for KIAA0090 gene, partial cds//0.0097:381:58//Hs.154797:D42044
R-PLACE1006368//ESTs//7.9e-85:412:97//Hs.150587:AI079284
R-PLACE1006371//ESTs//7.7e-74:442:88//Hs.143671:W61053
R-PLACE1006382
R-PLACE1006385//ESTs//5.3e-06:346:61//Hs.163706:AA515748
R-PLACE1006412//EST//7.7e-46:306:86//Hs.149580:AI281881
R-PLACE1006414//Homo sapiens UM protein mRNA, complete cds//4.1e-43:551:69//Hs.154103:AF061258
R-PLACE1006438//ESTs//1.1e-77:284:86//Hs.24545:AI278629
R-PLACE1006445//ESTs//4.4e-53:259:99//Hs.24481:AA573139
R-PLACE1006469//ESTs//9.4e-102:482:98//Hs.7218:AA936961
R-PLACE1006470//ESTs//1.0:271:57//Hs.144517:AA938297
R-PLACE1006482//ESTs//4.0e-61:354:92//Hs.51305:T47418
R-PLACE1006492//EST//1.8e-09:48:91//Hs.144451:AA827722
R-PLACE1006506//ESTs//0.012:161:61//Hs.145333:AI251374
R-PLACE1006521//Human mRNA for KIAA0013 gene, complete cds//2.1e-15:415:63//Hs.48824:D87717
R-PLACE1006531//ESTs//5.6e-31:213:87//Hs.125153:AA453723
R-PLACE1006534//ESTs//6.5e-101:512:95//Hs.27763:W46368
R-PLACE1006540//ESTs//7.3e-40:320:79//Hs.121659:H02532
R-PLACE1006552//EST//0.38:418:56//Hs.140470:AA765214
R-PLACE1006598//ESTs//4.0e-80:409:95//Hs.142868:AI128443
R-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//9.3e-118:590:95//Hs.155377:U97670
R-PLACE1006617//ESTs//8.1e-31:246:83//Hs.139128:AA205322
R-PLACE1006626//ESTs//0.90:98:68//Hs.96322:AA541615
R-PLACE1006629//Human mRNA for KIAA0386 gene, complete cds//5.3e-33:315:78//Hs.101359:AB002384
R-PLACE1006640//ESTs//3.7e-26:137:100//Hs.32672:W16522
R-PLACE1006673//Interleukin 10//8.4e-47:330:83//Hs.2180:M57627
R-PLACE1006678//ESTs//1.1e-13:87:98//Hs.34035:D87736
R-PLACE1006704//ESTs//2.6e-65:394:89//Hs.30582:D12214
R-PLACE1006731//Homo sapiens clone 23923 mRNA sequence/1.9e-102:486:98//Hs.12472:AF038172
R-PLACE1006754//EST//1.0e-61:381:89//Hs.14727:T83861
R-PLACE1006760//Homo sapiens clone 24800 mRNA sequence//3.8e-73:394:93//Hs.7252:AF070622
R-PLACE1006779//ESTs//1.4e-69:405:90//Hs.136235:AA262658
R-PLACE1006782//EST//1.8e-25:197:86//Hs.137257:N33234
R-PLACE1006792//ESTs//1.8e-43:317:84//Hs.139190:N55515
R-PLACE1006795//ESTs//6.4e-68:350:95//Hs.11092:AA916335
R-PLACE1006800//ESTs//1.9e-55:268:100//Hs.126695:AA917989
R-PLACE1006805//ESTs//6.6e-91:484:93//Hs.94262:AA768847
R-PLACE1006815//ESTs//2.1e-49:364:83//Hs.142031:AA809159
R-PLACE1006819//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//1.0e-87:481:92//Hs.141263:H64113
R-PLACE1006829//ESTs//5.7e-43:332:83//Hs.19906:AA456933
R-PLACE1006860//ESTs//0.96:138:63//Hs.136649:AA-828359
R-PLACE1006867//ESTs//1.4e-98:478:97//Hs.10299:N35008
R-PLACE1006878//EST//8.4e-48:243:97//Hs.54970:N93536

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R-PLACE1006883//EST//3.1e-46:300:88//Hs.162404:AA573131
R-nnnnnnnnnnnn//ESTs//3.0e-95:496:94//Hs.47546:AA181348
R-PLACE1006904//ESTs//5.8e-18:304:68//Hs.125816:AA806089
R-PLACE1006917//Endothelin receptor type B//0.00012:451:60//Hs.82002:D13168
R-PLACE1006932//ESTs//4.6e-56:285:96//Hs.114727:AI379514
R-PLACE1006935//ESTs//3.6e-12:157:73//Hs.161714:AA229078
R-nnnnnnnnnnnn//Human mRNA for KIAA0201 gene, complete cds//3.2e-25:494:63//Hs.36927:D86956
R-PLACE1006961//Tyrosine aminotransferase//2.5e-46:471:74//Hs.2999:X52520
R-PLACE1006962//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//9.0e-29:324:68//Hs.154257:AI275982
R-PLACE1006966//ESTs//4.5e-99:470:99//Hs.46913:AI017636
R-PLACE1006989//ESTs//2.2e-68:353:97//Hs.14394:R61257
R-PLACE1007014//ESTs//3.4e-86:457:94//Hs.129819:AA838366
R-PLACE1007021//ESTs//1.6e-93:539:90//Hs.7111:U55971
R-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//6.6e-83:584:82//Hs.23094:M19503
R-PLACE1007053//ESTs//4.2e-85:550:88//Hs.7984:AI202575
R-PLACE1007097//ESTs//6.4e-78:493:86//Hs.56406:N91027
R-PLACE1007105//ESTs//5.3e-70:381:91//Hs.22605:N74202
R-PLACE1007111//ESTs//8.6e-75:358:99//Hs.145629:AA398646
R-PLACE1007112//ESTs//6.9e-69:371:94//Hs.71922:AA148417
R-PLACE1007132//ESTs//1.2e-36:373:69//Hs.10762:W28948
R-PLACE1007140//ESTs//1.7e-70:360:96//Hs.56179:W56794
R-PLACE1007178//EST//0.68:85:65//Hs.147010:AI184765
R-PLACE1007226//ESTs//3.1e-78:452:90//Hs.8033:N94998
R-PLACE1007238//ESTs//5.2e-70:362:95//Hs.85636:AA740619
R-PLACE1007239//Human mRNA for transcription elongation factor S-II, hS-II-T1, complete cds//6.3e-93:534:89//Hs.80598:D50495
R-PLACE1007242//ESTS//1.2e-80:390:98//Hs.117325:AA699450
R-PLACE1007243//ESTs, Weakly similar to transporter protein [H. sapiens]//3.7e-73:357:98//Hs.18272:N78499
R-PLACE1007257//Homo sapiens mRNA for dia-156 protein//4.3e-85:487:91//Hs.121556:Y15909
R-PLACE1007274//ESTs//4.3e-79:430:93//Hs.146023 AI275071
R-PLACE1007276//ESTs//1.5e-33:338:74//Hs.142850:R38419
R-PLACE1007282//ESTs//4.8e-98:532:93//Hs.10071:AA100812
R-PLACE1007286//Human mRNA for KIAA0118 gene, partial cds//2.9e-50:518:74//Hs.154326:D42087
R-PLACE1007301
R-PLACE1007317
R-PLACE1007342
R-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds//1.2e-66:367:91//Hs.76596:AF096870
R-PLACE1007367//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-98:488:96//Hs.24359:AA699594
R-PLACE1007375//ESTs//2.3e-67:375:92//Hs.33368:AA206614
R-PLACE1007386//ESTs//0.020:242:62//Hs.42768:AI129945
R-PLACE1007402//ESTs//1.6e-91:441:97//Hs.26243:AA455877
R-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence//2.4e-113:590:94//Hs.14387:AF093771
R-PLACE1007416//ESTs, Weakly similar to DIPEPTIDYL PEPTIDASE IV [H.sapiens]//3.8e-115:579:95//Hs.72165:AI243857
R-PLACE1007450//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.7e-38:311:80//Hs.97203:U83171
R-PLACE1007452//EST//2.5e-42:386:77//Hs.140562:AA826514
R-PLACE1007460//ESTs//4.9e-87:434:95//Hs.28472:AI028230
R-PLACE1007478
R-PLACE1007484//ESTs//6.8e-08:64:92//Hs.100251:AA535975
R-PLACE1007488//Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272//0.26:411:60//Hs.79012:M18533
R-PLACE1007507//ESTs//2.2e-11:136:76//Hs.128815:AA678072
R-PLACE1007511//ESTs, Highly similar to KERATIN, TYPE I CYTOSKELETAL 14 [Homo sapiens]//1.5e-41:261:89//Hs.9029:W57657

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R-PLACE1007524//ESTs//5.8e-45:297:87//Hs.154923:AA491377
R-PLACE1007525//Human mRNA for KIAA0118 gene, partial cds//1.9e-44:422:75//Hs.154326:D42087
R-PLACE1007544//ESTs//8.4e-59:327:93//Hs.27410:N25612
R-PLACE1007547//EST//0.00010:107:71//Hs.146867:AI161404
R-PLACE1007557//ESTs//1.6e-43:356:79//Hs.44702:AI148840
R-PLACE1007583//ESTs//1.7e-41:214:97//Hs.155071:AA584257
R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence//4.8e-104:554:93//Hs.21838:AF038179
R-PLACE1007618//Lymphocyte cytosolic protein 1 (L-plastin)//0.54:161:65//Hs.76506:J02923
R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence//4.8e-105:537:94//Hs.151046:AF038176
R-PLACE1007632
R-PLACE1007645//ESTs//0.99:187:62//Hs.163453:AI344106
R-PLACE1007649//ESTs//2.2e-108:561:94//Hs.24398:AI262946
R-PLACE1007677//ESTs, Moderately similar to !!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!! [H.sapiens]// 9.0e-37:190:97//Hs.23437:AA707331
R-PLACE1007688//ESTs//7.5e-79:409:95//Hs.6166:AI376944
R-PLACE1007690//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Ascaris suum] //3.4e-61:384;89//Hs.92918:AA133274
R-PLACE1007697//ESTs, Highly similar to GCN20 PROTEIN [Saccharomyces cerevisiae]//1.8e-84:501:88//Hs. 91251:U66685
R-PLACE1007705//Human mRNA for apolipoprotein E receptor 2, complete cds//0.43:307:59//Hs.54481:D86407
R-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//5.7e-75:374:96//Hs.4812: AF061243
R-PLACE1007725//ESTs, Weakly similar to No definition line found [C.elegans]//3.1e-39:253:88//Hs.108797: AA476815
R-PLACE1007729//ESTs//2.7e-44:392:79//Hs.142375:AA398619
R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//6.7e-94:556:89//Hs.153121: AB014585
R-PLACE1007737//ESTs//1.1e-41:345:80//Hs.114671:N39322
R-PLACE1007743//ESTs//2.8e-17:98:100//Hs.124258:AA976778
R-PLACE1007746//ESTs//5.3e-69:413:90//Hs.5297:AA156903
R-PLACE1007791//ESTS, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]// 8.6e-27:143:98//Hs.144194:AA706337
R-PLACE1007807//Human Line-1 repeat mRNA with 2 open reading frames//9.9e-45:428:76//Hs.23094:M 9503
R-PLACE1007810//ESTs//5.9e-15:143:82//Hs.126257:AI279044
R-PLACE1007829//ESTs//2.2e-22:190:84//Hs.142707:W24050
R-PLACE1007843//ESTs//5.3e-110:556:95//Hs.107287:AI308839
R-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-95:525:91//Hs.23094:M19503
R-PLACE1007852//ESTs//4.5e-14:174:75//Hs.153419:N52017
R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//2.1e-111:574:94//Hs.28020: AB018309
R-PLACE1007866//EST//1.8e-48:262:96//Hs.141009:H01178
R-PLACE1007877//ESTs//1.2e-94:478:96//Hs.5999:AI207832
R-PLACE1007897//ESTs//2.3e-92:437:99//Hs.122843:AI189060
R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.8e-89:460:95//Hs. 92381:AB007956
R-PLACE1007946//ESTs//2.8e-28:172:78//Hs.126784:AA521510
R-PLACE1007954//ESTs//6.1e-72:366:95//Hs.27842:AI217966
R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//3.9e-103:509:96//Hs. 5671:AF084530
R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//7.2e-89: 465:93//Hs.78106:AF079529
R-PLACE1007969//ESTs, Weakly similar to F35C12.2 [C.elegans]//1.4e-113:534:99//Hs.44268:AA455900
R-PLACE1007990//ESTs, Highly similar to DOSAGE COMPENSATION REGULATOR [Drosophila melanogaster) //3.8e-97:493:95//Hs.6141:U69564
R-PLACE1008000//ESTs//0.00013:241:65//Hs.44369:AI206835
R-PLACE1008002//ESTs//2.2e-83:397:98//Hs.28780:AI263612
R-PLACE1008044//ESTs, Moderately similar to NUCLEAR PORE COMPLEX PROTEIN NUP107 [R.norvegicus] //2.0e-115:575:95//Hs.92395:AA779854

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R-PLACE1008045//EST//2.6e-89:465:94//Hs.47374:N51935
R-PLACE1008080//EST//0.27:118:65//Hs.144110:AI054269
R-PLACE1008095//ESTs//5.5e-23:268:73//Hs.152525:AA516469
R-PLACE1008111//ESTs, Weakly similar to oxidoreductase [H.sapiens]//4.4e-108:537:96//Hs.28877:AI309334
R-PLACE1008122//ESTs//6.5e-103:531:94//Hs.34737:AI028617
R-PLACE1008129//ESTs//0.76:96:66//Hs.65373:AA883511
R-PLACE1008132//ESTs//5.9e-05:113:72//Hs.13014:W26381
R-PLACE1008177//ESTs//7.2e-107:557:93//Hs.132851:AI028266
R-PLACE1008181//ESTs//5.3e-97:473:97//Hs.57483:AA776267
R-PLACE1008198//ESTs//3.9e-16:120:85//Hs.9142:AA662107
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds//1.6e-104:551:93//Hs.10801:AB011102
R-PLACE1008209//ESTs//L2e-72:366:96//Hs.92308:AI052701
R-PLACE1008231//ESTs//1.2e-70:363:94//Hs.25094:R80871
R-PLACE1008244//ESTs//1.3e-98:543:92//Hs.25130:AA218990
R-PLACE1008273//ESTs//6.1e-16:153:79//Hs.115987:AA483808
R-nnnnnnnnnnnn
R-PLACE1008280//ESTs//1.3e-66:353:94//Hs.156376:AI338705
R-PLACE1008309//ESTs//2.8e-100:511:95//Hs.45080:N49852
R-PLACE1008329//V-myc avian myelocytomatosis viral oncogene homolog//0.53:206:62//Hs.79070:K02276
R-PLACE1008330//ESTs, Weakly similar to EOSINOPHIL LYSOPHOSPHOLIPASE [H.sapiens]//8.6e-79:297:91//Hs.146477:AI128445
R-PLACE1008331//ESTs//0.98:156:62//Hs.108548:AA081656
R-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.1e-99:556:90//Hs.5734:AB014579
R-PLACE1008368//EST//0.0027:198:63//Hs.160868:AI359052
R-PLACE1008369//ESTs//5.4e-28:167:92//Hs.19530:AA480009
R-PLACE1008392//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//2.0e-41:448:72//Hs.139007:H74314
R-PLACE1008398//ESTs, Highly similar to Mig-6//1.4e-103:529:94//Hs.11169:AA156242
R-PLACE1008401//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-81:536:87//Hs.7570:W31010
R-nnnnnnnnnnnnn//Homo sapiens mRNA for p115, complete cds//5.1e-103:521:95//Hs.7763:D86326
R-PLACE1008405//ESTs//1.2e-89:485:92//Hs.138241:AA767440
R-PLACE1008424//ESTs//6.7e-97:508:93//Hs.6709:AI379778
R-PLACE1008426//ESTs//5.5e-30:174:92//Hs.7946:AA651757
R-PLACE1008429//ESTs//2.1e-12:188:71//Hs.140769:AA931562
R-PLACE1008437//ESTs//7.1e-54:266:98//Hs.13068:AA001928
R-PLACE1008455//ESTs//4.7e-69:471:85//Hs.28337:AA210761
R-PLACE1008457//EST//8.6e-14:202:71//Hs.149887:AI289387
R-PLACE1008465//ESTs//3.8e-80:426:93//Hs.153146:AI299636
R-PLACE1008488//ESTs//7.9e-73:388:94//Hs.97268:AA292180
R-PLACE1008524//ESTs//7.4e-107:545:95//Hs.10441:N62816
R-PLACE1008531//ESTs//3.8e-68:427:87//Hs.56607:H23560
R-PLACE1008532
R-PLACE1008533//ESTs//2.5e-52:318:88//Hs.7274:AA476850
R-PLACE1008568//ESTs//3.2e-99:486:97//Hs.84414:AI423223
R-PLACE1008584//EST//2.2e-18:154:68//Hs.141498:N50064
R-PLACE1008621//ESTS, Weakly similar to line-1 protein ORF1 [H.sapiens]//8.6e-67:483:82//Hs.140416:AA778649
R-nnnnnnnnnnnn
R-PLACE1008626//ESTs//4.7e-73:372:95//Hs.23491:AA642454
R-PLACE1008627//ESTS//1.6e-90:475:93//Hs.102401:AI004972
R-PLACE1008629//ESTs//8.0e-93:492:93//Hs.20843:AA699512
R-PLACE1008630//ESTs//1.0e-94:453:98//Hs.34840:AI279612
R-PLACE1008643//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:422:79//Hs.153014:AB002353
R-PLACE10086507/Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//7.9e-90:434:97//Hs.147967:AF044333
R-PLACE1008693//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.8e-41:505:71//Hs.51048:X68830
R-PLACE1008696//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.7e-51:316:

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76//Hs.1361:M55053
R-PLACE1008715//EST//0.63:114:64//Hs.121353:AA758600
R-PLACE1008748//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//2.3e-40:281:83//Hs.142209:AA873303
R-PLACE1008757//ESTs//1.4e-45:226:99//Hs.22822:H06408
R-PLACE1008790//ESTs//0.035:67:76//Hs.153554:AI286313
R-PLACE1008798//ESTs//4.9e-59:285:99//Hs.49018:N79930
R-PLACE1008807//ESTs//1.7e-82:413:96//Hs.130745:AA573217
R-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 mRNA, complete cds//1.1e-98:499:95//Hs.7179:AF011905
R-PLACE1008813//ESTs, Weakly similar to coded for by C. elegans cDNA cm10e3 [C.elegans]//4.2e-92:490:93//Hs.110454:H11810
R-PLACE1008851//ESTs//2.4e-84:421:95//Hs.158893:AI378428
R-nnnnnnnnnnnn
R-PLACE1008867//ESTs//1.1e-77:400:95//Hs.44198:AI093502
R-PLACE1008887//Oxytocin receptor//1.1e-43:601:67//Hs.2820:X64878
R-PLACE1008902//ESTs//0.023:208:61//Hs.154164:AI246893
R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.6e-56:344:89//Hs.62318:AB018308
R-PLACE1008925//ESTs//0.17:294:57//Hs.105113:AA457018
R-PLACE1008934//ESTs//2.0e-61:339:92//Hs.100448:AA622653
R-PLACE1008941//ESTs, Moderately similar to ATP-BINDING CASSETTE TRANSPORTER 2 [Mus musculus]//1.3e-19:488:63//Hs.15780:U66680
R-PLACE1008947//ESTs//1.3e-81:385:99//Hs.71574:AI376573
R-PLACE1009020//ESTs//2.9e-79:419:94//Hs.121816:AA775419
R-PLACE1009027//Homo sapiens mRNA for doublecortin//3.1e-82:434:94//Hs.34780:AJ003112
R-PLACE1009039//ESTs//2.8e-83:448:92//Hs.129179:AA988520
R-PLACE1009045//ESTs//1.6e-64:318:97//Hs.103423:AA814195
R-PLACE1009048//ESTs//2.7e-17:403:63//Hs.149343:AI249139
R-PLACE1009050//ESTs//2.0e-88:475:92//Hs.122925:AA909008
R-PLACE1009060//ESTs, Highly similar to HYPOTHETICAL 98.3 KD PROTEIN R10E12.1 IN CHROMOSOME III [Caenorhabditis elegans]//1.2e-112:555:96//Hs.9663:AA527142
R-PLACE1009090//ESTs//5.0e-13:175:75//Hs.140608:N53448
R-PLACE1009094//Human splicing factor SRp30c mRNA, complete cds//0.98:161:63//Hs.77608:AL021546
R-PLACE1009099//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//0.037:63:84//Hs.39943:AA203136
R-PLACE1009110//EST//5.8e-17:307:65//Hs.117264:AA682549
R-PLACE1009111//ESTs//1.9e-57:349:90//Hs.11260:N98983
R-PLACE1009130//ESTs, Weakly similar to hypothetical protein 2 [H.sapiens]//6.5e-97:501:94//Hs.11123:AA703945
R-PLACE1009150//LAMIN B1//0.064:393:60//Hs.89497:L37747
R-PLACE1009155/TESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//2.5e-36:163:82//Hs.93332:AA811920
R-PLACE1009158//ESTs//0.30:149:65//Hs.155796:R80005
R-PLACE1009166//ESTs//3.3e-34:292:77//Hs.140255:AA708322
R-PLACE1009172//EST//8.9e-21:364:67//Hs.142557:AA464948
R-PLACE1009174//ESTs//2.9e-18:274:70//Hs.139241:AA283707
R-PLACE1009183//ESTs//2.3e-44:297:87//Hs.136839:H93717
R-PLACE10091867/ESTs, Weakly similar to No definition line found [C.elegans]//1.5e-109:572:94//Hs.54943:Z78396
R-PLACE1009190//ESTs//2.6e-53:318:90//Hs.25245:AA176701
R-PLACE1009200//H.sapiens mRNA for sortilin//3.2e-33:195:92//Hs.104247:X98248
R-PLACE1009230//ESTs//3.0e-31:153:92//Hs.124116:AA772680
R-PLACE1009246//ESTs//2.7e-90:488:92//Hs.10706:AA909018
R-PLACE1009308//ESTs//0.022:46:97//Hs.36545:AA075423
R-PLACE1009319//ESTs//7.7e-99:533:92//Hs.109654:N91279
R-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//7.3e-82:578:82//Hs.23094:M19503
R-PLACE1009335//EST//1.3e-64:311:99//Hs.130558:AI004397
R-PLACE1009338//ESTs//6.0e-70:386:93//Hs.3542:AI015782
R-PLACE1009368//ESTs//1.4e-18:107:98//Hs.133303:W04760

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R-PLACE1009375//ESTs//8.9e-36:313:76//Hs.24608:AA161260
R-PLACE1009388//EST//4.4e-11:101:83//Hs.147074:AI188883
R-PLACE1009398//ESTs//5.7e-63:335:93//Hs.149003:AI243186
R-nnnnnnnnnnnnn//ESTs//3.6e-94:452:98//Hs.103177:W72798
R-PLACE1009410//ESTs//2.2e-112:553:96//Hs.61779:AA195255
R-PLACE1009434//EST//3.4e-15:109:74//Hs.103742:U48632
R-PLACE1009443//EST//7.5e-61:302:98//Hs.157787:AI361269
R-PLACE1099444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//6.6e-85:479:90//Hs.76987:AF012872
R-PLACE1009459//ESTs//9.3e-86:437:95//Hs.104871:AI161427
R-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1//1.3e-42:266:89//Hs.155049:AC004531
R-PLACE1009477//ESTs//2.0e-50:367:82//Hs.152788:AA630925
R-PLACE1009493//ESTs//4.5e-14:150:78//Hs.143918:AA699596
R-PLACE1009524//ESTs//2.9e-97:454:99//Hs.7189:AA767698
R-PLACE1009539//ESTs//9.1e-94:454:97//Hs.154706:AI262131
R-PLACE1009542//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.4e-10:289:63//Hs.77579:AF013263
R-PLACE1009571//ESTs//2.1e-23:125:100//Hs.41767:AA732326
R-PLACE1009581//ESTS, Weakly similar to FIBRINOGEN ALPHA AND ALPHA-E CHAIN PRECURSORS [H.sapiens]//0.0012:56:91//Hs.12151:AA001818
R-PLACE1009595//Homo sapiens mRNA for KIAA0635 protein, complete cds//6.0e-42:547:70//Hs.69157:AB014535
R-PLACE1009596//ESTs//1.9e-102:588:90//Hs.142395:AI374735
R-PLACE1009607//ESTs//0.0093:107:70//Hs.70932:AA126482
R-PLACE1009613//ESTs//7.5e-101:488:97//Hs.5905:AA946680
R-PLACE1009621//EST//0.99:261:60//Hs.149030:AI243338
R-PLACE1009622//ESTs//8.0e-93:508:92//Hs.20967:AI422858
R-PLACE1009637//EST//8.7e-90:442:97//Hs.121372:AA758701
R-PLACE1009639//EST//8.5e-49:279:93//Hs.117447:R27213
R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.3e-109:589:92//Hs.21862:AB011159
R-PLACE1009665//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//9.9e-62:483:79//Hs.140416:AA778649
R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//6.6e-63:310:97//Hs.109590:AF062534
R-PLACE1009708//ESTs//3.Oe-94:471:96//Hs.40091:N48582
R-PLACE1009721//ESTs, Weakly similar to MSF1 PROTEIN [S.cerevisiae]//4.2e-98:529:92//Hs.3945:AA004210
R-PLACE1009731/TESTs, Weakly similar to immune associated protein 38 [M.musculus]//6.8e-85:489:89//Hs.26194:AA033989
R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//2.0e-117:598:95//Hs.154320:AF046024
R-PLACE1009794//ESTs//7.9e-102:529:95//Hs.42927:N20989
R-nnnnnnnnnnnn//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs//1.1e-113:549:97//Hs.16411:AL030996
R-PLACE1009845//ESTs//9.5e-106:560:93//Hs.117751:AI056868
R-PLACE1009879//ESTs//1.8e-61:399:86//Hs.141012:R68748
R-PLACE1009886//EST//0.54:153:64//Hs.144281:AA081328
R-PLACE1009888//ESTs//2.7e-105:520:97//Hs.108646:AA613031
R-nnnnnnnnnnnn//ESTs, Weakly similar to similar to mouse MMR1 [C.elegans]//1.6e-114:594:94//Hs.67466:AI219740
R-PLACE1009921//ESTs//7.6e-05:291:60//Hs.124786:AA825563
R-PLACE1009924//EST//1.2e-42:216:98//Hs.31742:H20276
R-PLACE1009925//ESTs//5.4e-30:154:100//Hs.114605:AI04317
R-PLACE1009935//ESTs//1.4e-83:417:97//Hs.131755:AA496543
R-PLACE1009947//Keratin 9//1.0:273:61//Hs.2783:Z29074
R-PLACE1009971//ESTs//1.5e-87:424:98//Hs.13781:AI160540
R-PLACE1009992//ESTs//1.3e-87:531:87//Hs.55044:AA460698

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R-PLACE1009995//ESTs//1.3e-103:575:91//Hs.71218:C75347
R-PLACE1009997//Small inducible cytokine A5 (RANTES)//1.1e-42:286:86//Hs.155464:AF088219
R-PLACE1010023//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//1.7e-17:137:86//Hs.7049:AI141736
R-PLACE1010031//ESTs//0.22:191:62//Hs.127787:AA832204
R-PLACE1010053//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spur [M.musculus]//7.6e-104:546:94//Hs.8215:AA521150
R-PLACE1010069//ESTs//0.99:173:59//Hs.21415:AI150905
R-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.5e-88:543:88//Hs.11183AF065482
R-PLACE1010076//ESTs//3.4e-106:530:95//Hs.28005:AA604375
R-PLACE1010083//ESTs//4.1e-65:395:88//Hs.6103:AA496424
R-PLACE1010089//ESTs//1.6e-70:348:97//Hs.9011:AA418615
R-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.norvegicus]//2.8e-104:565:92//Hs.11469:U69567
R-PLACE1010102//ESTs//7.7e-50:311:89//Hs.5518:AI052015
R-PLACE1010105//ESTs//6.0e-94:483:94//Hs.62684:AA806103
R-PLACE1010106//ESTs, Weakly similar to putative p150 [H.sapiens]//1.6e-107:575:93//Hs.48301:AA122270
R-PLACE1010134//EST//8.5e-59:314:94//Hs.135005:AI095130
R-PLACE1010148//A-KINASE ANCHOR PROTEIN 79//0.52:351:56//Hs.48714:M90359
R-PLACE1010152//ESTS//1.9e-40:240:90//Hs.17054:AI139897
R-PLACE1010181//ESTs//3.6e-64:307:99//Hs.154163:AJ003313
R-PLACE1010194//ESTs//2.7e-70:366:96//Hs.5301:T58466
R-PLACE1010202//ESTs//0.57:120:67//Hs.58873:W95037
R-PLACE1010231
R-PLACE1010261//EST//6.9e-50:251:98//Hs.148208:AA897478
R-PLACE1010270//ESTs//1.9e-87:430:96//Hs.25252:AI079545
R-PLACE1010274//ESTs//1.9e-57:439:81//Hs.30078:H04535
R-PLACE1010293//ESTs//8.1e-41:310:81//Hs.146811:AA410788
R-PLACE1010321//ESTs//5.7e-50:246:99//Hs.151445:AA351081
R-PLACE1010324//ESTs//0.00025:377:60//Hs.97430:AA398568
R-PLACE1010329//Small inducible cytokine A5 (RANTES)//2.4e-40:300:82//Hs.155464:AF088219
R-PLACE1010341//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//9.9e-32:190:77//Hs.152369:AA504818
R-PLACE1010362//ESTs//8.2e-86:404:99//Hs.25625:AA669327
R-PLACE1010364//ESTs//1.5e-105:556:93//Hs.12229:AA149594
R-PLACE1010383//Homo sapiens mRNA for putative lipoic acid synthetase, partial//4.9e-35:166:86//Hs.53531:AJ224162
R-PLACE1010401//ESTs//2.3e-85:450:93//Hs.23193:AA418152
R-PLACE1010481//ESTs//0.012:280:59//Hs.5579:AI392816
R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds//2.4e-89:438:96//Hs.13313:AF039081
R-PLACE1010492
R-PLACE1010522//EST//0.43:82:68//Hs.89303:AA284031
R-nnnnnnnnnnnn//ESTs//3.4e-36:228:89//Hs.128724:AA215455
R-PLACE1010562//ESTs//4.8e-68:408:90//Hs.17244:W86306
R-PLACE1010579//EST//0.015:193:63//Hs.67093:C14033
R-PLACE1010580//ESTs//2.4e-93:445:98//Hs.127325:AA234116
R-PLACE1010599
R-PLACE1010616//ESTs//2.9e-101:497:97//Hs.142197:AA573418
R-PLACE1010622//ESTs//7.1e-23:157:91//Hs.159877:N57895
R-PLACE1010624//ESTs//1.4e-89:428:98//Hs.116561:AA658475
R-PLACE1010628//ESTS, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.4e-74:391:95//Hs.163495:W57637
R-PLACE1010629//ESTs//5.8e-75:359:99//Hs.123630:AI250805
R-PLACE1010630//ESTs//9.5e-101:519:94//Hs.77873:AA731719
R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//8.3e-94:497:93//Hs.10801:AB011102
R-PLACE1010661//ESTs, Highly similar to TESTIS-SPECIFIC PROTEIN PBS13 [Mus musculus]//4.8e-83:467:

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91//Hs.22383:R51067
R-PLACE1010662//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]//8.3e-103:538:94//Hs.105794:AA701659
R-PLACE1010702//Homo sapiens DNA from chromosome 19, BAC 33152//4.8e-46:531:71//Hs.55452:AC003973
R-PLACE1010714//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.0074:351:60//Hs.46440:U21943
R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//1.2e-56:300:95//Hs.50758:AF092564
R-PLACE1010739//Homo sapiens mRNA for oligophrenin 1//2.6e-84:501:88//Hs.158122:AJ001189
R-PLACE1010743
R-PLACE1010761//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//5.2e-94:442:96//Hs.3688:AF069250
R-PLACE1010771//ESTs//3.8e-54:264:99//Hs.27299:AI074024
R-PLACE1010786//ESTs, Highly similar to MYOSIN HEAVY CHAIN IB [Acanthamoeba castellanii]//7.6e-111:575:94//Hs.10260:AI126627
R-PLACE1010800//ESTs//1.9e-109:557:95//Hs.11460:AA057558
R-PLACE1010802//ESTs//0.00021:428:5 8//Hs.70258:AI091203
R-PLACE1010811//ESTs//7.4e-73:394:93//Hs.48499:AA428896
R-PLACE1010833//ESTs//9.0e-33:274:78//Hs.24391:W27472
R-PLACE1010856//ESTs//5.8e-41:351:81//Hs.17401:W81048
R-PLACE1010857//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//1.4e-71:326:92//Hs.3385:N25917
R-PLACE1010870//ESTs//5.8e-57:303:96//1Hs.30503:H05090
R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//2.3e-101:501:96//Hs.118087:AB011182
R-PLACE1010891
R-PLACE1010896//EST//0.0039:249:57//Hs.126090:AA867983
R-PLACE1010900//Human Xq28 mRNA, complete cds//3.3e-07:106:76//Hs.20136:U46023
R-PLACE1010916//Plasminogen activator inhibitor, type II (arginine-serpin)//0.25:190:61//Hs.75716:Y00630
R-PLACE1010917//ESTs//1.3e-82:452:92//Hs.68055:AA081093
R-PLACE1010925//ESTs//1.1e-92:471:95//Hs.17448:AI125479
R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//1.3e-66:402:89//Hs.74750:AB011126
R-nnnnnnnnnnnn//Homo sapiens intersectin short form mRNA, complete cds//8.9e-82:441:93//Hs.66392:AF064244
R-PLACE1010944
R-PLACE1010947//ESTs//6.7e-15:102:91//Hs.116808:AA211519
R-PLACE1010954//Small inducible cytokine A5 (RANTES)//8.8e-51:278:93//Hs.155464:AF088219
R-PLACE1010960//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]//1.0e-103:565:92//Hs.23259:AA532437
R-PLACE1010965//EST//6.3e-80:447:91//Hs.139529:AA219580
R-PLACE1011026//ESTs//4.6e-99:463:99//Hs.149732:AI199846
R-PLACE1011032//ESTs//6.3e-56:295:94//Hs.143576:AI147867
R-PLACE1011041//ESTs//5.3e-27:168:91//Hs.7936:AA923249
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0581 protein, partial cds//9.4e-102:563:91//Hs.41143:AB011153
R-PLACE1011054//EST//1.1e-15:245:69//Hs.112648:AA609135
R-PLACE1011056//Small inducible cytokine A5 (RANTES)//3.5e-38:285:82//Hs.155464:AF088219
R-PLACE1011057//ESTs//3.5e-81:410:96//Hs.96499:AA252537
R-PLACE1011090//ESTS. Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.6e-54:398:84//Hs.108740:W20094
R-PLACE1011109//EST//1.3e-48:321:85//Hs.146794:AI149478
R-PLACE101111 4//ESTs//5.4e-90:475:94//Hs.69331:AA099587
R-PLACE1011133//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]//3.0e-105:552:93//Hs.31257:AA875998
R-PLACE1011143//ESTs//0.40:127:65//Hs.118701:AA420795
R-PLACE1011160//Homa sapiens mRNA for HRIHFB2038, partial cds//7.7e-97:534:91//Hs.28719:AB015333
R-PLACE1011165//ESTs//1.0:135:69//Hs.32163:AI374673
R-PLACE1011185//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//3.4e-85:442:95//Hs.136910:AA810782
R-PLACE1011203//EST//0.0047:268:60//Hs.68832:AA088438

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R-PLACE1011219//ESTs//7.6e-96:504:93//Hs.124834:AI138671
R-PLACE1011221//ESTs//5.2e-23:241:78//Hs.26761:AA203299
R-PLACE1011229//ESTs//1.9e-90:461:95//Hs.132288:AI027693
R-PLACE1011263//ESTs//6.6e-56:321:93//Hs.158787:W79602
R-PLACE1011273//ESTs//0.016:131:65//Hs.140466:AA766772
R-PLACE1011291//EST//8.7e-47:267:91//Hs.158806:AI376913
R-PLACE1011296//EST//2.7e-38:225:92//Hs.160934:AI376849
R-PLACE1011310//ESTs//9.1e-37:196:96//Hs.39328:H71807
R-PLACE1011325//Human clone 23721 mRNA sequence//0.0012:486:58//Hs.83572:U79291
R-PLACE1011332//ESTs//8.4e-44:217:99//Hs.101365:R60578
R-PLACE1011340//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//3.4e-92:452:97//Hs.144194:AA706337
R-PLACE1011375//ESTs//2.2e-35:195:96//Hs.106486:H11376
R-PLACE1011399//ESTs//0.00096:224:67//Hs.151643:AA001194
R-PLACE1011419//ESTs//4.9e-50:267:95//Hs.7045:AA167337
R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds//4.8e-114:600:94//Hs.10801:AB011102
R-PLACE1011452//Homo sapiens mRNA for KIAA0707 protein, partial cds//3.7e-32:310:76//Hs.138488:AB014607
R-PLACE1011465//ESTs//4.5e-86:471:93//Hs.144519:R70887
R-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds//2.6e-104:515:96//Hs.111138:AB018255
R-PLACE1011492//ESTs//1.7e-96:488:95//Hs.116555:AA639278
R-PLACE1011503//Homo sapiens clone 23597 mRNA sequence//1.0:193:60//Hs.28197:AF035294
R-PLACE1011520//ESTs//6.8e-99:477:97//Hs.85077:AA968576
R-PLACE1011563//ESTs//1.4e-94:514:92//Hs.16471:AA206421
R-PLACE1011567//EST//2.8e-89:417:100//Hs.149770:AI285985
R-PLACE1011576//Zinc finger protein 91 (HPF7, HTF10)//4.7e-55:267:81//Hs.8597:L11672
R-PLACE1011586//Myosin, heavy polypeptide 11, smooth muscle//0.98:168:61//Hs.78344:AF001548
R-PLACE1011635//ESTs//2.5e-67:332:98//Hs.108194:AA780067
R-PLACE1011641//ESTs//2.5e-71:J38:100//Hs.153085:AA993965
R-PLACE1011643//EST//1.9e-18:181:78//Hs.160879:AI361900
R-PLACE1011649//Homo sapiens clone 24432 mRNA sequence//2.5e-73:414:91//Hs.78019:AF070535
R-PLACE1011650//EST//5.8e-18:118:92//Hs.124486:AA846036
R-PLACE1011664//Restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)//0.50:178:62//Hs.31638:X64838
R-PLACE1011675
R-PLACE1011682//ESTs//2.4e-90:465:94//Hs.57830:AI312025
R-PLACE1011719//Human Line-1 repeat mRNA with 2 open reading frames//8.5e-57:410:83//Hs.23094:M19503
R-PLACE1011725//ESTs//2.0e-70:340:98//Hs.161725:AA251392
R-PLACE1011729//ESTs//7.5e-19:180:79//Hs.119516:AA443426
R-PLACE1011749//Myelin oligodendrocyte glycoprotein {alternative products}//7.3e-40:361:77//Hs.53217:Z48051
R-PLACE1011762//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//3.0e-60:319:76//Hs.103948:K00627
R-PLACE1011778//ESTs//8.0e-70:372:94//Hs.46765:AA521080
R-PLACE1011783//Calcium modulating ligand//8.4e-41:279:85//Hs.13572:AF068179
R-PLACE1011858//ESTs//2.6e-69:396:91//Hs.55220:D11563
R-PLACE1011874//Human mRNA for KIAA0033 gene, partial cds//1.2e-53:439:80//Hs.22271:D26067
R-PLACE1011875//ESTs//9.0e-88:420:98//Hs.70897:AA987648
R-PLACE1011891//ESTs//3.9e-17:97:100//Hs.84698:AA725913
R-PLACE1011896//ESTs//2.8e-23:176:84//Hs.121540:AI275497
R-PLACE1011922//ESTs//6.6e-35:415:73//Hs.10972:AA164268
R-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//2.3e-99:546:92//Hs.3838:AF059617
R-PLACE1011962//ESTs//3.3e-49:294:90//Hs.106800:AI031969
R-PLACE1011964//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//2.6e-06:284:63//Hs.124102:AA701285
R-PLACE1011982//ESTs//2.9e-51:291:93//Hs.20792:R14890

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R-PLACE1011995//ESTs//4.5e-39:304:81//Hs.138852:AA284247
R-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//8.0e-106:540:95//Hs.88756:AB018256
R-PLACE2000003//ESTs//2.0e-103:488:98//Hs.8341:AA490069
R-PLACE2000007//ESTs//2.4e-110:564:95//Hs.65135:W89120
R-PLACE2000011//Homo sapiens clone 614 unknown mRNA, complete sequence//4.8e-105:524:95//Hs.21811:AF091080
R-PLACE2000015//ESTs//7.1e-111:543:96//Hs.32178:AA083211
R-PLACE2000017//EST//8.2e-46:404:79//Hs.133006:AI049504
R-PLACE2000021//EST//4.5e-19:221:71//Hs.150830:AI302868
R-PLACE2000033//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.6e-43:355:79//Hs.154069:U06452
R-PLACE2000034//ESTs//2.2e-21:314:70//Hs.107697:W29013
R-PLACE2000039//H.sapiens mRNA for translin associated protein X//2.9e-45:514:72//Hs.96247:X95073
R-PLACE2000047//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//4.1e-45:358:81//Hs.159523:AF001622
R-PLACE2000050//ESTs//4.5e-65:322:98//Hs.155820:N67652
R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.2e-41:429:72//Hs.153468:AB011147
R-PLACE2000062//Human mRNA for KIAA0392 gene, partial cds//2.0e-43:296:86//Hs.40100:AB002390
R-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//6.2e-111:550:95//Hs.9443:AF027219
R-PLACE2000097//Calcium modulating ligand//6.2e-47:372:80//Hs.13572:AF068179
R-PLACE2000100//ESTs//8.8e-42:281:86//Hs.150727:AI292236
R-PLACE2000103//ESTs//4.7e-97:518:93//Hs.118727:W26941
R-PLACE2000111//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//0.00043:127:71//Hs.42400:AF022789
R-PLACE2000115//ESTs//7.8e-93:458:96//Hs.104520:AA481662
R-PLACE2000132//ESTs//3.8e-69:409:91//Hs.98502:AA433988
R-PLACE2000136//ESTs//6.2e-05:274:61//Hs.114067:AA701558
R-PLACE2000140//Homo sapiens mRNA for KIAA0562 protein, complete cds//4.7e-44:302:85//Hs.118401:AB011134
R-PLACE2000164//ESTs//6.3e-106:506:98//Hs.16390:AI052357
R-PLACE2000170//Small inducible cytokine A5 (RANTES)//3.7e-42:326:79//Hs.155464:AF088219
R-PLACE2000172//ESTs//9.6e-43:232:94//Hs.6709:AI379778
R-PLACE2000176//EST//1.6e-24:154:91//Hs.157734:AI360292
R-PLACE2000187//Human mRNA for KIAA0033 gene, partial cds//2.0e-49:292:90//Hs.22271:D26067
R-PLACE2000216//ESTS//0.0041:166:64//Hs.159476:AI382378
R-PLACE2000223//ESTs//0.49:171:60//Hs.86154:AA207191
R-PLACE2000235//ESTs//2.9e-39:264:85//Hs.136839:H93717
R-PLACE2000246//NAD(P)H:menadione oxidoreductase//4.0e-44:331:82//Hs.80706:M81600
R-PLACE2000264//Human mRNA for KIAA0365 gene, partial cds/4.0e-38:311:81//Hs.84123:AB002363
R-PLACE2000274//ESTs, Weakly similar to dynein-related protein [H.sapiens]//1.9e-87:422:98//Hs.9740:AI004779
R-PLACE2000302//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [Homo sapiens]//4.8e-68:380:92//Hs.107365:AA720664
R-PLACE2000305//ESTs//2.6e-43:413:75//Hs.118732:AI344055
R-PLACE2000317//ESTs//2.8e-92:501:92//Hs.28432:R83380
R-PLACE2000335//ESTs//4.3e-32:300:77//Hs.163035:AA748058
R-PLACE2000342//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//0.00071:117:73//Hs.42400:AF022789
R-PLACE2000347//ESTs//1.6e-30:214:86//Hs.135272:AI347618
R-PLACE2000359//Zinc finger protein 139 (clone pHZ-37)//5.5e-42:288:86//Hs.140090:U09848
R-PLACE2000366//Thromboxane A2 receptor//6.7e-53:392:82//Hs.89887:D38081
R-PLACE2000371//ESTs//3.6e-81:409:97//Hs.155138:AA158731
R-PLACE2000373//Homo sapiens mRNA for KIAA0734 protein, partial cds//0.89:186:62//Hs.101516:AB018277
R-PLACE2000379//ESTs//3.4e-10:228:64//Hs.57842:W63781
R-PLACE2000394//ESTs//6.7e-41:462:74//Hs.107657:AA126814

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R-PLACE2000398//ESTs//4.2e-33:373:74//Hs.155184:AA573189
R-PLACE2000399
R-PLACE2000404//ESTs, Highly similar to LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC [Saccharomyces cerevisiae]//4.2e-109:540:96//Hs.6762:AA088424
R-PLACE2000411//ESTs//1.6e-89:459:95//Hs.117589:N25941
R-PLACE2000419//ESTs, Weakly similar to F25H9.6 [C.elegans]//1.6e-97:436:95//Hs.24647:W19739
R-PLACE2000425//Homo sapiens PEC-205 mRNA, complete cds//2.2e-44:287:88//Hs.153563:AF011333
R-PLACE2000427//ESTs, Weakly similar to coded for by C. elegans cDNA CEESI42F [C.elegans]//3.0e-113:543:97//Hs.16933:AA976002
R-PLACE2000433//ESTs//1.8e-46:311:85//Hs.145032:AA343523
R-PLACE2000435//ESTs//2.9e-33:243:87//Hs.90964:AA393986
R-PLACE2000438//ESTs//2.8e-09:66:96//Hs.59548:AI279887
R-PLACE2000450//Human mRNA for KIAA0392 gene, partial cds//3.3e-39:394:74//Hs.40100:AB002390
R-PLACE2000455//ESTs//1.2e-62:301:99//Hs.151708:AA554714
R-PLACE2000458//ESTs//6.8e-92:473:96//Hs.115897:AA156638
R-PLACE2000465//ESTs//1.3e-45:435:76//Hs.141635:N79228
R-PLACE2000477//ESTs//2.6e-100:536:94//Hs.77822:AA532642
R-PLACE3000004//ESTs//9.1e-114:558:97//Hs.13035:AA151838
R-PLACE3000029//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.3e-64:350:86//Hs.153468:AB011147
R-PLACE3000059//EST//0.028:175:61//Hs.159873:R92763
R-PLACE3000070//ESTs//3.8e-16:200:74//Hs.138771:N70979
R-PLACE3000103//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.7e-48:468:75//Hs.51048:X68830
R-PLACE3000119//ESTs//1.2e-45:330:83//Hs.35254:AI133727
R-PLACE3000124//EST//3.1e-75:391:96//Hs.161515:N71739
R-PLACE3000136//ESTs//8.3e-18:152:84//Hs.10043:D81792
R-PLACE3000142//ESTs//0.047:183:62//Hs.43102:AA131369
R-PLACE3000147//ESTs//6.6e-53:310:90//Hs.8230:W07142
R-PLACE3000148//EST//1.9e-16:184:76//Hs.146570:AI139815
R-PLACE3000155//ESTS//1.2e-19:192:79//Hs.131350:AA805223
R-PLACE3000156//ESTs, Highly similar to ENV POLYPROTEIN [Avian spleen necrosis virus]//4.8e-36:262:88//Hs.31532:H18272
R-PLACE3000157
R-PLACE3000158//Small inducible cytokine A5 (RANTES)//8.2e-39:296:81//Hs.155464:AF088219
R-PLACE3000160
R-PLACE3000169//ESTs//1.5e-64:329:97//Hs.129864:R20798
R-PLACE3000194
R-PLACE3000197//ESTs//1.4e-3 8:197:98//Hs.146341:AI269930
R-PLACE3000199//ESTs, Highly simrilar to APOLIPOPROTEIN E PRECURSOR [Sus scrofa]//0.018:261:61//Hs.131370:AA927516
R-PLACE3000207//EST//1.3e-15:154:78//Hs.136617:AA630476
R-PLACE3000208//ESTS//1.6e-18:151:82//Hs.155498:W27084
R-PLACE3000218//ESTs//1.8e-85:463:93//Hs.7849:AI129964
R-PLACE3000220//ESTs//6.4e-44:308:84//Hs.136839:H93717
R-PLACE3000226//ESTs//L3e-49:269:95//Hs.9059:AI359014
R-PLACE3000230//EST//2.3e-34:258:83//Hs.4382:T02878
R-PLACE3000242//Human trophinin mRNA, complete cds//1.1e-63:546:78//Hs.76313:U04811
R-PLACE3000244//ESTs, Highly similar to NEGATIVE REGULATOR OF MITOSIS [Emericella nidulans]//7.5e-110:549:95//Hs.13692:AA632002
R-PLACE3000254//Human mRNA for KIAA0309 gene, partial cds//2.4e-29:174:94//Hs.87908:AB002307
R-PLACE3000271//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.3e-62:287:82//Hs.97203:U83171
R-PLACE3000276//ESTs//7.5e-07:187:64//Hs.80720:AA031782
R-PLACE3000304//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//4.0e-59:456:80//Hs.108966:U48696
R-PLACE3000310//ISLET AMYLOID POLYPEPTIDE PRECURSOR//6.0e-45:302:86//Hs.51048:X68830
R-PLACE3000320//Interleuldn 10//9.6e-42:288:85//Hs.2180:M57627
R-PLACE3000322//ESTs, Highly similar to ARGININOSUCCINATE LYASE [Homo sapiens]//5.8e-34:190:95//Hs.

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114531:N74103
R-PLACE3000331//Homo sapiens mRNA for KIAA0772 protein, complete cds//3.7e-32:239:84//Hs.15519:AB018315
R-PLACE3000339//ESTs//1.3e-109:548:96//Hs.7871:AI041837
R-PLACE3000341//EST//1.1e-11:231:68//Hs.131328:AA922688
R-PLACE3000350//Human mRNa for adipogenesis inhibitory factor//8.0e-40:291:76//Hs.1721:X58377
R-PLACE3000352//EST//1.8e-72:343:100//Hs.144871:AI202380
R-PLACE3000353//ESTs//2.0e-75:395:95//Hs.107260:W52683
R-PLACE3000362//EST//2.8e-80:381:99//Hs.136233:AA261888
R-PLACE3000363
R-PLACE3000365//EST//4.8e-50:307:88//Hs.149580:AI281881
R-PLACE3000373//ESTs//5.8e-60:422:83//Hs.142826:W87430
R-PLACE3000388//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-35:427:73//Hs.138795:R98534
R-PLACE3000399//ESTs//6.5e-05:162:66//Hs.149440:AI274570
R-PLACE3000400//ESTs//8.3e-05:310:63//Hs.17697:AA287528
R-PLACE3000401//ESTs//4.6e-60:326:80//Hs.139555:N48230
R-PLACE3000402//Homo sapiens clone 24629 mRNA sequence//0.50:227:62//Hs.142570:AF052160
R-PLACE3000405//Human HsLIM15 mRNA for HsLim15, complete cds//5.3e-43:315:82//Hs.37181:D64108
R-PLACE3000406//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.4e-47:302:87//Hs.73614:U83460
R-PLACE3000413//ESTs//1.6e-116:571:97//Hs.10235:H93077
R-PLACE3000416//Small inducible cytokine A5 (RANTES)//1.8e-41:300:85//Hs.155464:AF088219
R-PLACE3000425//Homo sapiens 4F5S mRNA, complete cds//1.6e-46:307:85//Hs.32567:AF073519
R-PLACE3000455//ESTs//1.0:160:64//Hs.156045:AA884461
R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA, complete cds//6.1e-84:440:92//Hs.153487:U43899
R-PLACE3000477//ESTs//2.4e-113:568:96//Hs.24557:AA142980
R-PLACE4000009//ESTs//1.5e-72:361:96//Hs.10119:AA700227
R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//8.8e-85:433:95//Hs.105399:AB018352
R-PLACE4000034//ESTs//7.0e-110:550:96//Hs.76607:AA156240
R-PLACE4000049//EST//0.028:87:75//Hs.89303:AA284031
R-PLACE4000052//ESTs//5.6e-116:553:98//Hs.19067:AA521292
R-PLACE4000063//ESTs//5.0e-80:388:98//Hs.135028:AI096444
R-PLACE4000089//ESTs//2.3e-97:479:97//Hs.102425:AA807547
R-PLACE4000093//ESTs//1.5e-82:391:99//Hs.160730:AI142739
R-PLACE4000100
R-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.7e-98:419:91//Hs.129937:AB007931
R-PLACE4000128//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.8e-11:184:71//Hs.154278:N45985
R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//5.2e-21:118:100//Hs.118164:AB007969
R-PLACE4000147//EST//1.6e-23:175:79//Hs.162236:AA551582
R-PLACE4000156//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.0e-47:306:88//Hs.153468:AB011147
R-PLACE4000192//ESTs, Weakly similar to similar to Human zinc finger protein(ZNF142) [H.sapiens]//6.7e-31:232:82//Hs.16493:T92186
R-PLACE4000222//ESTs//2.2e-53:195:85//Hs.141575:AA211734
R-PLACE4000233//ESTs//2.9e-81:456:93//Hs.124964:R81949
R-PLACE4000247//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.5e-72:307:85//Hs.113283:AF018080
R-PLACE4000250//Small inducible cytokine A5 (RANTES)//7.1e-43:301:83//Hs.155464:AF088219
R-PLACE4000252//EST//1.6e-40:275:85//Hs.162197:AA535216
R-PLACE4000261//EST//0.0063:384:58//Hs.136284:AA400442
R-PLACE4000269//ESTs//7.3e-67:345:97//Hs.5000:R44586
R-PLACE4000270//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//2.1e-37:352:77//Hs.77579:AF013263

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R-PLACE4000300//EST//0.26:103:68//Hs.144438:AA780782
R-PLACE4000320//EST//2.7e-44:298:85//Hs.162404:AA573131
R-PLACE4000323//ESTs//8.8e-38:178:79//Hs.155475:AA761454
R-PLACE4000326//ESTs//7.4e-103:516:96//Hs.55042:AA150460
R-PLACE4000344//ESTs//9.9e-94:463:96//Hs.100057:AA001414
R-PLACE4000367//ESTs//0.81:102:73//Hs.107692:H38478
R-PLACE4000369//ESTs//1.5e-69:390:92//Hs.13733:AA418656
R-PLACE4000379//ESTs//1.3e-67:373:91//Hs.48569:AA905425
R-PLACE4000387//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.9e-44:379:78//Hs.152369:AA504818
R-PLACE4000392//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//2.3e-70:482:83//Hs.140416:AA778649
R-PLACE4000401//ESTs//1.3e-18:151:84//Hs.150355:AI273502
R-PLACE4000411//ESTs//1.1e-108:543:96//Hs.23901:AA169780
R-PLACE4000445//ESTs, Weakly similar to C05D9.6 gene product [C.elegans]//2.6e-111:530:98//Hs.12003:AA643063
R-PLACE4000465//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//8.5e-58:409:72//Hs.1361:M55053
R-PLACE4000489//ESTs//5.0e-70:342:98//Hs.72865:AI380932
R-PLACE4000494//EST&//1.4e-109:525:98//Hs.22539:AI334210
R-PLACE4000522//ESTs//6.3e-88:471:93//Hs.8121:AA521290
R-PLACE4000548//ESTs//3.3e-86:441:96//Hs.5070:AA149527
R-PLACE4000558//Human putative monocarboxylate transporter (MCT) mRNA, complete cds//5.7e-46:425:76//Hs.23590:U59185
R-THYRO1000026//ESTs//2.6e-42:331:82//Hs.137875:AA993532
R-THYRO1000034//ESTs//2.1e-43:214:100//Hs.153018:AI243524
R-THYRO1000035//ESTs//7.6e-52:325:90//Hs.49817:AA001249
R-THYRO1000040//ESTs//1.7e-94:459:98//Hs.48712:AI027889
R-THYRO1000070//ESTs//6.7e-43:283:86//Hs.37573:H59651
R-THYRO1000072//ESTs//1.3e-57:313:96//Hs.127827:H13438
R-THYRO1000085//ESTs//1.1e-90:439:98//Hs.150539:AA908435
R-THYRO1000092//Human mRNA for KIAA0355 gene, complete cds//1.3e-41:344:79//Hs.153014:AB002353
R-THYRO1000107//Interieuldn 10//2.8e-43:292:84//Hs.2180:M57627
R-THYRO1000111//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//1.0e-52:413:80//Hs.140385:AA773359
R-THYRO1000121//EST//0.24:78:74//Hs.156632:AI345108
R-THYRO1000124//ESTs//2.8e-86:428:96//Hs.141634:AI122764
R-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds//6.8e-90:449:96//Hs.87619:AF087142
R-THYRO1000132//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//5.2e-49:486:77//Hs.24164:N95217
R-THYRO1000156//ESTs//6.1e-36:344:75//Hs.70279:AA757426
R-THYRO1000163//Homo sapiens LIM protein mRNA, complete cds//4.8e-38:278:84//Hs.154103:AF061258
R-THYRO1000173//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [Mus musculus]//1.1e-111:554:96//Hs.18894:AA910946
R-THYRO1000186//ESTs//1.0e-44:339:83//Hs.155184:AA573189
R-THYRO1000187//Small inducible cytokine A5 (RANTES)//1.1e-41:305:81//Hs.155464:AF088219
R-THYRO1000190//Small inducible cytokine A5 (RANTES)//2.3e-44:301:85//Hs.155464:AF088219
R-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//3.6e-110:535:97//Hs.43445:AJ005698
R-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.3e-115:559:97//Hs.79672:AB014552
R-THYRO1000206//ESTs//3.1e-90:507:90//Hs.32456:W29063
R-THYRO1000221//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.1e-72:357:98//Hs.140002:AA635349
R-THYRO1000241//Homo sapiens mRNA for KIAA0688 protein, complete cds//7.8e-69:524:82//Hs.141874:AB014588
R-THYRO1000242//ESTs//4.2e-27:222:85//Hs.77554:W87927

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R-THYRO1000253//Sialophorin (gpL115, leukosialin, CD43)//7.3e-40:318:80//Hs.80738:X52075
R-THYRO1000270//ESTs//1.9e-99:531:94//Hs.17767:N62925
R-THYRO1000279//EST//2.7e-54:266:99//Hs.149527:AI280674
R-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds//3.5e-100:566:91//Hs.25846:AB016068
R-THYRO1000320//POLYPOSIS LOCUS PROTEIN 1//1.0:321:58//Hs.74648:M73547
R-THYRO1000327//Autocrine motility factor receptor//9.2e-54:289:93//Hs.80731:M63175
R-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//3.4e-113:559:96//Hs.12002:AB018333
R-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds//1.5e-48:317:87//Hs.7833:U29091
R-THYRO1000368//ESTs//4.7e-88:430:98//Hs.146085:AA021064
R-nnnnnnnnnnnn//ESTs//1.0:253:57//Hs.128783:AA436250
R-THYRO1000387//Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds//4.6e-69:294:84//Hs.151614:AF032456
R-THYRO1000394//Thromboxane A2 receptor//4.1e-40:232:87//Hs.89887:D38081
R-THYRO1000395//ESTs//3.3e-20:160:83//Hs.101570:AA505429
R-THYRO1000401//ESTs//1.3e-109:516:99//Hs.78524:AI140601
R-THYRO1000438//ESTs//2.1e-48:360:83//Hs.141203:H52638
R-THYRO1000452//ESTs, Weakly similar to No definition line found [C.elegans]//8.5e-40:239:90//Hs.84009:AI309761
R-THYRO1000471//ESTs//3.3e-36:302:80//Hs.70279:AA757426
R-THYRO1000484//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.2e-49:479:75//Hs.17630:AB018280
R-THYRO1000488//Homa sapiens mRNA for HRIHFB2038, partial cds//4.1e-89:471:94//Hs.28719:AB015333
R-THYRO1000501//ESTs//L5e-46:287:89//Hs.125300:R62360
R-THYRO1000502//ESTs//1.7e-08:63:96//Hs.116319:AI208005
R-THYRO1000505//ESTs, Weakly similar to KIAA0281 [H. sapiens]//3.9e-57:286:96//Hs.105861:AI206965
R-THYRO1000558//ESTs//1.7e-95:454:99//Hs.125063:AA648511
R-THYRO1000569//ESTs//3.2e-89:463:94//Hs.20555:W22193
R-THYRO1000570//ESTs//2.8e-97:471:97//Hs.8245:AA115485
R-nnnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds//2.6e-108:533:97//Hs.151411:AF075587
R-THYRO1000596//ESTs//3.1e-99:527:94//Hs.6084:AA045247
R-THYRO1000602//EST//6.9e-50:381:83//Hs.161917:AA483223
R-THYRO1000605//ESTs, Weakly similar to monocytic leukaemia zinc finger protein [H.sapiens]//1.2e-96:483:96//Hs.21907:N24415
R-THYRO1000625//ESTs//5.6e-36:257:84//Hs.139657:AA191742
R-THYRO1000637
R-THYRO1000641//ESTs, Weakly similar to ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN [H. sapiens]//4.9e-46:245:95//Hs.97398:AA398634
R-THYRO1000658//ESTs//5.8e-48:281:90//Hs.142259:AA828840
R-nnnnnnnnnnnn//ESTs//1.5e-82:389:99//Hs.155573:AA487384
R-THYRO1000666//ESTs//1.4e-26:179:88//Hs.98382:AA779866
R-THYRO1000676//EST//6.4e-05:88:77//Hs.133424:AI061063
R-THYRO1000684//ESTs//1.9e-69:374:94//Hs.144617:R77109
R-THYRO1000699//ESTs//1.7e-58:394:86//Hs.26373:AA700713
R-THYRO1000712
R-THYRO1000734//EST//2.0e-06:95:73//Hs.156201:AA724287
R-THYRO1000748//EST//4.1e-12:155:74//Hs.118694:AA148713
R-THYRO1000756//ESTs, Weakly similar to CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE [H.sapiens]//8.1e-82:497:87//Hs.109672:W22624
R-THYRO1000777
R-THYRO1000783//EST//5.6e-100:470:99//Hs.123515:AA812932
R-THYRO1000787//EST//8.0e-34:175:99//Hs.99607:AA463897
R-THYRO1000793//ESTs//2.2e-106:505:99//Hs.50929:AA443144
R-THYRO1000796//ESTs//4.3e-44:445:75//Hs.55855:AA621381
R-THYRO1000805//EST//2.6e-32:407:67//Hs.123424:AA813594
R-THYRO1000815//Human mRNA for KIAA0033 gene, partial cds//2.0e-56:307:87//Hs.22271:D26067

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R-THYRO1000829
R-THYRO1000843//Interleukin 10//1.1e-44:285:87//Hs.2180:M57627
R-THYRO1000852//EST//2.3e-20:157:85//Hs.149580:AI281881
R-THYRO1000855//ESTs//2.6e-44:359:81//Hs.140329:AA714011
R-THYRO1000865//Protein kinase, interferon-inducible double stranded RNA dependent//2.8e-44:374:79//Hs.73821:M35663
R-THYRO1000895//ESTs//1.0e-32:196:85//Hs.138630:H97871
R-THYRO1000916//ESTs//4.6e-99:492:96//Hs.152442:AA528234
R-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//3.1e-110:566:94//Hs.78106:AF079529
R-THYRO1000934//ESTs//7.4e-102:535:95//Hs.58194:W72182
R-THYRO1000951//ESTs//4.2e-11:91:89//Hs.6278:T15859
R-THYRO1000952//ESTs//3.9e-93:489:94//Hs.48928:AA211761
R-THYRO1000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds//1.1e-60:321:95//Hs.14454:AF047440
R-THYRO1000975//EST//9.8e-49:303:89//Hs.149580:AI281881
R-THYRO1000983//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 [Arabidopsis thaliana]//1.6e-90:474:93//Hs.106616:AI027524
R-THYRO1000984//ESTs//5.9e-97:481:96//Hs.142457:AI202777
R-THYRO1000988//EST//3.5e-42:241:83//Hs.162404:AA573131
R-THYRO1001003//ESTs, Weakly similar to ubiquitin-conjugating enzyme [H.sapiens]//3.0e-57:341:91//Hs.44049:AA521489
R-THYRO1001031//ESTs//5.5e-47:322:85//Hs.136839:H93717
R-THYRO1001033//ESTs//5.7e-89:427:98//Hs.71508:AA809070
R-THYRO1001062//EST//1.5e-46:291:89//Hs.161917:AA483223
R-THYRO1001093//ESTs//2.7e-80:468:90//Hs.124601:AA203497
R-THYRO1001100
R-THYRO1001120//ESTs, Moderately similar to fractionated X-irradiation-induced 29 thymoma [M.musculus]//6.6e-86:491:89//Hs.89135:AI138834
R-THYRO1001121//Homo sapiens mRNA for beta-tubulin folding cofactor D//2.6e-82:429:94//Hs.12570:AJ006417
R-THYRO1001133//ESTs//2.9e-39:242:90//Hs.152340:AA521399
R-THYRO1001134//ESTs//1.8e-102:521:95//Hs.108408:N31922
R-THYRO1001142//ESTs//0.26:84:69//Hs.153434:AI287853
R-THYRO1001173//Human mRNA for KIAA0238 gene, partial cds//0.0012:305:62//Hs.82042:D87075
R-THYRO1001177
R-THYRO1001189//H.sapiens F11 mRNA//1.5e-59:260:83//Hs.159639:X77744
R-THYRO1001204//ESTs, Weakly similar to TH1 protein [D.melanogaster]//1.0e-75:431:91//Hs.5184:AA709151
R-THYRO1001213//ESTs//1.3e-75:409:92//Hs.140213:AA828932
R-THYRO1001262//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//1.3e-48:349:83//Hs.139107:K00629
R-THYRO1001271//PUTATIVE PROTEIN PHOSPHATASE 2C//1.0:128:64//Hs.118728:D13640
R-THYRO1001290//ESTs//2.1e-89:424:99//Hs.118152:AA702561
R-THYRO1001313//ESTs//3.5e-17:139:87//Hs.15827:H16269
R-THYRO1001320//ESTs//1.4e-61:403:79//Hs.139555:N48230
R-THYRO1001321//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)//8.5e-05:326:60//Hs.82314:M31642
R-nnnnnnnnnnnnn//ESTs//0.16:422:5.9//Hs.23876:AA082935
R-THYRO1001347//ESTs, Weakly similar to C35A5.8 [C.elegans]//1.1e-106:562:94//Hs.15032:AA774250
R-THYRO1001363//ESTs//1.4e-99:508:95//Hs.5028:D51033
R-THYRO1001365
R-THYRO1001374
R-THYRO001401//Human HsLIM15 mRNA for HsLiml5, complete cds//2.5e-48:467:75//Hs.37181:D64108
R-THYRO1001403//Interleukin 10//2.1e-46:305:85//Hs.2180:M57627
R-THYRO1001405//ESTs//4.8e-25:197:84//Hs.6907:W72733
R-THYRO1001406//EST//0.0023:117:66//Hs.162931:AA633197
R-THYRO1001411//ESTs//6.1e-77:421:93//Hs.22973:R40979
R-THYRO1001426//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//9.1e-49:305:86//Hs.159187:AB007977

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R-THYRO1001434//ESTs//0.40:161:61//Hs.161993:AA503172
R-THYRO1001458//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//1.7e-05:159:66//Hs.104239:AA488082
R-THYRO1001480//Small inducible cytokineA5 (RANTES)//1.3e-40:331:79//Hs.155464:AF088219
R-THYRO1001487//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.1e-17:134:76//Hs.15731:AB011135
R-THYRO1001534//ESTs//4.6e-96:447:100//Hs.135204:AI093110
R-THYRO1001537//ESTS, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.0e-33:304:80//Hs.108740:W20094
R-THYRO1001541//Human peptide transporter (HPEPT1) mRNA, complete cds//9.0e-49:427:76//Hs.2217:U21936
R-THYRO1001559//ESTs//0.99:210:62//Hs.33619:AA021594
R-THYRO1001570//ESTs//4.9e-48:287:91//Hs.27131:AA442413
R-THYRO1001573//ESTs//2.1e-87:446:95//Hs.143669:AA621958
R-THYRO1001584//ESTs//1.5e-64:354:95//Hs.146222:AA397741
R-THYRO1001595//ESTs//5.7e-39:366:78//Hs.22562:R54247
R-THYRO1001602//Insulin-like growth factor 1 (somatomedia C)//7.4e-12:288:67//Hs.85112:X57025
R-THYRO1001605//Human GS2 mRNA, complete cds//6.9e-49:359:83//Hs.264:U03886
R-THYRO1001617//Homo sapiens peroxisomal acyl-CoA:dihydroxyacetonephosphate acyltransferase (DHAPAT) mRNA, complete cds//1.3e-82:434:93//Hs.12482:AJ002190
R-THYRO1001637//Homo sapiens KIAA0414 mRNA, partial cds//7.1e-58:331:83//Hs.127649:AB007874
R-THYRO1001656//ESTs//3.8e-19:209:75//Hs.92186:AI080282
R-THYRO1001661//ESTs//1.4e-56:323:91//Hs.24984:AA534446
R-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform//-1.6e-111:562:95//Hs.118633:AJ225089
R-THYRO1001673//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-17:246:73//Hs.67619:AB007957
R-THYRO1001703//ESTs//1.1e-39:142:97//Hs.110748:AI341726
R-THYRO1001706//ESTs//2.2e-42:214:99//Hs.112536:AI147691
R-THYRO1001721
R-nnnnnnnnnnnnn//ESTs, Weakly similar to ZK1128.6 [C.elegans]//1.7e-10:147:77//Hs.158196:R53184
R-THYRO1001745//ELK1, member of ETS oncogene family//1.8e-12:282:65//Hs.116549:AL009172
R-THYRO1001746//EST//0.0073:226:61//Hs.146544:AI125323
R-THYRO1001772//ESTs//8.2e-100:495:97//Hs.144993:AA243474
R-THYRO1001793//ESTs//2.5e-89:430:97//Hs.58127:AA534224
R-THYRO1001809//ESTs//1.0e-41:327:80//Hs.146811:AA410788
R-THYRO1001854//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//5.7e-38:242:83//Hs.92381:AB007956
R-THYRO1001895//ESTs//1.7e-08:213:64//Hs.156056:AI352123
R-THYRO1001907//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3.7e-41:362:79//Hs.139007:H74314
R-VESEN1000122
R-Y79AA1000013//ESTs//0.99:233:57//Hs.132216:AA923289
R-Y79AA1000033//EST//1.9e-62:324:95//Hs.157692:AI359321
R-Y79AA1000037//ESTs//6.1e-47:234:98//Hs.30773:AA557178
R-Y79AA1000059//Homo sapiens mRNA for KIAA0640 protein, partial cds//2.8e-51:330:89//Hs.153026:AB014540
R-Y79AA1000065//ESTs//2.0e-91:497:94//Hs.37759:H59629
R-Y79AA1000131//EST//2.3e-16:184:75//Hs.141501:N50792
R-Y79AA1000181//ESTs, Weakly similar to No definition line found [C.elegans]//2.4e-110:553:95//Hs.23159:AA113849
R-Y79AA1000202//Human mRNA for KIAA0169 gene, partial cds//0.094:185:62//Hs.79414:D79991
R-Y79AA1000214//ESTs//1.7e-93:495:94//Hs.11673:W68103
R-Y79AA1000230//ESTs//3.5e-114:553:98//Hs.47125:AI421812
R-Y79AA1000231//ESTs//1.1e-106:526:97//Hs.82856:AI246624
R-Y79AA1000258//ESTs//1.5e-99:490:97//Hs.6459:AI092936
R-Y79AA1000268//Human mRNA for KIAA0365 gene, partial cds//1.3e-44:320:84//Hs.84123:AB002363
R-Y79AA1000313//ESTs//1.7e-105:558:93//Hs.18851:AA857826

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R-Y79AA1000328//ESTs//1.9e-76:448:91//Hs.16470:AA121635
R-Y79AA1000342//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//2.0e-37:239:88//Hs.23476:AA401210
R-Y79AA1000346//ESTs//7.9e-12:139:76//Hs.115987:AA483808
R-Y79AA1000349//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spnr [M.musculus]//4.4e-66:339:97//Hs.8215:AA521150
R-Y79AA1000355//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3.2e-44:279:88//Hs.139007:H74314
R-Y79AA1000368//ESTs//3.8e-97:513:94//Hs.68090:AA641018
R-Y79AA1000405//ESTs//4.4e-47:267:94//Hs.125304:R51613
R-Y79AA1000410//ESTs//7.4e-49:359:82//Hs.158107:AA707758
R-Y79AA1000420//EST//0.17:99:69//Hs.160859:AI352292
R-Y79AA1000469//ESTs, Highly similar to ancient ubiquitous 46 kDa protein AUP46 precursor [M.musculus]//3.1e-60:362:88//Hs.6381:AI188509
R-Y79AA1000480//ESTs//1.0e-75:433:91//Hs.78110:AA741320
R-Y79AA1000538//EST//7.9e-48:307:87//Hs.149580:AI281881
R-Y79AA1000539//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds//0.95:172:62//Hs.41723:U37426
R-Y79AA1000540//ESTs//1.5e-97:534:93//Hs.67991:AA147848
R-Y79AA1000560//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicus]//8.2e-97:482:97//Hs.19121:AI125280
R-Y79AA1000574//ESTs, Weakly similar to M04B2.4 [C.elegans]//1.3e-107:564:93//Hs.16361:AI147455
R-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//3.4e-99:517:94//Hs.60580:AF060503
R-Y79AA1000705//ESTs, Weakly similar to HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC REGION [Saccharomyces cerevisiae]//8.1e-27:140:100//Hs.129049:H28818
R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds//8.7e-114:586:95//Hs.83023:AF093670
R-Y79AA1000748//ESTs, Weakly similar to HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III [C.elegans]//9.8e-111:563:95//Hs.19845:AI005330
R-Y79AA1000752//Homo sapiens (huc) mRNA, complete cds//0.97:235:59//Hs.1701:L26405
R-Y79AA1000774//ESTs//5.9e-109:559:95//Hs.17138:N91463
R-Y79AA1000782//Human mRNA for KIAA0246 gene, partial cds//1.6e-18:107:100//Hs.84753:D87433
R-Y79AA1000784//EST//0.80:87:67//Hs.158558:AI368359
R-Y79AA1000794//ESTs//2.7e-99:498:96//Hs.25441:AA580512
R-Y79AA1000800//ESTs//1.2e-97:532:93//Hs.77822:AA532642
R-nnnnnnnnnnn//Carboxypeptidase E//0.018:354:59//Hs.75360:X51405
R-Y79AA1000805
R-Y79AA1000824//ESTs//0.99:276:61//Hs.153992:AA280227
R-Y79AA1000827//ESTs//1.2e-55:326:92//Hs.158127:AI334650
R-Y79AA1000850//Homo sapiens small optic lobes homolog (SOLH) mRNA, complete cds//0.016:386:59//Hs.55836:U85647
R-Y79AA1000962//EST//0.024:177:63//Hs.25214:R37079
R-Y79AA1000968
R-Y79AA1000969//ESTs//2.9e-70:251:98//Hs.120858:AA417181
R-Y79AA1000976//ESTs//7.8e-56:299:95//Hs.120125:M86049
R-Y79AA1000985
R-Y79AA1001023//ESTs//5.7e-66:379:90//Hs.64616:W22851
R-Y79AA1001041//ESTs//8.6e-06:54:100//Hs.8980:AA629067
R-Y79AA1001048//ESTs//4.4e-97:461:99//Hs.7010:AA837407
R-Y79AA1001061//ESTs//3.8e-105:493:99//Hs.128419:AI271325
R-Y79AA1001068//Homo sapiens mRNA for KIAA0563 protein, complete cds//4.8e-53:279:83//Hs.15731:AB011135
R-Y79AA1001077//ESTs//1.9e-51:339:87//Hs.11197:AA309047
R-Y79AA1001078//ESTs//8.3e-98:528:92//Hs.24608:AA161260
R-Y79AA1001105//ESTs//6.0e-77:393:96//Hs.30837:H08155
R-Y79AA1001145//ESTs//1.7e-13:285:64//Hs.128259:AA343015
R-Y79AA1001167
R-Y79AA1001177//EST//1.2e-05:92:76//Hs.65277:T15884

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R-Y79AA1001185
R-Y79AA1001211//ESTs//1.3e-70:344:97//Hs.49760:AA741051
R-Y79AA1001216//ESTs//5.8e-63:416:88//Hs.8595:W60933
R-Y79AA1001228//ESTs//9.3e-101:483:98//Hs.13916:AI025750
R-Y79AA1001233//EST//0.00027:232:62//Hs.132431:AA909674
R-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin))//1.1e-110:549:95//Hs.23170:AJ005892
R-Y79AA1001281//ESTs//3.6e-98:466:99//Hs.104442:AA481271
R-Y79AA1001299//Human Ini1 mRNA, complete cds//9.6e-25:133:100//Hs.155626:U04847
R-Y79AA1001312//ESTs//3.4e-92:454:97//Hs.127319:AI191149
R-Y79AA1001323//ESTs//1.6e-67:422:89//Hs.118559:AA887084
R-Y79AA1001384//ESTs//3.1e-104:496:98//Hs.153692:AA604143
R-Y79AA1001391//ESTs//2.2e-77:418:94//Hs.118608:AA101819
R-Y79AA1001394//ESTs//2.1e-78:409:95//Hs.23413:AA579859
R-Y79AA1001402//EST//9.3e-08:128:75//Hs.141607:N63891
R-Y79AA1001493//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 [Arabidopsis thaliana]//4.4e-109:553:95//Hs.106616:AI027524
R-Y79AA1001511//ESTs//4.9e-49:271:92//Hs.109045:AA523704
R-Y79AA1001533//ESTs, Moderately similar to RNA polymerase I associated factor [M.musculus]//6.2e-46:260:94//Hs.24884:AA176812
R-nnnnnnnnnnnn//EST//0.62:126:67//Hs.137020:AA868563
R-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//3.5e-95:517:91//Hs.76987:AF012872
R-Y79AA1001555//Collagen, type XI, alpha 1//1.0:157:64//Hs.82772:J04177
R-Y79AA1001585//ESTs//1.9e-90:430:98//Hs.48333:AA704508
R-Y79AA1001594//ESTs//9.6e-23:122:100//Hs.63795:AI126237
R-Y79AA1001603//ESTs//1.0e-50:193:100//Hs.25635:AI336204
R-Y79AA1001613//ESTs, Weakly similar to zinc finger protein [H.sapiens]//7.2e-81:400:97//Hs.13323:AA897542
R-Y79AA1001647//ESTs//6.8e-92:479:95//Hs.154270:N26486
R-Y79AA1001665//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//2.5e-19:112:97//Hs.26252:AA643235
R-Y79AA1001679//ESTs, Highly similar to LAMBDA-CRYSTALLIN [Oryctolagus cuniculus]//9.7e-99:553:92//Hs.108896:R54040
R-nnnnnnnnnnnn
R-Y79AA1001696//ESTs//1.4e-84:478:91//Hs.6606:AA211783
R-Y79AA1001705//ESTs//6.7e-107:546:95//Hs.106805:AA418490
R-Y79AA1001711//Human DNA sequence from clone 1119D9 on chromosome 20p12. Contains part of a gene for a PAK1 LIKE Serine/Threonine-Protein Kinase and part of the PLCB4 gene for Phopholipase C, beta (1-Phosphatidylinositol -4,5-Bisphosphate Phosphodiesterase Beta 4). Contains ESTs, STSs and GSSs//0.0085:251:63//Hs.21864:AL031652
R-Y79AA1001781//ESTs, Weakly similar to partial CDS [C.elegans]//9.4e-87:427:97//Hs.18645:AI023798
R-nnnnnnnnnnnn//ESTs//1.1e-112:558:97//Hs.109755:AA180809
R-Y79AA1001827//ESTs, Weakly similar to Similar to S.cerevisiae YD9335.03c protein [H.sapiens]//8.1e-95:530:91//Hs.72444:W23217
R-Y79AA1001846//EST//2.8e-41:312:81//Hs.162236:AA551582
R-Y79AA1001848//Human adhalin (DAG2) mRNA, complete cds//0.54:221:58//Hs.99931:L34355
R-Y79AA1001866//ESTs//2.2e-102:498:97//Hs.130683:AI278630
R-Y79AA1001874//ESTs//1.9e-76:377:98//Hs.79707:AA354094
R-Y79AA1001875//ESTs//0.64:152:63//Hs.156159:AI333652
R-Y79AA1001923//EST//0.19:180:58//Hs.148290:AA908404
R-Y79AA1002027//ESTs//1.6e-104:497:98//Hs.21275:N73275
R-Y79AA1002083//Homo sapiens mRNA for KIAA0563 protein, complete cds//0.69:93:73//Hs.15731:AB011135
R-Y79AA1002089//Homo sapiens PYRJN (MEFV) mRNA, complete cds//1.1e-46:392:80//Hs.113283:AF018080
R-Y79AA1002093//Homo sapiens GT198 mRNA, complete ORF//1.2e-12:80:100//Hs.78185:L38933
R-Y79AA1002103//ESTs//1.3e-52:535:76//Hs.142167:AI417785
R-Y79AA1002115//ESTs//4.2e-101:519:96//Hs.23977:AA115275
R-Y79AA1002125//ESTs//9.8e-68:363:94//Hs.72085:AA193399
R-Y79AA1002139//ESTs//1.2e-100:498:96//Hs.72020:AA149858
R-Y79AA1002204//ESTs//2.1e-83:434:95//Hs.22979:R43725

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R-nnnnnnnnnnnn//ESTs//1.7e-55:478:76//Hs.154554:AA552715
R-Y79AA1002209//ESTs, Weakly similar to similar to tyrosyl-tRNA synthetase. [C.elegans]//3.5e-108:553:95//Hs.50441:AA747428
R-Y79AA1002210//ESTs//4.2e-16:92:100//Hs.54862:AA248349
R-Y79AA1002211//ESTs, Weakly similar to PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN [H.sapiens]//6.5e-86:518:90//Hs.25682:AA857843
R-Y79AA1002220//EST//1.3e-68:326:100//Hs.131052:AI016274
R-Y79AA1002229//ESTs//1.9e-98:467:98//Hs.132002:AI039977
R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//2.0e-118:564:98//Hs.100729:AB014592
R-Y79AA1002246//ESTs, Weakly similar to PROTEIN KINASE C, BRAIN ISOZYME [D.melanogaster]//9.0e-102:507:96//Hs.25895:AI341537
R-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.4e-93:453:97//Hs.96731:AB014555
R-Y79AA1002298//ESTs//0.022:241:62//Hs.118272:N90288
R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//8.1e-110:403:99//Hs.30898:AB014534
R-Y79AA1002311//EST//2.6e-27:214:85//Hs.144721:AI187985
R-Y79AA1002351//ESTs//5.6e-100:489:97//Hs.30318:AA913371
R-Y79AA1002361
R-Y79AA1002399//ESTs//0.029:149:65//Hs.43872:N26908
R-Y79AA1002407//ESTs//2.8e-117:552:99//Hs.99519:AI042000
R-Y79AA1002416//ESTs//2.6e-107:531:96//Hs.6716:AA502753
R-Y79AA100243//EST//6.6e-23:128:98//Hs.128417:AA975026
R-nnnnnnnnnnnn//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 68 [Saccharomyces cerevisiae]//4.4e-62:390:88//Hs.143930:AI207821
R-Y79AA1002472//ESTs//1.1e-39:234:78//Hs.117969:H94870
R-Y79AA1002482//ESTs//3.4e-45:312:85//Hs.146811:AA410788
R-Y79AA1002487//ESTs//1.7e-80:427:94//Hs.49210:N66499

Homology Search Result Data 6

[0314] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences. In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be compared. Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.

C-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.9E-250//554aa//85%//Q61712
C-HEMBA1000030
C-HEMBA1000046
C-HEMBA1000050
C-HEMBA1000076
C-HEMBA1000156//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//1.9E-12//368aa//24%//P08553
C-HEMBA1000158//HEPATOCYTE NUCLEAR FACTOR 3.-GAMMA (HNF-3G).//5E-16//166aa//36%//P35584
C-HEMBA1000168//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//2.9E-14//303aa//25%//P35662
C-HEMBA1000185//RAS-RELATED PROTEIN RAL-A.//3.4E-12//125aa//31%//P48555
C-HEMBA1000193
C-HEMBA1000227
C-HEMBA1000288
C-HEMBA1000302
C-HEMBA1000304
C-HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1//5.2E-49//107aa//91 %//035594
C-HEMBA1000369//Novel human mRNA similar to mouse gene PICK1 (TR:Q62083).//0//1950bp//98%//AL049654
C-HEMBA1000387
C-HEMBA1000392

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C-HEMBA1000460
C-HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).//3.3E-45//481aa//29%//Q04652
C-HEMBA1000491//RAS-LIKE PROTEIN 2.//2E-22//188aa//31%//P22279
C-HEMBA1000501
C-HEMBA1000508
C-HEMBA1000520
C-HEMBA1000531//HEAT SHOCK 70 KD PROTEIN COGNATE 1 (HEAT SHOCK 70 KD PROTEIN 70C) (FRAGMENTS).//2.6E-12//73aa//41%//P02826
C-HEMBA1000534
C-HEMBA1000555
C-HEMBA1000568
C-HEMBA1000588
C-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8E-55//179aa//61%//O43295
C-HEMBA1000636
C-HEMBA1000682
C-HEMBA1000686
C-HEMBA1000719
C-HEMBA1000727
C-HEMBA1000752
C-HEMBA1000817
C-HEMBA1000851
C-HEMBA1000867
C-HEMBA1000869
C-HEMBA1000872
C-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN)//1.6E-30//127aa//40%//P43366
C-HEMBA1000918
C-HEMBA1000919//HYPOTHETICAL 65.5 KD TRP-ASP REPEATS CONTAINING PROTEIN F02E8.5 IN CHROMOSOME X.//1E-10//288aa//23%//Q19124
C-HEMBA1000946
C-HEMBA1000968
C-HEMBA1000971
C-HEMBA1000975
C-HEMBA1001009
C-HEMBA1001022
C-HEMBA1001043//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)(FRAGMENT).//1.4E-12//131aa//38%//Q01485
C-HEMBA1001052
C-HEMBA1001080
C-HEMBA1001085
C-HEMBA1001088//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//3.5E-50//176aa//57%//P48059
C-HEMBA1001109
C-HEMBA1001122
C-HEMBA1001133
C-HEMBA1001137//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) (FRAGMENT).//1.5E-116//197aa//58%//Q06730
C-HEMBA1001140
C-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//6.8E-79//179aa//80%//P51646
C-HEMBA1001197//Homo sapiens mRNA for KIAA0871 protein, complete cds.//9.5E-257//1307bp//94%//AB020678
C-HEMBA1001235
C-HEMBA1001257//Homo sapiens mRNA 2-methylacyl-CoA racemase.//0//1672bp//99%//AJ130733
C-HEMBA1001281
C-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//0.00000002//198aa//29%//Q60401
C-HEMBA1001303
C-HEMBA1001310

BNSDOCID: <EP___1074617A2_I_>

C-HEMBA1001326
C-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//1.4E-133//614bp//99%//AF057358
C-HEMBA1001387//GTP-BINDING PROTEIN TC10.//2.9E-64//104aa//82%//P17081
C-HEMBA1001388
C-HEMBA1001398
C-HEMBA1001405
C-HEMBA1001407
C-HEMBA1001413
C-HEMBA1001415
C-HEMBA1001446
C-HEMBA1001450
C-HEMBA1001455
C-HEMBA1001510//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).//1.7E-16//63aa//61%//P18850
C-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//4.9E-37//399aa//29%//P29166
C-HEMBA1001533
C-HEMBA1001579//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1662bp//99%//AB020657
C-HEMBA1001581
C-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//4.9E-156//348aa//83%//Q14141
C-HEMBA1001635//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA).//1.6E-10//155aa//28%//Q63679
C-HEMBA1001661//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//4.6E-36//365aa//33%//P33450
C-HEMBA1001702
C-HEMBA1001714//Homo sapiens mRNA; cDNA DKFZp564G0422 (from clone DKFZp564G0422).//0//1845bp//99%//AL050386
C-HEMBA1001731
C-HEMBA1001744//SCY1PROTEIN.//9.9E-32//481aa//25%//P53009
C-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//3.8E-11//206aa//36%//P11675
C-HEMBA1001815
C-HEMBA1001819//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.9E-135//459aa//52%//Q99676
C-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//7.6E-64//221aa//55%//Q07230
C-HEMBA1001864
C-HEMBA1001869//TRITHORAX PROTEIN.//0.000096//166aa//27%//P20659
C-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (ME2GLYDH).//9.3E-36//395aa//26%//Q63342
C-HEMBA1001987
C-HEMBA1002018
C-HEMBA1002049
C-HEMBA1002084
C-HEMBA1002125
C-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.4E-51//180aa//56%//P79293
C-HEMBA1002177//TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).//6E-13//190aa//36%//P43694
C-HEMBA1002191
C-HEMBA1002199
C-HEMBA1002212//TYROSINE-PROTEIN KINASE 2 (EC 2.7.1.112) (FRAGMENT).//3E-17//267aa//29%//P18161
C-HEMBA1002237
C-HEMBA1002265
C-HEMBA1002267//Sus scrofa decorin mRNA, complete cds.//1.1E-46//302bp//90%//AF125537
C-HEMBA1002349
C-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//1847bp//99%//AF092563
C-HEMBA1002419//TRICHOHYALIN.//1.9E-09//299aa//24%//P22793
C-HEMBA1002430

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C-HEMBA1002439
C-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.//4.2E-24//109aa//55%//Q00994
C-HEMBA1002460
C-HEMBA1002462
C-HEMBA1002469//DXS8237E PROTEIN (FRAGMENT).//3.5E-50//199aa//61%//P98175
C-HEMBA1002475//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.1E-12//285aa//31%//P17437
C-HEMBA1002477
C-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1.//6.8E-53//257aa//36%//P48732
C-HEMBA1002515
C-HEMBA1002542
C-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds.//6.8E-305//951bp//99%//AF075587
C-HEMBA1002583
C-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds.//1.4E-253//1149bp//99%//AB011169
C-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//0//1539bp//99%//AB018351
C-HEMBA1002688
C-HEMBA1002696
C-HEMBA1002750
C-HEMBA1002768//Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4).//1E-80//882bp//61%//AJ000414
C-HEMBA1002770//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//1532bp//99%//AB020636
C-HEMBA1002777
C-HEMBA1002794
C-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//8.2e-314//1437bp//99%//AF071185
C-HEMBA1002818//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819
C-HEMBA1002850
C-HEMBA1002863
C-HEMBA1002876//HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II.//1.5E-44//188aa//52%//Q09297
C-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//1483bp//100%//AB011148
C-HEMBA1002937
C-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//2E-34//300aa//34%//P16157
C-HEMBA1002951//Homo sapiens mRNA for KIAA0903 protein, partial cds.//0//1752bp//99%//AB020710
C-HEMBA1002954
C-HEMBA1002971
C-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17) (DPDE4).//1.2E-27//63aa//100%//P14646
C-HEMBA1002997//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//3.8E-25//5 34aa//24%//Q02224
C-HEMBA1003033
C-HEMBA1003035
C-HEMBA1003041
C-HEMBA1003046//MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT PRECURSOR (EC 3.4.24.64) (BETA-MPP) (P-52).//2.5E-263//489aa//99%//O75439
C-HEMBA1003067
C-HEMBA1003096
C-HEMBA1003117
C-HEMBA1003129
C-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//8.5E-51//221aa//33%//P41940
C-HEMBA1003148//Homo sapiens mRNA full-length insert cDNA clone EUROIMAGE 381801.//0//1583bp//99%//AL079278
C-HEMBA1003175
C-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE (EC 2.1.1.61).//5.9E-74//134aa//53%//P44551
C-HEMBA1003199

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C-HEMBA1003222
C-HEMBA1003235//TROPOMYOSIN.//0.0000023//109aa//33%//Q02088
C-HEMBA1003250//PROTEIN KINASE APK1A (EC 2.7.1.-).//7.2E-41//245aa//42%//Q06548
C-HEMBA1003257
C-HEMBA1003281//POLIOVIRUS RECEPTOR PRECURSOR.//6E-11//239aa//32%//P32506
C-HEMBA1003286//Homo sapiens mRNA for beta-1,4-galactosyltransferase IV, complete cds.//5.4E-229//1043bp//99%//AB024436
C-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//0//791bp//99%//AB011109
C-HEMBA1003322
C-HEMBA1003327
C-HEMBA1003369//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//0.00000002//248aa//23%//Q02224
C-HEMBA1003370
C-HEMBA1003380
C-HEMBA1003395
C-HEMBA1003402
C-HEMBA1003408//Homo sapiens mRNA for KIAA0905 protein, complete cds.//0//1732bp//98%//AB020712
C-HEMBA1003417//Homo sapiens mRNA; cDNA DKFZp586C021 (from clone DKFZp586C021).//1.6e-312//1414bp//99%//AL050287
C-HEMBA1003418//TRICHOHYALIN.//8.7E-19//281aa//31%//P37709
C-HEMBA1003433//Homo sapiens gene for NBS1, complete cds.//0//511bp//94%//AB013139
C-HEMBA1003447
C-HEMBA1003461
C-HEMBA1003463
C-HEMBA1003528
C-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (ISLET-2).//8.8E-189//360aa//96%//P50480
C-HEMBA1003555//NUCLEOTIDE-BINDING PROTEIN (NBP).//2.1E-68//251aa//52%//P53384
C-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAMMA-I).//1.2E-31//71aa//100%//P16874
C-HEMBA1003568//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//7.9E-49//279aa//32%//P19474
C-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1.//6.9E-206//445aa//74%//Q13330
C-HEMBA1003581//TALIN.//4.4E-45//52aa//98%//P26039
C-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP).//4.4E-10//118aa//35%//P19682
C-HEMBA1003615
C-HEMBA1003617//Homo sapiens HRIHFB2157 mRNA, partial cds.//8.2E-178//501bp//97%//AB015344
C-HEMBA1003621
C-HEMBA1003662//TBX2 PROTEIN (T-BOX PROTEIN 2).//1.2E-75//151aa//99%//Q13207
C-HEMBA1003690//HISTONE DEACETYLASE HDA1.//2.1E-59//249aa//47%//P53973
C-HEMBA1003711
C-HEMBA1003807
C-HEMBA1003864
C-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//3.8E-16//89aa//46%//P16372
C-HEMBA1003959
C-HEMBA1003989
C-HEMBA1004074
C-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//8.5E-221//1188bp//78%//AF091234
C-HEMBA1004146
C-HEMBA1004199//Homo sapiens mRNA for KIAA0928 protein, partial cds.//0//1893bp//98%//AB023145
C-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//0//1892bp//99%//U50748
C-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//5.7E-217//1217bp//88%//AF095927
C-HEMBA1004246
C-HEMBA1004276//Homo sapiens AP-4 adaptor complex beta4 subunit mRNA, complete cds.//4.8E-257//738bp//99%//AF092094
C-HEMBA1004289

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C-HEMBA1004509//Homo sapiens CGI-21 protein mRNA, complete cds.//0//1512bp//96%//AF132955
C-HEMBA1004534//Homo sapiens gamma-filamin (ABPL) mRNA, complete cds.//1.2e-316//1445bp//99%//AF089841
C-HEMBA1004596
C-HEMBA1004693
C-HEMBA1004736
C-HEMBA1004753
C-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds.//9.1E-34//515bp//66%//U49082
C-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds.//2.6E-246//1249bp//94%//L39060
C-HEMBA1004763
C-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.4E-111//314aa//58%//P08547
C-HEMBA1004771
C-HEMBA1004776
C-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).//3.8E-69//198aa//66%//P50851
C-HEMBA1004806
C-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//8.2E-154//317aa//94%//Q00004
C-HEMBA1004850
C-HEMBA1004863//Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp586M2022).//0//1443bp//100%//AL080114
C-HEMBA1004923
C-HEMBA1004929
C-HEMBA1004930//26S PROTEASOME SUBUNIT S5B (KIAA0072) (HA1357).//3.3E-27//65aa//100%//Q16401
C-HEMBA1004933
C-HEMBA1004954
C-HEMBA1004972//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//0.00000096//286aa//23%//P12036
C-HEMBA1005475
C-HEMBA1005581//Homo sapiens SLIT2 (SUL2) mRNA, complete cds.//0//1721bp//100%//AF133270
C-HEMBA1006248//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//8.6E-23//151aa//37%//P16372
C-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//3.7E-225//1189bp//88%//AF076183
C-HEMBA1006344//RADIXIN.//1.5E-31//333aa//28%//P26043
C-HEMBA1006377
C-HEMBA1006467
C-HEMBA1006474//40 KD PROTEIN.//1.4E-39//292aa//34%//Q01552
C-HEMBA1006530
C-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//0.000000043//111aa//40%//Q01485
C-HEMBA1006795
C-HEMBA1006877//OXYSTEROL-BINDING PROTEIN.//2E-59//378aa//39%//P16258
C-HEMBA1006936
C-HEMBA1007018//Homo sapiens dynein light chain-A mRNA, complete cds.//1.5E-267//1215bp//99%//AP078849
C-HEMBA1007342
C-HEMBB1000008
C-HEMBB1000018
C-HEMBB1000024
C-HEMBB1000025
C-HEMBB1000036
C-HEMBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//2.8E-187//1582bp//80%//AF084928
C-HEMBB1000083//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//1.9E-22//426aa//25%//P11799
C-HEMBB1000103
C-HEMBB1000119//Homo sapiens ASMTL gene.//0//1891bp//99%//Y15521

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C-HEMBB1000136
C-HEMBB1000215
C-HEMBB1000226//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE EEED8.5.// 2.7E-12//112aa//47%//Q09530
C-HEMBB1000244
C-HEMBB1000266//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHROMOSOME V.//6.1E-09//242aa//26%//Q23256
C-HEMBB1000338
C-HEMBB1000339
C-HEMBB1000391
C-HEMBB1000438
C-HEMBB1000449
C-HEMBB1000589
C-HEMBB1000591
C-HEMBB1000623
C-HEMBB1000630
C-HEMBB1000631//LONGEVITY-ASSURANCE PROTEIN 1 (LONGEVITY ASSURANCE FACTOR 1).//4.1E-19// 232aa//28%//P78970
C-HEMBB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//2.2E-28//273aa//31%//P27671
C-HEMBB1000671
C-HEMBB1000673
C-HEMBB1000705
C-HEMBB1000706
C-HEMBB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//6.2E-130//692bp//93%// U53475
C-HEMBB1000763//Homo sapiens CGI-89 protein mRNA, complete cds.//0//1676bp//96%//AF151847
C-HEMBB1000781//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.// 1.2E-126//613bp//97%//AF111105
C-HEMBB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//5.1E-54//232aa//43%//P39956
C-HEMBB1000807
C-HEMBB1000810
C-HEMBB1000848
C-HEMBB1000852
C-HEMBB1000870
C-HEMBB1000887
C-HEMBB1000908
C-HEMBB1000927//Homo sapiens calsenilin mRNA, complete cds.//1.1E-70//595bp//76%//AF120102
C-HEMBB1000947//Homo sapiens clone HAW 100 putative ribonuclease III mRNA, complete cds.//0//2292bp// 99%//AF116910
C-HEMBB1000973//Mus musculus schlafen3 (Slfn3) mRNA, complete cds.//3.4E-120//580bp//67%//AF099974
C-HEMBB1000975
C-HEMBB1000985//MEPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//8.6E-18//178aa//30%//P28575
C-HEMBB1000991
C-HEMBB1001011//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.4E-73//230aa//45%// P51523
C-HEMBB1001014
C-HEMBB1001024
C-HEMBB1001056//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//2.9E-19//264aa//34%//P46087
C-HEMBB1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//3.6E-52//331bp// 80%//AF010144
C-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.4E-307//1447bp//97%//AF034803
C-HEMBB1001096
C-HEMBB1001105
C-HEMBB1001117
C-HEMBB1001126

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C-HEMBB1001137//Homo sapiens mRNA for putative phospholipase, complete cds.//0//3069bp//99%//AB019435
C-HEMBB1001151//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//4.2E-210//1835bp//76%//AF110267
C-HEMBB1001153
C-HEMBB1001169
C-HEMBB1001175//ANKYRIN.//6.9E-11//169aa//31%//Q02357
C-HEMBB1001182
C-HEMBB1001199
C-HEMBB1001210//Homo sapiens mRNA for KIAA0970 protein, complete cds.//0//1816bp//99%//AB023187
C-HEMBB1001242//Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds.//1.8E-284//713bp//100%//AF089897
C-HEMBB1001288//Homo sapiens CGI-32 protein mRNA, complete cds.//1.8E-274//642bp//99%//AF132966
C-HEMBB1001289
C-HEMBB1001294//GTP-BINDING PROTEIN TC10.//1.2E-79//196aa//80%//P17081
C-HEMBB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.3E-129//724bp//86%//U92703
C-HEMBB1001331
C-HEMBB1001339//DXS8237E PROTEIN (FRAGMENT).//0.0000046//124aa//37%//P98175
C-HEMBB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.1E-58//292bp//99%//AF097441
C-HEMBB1001369
C-HEMBB1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%//AF100757
C-HEMBB1001387
C-MAMMA1002317
C-MAMMA1002319
C-MAMMA1002385//RIBONUCLEOPROTEIN RB97D.//0.00000015//206aa//29%//Q02926
C-NT2RM1000080//UNC-1 PROTEIN.//5.9E-25//211aa//31%//Q21190
C-NT2RM1000242
C-NT2RM1000257//MAGO NASHI PROTEIN.//7.9E-69//143aa//91%//P49028
C-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V- ATPASE 28 KD ACCESSORY PROTEIN).//1.5E-106//118aa//97%//P39942
C-NT2RM1000669
C-NT2RM1000781
C-NT2RM1000867//Homo sapiens HSPC033 mRNA, complete cds.//6.3E-172//798bp//99%//AF092138
C-NT2RM1001008
C-NT2RM1001044//Homo sapiens HSPC031 mRNA, complete cds.//0.000000002//980bp//95%//AF085360
C-NT2RM1001074
C-NT2RM1001115//ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14).//0.0000056//239aa//27%//
C-NT2RM2000006//Human DNA sequence from clone 796F18 on chromosome 1p36.11-36.33 Contains a pseudogene similar to MMS2, ESTs and GSSs, complete sequence.//0//1740bp//99%//AL031291
C-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//2.2E-144//362aa//71%//P25167
C-NT2RM2000030//DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DH IC) (CYTOPLASMIC DYNEIN INTERMEDIATE CHAIN).//0.00000043//136aa//31%//P54703
C-NT2RM2000032
C-NT2RM2000042
C-NT2RM2000092//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUTTIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//1.3E-36//160aa//40%//P50102
C-NT2RM2000093
C-NT2RM2000101
C-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1574bp//99%//AF067223
C-NT2RM2000192
C-NT2RM2000239
C-NT2RM2000250//Homo sapiens mRNA; cDNA DKFZp564L232 (from clone DKFZp564L232).//4.2e-314//1416bp//100%//AL080069
C-NT2RM2000259

BNSDOCID: <EP___1074617A2_I_>

C-NT2RM2000260//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//3.6E-19//181-aa//34%//P14918
C-NT2RM2000287
C-NT2RM2000322//Homo sapiens mRNA for KIAA0859 protein, complete cds.//3.4E-294//863bp//99%//AB020666
C-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds.//0//1637bp//99%//AB011132
C-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN.//1.8E-14//245aa//29%//P11274
C-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//0//1506bp//99%//U48251
C-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLEOTIDE//1.7E-68//419aa//36%//P50849
C-NT2RM2000374
C-NT2RM2000395
C-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).//1.6E-54//344aa//33%//P32802
C-NT2RM2000407
C-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//1E-222//237aa//89%//Q08469
C-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION.//0.0000001//157aa//28%//P36113
C-NT2RM2000469//NITROGEN PERMEASE REACTIVATOR PROTEIN (EC 2.7.1.-).//0.0000089//377aa//24%//P22211
C-NT2RM2000490//SYNAPTOTAGMIN(P65).//1.8E-13//166aa//34%//P41823
C-NT2RM2000502
C-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//1673bp//99%//AF061243
C-NT2RM2000522//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.3E-12//282aa//32%//P17437
C-NT2RM2000540
C-NT2RM2000567
C-NT2RM2000569
C-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS).//1.7E-187//741aa//46%//P73505
C-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds.//0//3001bp//99%//D86987
C-NT2RM2000588//HISTONE DEACETYLASE HDA1.//2.8E-60//384aa//40%//P53973
C-NT2RM2000594//Homo sapiens DNA cytosine-5 methyltransferase 3 beta 3 (DNMT3B) mRNA, complete cds.//0//2712bp//99%//AF156487
C-NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.//4.9E-70//838bp//69%//AF179221
C-NT2RM2000624//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//4.4E-32//319aa//35%//Q08170
C-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds.//0//3791bp//99%//AB018272
C-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds.//0//2530bp//99%//AB014558
C-NT2RM2000639
C-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1543bp//99%//AB014576
C-NT2RM2000669
C-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//3.7E-142//285aa//90%//P32391
C-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP1).//3.8E-23//184aa//36%//Q15404
C-NT2RM2000718//Homo sapiens HRIHFB2436 mRNA, partial cds.//4.4E-231//1065bp//99%//AB015342
C-NT2RM2000740//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//5.7E-53//266aa//43%//P41877
C-NT2RM2000795
C-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETACOP).//9.5E-279//545aa//98%//P23514
C-NT2RM2000837
C-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//1.7E-200//927bp//99%//AB015046

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C-NT2RM2000952
C-NT2RM2000984
C-NT2RM2001004
C-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//8.2E-154//285aa//99%//Q60809
C-NT2RM2001065
C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//2.4E-15//266aa//26%//P46577
C-NT2RM2001131
C-NT2RM2001141
C-NT2RM2001152
C-NT2RM2001177//Homo sapiens mRNA; cDNA DKFZp586G1822 (from clone DKFZp586G1822).//2.1E-293//1335bp//99%//AL080109
C-NT2RM2001194
C-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.3E-20//267aa//35%//P05143
C-NT2RM2001201//EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF5).//0.00000015//95aa//35%//P48724
C-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (PCIP10).//3.6E-10//177aa//32%//P97924
C-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMIDOHYDROLASE).//1.3E-180//328aa//99%//P13264
C-NT2RM2001243
C-NT2RM2001247
C-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.6E-166//312aa//98%//P53995
C-NT2RM2001291
C-NT2RM2001306//Homo sapiens mRNA; cDNA DKFZp564I052 (from clone DKFZp564I052).//0//1694bp//99%//AL080063
C-NT2RM2001312
C-NT2RM2001319
C-NT2RM2001324//ZYXIN.//6.8E-55//200aa//41%//Q04584
C-NT2RM2001345//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E1.//0.000000029//334aa//22%//000808
C-NT2RM2001370
C-NT2RM2001393
C-NT2RM2001420
C-NT2RM2001424//Homo sapiens mRNA; cDNA DKFZp586D0920 (from clone DKFZp586D0920).//0//1621bp//100%//AL050146
C-NT2RM2001499//LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2).//7.4E-121//437aa//57%//P52569
C-NT2RM2001504
C-NT2RM2001524
C-NT2RM2001544
C-NT2RM2001547//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.9E-27//90aa//42%//P38660
C-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SSA)) (RO(SS-A)).//4.3E-61//312aa//44%//P19474
C-NT2RM2001582
C-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds.//0//1000bp//100%//AB014610
C-NT2RM2001896//CELL DIVISION PROTEIN FTSJ.//5.1E-26//204aa//34%//P28692
C-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds.//0//2390bp//99%//AB007931
C-NT2RM2001930
C-NT2RM2001935
C-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//2.7E-27//216aa//34%//P28320
C-NT2RM2001950//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION.//0.0000001//212aa//23%//P38250
C-NT2RM2001982
C-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//1.9E-39//253aa//35%//P37838
C-NT2RM2001997//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//1.3E-10//232aa//

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28%//Q12730
C-NT2RM2001998//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//3.1E-12//206aa//30%//Q09782
C-NT2RM2002004//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//0.000000029//83aa//44%//P40796
C-NT2RM2002014//HYPOTHETICAL 81.4 KD PROTEIN IN GREB-FEOA INTERGENIC REGION.//1.1E-89//425aa//41%//P46837
C-NT2RM2002030//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.//0//1959bp//99%//AB016789
C-NT2RM2002049
C-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.00000099//338aa//24%//Q07878
C-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//5E-62//104aa//57%//Q61990
C-NT2RM2002091
C-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//0//1807bp//99%//AJ010840
C-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//0//1868bp//99%//AF030435
C-NT2RM2002128//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//4.9E-13//487aa//26%//P49695
C-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//8E-31//105aa//47%//P47805
C-NT2RM2002178//Homo sapiens mRNA; cDNA DKFZp434E0335 (from clone DKFZp434E0335).//0//1683bp//99%//AL117402
C-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//7.1E-155//381aa//72%//P25167
C-NT2RM4000061
C-NT2RM4000104//ZINC FINGER PROTEIN 135.//1.5E-81//251aa//53%//P52742
C-NT2RM4000139//R.norvegicus trg mRNA.//2.3E-114//1161bp//72%//X68101
C-NT2RM4000169//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//4.8E-13//686aa//23%//P25386
C-NT2RM4000191//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.//9.2E-75//439aa//41%//P16381
C-NT2RM4000197
C-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//0//1926bp//100%//AB018255
C-NT2RM4000229//Gallus gallus actin filament-associated protein (AFAP-110) mRNA, complete cds.//1.1E-27//633bp//64%//L20303
C-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//2.2E-276//1124bp//97%//M99438
C-NT2RM4000344//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//0//2030bp//99%//AJ132637
C-NT2RM4000349//Homo sapiens HSPC028 mRNA, complete cds.//0//1827bp//99%//AF083246
C-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//1.5E-21//208aa//35%//Q24371
C-NT2RM4000386//Mus musculus mRNA for Ten-m3, complete cds.//0//2156bp//86%//AB025412
C-NT2RM4000395
C-NT2RM4000421//Homo sapiens mRNA for nuclear transport receptor.//0//1730bp//99%//AJ133769
C-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//8E-20//393aa//24%//Q10297
C-NT2RM4000471//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2092bp//99%//AF097025
C-NT2RM4000486//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.8E-11//242aa//31%//P04280
C-NT2RM4000496//SAP1 PROTEIN.//8.3E-53//434aa//29%//P39955
C-NT2RM4000511
C-NT2RM4000515//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H) (FRAGMENT).//1.1E-11//394aa//24%//P16884
C-NT2RM4000520
C-NT2RM4000585
C-NT2RM4000595//Homo sapiens leucine-rich repeats containing F-box protein FBL3 mRNA, complete cds.//1.1E-285//1293bp//99%//AF186273
C-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds.//0//1940bp//95%//AB014587

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C-NT2RP1000035//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657
C-NT2RP1000040
C-NT2RP1000063
C-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsal2.//0//1162bp//99%//X98834
C-NT2RP1000101
C-NT2RP1000111//COP1 REGULATORY PROTEIN.//4E-116//296aa//51%//P93471
C-NT2RP1000112
C-NT2RP1000124
C-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//4.5E-50//181aa//60%//P51859
C-NT2RP1000163//Homo sapiens mRNA for KIAA0948 protein, complete cds.//0//1889bp//98%//AB023165
C-NT2RP1000170
C-NT2RP1000191
C-NT2RP1000202//ANKYRIN.//1E-25//302aa//34%//Q02357
C-NT2RP1000243
C-NT2RP1000259
C-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//5.8E-114//616bp//93%//AF067730
C-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.3E-275//1249bp//99%//AF053551
C-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//8.7E-47//155aa//58%//P32447
C-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.7E-15//162aa//30%//P25343
C-NT2RP1000357
C-NT2RP1000376//Homo sapiens mRNA; cDNA DKFZp434A102 (from clone DKFZp434A102).//0//2265bp//95%//AL080187
C-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds.//0//1056bp//99%//AB011159
C-NT2RP1000416
C-NT2RP1000439//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//1.8E-94//1019bp//63%//AF111423
C-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN).//2.4E-10//227aa//25%//Q08257
C-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//2.6E-94//254aa//47%//P34580
C-NT2RP1000478//TUBULIN BETA-5 CHAIN (CLASS-V).//4.5E-240//445aa//97%//P09653
C-NT2RP1000481
C-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds.//0//2728bp//99%//D87686
C-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.1E-27//193aa//35%//P49020
C-NT2RP1000574//HOMEOBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//3.5E-75//151aa//94%//P97367
C-NT2RP1000581
C-NT2RP1000630//NECDIN.//2.4E-44//227aa//41%//P25233
C-NT2RP1000688
C-NT2RP1000695
C-NT2RP1000733//Human mRNA for GSPT1-TK protein,complete cds.//0//2057bp//99%//E14379
C-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds.//0//2186bp//99%//AF101434
C-NT2RP1000782//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%//O35566
C-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//8.2E-83//334aa//50%//Q07960
C-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1494bp//99%//AF067223
C-NT2RP1000846
C-NT2RP1000851
C-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%//035566
C-NT2RP1000915//AUTOANTIGEN NGP-1.//1.7E-19//343aa//25%//Q13823
C-NT2RP1000947//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds.//4.6E-

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105//504bp//99<%//U39317
C-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//1.4E-23//370aa//28%//Q04652
C-NT2RP1000958//AUTOANTIGEN NGP-1.//1.4E-19//343aa//25%//Q13823
C-NT2RP1000959//Human acidic ribosomal phosphoprotein P0 mRNA, complete cds.//2.5E-236//966bp//99%//M17885
C-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//8.9E-299//554aa//99%//P19338
C-NT2RP1000980
C-NT2RP1000988
C-NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds.//2.2E-78//1529bp//61%//L01790
C-NT2RP1001014
C-NT2RP1001395
C-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//8.9E-141//396aa//67%//P91917
C-NT2RP1001424
C-NT2RP1001449
C-NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).//1.2E-137//629bp//100%//AJ005257
C-NT2RP1001466
C-NT2RP1001475
C-NT2RP1001482
C-NT2RP1001494//MALE STERILITY PROTEIN 2.//7.2E-40//261aa//27%//Q08891
C-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.6E-166//506aa//60%//P42803
C-NT2RP1001546//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.6E-30//232aa//30%//035566
C-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//5.8E-121//271aa//89%//P47758
C-NT2RP1001616
C-NT2RP1001665//CALMODULIN.//0.00000051//83aa//30%//P02594
C-NT2RP2000006//DNAJ PROTEIN (40 KD HEAT SHOCK CHAPERONE PROTEIN) (HSP40).//9.8E-17//79aa//55%//O34136
C-NT2RP2000007
C-NT2RP2000008//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.4E-177//726aa//47%//P51523
C-NT2RP2000032//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP1).//1.8E-22//184aa//34%//Q01730
C-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//0//1390bp//98%//AF061749
C-NT2RP2000054
C-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EPSILON).//9.4E-16//45aa//100%//P49446
C-NT2RP2000067
C-NT2RP2000070//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//3.4E-51//383aa//32%//P33450
C-NT2RP2000079
C-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//0//2286bp//100%//AB018338
C-NT2RP2000091
C-NT2RP2000097
C-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//0//2244bp//99%//AB018356
C-NT2RP2000120
C-NT2RP2000126//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//2.5E-117//541aa//42%//P41877
C-NT2RP2000133//Homo sapiens mRNA for KIAA0989 protein, partial cds.//0//2286bp//99%//AB023206
C-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1-47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//4.4E-226//423aa//99%//P35585
C-NT2RP2000153//GAR2 PROTEIN.//9.8E-23//311aa//28%//P41891
C-NT2RP2000157//MLO2 PROTEIN.//2.6E-11//62aa//40%//Q09329

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C-NT2RP2000161//Homo sapiens mRNA for KIAA1008 protein, complete cds.//3.4e-315//1430bp//99%// AB023225
C-NT2RP2000173
C-NT2RP2000175
C-NT2RP2000195
C-NT2RP2000205
C-NT2RP2000208//Homo sapiens mRNA for KIAA0892 protein, partial cds.//0//2898bp//99%//AB020699
C-NT2RP2000224//INSULIN RECEPTOR SUBSTRATE-1 (IRS1).//0.000043//103aa//28%//P35568
C-NT2RP2000232
C-NT2RP2000233
C-NT2RP2000239
C-NT2RP2000248//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//3.4E-21//210aa//33%//P56558
C-NT2RP2000270
C-NT2RP2000274
C-NT2RP2000283
C-NT2RP2000288//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//1.6E-27//576aa// 25%//Q10297
C-NT2RP2000297//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.3E-186//256aa//60%//Q99676
C-NT2RP2000298
C-NT2RP2000310//Human proline-dehydrogenase/proline oxidase (PRODH) mRNA, complete cds.//4.3E-279// 1193bp//99%//U82381
C-NT2RP2000328
C-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//. 226aa//92%//P08760
C-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//6.3E-115// 674aa//46%//P17564
C-NT2RP2000369
C-NT2RP2000412
C-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F).//4.3E-228//415aa// 100%//P52597
C-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//0//1757bp// 99%//AF102265
C-NT2RP2000438
C-NT2RP2000448//KES1 PROTEIN.//8.7E-54//392aa//38%//P35844
C-NT2RP2000503
C-NT2RP2000510
C-NT2RP2000516
C-NT2RP2000603
C-NT2RP2000617
C-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//0//2482bp//99%//AB014514
C-NT2RP2000656
C-NT2RP2000658
C-NT2RP2000668//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E-27//349aa//32%//Q01577
C-NT2RP2000704
C-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE)//2.7E-100// 488aa//44%//O32038
C-NT2RP2000764//NIFS PROTEIN.//6.6E-36//252aa//42%//P12623
C-NT2RP2000809//Homo sapiens mRNA for KIAA0873 protein, partial cds.//0//3347bp//99%//AB020680
C-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//0.000000056//179aa// 29%//Q99104
C-NT2RP2000814//GELATION FACTOR (ACTIN BINDING PROTEIN 120) (ABP-120).//0.00000011//96aa//29%// P13466
C-NT2RP2000816//MAGNESIUM-CHELATASE 30 KD SUBUNIT.//0.000000079//172aa//28%//P26174
C-NT2RP2000819
C-NT2RP2000841
C-NT2RP2000845
C-NT2RP2000863

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C-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2.//0//694aa//99%//060841
C-NT2RP2000892
C-NT2RP2000931//MATRIN 3.//2.4E-289//467aa//95%//P43244
C-NT2RP2000932//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp5640043).//0//2487bp//99%// AL050390
C-NT2RP2000938
C-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//0//3458bp//99%//AB018298
C-NT2RP2000965//Homo sapiens mRNA for fls353, complete cds.//0//1989bp//96%//AB024704
C-NT2RP2000985
C-NT2RP2001036
C-NT2RP2001044
C-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488.//0//2749bp//99%// AB007957
C-NT2RP2001065
C-NT2RP2001070//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE).// 5.8E-46//222aa//45%//Q20939
C-NT2RP2001081//SYNAPTOTAGMIN IV.//4.2E-118//430aa//54%//P50232
C-NT2RP2001094
C-NT2RP2001119
C-NT2RP2001127//Homo sapiens mRNA for PLU-1 protein.//0//2514bp//99%//AJ132440
C-NT2RP2001218
C-NT2RP2001245//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHAIN) (NMMHC).// 2.2E-10//366aa//28%//P14105
C-NT2RP2001381
C-NT2RP2001397//Homo sapiens mRNA; cDNA DKFZp434B174 (from clone DKFZp434B174).//0//1495bp// 100%//AL080146
C-NT2RP2001427
C-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds.//0//1748bp//99%//AB018340
C-NT2RP2001675
C-NT2RP2001721
C-NT2RP2001907
C-NT2RP2001969
C-NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA, complete cds.//4.7E-177// 1538bp//74%//AF062378
C-NT2RP2002046
C-NT2RP2002154
C-NT2RP2002208
C-NT2RP2002270//AF-9 PROTEIN.//0.00000012//74aa//36%//P42568
C-NT2RP2002312//Homo sapiens mRNA for CDS2 protein.//0//2333bp//99%//Y16521
C-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds.//8.4E-254//1158bp//99%//AB015594
C-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//4.3E-240// 1105bp//99%//AF038958
C-NT2RP2002426
C-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//0//2180bp//99%// AB005289
C-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//6.2E-19//288aa//26%// Q11073
C-NT2RP2002595//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//7.5E-35//181aa// 42%//P12815
C-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.-).//1.7E-51//326aa//38%// P55345
C-NT2RP2002621
C-NT2RP2002672
C-NT2RP2002701//HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME II.//1.9E-14//210aa// 30%//O14345
C-NT2RP2002769
C-NT2RP2002862//60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN).//8.8E-10// 203aa//27%//P29764

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C-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//1.9E-136//623bp//100%//AF038392
C-NT2RP2002954
C-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//4.6E-80//147aa//100%//P51669
C-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//0.00000001//98aa//36%//P10129
C-NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds.//0//2209bp//99%//AB026190
C-NT2RP2003108
C-NT2RP2003117
C-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete eds.//2.3E-82//642bp//68%//AF079765
C-NT2RP2003125//RING CANAL PROTEIN (KELCH PROTEIN).//2.4E-38//539aa//25%//004652
C-NT2RP2003177
C-NT2RP2003194
C-NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.//0//1580bp//99%//AF151811
C-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds.//0//1526bp//99%//AB006572
C-NT2RP2003329//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//3.6E-14//332aa//32%//P26337
C-NT2RP2003367
C-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//5E-131//269aa//91%//P38378
C-NT2RP2003446
C-NT2RP2003533
C-NT2RP2003543//HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE SLR1673 (EC 2.1.1.-).//1.7E-17//148aa//34%//P74261
C-NT2RP2003596
C-NT2RP2003629
C-NT2RP2003687
C-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//5.4E-29//85aa//72%//Q05481
C-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//1.7E-75//147aa//93%//P51669
C-NT2RP2003793
C-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//1.5E-23//200aa//30%//O09175
C-NT2RP2003986
C-NT2RP2004042
C-NT2RP2004316//Homo sapiens chromosome 1 clone J549L20, WORKING DRAFT SEQUENCE, in unordered pieces.//8.2E-202//926bp//100%//AL096820
C-NT2RP2004389//PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR.//9.3E-15//126aa//39%//P38120
C-NT2RP2004392//MNN4 PROTEIN.//1.4E-11//143aa//27%//P36044
C-NT2RP2004463
C-NT2RP2004602
C-NT2RP2004614//Homo sapiens mRNA for KIAA0922 protein, partial cds.//0//2040bp//99%//AB023139
C-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//8.5E-233//1061bp//99%//AJ006291
C-NT2RP2004689//HYPOTHETICAL 192.5 KD PROTEIN C6G9.10C IN CHROMOSOME I.//5.6E-64//616aa//33%//Q92355
C-NT2RP2004791//PUTATIVE LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.4) (LEUCINE-- TRNA LIGASE) (LEURS).//9.5E-73//153aa//59%//Q10490
C-NT2RP2004799//PROBABLE SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//3.7E-135//414aa//62%//P53588
C-NT2RP2004802
C-NT2RP2004841
C-NT2RP2004936
C-NT2RP2004959//P54 PROTEIN PRECURSOR.//0.00000095//297aa//20%//P13692
C-NT2RP2004999

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C-NT2RP2005000
C-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//0//1694bp//99%//AB014515
C-NT2RP2005012//Homo sapiens mRNA for SEC63 protein.//0//1693bp//99%//AJ011779
C-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//3.3E-47//155aa//59%//P32447
C-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//0//2388bp//98%//X98743
C-NT2RP2005140
C-NT2RP2005147
C-NT2RP2005159
C-NT2RP2005239//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2087bp//99%//AF097025
C-NT2RP2005270
C-NT2RP2005276//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2122bp//99%//D89053
C-NT2RP2005293
C-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1515bp//99%//AB014576
C-NT2RP2005358//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds.//0//2199bp//99%//AF072247
C-NT2RP2005393//AUTOANTIGEN NGP-1.//7.2E-39//224aa//35%//Q13823
C-NT2RP2005436//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.2E-13//185aa//38%//Q08170
C-NT2RP2005441
C-NT2RP2005453
C-NT2RP2005464
C-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2.//3E-44//252aa//41%//P38127
C-NT2RP2005472
C-NT2RP2005495
C-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55).//5.2E-81//166aa//88%//P36876
C-NT2RP2005509//Homo sapiens CGI-45 protein mRNA, complete cds.//0//1825bp//99%//AF151803
C-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//3994bp//99%//AF092563
C-NT2RP2005525//Mus musculus kanadaptin mRNA, complete cds.//2.4E-304//1687bp//85%//AF035526
C-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//0//2856bp//99%//AB007963
C-NT2RP2005549//PUTATIVE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE).//2E-20//181aa//36%//Q39366
C-NT2RP2005555
C-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds.//1E-46//576bp//70%//AF062529
C-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//8.9e-313//1455bp//98%//AF062085
C-NT2RP2005622
C-NT2RP2005635//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1E-11//128aa//36%//P47623
C-NT2RP2005637
C-NT2RP2005640
C-NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).//1.2E-13//74aa//45%//P56101
C-NT2RP2005669//Homo sapiens mRNA for DEDD protein.//3.9E-209//957bp//99%//AJ010973
C-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.4E-200//908bp//99%//AF089814
C-NT2RP2005683
C-NT2RP2005690
C-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//0//1684bp//99%//AB018342
C-NT2RP2005723//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN).//0.000000003//169aa//28%//P38074
C-NT2RP2005748
C-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//0//1968bp//99%//AF068868
C-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//1966bp//99%//AF082516

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C-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A (EIF-4A).//1.7E-61//374aa//38%//P47943
C-NT2RP2005767//G.gallus PB1 gene.//5E-163//1158bp//81%//X90849
C-NT2RP2005773//Homo sapiens pyrroline 5-carboxylate reductase isoform (P5CR2) mRNA, complete cds.//2.7E-180//656bp//99%//AF151351
C-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN-BINDING PROTEIN) (SABP).//2.1E-213//249aa//85%//Q02038
C-NT2RP2005781
C-NT2RP2005804
C-NT2RP2005835//SHP1 PROTEIN.//1.8E-28//208aa//32%//P34223
C-NT2RP2005853
C-NT2RP2005868
C-NT2RP2005886
C-NT2RP2005890
C-NT2RP2005901//Homo sapiens mRNA for KIAA0971 protein, complete cds.//0//1977bp//99%//AB023188
C-NT2RP2005933//NUCLEOPORIN NUP57 (NUCLEAR PORE PROTEIN NUP57).//5E-11//155aa//34%//P48837
C-NT2RP2006038
C-NT2RP2006043//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.5E-13//185aa//38%//Q08170
C-NT2RP2006052
C-NT2RP2006069
C-NT2RP2006071
C-NT2RP2006100//Homo sapiens mRNA; cDNA DKFZp564B102 (from clone DKFZp564B102).//0//1759bp//99%//AL049970
C-NT2RP2006106
C-NT2RP2006141
C-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//3.3E-189//899bp//97%//AB014554
C-NT2RP2006196
C-NT2RP2006200
C-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.1E-214//1026bp//97%//X96484
C-NT2RP2006237
C-NT2RP2006238
C-NT2RP2006275//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//2E-59//388aa//32%//P46821
C-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.8E-274//1236bp//99%//AF035262
C-NT2RP2006333
C-NT2RP2006365
C-NT2RP2006393
C-NT2RP2006436//ANTERIOR-RESTRICTED HOMEOBOX PROTEIN (RATHKE POUCH HOMEO BOX).//0.00000034//50aa//50%//Q61658
C-NT2RP2006456
C-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//0//2181bp//99%//AJ006266
C-NT2RP2006467
C-NT2RP2006472
C-NT2RP2006565//Sus scrofa mRNA for SCAMPI protein.//0//1276bp//84%//Y15710
C-NT2RP2006571//CYTOCHROME P450 2G1 (EC 1.14.14.1) (CYPIIG1) (P450-NMB) (OLFACTIVE).//4.2E-134//486aa//50%//P24461
C-NT2RP2006573//2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37) (CNP).//0.0000055//169aa//25%//P09543
C-NT2RP3000031//Homo sapiens mRNA for KIAA0901 protein, complete cds.//0//2547bp//99%//AB020708
C-NT2RP3000072
C-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//0//1404bp//97%//AB011164
C-NT2RP3000220
C-NT2RP3000251
C-NT2RP3000252//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2388bp//99%//AF120334
C-NT2RP3000312
C-NT2RP3000320//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//100%//AJ242978

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C-NT2RP3000333
C-NT2RP3000348
C-NT2RP3000350//PROBABLE GTP-BINDING PROTEIN HP0303.//0.000000028//185aa//31%//O25074
C-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//226aa//92%//P08760
C-NT2RP3000361//Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1/Zer1 and Prp6.//0//2072bp//98%//AB019219
C-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.1E-107//206aa//99%//P35293
C-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)//1.7E-139//679aa//41%//O43143
C-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//0//2364bp//99%//AF071185
C-NT2RP3000484
C-NT2RP3000527//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//4.8E-28//536aa//27%//P28160
C-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//1.9E-12//192aa//30%//P15151
C-NT2RP3000596/TRICHOHYALIN.//2.5E-17//304aa//28%//Q07283
C-NT2RP3000599
C-NT2RP3000632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3E-140//499aa//46%//P51523
C-NT2RP3000644
C-NT2RP3000661
C-NT2RP3000665
C-NT2RP3000690
C-NT2RP3000759//ADP-RIBOSYLATION FACTOR.//7E-28//176aa//34%//Q94650
C-NT2RP3000825//NEUROGENIC LOCUS NOTCH 3 PROTEIN.//2.5E-36//417aa//31%//Q61982
C-NT2RP3000836
C-NT2RP3000841
C-NT2RP3000850
C-NT2RP3000852
C-NT2RP3000859
C-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//6.9E-69//1611bp//61%//U53445
C-NT2RP3000869
C-NT2RP3000901
C-NT2RP3000917//Homo sapiens Dhm1-like protein mRNA, complete cds.//0//3199bp//99%//AF064257
C-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//2.7E-185//585bp//88%//AF015264
C-NT2RP3000980
C-NT2RP3000994//MATERNAL EFFECT PROTEIN STAUFEN.//0.00000006//78aa//48%//P25159
C-NT2RP3001004
C-NT2RP3001081
C-NT2RP3001084
C-NT2RP3001096//Rattus norvegicus leprecan (lepre1) mRNA, complete cds.//1.7E-94//787bp//66%//AF087433
C-NT2RP3001107//PEREGRIN (BR140 PROTEIN).//3E-44//260aa//40%//P55201
C-NT2RP3001109
C-NT2RP3001116
C-NT2RP3001119
C-NT2RP3001133
C-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//0//2802bp//99%//AB018305
C-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//0//2732bp//99%//AJ006266
C-NT2RP3001176//HYPOTHETICAL 65.3 KD PROTEIN IN MAD1-SCY1 INTERGENIC REGION.//1.7E-10//196aa//27%//P53154
C-NT2RP3001214
C-NT2RP3001216//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT).//0.0000023//137aa//33%//P35663
C-NT2RP3001221//GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-BUTYROBETAINE HYDROXYLASE).//1.9E-31//353aa//30%//P80193

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C-NT2RP3001236
C-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CONTAINS: LIGHT CHAIN LC1].//1.2E-166//395aa//51%//P14873
C-NT2RP3001260//Homo sapiens mRNA for KIAA0911 protein, complete cds.//0//2497bp//99%//AB020718
C-NT2RP3001307
C-NT2RP3001325
C-NT2RP3001384//Homo sapiens NAKAP95 mRNA for neighbor of A-kinase anchoring protein 95, complete cds.//0//1213bp//99%//AB025905
C-NT2RP3001392
C-NT2RP3001396
C-NT2RP3001398//TRANSCRIPTIONAL REPRESSOR CTCF.//1.3E-61//374aa//36%//P49711
C-NT2RP3001407//SCY1 PROTEIN.//0.00000033//143aa//25%//P53009
C-NT2RP3001420
C-NT2RP3001426//DNAJ PROTEIN (FRAGMENT).//1E-16//77aa//46%//O33529
C-NT2RP3001427//WERNER SYNDROME HELICASE HOMOLOG.//2.7E-10//159aa//33%//O09053
C-NT2RP3001457
C-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A.//9.1E-13//87aa//43%//P11632
C-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//0//1475bp//99%//U13395
C-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//0//2295bp//99%//AF064801
C-NT2RP3001529//SPO0B-ASSOCIATED GTP-BINDING PROTEIN.//1E-61//345aa//42%//P20964
C-NT2RP3001621
C-NT2RP3001629
C-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210.//6.8E-18//91aa//38%//Q92609
C-NT2RP3001646//WD-40 REPEAT PROTEIN MSI2.//8.8E-09//132aa//31%//O22468
C-NT2RP3001676
C-NT2RP3001679
C-NT2RP3001799//MYOSIN HEAVY CHAIN, STRIATED MUSCLE.//1.6E-11//348aa//27%//P24733
C-NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN).//7.4E-18//249aa//30%//Q04652
C-NT2RP3001896
C-NT2RP3001915
C-NT2RP3001929
C-NT2RP3003193//ZINC FINGER PROTEIN 135.//7.3E-98//269aa//62%//P52742
C-NT2RP3004466
C-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//3.3E-113//466aa//42%//P34110
C-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds.//0//1520bp//99%//AB014532
C-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds.//0//974bp//95%//AB011126
C-NT2RP3004569//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).//0.000000038//150aa//28%//Q01484
C-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds.//0//1770bp//99%//AF026445
C-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//0//1639bp//99%//AB007946
C-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//0//1807bp//99%//AJ006266
C-NT2RP3004617//ZINC-BINDING PROTEIN A33.//7.2E-75//464aa//35%//Q02084
C-NT2RP3004618//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//3972bp//98%//AF093097
C-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN).//1.7E-72//254aa//45%//P54352
C-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64.//2.6E-98//239aa//64%//P35526
C-NT2RP4000051//SYNAPTONEMAL COMPLEX-PROTEIN SC65.//4.9E-51//335aa//37%//Q64375
C-NT2RP4000078//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//3013bp//99%//AB020657
C-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//0//2161bp//99%//AB011538
C-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//728aa//99%//Q10568
C-NT2RP4000129
C-NT2RP4000147//Drosophila melanogaster putative ARF1 GTPase activating protein (ARF1-GAP) mRNA, complete cds.//3.8E-28//528bp//67%//AF011427

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C-NT2RP4000150
C-NT2RP4000151
C-NT2RP4000159
C-NT2RP4000185
C-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//0//4149bp//99%//AB014600
C-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//5.9E-15//104aa//40%//P15287
C-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//0//1932bp//99%//AJ006470
C-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//2.7E-84//208aa//76%//Q03173
C-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).//5.5E-29//153aa//43%//O23968
C-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//3.5E-297//1024aa//55%//P87115
C-NT2RP4000312//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//1.5E-26//237aa//28%//Q01631
C-NT2RP4000323//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.0000003//101aa//32%//P26372
C-NT2RP4000355
C-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//0//4074bp//99%//AB018281
C-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//0//4782bp//99%//AF044195
C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1).//2.6E-77//262aa//54%//O75570
C-NT2RP4000376//Homo sapiens mRNA for phospholipase A2 activating protein.//0//2412bp//99%//AJ238243
C-NT2RP4000381
C-NT2RP4000398//ZINC FINGER PROTEIN 140.//2.9E-110//435aa//50%//P52738
C-NT2RP4000415
C-NT2RP4000417//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113)(MAN(9)-ALPHA-MANNOSIDASE) (FRAGMENT).//2.6E-51//438aa//33%//P45701
C-NT2RP4000448//Homo sapiens mRNA; cDNA DKFZp566G0746 (from clone DKFZp566G0746).//0//3991bp//99%//AL050078
C-NT2RP4000449
C-NT2RP4000455//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//0.0000003//175aa//27%//P09309
C-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15)(DEUBIQUITINATING ENZYME 15).//2.5E-37//291aa//38%//P50101
C-NT2RP4000480
C-NT2RP4000481//ATP-DEPENDENT RNA HELICASE DOB1 (MRNA TRANSPORT REGULATOR MTR4).//1.9E-67//721aa//29%//Q09475
C-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//8.8E-50//214aa//50%//P40484
C-NT2RP4000500
C-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.5E-106//495aa//45%//P45818
C-NT2RP4000524
C-NT2RP4000541
C-NT2RP4000556//SUR4 PROTEIN (SRE1 PROTEIN).//7.4E-14//233aa//31%//P40319
C-NT2RP4000560
C-NT2RP4000588
C-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//2.9E-188//863bp//99%//AF067730
C-NT2RP4000638
C-NT2RP4000648//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//0.00000037//175aa//27%//P09309
C-NT2RP4000657//SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN SPSE.//1.1E-32//350aa//30%//P39625
C-NT2RP4000704
C-NT2RP4000713//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//1.1E-13//295aa//27%//Q11073
C-NT2RP4000724//RETROVIRUS-RELATED ENV POLYPROTEIN.//3.2E-191//199aa//78%//P10267
C-NT2RP4000728//Homo sapiens mRNA for KIAA0931 protein, partial cds.//0//3392bp//95%//AB023148
C-NT2RP4000737

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C-NT2RP4000739//Homo sapiens mRNA for KIAA1012 protein, complete cds.//0//3574bp//99%//AB023229
C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.// 0.000000032//67aa//31%//P53915
C-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds.//0//1927bp//99%//AB007939
C-NT2RP4000833
C-NT2RP4000837//Homo sapiens mRNA for zinc finger protein SALL1.//4.3E-94//810bp//65%//Y18265
C-NT2RP4000839//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.5E-21//271 aa//28%//Q00808
C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE)(ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV)(AP-B).//5.7E-82//324aa//48%//O09175
C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//4.1E-85//174aa//55%//P16415
C-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//6.2E-91//173aa//87%//O35682
C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN).//9.6E-96//513aa//42%//P22314
C-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//2.6E-26// 227aa//36%//Q06828
C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//1.5E-76//346aa//43%//Q61068
C-NT2RP4000928//Homo sapiens mRNA for CDS2 protein.//0//2487bp//99%//Y16521
C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HELICASE MJ1505.//0.00000014//185aa//25%//Q58900
C-NT2RP4000955
C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//1.4E-26// 90aa//42%//P38660
C-NT2RP4000975
C-NT2RP4000979
C-NT2RP4000984
C-NT2RP4000989//UNC-47 PROTEIN.//0.0000082//173aa//25%//P34579
C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//838aa//87%//P70700
C-NT2RP4001004//VACUOLAR PROTEIN 8.//3.7E-16//401aa//26%//P39968
C-NT2RP4001006
C-NT2RP4001010//Homo sapiens mRNA for KIAA0964 protein, complete cds.//0//2482bp//99%//AB023181
C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE)//1.5E-92//443aa//44%//Q09996
C-NT2RP4001057
C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65.//6.7E-51//335aa//37%//Q64375
C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA^{2+}-ATPASE).//1.3E-123// 563aa//46%//P13586
C-NT2RP4001080//Homo sapiens mRNA for Rodi, complete cds.//0//1439bp//99%//AB023967
C-NT2RP4001086
C-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//2.6E-17//121aa//36%//P51400
C-NT2RP4001100
C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.9E-115//224aa//100%// P38378
C-NT2RP4001122//TIPD PROTEIN.//1.4E-65//253aa//41%//O15736
C-NT2RP4001126//TRICHOHYALIN.//2.9E-18//380aa//26%//Q07283
C-NT2RP4001138
C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE (EC 3.5.1.18) (SDAP).//0.00000021// 93aa//33%//P44514
C-NT2RP4001148//SOF1 PROTEIN.//1.3E-104//236aa//52%//P33750
C-NT2RP4001149
C-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).// 3.4E-29//385aa//29%//P35331
C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).// 4.7E-29//227aa//35%//P52178
C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//4.4E-104//1460bp// 65 %//U95760
C-NT2RP4001207

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C-NT2RP4001210
C-NT2RP4001219//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.2E-27//90aa//42%//P38660
C-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//1.8E-103//508aa//43%//Q04652
C-NT2RP4001235
C-NT2RP4001256
C-NT2RP4001260//Homo sapiens mRNA for KIAA0875 protein, partial cds.//0//2876bp//99%//AB020682
C-NT2RP4001274//Human transporter protein (g17) mRNA, complete cds.//4.4E-58//1196bp//61%//U49082
C-NT2RP4001276//TRICHOHYALIN.//7.9E-09//126aa//32-%//Q07283
C-NT2RP4001313//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT).//5.9E-17//296aa//29%//P24391
C-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//8.5E-213//1129bp//92%//AJ001119
C-NT2RP4001339//Homo sapiens mRNA for AMMERC1 protein.//9.2E-160//736bp//99%//AJ007014
C-NT2RP4001343
C-NT2RP4001345//Homo sapiens mRNA for LCAT-like lysophospholipase (LLPL), complete cds.//2.7e-310//1400bp//100%//AB017494
C-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//1.4E-58//2425bp//59%//U53445
C-NT2RP4001353
C-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN).//1.6E-19//222aa//30%//Q08180
C-NT2RP4001373
C-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PROTEIN KINASE 1).//9.2E-17//146aa//35%//P18160
C-NT2RP4001379//HYPOTHETICAL 49.1 KD PROTEIN C11D3.06 IN CHROMOSOME I.//2E-53//436aa//30%//Q10085
C-NT2RP4001407//Homo sapiens mRNA for KIAA0923 protein, complete cds.//0//2716bp//99%//AB023140
C-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//7.7E-190//422aa//82%//Q14141
C-NT2RP4001433//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.2E-138//419aa//54%//Q99676
C-NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//2.7E-66//738bp//71%//AF129131
C-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE).//0//962aa//78%//Q02218
C-NT2RP4001498//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//1E-27//374aa//29%//P39010
C-NT2RP4001502
C-NT2RP4001507
C-NT2RP4001524
C-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENIC REGION.//5.7E-54//242aa//3 8%//P25656
C-NT2RP4001551//Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit mRNA, complete cds.//0//3202bp//99%//AF152961
C-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//4.7E-09//216aa//24%//P96902
C-NT2RP4001567//ARMADILLO SEGMENT POLARITY PROTEIN.//0.00000054//213aa//26,%//Q02453
C-NT2RP4001568//ZINC FINGER PROTEIN GCS1.//1.8E-10//109aa//36%//P35197
C-NT2RP4001571
C-NT2RP4001574//Homo sapiens coat protein gamma-cop mRNA, complete cds.//0//3046bp//99%//AF100756
C-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//0//1087bp//87%//AJ223830
C-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS).//1.7E-141//373aa//47%//P73505
C-NT2RP4001610//Homo sapiens mRNA for KIAA0869 protein, partial cds.//0//1897bp//99%//AB020676
C-NT2RP4001614
C-NT2RP4001634
C-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19.//5.1E-46//234aa//32%//P40469
C-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//6.4E-19//111aa//45%//P25323
C-NT2RP4001677
C-NT2RP4001679
C-NT2RP4001696//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF

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100 KD SUBUNIT).//4E-10//243aa//25%//Q10568
C-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//3E-10//128aa//32%//Q10282
C-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//6.4E-170//1168aa//33%//Q09332
C-NT2RP4001739
C-NT2RP4001753//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.9E-236//665aa//58%//P51523
C-NT2RP4001760//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN).//4.1E-16//263aa//27%//P98174
C-NT2RP4001790//Homo sapiens mRNA for KIAA1015 protein, complete cds.//0//3144bp//99%//AB023232
C-NT2RP4001803
C-NT2RP4001822//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//241aa//30%//O35566
C-NT2RP4001823//MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.//1.1E-19//77aa//54%//P55083
C-NT2RP4001828
C-NT2RP4001838//Homo sapiens CoREST protein (COREST) mRNA, complete cds.//6.3E-99//555.bp//73%//AF155595
C-NT2RP4001861//TRICHOHYALEN.//1E-35//307aa//34%//P37709
C-NT2RP4001893//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp5640043).//0//1306bp//98%//AL050390
C-NT2RP4001896//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E1.//0.000000014//345aa//25%//Q00808
C-NT2RP4001901
C-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.3E-38//258aa//32%//Q12024
C-NT2RP400193 8//TRANSCRIPTIONAL REPRESSOR CTCF.//9.8E-60//303aa//38%//P49711
C-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE).//1.5E-13//211aa//28%//Q43209
C-NT2RP4001950//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//1.2E-13//356aa//27%//P13816
C-NT2RP4001953
C-NT2RP4001966
C-NT2RP4001975
C-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//6.9E-24//370aa//27%//Q04652
C-NT2RP4002052
C-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)//1E-137//679aa//40%//O43143
C-NT2RP4002071
C-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3E-150//722aa//39%//Q05481
C-NT2RP4002081//TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA CHAINS (TFIIA P35 AND P19 SUBUNITS) (TFIIA-42) (TFIIAL).//0.0000067//250aa//31%//P52655
C-NT2RP4002298
C-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.5E-63//159aa//53%//P38938
C-NT2RP4002791
C-NT2RP4002888//Homo sapiens mRNA; cDNA DKFZp434FI 72 (from clone DKFZp434F172).//0//2557bp//99%//AL080202
C-NT2RP4002905
C-NT2RP5003461//RLR1 PROTEIN.//9.7E-22//177aa//27%//P53552
C-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.5E-15//280aa//27%//Q00808
C-NT2RP5003492
C-NT2RP5003500
C-NT2RP5003506
C-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//3.3E-23//219aa//40%//P37116
C-NT2RP5003524
C-NT2RP5003534
C-OVARC1000006//HISTONE H2A.1.//1.1E-55//117aa//99%//P02262
C-OVARC1000013//APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1).//0.0000042//102aa//32%//

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O14727
C-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//2.6E-295//1393bp//97%//AF058922
C-OVARC1000035
C-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE).// 0.00000032//60aa//45 %//P80022
C-OVARC1000087//HISTONE MACRO-H2A.1.//1.6E-12//174aa//26%//Q02874
C-OVARC1000091//HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1) (VCAF) (CFF).// 8.4E-14//259aa//30%//P51610
C-OVARC1000113
C-OVARC1000139//Homo sapiens CGI-21 protein mRNA, complete cds.//0//1562bp//99%//AF132955
C-OVARC1000148
C-OVARC1000151//Homo sapiens partial mRNA for putative protein p38 interacting with transcription factor Sp1.// 2.5E-95//461bp//98%//AJ242975
C-OVARC1000168
C-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//1.8E-32//511bp//65%// AF068332
C-OVARC1000212
C-OVARC1000241//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//8.2E-120//351aa//54%//Q16665
C-OVARC1000288//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)(LEUCINE AMINOPEPTIDASE IV) (LAPIV) (AMINOPEPTIDASE III)(AMINOPEPTIDASE YSCI).//5.4E-53//384aa// 30%//P14904
C-OVARC1000304//PROTEIN MOV-10.//1.1E-249//519aa//87%//P23249
C-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//2.7E-40//154aa//38%//P29363
C-OVARC1000321
C-OVARC1000326
C-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//5.9E-14// 200aa//27%//P40004
C-OVARC1000347
C-OVARC1000384
C-OVARC1000411
C-OVARC1000420
C-OVARC1000437//TENSIN.//7.9E-181//340aa//84%//Q04205
C-OVARC1000443//Homo sapiens mRNA; cDNA DKFZp434A073 (from clone DKFZp434A073).//0//1216bp// 99%//AL080126
C-OVARC1000461
C-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//1.2E-25//227aa//25%//P11075
C-OVARC1000466
C-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE VHR).//3.1E-10//125aa//35%//P51452
C-OVARC1000479//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//1919bp//99%//AB020636
C-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.2E-157//892bp//91 %//AF051850
C-OVARC1000564
C-OVARC1000576
C-OVARC1000588
C-OVARC1000605
C-OVARC1000640
C-OVARC1000649//Human squamous cell carcinama of esophagus mRNA for GRB-7 SH2 domain protein, complete cds.//0//1812bp//98%//D43772
C-OVARC1000661
C-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.1E-46//121aa//79%//P08886
C-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//1.2E-17//127aa//33%//Q58343
C-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//1.5E-178//1113bp//86%//AF001533
C-OVARC1001038//Homo sapiens mRNA for Ariadne-2 protein.//01/1172bp//97%//AJ130978
C-OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.//1E-215//1027bp//98%//AF132946
C-OVARC1001162
C-OVARC1001243
C-OVARC1001296

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C-OVARC1001360
C-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL.//6E-148//683bp//99%//AJ224819
C-OVARC1001425
C-PLACE1000005
C-PLACE1000066//SSU72 PROTEIN.//1.1E-39//206aa//43%//P53538
C-PLACE1000142//3-HYDROXYBUTYRYL-COA DEHYDRATASE (EC 4.2.1.55) (CROTONASE).//2.8E-29//134aa//43%//P52046
C-PLACE1000184//Homo sapiens mRNA for KIAA0832 protein, complete cds.//5.5e-312//1411bp//99%//AB020639
C-PLACE1000185
C-PLACE1000213//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//1904bp//99%//AB023194
C-PLACE1000347
C-PLACE1000374
C-PLACE1000380//Homo sapiens mRNA for KIAA0853 protein, partial cds.//0//2208bp//99%//AB020660
C-PLACE1000383//Homo sapiens mRNA for MTMR1 protein.//0//753bp//99%//AJ224979
C-PLACE1000401//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//2.7E-30//352aa//31%//P15151
C-PLACE1000406//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.2E-132//334aa//72%//P23246
C-PLACE1000420//7.8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE).//0.0000028//134aa//29%//P53368
C-PLACE1000435
C-PLACE1000444
C-PLACE1000562
C-PLACE1000564
C-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-BINDING PROTEIN 1).//1.6E-270//437aa//86%//P32455
C-PLACE1000596//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//2393bp//99%//AB020657
C-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2E-55//779bp//67%//AF044201
C-PLACE1000636//MALE STERILITY PROTEIN 2.//1.2E-39//261aa//27%//Q08891
C-PLACE1000716
C-PLACE1000748
C-PLACE1000755//Homo sapiens mRNA for Helicase-MOI, complete-cds.//4.6E-250//1189bp//97%//AB028449
C-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0//2002bp//99%//AB014548
C-PLACE1000798
C-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR148W.//2.5E-49//181aa//54%//P32899
C-PLACE1000909//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//2.6E-19//404aa//26%//P39010
C-PLACE1000948
C-PLACE1000972
C-PLACE1000977//BETA-CHIMAERIN (BETA-CHIMERIN).//4.4E-22//129aa//35%//Q03070
C-PLACE1001000
C-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//0//1500bp//99%//AF065485
C-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.3E-54//257aa//46%//Q04652
C-PLACE1001383//ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUIEM).//3E-33//138aa//42%//Q61103
C-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//2.3E-61//132aa//46%//Q12929
C-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22_N_12, complete sequence.//0//2118bp//99%//AC005412
C-PLACE1001412
C-PLACE1001484//Homo sapiens chromosome 20 clone 387E22, WORKING DRAFT SEQUENCE, in unordered pieces.//0//1440bp//99%//AL031660
C-PLACE1001503
C-PLACE1001570
C-PLACE1001610
C-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14)

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(THIOESTERASE n).//4E-81//263aa//56%//P08635
C-PLACE1001729
C-PLACE1001739//PUTATIVE ATP-DEPENDENT RNA HEUCASE PL10.//3.5E-75//439aa//41%//P16381
C-PLACE1001781//PROBABLE PHOSPHOMANNOMUTASE (EC 5.4.2.8) (PMM).//5.4E-63//427aa//35%//Q57290
C-PLACE1001810
C-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//0//1995bp//99%//AF058953
C-PLACE1001869//L-RIBULOKINASE (EC 2.7.1.16).//2E-27//270aa//31%//P94524
C-PLACE1001912//Homo sapiens clone 24963 mRNA sequence, complete cds.//0//1196bp//99%//AF131737
C-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1729bp//99%//AF099935
C-PLACE1001928
C-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//1.4E-78//496aa//37%//Q49091
C-PLACE1002046//LIGATIN (FRAGMENT).//1.7E-240//560aa//80%//Q61211
C-PLACE1002072
C-PLACE1002073//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//0.00000053//188aa//29%//P49606
C-PLACE1002140
C-PLACE1002163
C-PLACE1002170
C-PLACE1002433
C-PLACE1002438//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//0.0000042//133aa//29%//Q13105
C-PLACE1002465
C-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//6.7E-214//956bp//94%//AB018256
C-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//0//1750bp//99%//AF068180
C-PLACE1002722//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//9E-45//305aa//33%//Q15391
C-PLACE1002794
C-PLACE1002815
C-PLACE1002839
C-PLACE1002851
C-PLACE1002941
C-PLACE1002996
C-PLACE1003045
C-PLACE1003092
C-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//2.6E-79//253aa//60%//Q13268
C-PLACE1003108
C-PLACE1003145
C-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//3.8E-37//143aa//51%//P42743
C-PLACE1003190//SOF1 PROTEIN.//1.9E-110//325aa//48%//P33750
C-PLACE1003200
C-PLACE1003296//Homo sapiens mRNA; cDNA DKFZp434G173 (from clone DKFZp434G173).//0//1706bp//99%//AL080133
C-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//6.9E-206//396aa//86%//P51522
C-PLACE1003334
C-PLACE1003342
C-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//0//2435bp//99%//U92715
C-PLACE1003369
C-PLACE1003602//Homo sapiens mRNA expressed in placenta.//5.9E-278//1275bp//99%//D83200
C-PLACE1003611
C-PLACE1003625//ARMADILLO SEGMENT POLARITY PROTEIN.//3.2E-10//380aa//25%//P18824
C-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//8E-19//209aa//34%//Q08170
C-PLACE1003711
C-PLACE1003723

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C-PLACE1003762
C-PLACE1003771
C-PLACE1003784
C-PLACE1003923
C-PLACE1003936
C-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN).// 2.4E-124//326aa//73%//P80385
C-PLACE1004104
C-PLACE1004114
C-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA CHAIN 4).//6.1E-181//340aa//96%//P29387
C-PLACE1004149
C-PLACE1004156
C-PLACE1004161
C-PLACE1004183//Homo sapiens for TOM1-like protein.//0//1279bp//97%//AJ010071
C-PLACE1004197//BUTYROPHILIN PRECURSOR (BT).//4.5E-10//208aa//27%//Q62556
C-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.// 0//1882bp//99%//AF069493
C-PLACE1004258
C-PLACE1004270//TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21.-).//9.7E-36//389aa//31%//O15393
C-PLACE1004277//Homo sapiens two pore domain K^+ channel (TASK-2) mRNA, complete cds.//0//1498bp//99%// AF084830
C-PLACE1004289
C-PLACE1004302//SOF1 PROTEIN.//1.9E-110//325aa//48%//P33750
C-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//0//1767bp//99%//Y11588
C-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//0// 2512bp//99%//AF100153
C-PLACE1004376
C-PLACE1004388
C-PLACE1004405
C-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-).//1.2E-39//385aa//33%//Q63448
C-PLACE1004437//Human NAD^+-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//0//985bp//99%//U49283
C-PLACE1004451
C-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0000002//218aa//23%//P25823
C-PLACE1004473
C-PLACE1004510//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete//1.3E-209//954bp// 99%//AF026445
C-PLACE1004516
C-PLACE1004548
C-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//525aa//99%//Q10568
C-PLACE1004629//PROTEIN OS-9 PRECURSOR.//7.7E-18//264aa//32%//Q13438
C-PLACE1004645
C-PLACE1004646//B.taurus mRNA for retinal pigment epithelial membrane receptor p63.//4.4E-42//985bp//59%// X66277
C-PLACE1004664
C-PLACE1004672
C-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//1.6E-95//191aa// 96%//P12815
C-PLACE1004691
C-PLACE1004722
C-PLACE1004736
C-PLACE1004740
C-PLACE1004743//PROBABLE N-END-RECOGNIZING PROTEIN (UBIQUITIN-PROTEIN LIGASE E3 COMPONENT) (N- RECOGNIN).//4.4E-35//578aa//27%//O60152
C-PLACE1004751//Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds.//7.1E-224// 790bp//98%//AB022918

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C-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//1.9E-32//259aa//32%//P30337
C-PLACE1004804//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//4.7E-65//695aa//29%//Q01631
C-PLACE1004814//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//5.9E-19//196aa//36%//Q08170
C-PLACE1004824
C-PLACE1004868//MALE STERILITY PROTEIN 2.//3.9E-39//261aa//27%//Q08891
C-PLACE1004885
C-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//9.3E-11//94aa//47%//O42643
C-PLACE1004918//L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDHA).//4.9E-48//198aa//44%//P06151
C-PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds//0//1853bp//98%//AF099936
C-PLACE1004934
C-PLACE1004937//SEL-10 PROTEIN.//6.3E-125//357aa//58%//Q93794
C-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//2E-14//205aa//26%//Q11073
C-PLACE1004982
C-PLACE1005026
C-PLACE1005027
C-PLACE1005046
C-PLACE1005077
C-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds.//1E-209//1031bp//96%//L40401
C-PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).//2.6E-56//565aa//30%//Q04652
C-PLACE1005111
C-PLACE1005181
C-PLACE1005187//APAG PROTEIN.//3.8E-13//122aa//36%//P05636
C-PLACE1005206
C-PLACE1005232
C-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E-27//349aa//32%//Q01577
C-PLACE1005261
C-PLACE1005266
C-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds.//3.2E-297//1341bp//100%//AB011182
C-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.3E-13//269aa//28%//P53352
C-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//226aa//92%//P08760
C-PLACE1005308
C-PLACE1005313
C-PLACE1005327
C-PLACE1005335
C-PLACE1005373//TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//8.6E-09//194aa//27%//O33335
C-PLACE1005374
C-PLACE1005480
C-PLACE1005481
C-PLACE1005494//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//1649bp//99%//AJ006276
C-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//5.6E-52//173aa//57%//Q09251
C-PLACE1005550
C-PLACE1005554
C-PLACE1005623
C-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//0//2130bp//99%//AF083255
C-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE).//2.1E-148//321aa//83%//P31350

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C-PLACE1005730
C-PLACE1005755
C-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//2.5E-79//209aa//53%//P08635
C-PLACE1005803
C-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.1E-217//994bp//99%//AF027156
C-PLACE1005851
C-PLACE1005921//AIG1 PROTEIN.//3E-31//284aa//31%//P54120
C-PLACE1005923
C-PLACE1005925
C-PLACE1005934
C-PLACE1005936
C-PLACE1005951
C-PLACE1005953//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//6.7E-30//198aa//37%//P43636
C-PLACE1005955//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)//5.4E-54//455aa//32%//P14904
C-PLACE1005966//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAFII-90).//0.00000014//254aa//25%//P38129
C-PLACE1005990
C-PLACE1006011//Homo sapiens mRNA for poly(ADP-ribose) polymerase-2.//0//1564bp//99%//AJ236876
C-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.7E-161//744bp//99%//X99906
C-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.5E-148//681bp//99%//AF039023
C-PLACE1006139
C-PLACE1006159
C-PLACE1006167
C-PLACE1006170//Homo sapiens mRNA for KIAA0899 protein, partial cds.//4.5E-293//953bp//99%//AB020706
C-PLACE1006195
C-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//2.7E-116//496aa//48%//Q09747
C-PLACE1006225
C-PLACE1006236
C-PLACE1006239//BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).//2E-16//244aa//31%//P28675
C-PLACE1006246
C-PLACE1006325//Homo sapiens mRNA; cDNA DKFZp564J142 (from clone DKFZp564J142).//3.8E-278//1271-bp//99%//AL080066
C-PLACE1006335
C-PLACE1006357
C-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//0//1168bp//99%//AF062085
C-PLACE1006412
C-PLACE1006414
C-PLACE1006438//ZINC FINGER PROTEIN 165.//2.5E-45//122aa//43%//P49910
C-PLACE1006445
C-PLACE1006470
C-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//7.7E-55//142aa//85%//Q90595
C-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.1E-229//367aa//96%//Q00004
C-PLACE1006492
C-PLACE1006531
C-PLACE1006552
C-PLACE1006598//Homo sapiens clone NH0310K15, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0//2182bp//99%//AC007383
C-PLACE1006615
C-PLACE1006626//Homo sapiens mRNA for KIAA0928 protein, partial cds.//0//1760bp//99%//AB023145
C-PLACE1006673
C-PLACE1006678//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.8E-24//734bp//62%//AB015630

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C-PLACE1006704
C-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//6.9E-13//177aa//33%//Q59263
C-PLACE1006782
C-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.8E-213//232aa//80%//P08547
C-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN).//2E-15//188aa//29%//P35123
C-PLACE1006883
C-PLACE1006901
C-PLACE1006917//HSH49 PROTEIN.//5.5E-12//97aa//35%//Q99181
C-PLACE1006932
C-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III.//6.7E-48//278aa//41%//Q10000
C-PLACE1006956//ATP-DEPENDENT PERMEASE MDL1.//1.3E-86//522aa//36%//P97998
C-PLACE1006958//Homo sapiens mRNA for heat shock protein apg-1, complete cds.//0//1770bp//99%//AB023421
C-PLACE1006961
C-PLACE1006962
C-PLACE1006966
C-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12) (DER12).//3.2E-35//180aa//33%//Q14542
C-PLACE1007021
C-PLACE1007105
C-PLACE1007178
C-PLACE1007226//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.-) (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1E-42//370aa//31%//P54304
C-PLACE1007238
C-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//6.5E-216//1068bp//96%//D50495
C-PLACE1007242
C-PLACE1007243//UNC-47 PROTEIN.//0.00000017//211aa//27%//P34579
C-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//0//2052bp//99%//Y15908
C-PLACE1007274
C-PLACE1007282
C-PLACE1007301
C-PLACE1007317//Drosophila melanogaster Adrift (adrift) mRNA, complete cds.//4.1E-17//1037bp//56%//AF117649
C-PLACE1007342
C-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//0//2366bp//99%//AF096870
C-PLACE1007367
C-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13.//0.00000044//127aa//30%//P27715
C-PLACE1007386
C-PLACE1007402
C-PLACE1007409//WHITE PROTEIN.//1.1E-64//428aa//32%//Q17320
C-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP).//8.8E-25//140aa//35%//P27487
C-PLACE1007450
C-PLACE1007452
C-PLACE1007460
C-PLACE1007484
C-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//5.4E-53//426aa//33%//P52734
C-PLACE1007507
C-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19).//1.4E-85//385aa//45%//P08728

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C-PLACE1007524
C-PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds.//8.9e-316//1485bp//98%//AF159164
C-PLACE1007544
C-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1E-49//361aa//36%//P34537
C-PLACE1007583
C-PLACE1007598//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.6E-143//666aa//44%//Q99676
C-PLACE1007618//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//713bp//99%//AB023194
C-PLACE1007621
C-PLACE1007632//POLIOVIRUS RECEPTOR PRECURSOR.//0.0000001//228aa//31%//P32506
C-PLACE1007645
C-PLACE1007649//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//1952-bp//99%//AB023194
C-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//8.7E-09//279aa//28%//Q26457
C-PLACE1007690
C-PLACE1007697//GCN20 PROTEIN.//7.6E-119//717aa//38%//P43535
C-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//3431bp//99%//AF061243
C-PLACE1007725
C-PLACE1007729//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.5E-44//231aa//42%//P10265
C-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//9.2E-294//1504bp//94%//AB014585
C-PLACE1007746
C-PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds.//0//1836bp//99%//AB019602
C-PLACE1007810
C-PLACE1007843
C-PLACE1007846//Homo sapiens genomic DNA of 21q22.2 Down Syndrome region, segment 3/13.//0//1751bp//99%//AP000010
C-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//0//3112bp//99%//AB018309
C-PLACE1007897
C-PLACE1007946//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//2.6E-14//370aa//25%//Q99323
C-PLACE1007954
C-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//0//2252bp//99%//AF084530
C-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//0//2300bp//99%//AF079529
C-PLACE1007969//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.1E-36//202aa//48%//P52272
C-PLACE1007990
C-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSYN-110) (SYNAPTIC DENSITY PROTEIN PSD-93).//6.1E-14//128aa//39%//Q63622
C-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0//1833bp//99%//AC005628
C-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NUCLEOPORIN) (P105).//4.6e-318//613aa//94%//P52590
C-PLACE1008095
C-PLACE1008122
C-PLACE1008129
C-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//1.3E-24//395aa//31%//Q09531
C-PLACE1008177/TRICHOHYALIN.//2.3E-29//487aa//26%//P37709
C-PLACE1008209
C-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.3E-283//671aa//77%//P53620
C-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-).//2.3E-18//162aa//37%//P12689
C-PLACE1008280
C-PLACE1008309

BNSDOCID: <EP___1074617A2_I_>

C-PLACE1008329
C-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds.//0//1853bp//100%//AB014579
C-PLACE1008398//GENE 33 POLYPEPTIDE.//7.3E-114//243aa//87%//P05432
C-PLACE1008401
C-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED PROTEIN) (TAP).//0//698aa//95%//P41541
C-PLACE1008429//ANKYRIN HOMOLOG PRECURSOR.//3.1E-11//189aa//32%//Q06527
C-PLACE1008457
C-PLACE1008465
C-PLACE1008488
C-PLACE1008524//Human DNA sequence from clone 34B21 on chromosome 6p12.1-21.1. Contains part of a gene for a novel protein with ZU5 domain similar to part of Tight Junction Protein ZO1 (TJP1) and UNC5 Homologs, the gene for a novel BZRP (peripheral benzodiazapine recepto//0//1980bp//99%//AL031778
C-PLACE1008531
C-PLACE1008532
C-PLACE1008533//101 KD MALARIA ANTIGEN (P101) (ACIDIC BASIC REPEAT ANTIGEN).//1.1E-09//62aa//48%//P22620
C-PLACE1008568
C-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//7.8E-236//453aa//96%//P37199
C-PLACE1008621
C-PLACE1008626
C-PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.//0//1850bp//99%//AJ006591
C-PLACE1008629
C-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//0//1548bp//100%//AF044333
C-PLACE1008693
C-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//0//3002bp//99%//AF038406
C-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBUNIT) (IMPORTIN ALPHA S2).//3.1E-280//533aa//98%//O35345
C-PLACE1008808//Homo sapiens mRNA for cell cycle checkpoint protein rad1A.//2.3E-269//1225bp//99%//AJ004974
C-PLACE1008813
C-PLACE1008854
C-PLACE1008867
C-PLACE1008887
C-PLACE1008902
C-PLACE1008925
C-PLACE1009020//NIFS PROTEIN.//3.9E-55//279aa//41%//P12623
C-PLACE1009027//Homo sapiens mRNA for doublecortin.//0//1919bp//99%//AJ003112
C-PLACE1009045
C-PLACE1009060//BRO1 PROTEIN.//6.7E-19//567aa//24%//P48582
C-PLACE1009090
C-PLACE1009091
C-PLACE1009094//FURIN-LIKE PROTEASE 2 PRECURSOR (EC 3.4.21.75) (FURIN 2).//1.9E-44//480aa//30%//P30432
C-PLACE1009099//ZINC FINGER PROTEIN 41 (FRAGMENT).//1.1E-179//452aa//67%//P51814
C-PLACE1009110
C-PLACE1009111
C-PLACE1009130//UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.2.-) (ONCOGENIC PROTEIN-ASSOCIATED PROTEIN E6-AP).//2E-68//181aa//43%//Q05086
C-PLACE1009158
C-PLACE1009166
C-PLACE1009174
C-PLACE1009186
C-PLACE1009190
C-PLACE1009230

BNSDOCID: <EP___1074617A2_I_>

C-PLACE1009319//Rattus norvegicus outer membrane protein (OMP25) mRNA, complete cds; nuclear gene for mitochondrial product.//2.1E-132//1229bp//75%//AF107295
C-PLACE1009328
C-PLACE1009335
C-PLACE1009338
C-PLACE1009368//METAL HOMEOSTASIS FACTOR ATX2.//2.5E-10//151aa//29%//Q12067
C-PLACE1009375
C-PLACE1009388
C-PLACE1009404//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I.//0.000000047// 165aa7/33%//Q09820
C-PLACE1009434
C-PLACE1009443
C-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//7.8E-71//82aa//89%//P42356
C-PLACE1009459
C-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.1E-289//550aa//93%//P54319
C-PLACE1009476//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//3.9E-40// 179aa//37%//P34580
C-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FACTOR).//8.1E-99//228aa//75%//Q99418
C-PLACE1009542
C-PLACE1009571
C-PLACE1009581
C-PLACE1009596//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.1E-54//291aa//40%//Q00808
C-PLACE1009607
C-PLACE1009621
C-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.3E-60//209aa//41%//P25159
C-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAPI PROTEIN).//1.5E-285//538aa//99%// P55161
C-PLACE1009665
C-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//0//1854bp//100%//AF062534
C-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN CHROMOSOME I.//7E-33//166aa//43%//Q09876
C-PLACE1009721//MSF1 PROTEIN.//1.7E-22//176aa//33%//P35200
C-PLACE1009731//AIG1 PROTEIN.//1.6E-22//274aa//28%//P54120
C-PLACE1009763//Homo sapiens mRNA for Nedd8-activating enzyme hUba3, complete cds.//4.3E-294//1329bp// 100%//AB012190
C-PLACE1009794
C-PLACE1009845//Homo sapiens mRNA for KIAA0905 protein, complete cds.//0//2685bp//99%//AB020712
C-PLACE1009886
C-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC REGION.//1.9E-108//277aa//43%//P53145
C-PLACE1009971
C-PLACE1009992//LIMULUS CLOTTING FACTOR C PRECURSOR (EC 3.4.21.84).//4.6E-59//450aa//34%// P28175
C-PLACE1009995//Homo sapiens mRNA; cDNA DKFZp5640123 (from clone DKFZp5640123).//0//1962bp//99%// AL080122
C-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds.//5.2E-70// 736bp//73%//U48288
C-PLACE1010023
C-PLACE1010031
C-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//6E-279//1402bp//94%//X84692
C-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2019bp//99%//AF065482
C-PLACE1010076
C-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.4E-268//506aa//98%//Q62671
C-PLACE1010102
C-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//7.3E-114//537aa//44%//O04652
C-PLACE1010106//Homo sapiens mRNA; cDNA DKFZp586M1418 (from clone DKFZp586M1418).//0//1974bp//

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99%//AL049385
C-PLACE1010134//TRANSCRIPTION REGULATORY PROTEIN SNF2 (SWI/SNF COMPLEX COMPONENT SNF2) (REGULATORY PROTEIN SWI2) (REGULATORY PROTEIN GAM1) (TRANSCRIPTION FACTOR TYE3).//1.7E-20//156aa//42%//P22082
C-PLACE1010148//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//0.00000046//431aa//23%//P35662
C-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//9.8E-11//95aa//49%//Q01130
C-PLACE1010202
C-PLACE1010261//SEGREGATION DISTORTER PROTEIN.//1.6E-77//214aa//62%//P25722
C-PLACE1010274//Homo sapiens mRNA; cDNA DKFZp5640123 (from clone DKFZp5640123).//0//1964bp//99%//AL080122
C-PLACE1010293
C-PLACE1010321//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//1.1E-09//350aa//22%//P52178
C-PLACE1010324
C-PLACE1010329
C-PLACE1010362//1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE PRECURSOR (EC 3.1.4.10) (PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC).//0.000000002//126aa//29%//P34024
C-PLACE1010364
C-PLACE1010383
C-PLACE1010481//Homo sapiens mRNA for KIAA0836 protein, partial cds.//0//2121bp//99%//AB020643
C-PLACE1010491
C-PLACE1010492
C-PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induced by progesterone), complete cds.//0//1981bp//99%//AB022718
C-PLACE1010529
C-PLACE1010547//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.00000012//616aa//24%//P253 86
C-PLACE1010599//Homo sapiens Pex14 mRNA for peroxisomal membrane anchor protein, complete cds.//0//1904bp//99%//AB017546
C-PLACE1010616
C-PLACE1010622//TROPONIN T, CARDIAC MUSCLE ISOFORMS (TNTC).//0.00000016//120aa//28%//P02642
C-PLACE1010629
C-PLACE1010630
C-PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS13.//5.7E-75//423aa//39%//Q01755
C-PLACE1010714
C-PLACE1010720//Homo sapiens mRNA for chromosome-associated polypeptide-C, complete cds.//4E-299//1091bp//99%//AB019987
C-PLACE1010743//Homo sapiens myosin-IXb splice variant (Myo9b) mRNA, partial cds.//8.9E-91//668bp//82%//AF020267
C-PLACE1010771//M.musculus HCNGP mRNA.//7.4E-168//966bp//89%//X68061
C-PLACE1010786
C-PLACE1010800
C-PLACE1010811
C-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.3E-143//407aa//58%//Q05481
C-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//0//1885bp//99%//AB011182
C-PLACE1010900
C-PLACE2000050
C-PLACE4000522//NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (XOTCH PROTEIN)-//2.4E-191//828aa//48%//P21783
C-PLACE4000590
C-PLACE4000638
C-PLACE4000650//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).//7.9E-17//201aa//34%//P49816
C-Y79AA1001647

BNSDOCID: <EP___1074617A2_I_>

Homology Search Result Data 7.

[0315] The result of the homology search of the SwissProt using the 5'-end sequence (54 clones selected in EXAMPLE 16).

[0316] Data include

the name of clone,
definition of the top hit data,
the P-value: the length of the compared sequence: identity (%), and
the organism and the Accession No. of the top hit data, as in the order separated by //.

[0317] Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000497//METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G).//0.13//52//38//P25860
F-HEMBA1001750//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E).//2.2e-28//104//59//Q24574
F-HEMBA1003854//VERPROLIN.//0.012//138//31//P37370
F-HEMBA1004193//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3) (FRAGMENT).//0.93//39//33//Q37131
F-HEMBA1004860//HIGH POTENTIAL IRON-SULFUR PROTEIN, ISOZYME 2 (HIPIP 2).//0.90//20//50//P38524
F-HEMBA1005572//ZINC FINGER PROTEIN 124 (HZF-16).//7.6e-46//141//58//Q15973
F-HEMBA1006038//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENT).//0.0033//32//46//P70560
F-HEMBA1006092//VERPROLIN.//1.0//62//35//P37370
F-HEMBA1006406//MATING PHEROMONE ER-10 PRECURSOR (EUPLOMONE R10).//0.30//41//36//P12350
F-HEMBA1006650//MATING-TYPE PHEROMONE BAP1(2) PRECURSOR.//0.089//21//52//Q02593
F-HEMBA1006812//HEAT SHOCK PROTEIN HTGA (HEAT SHOCK PROTEIN HTPY).//0.38//156//30//P28697
F-HEMBB1000672
F-HEMBB1001197//DNA-BINDING PROTEIN 65 (PROTEIN GP65).//1.0//30//36//P16012
F-HEMBB1001871//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S1).//3.7e-54//241//47//P47853
F-MAMMA1001252//HYPOTHETICAL 9.1 KD PROTEIN IN NIRQ 3'REGION (ORF3).//0.59//48//39//Q51483
F-MAMMA1002094
F-NT2RM4000634//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).//0.26//58//27//P06333
F-NT2RM4000657//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).//8.9e-20//83//48//P10895
F-NT2RM4000783//ZINC FINGER PROTEIN (FRAGMENT).//1.0//42//40//P19326
F-NT2RM4000857//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR (ALS).//6.0e-23//207//32//O02833
F-NT2RM4001178//HOMEOBOX PROTEIN OTX3 (ZOTX3).//0.012//156//28//Q90267
F-NT2RM4002420//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//0.0012//81//37//P13816
F-NT2RP2000198//CREB-BINDING PROTEIN.//0.29//98//37//Q92793
F-NT2RP2000551//PROTEIN Q300.//0.00017//23//60//Q02722
F-NT2RP2000660//HYPOTHETICAL PROTEIN MJ0401.//1.0//41//29//Q57844
F-NT2RP2001214//MALE SPECIFIC SPERM PROTEIN MST84DC.//0.27//13//61//Q01644
F-NT2RP2001460//PROTEIN KINASE C-LIKE (EC 2.7.1.-).//0.089//99//29//Q99014
F-NT2RP2001756//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT)-//4.0e-13//177//28//P16372
F-NT2RP2002056//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5'REGION.//0.37//12//75//P53820
F-NT2RP2002677//NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3).//0.99//61//32//Q42616
F-NT2RP2002755//OCTAPEPTIDE-REPEAT PROTEIN T2.//3.3e-10//90//35//Q06666
F-NT2RP2002843//CYTOCHROME B.//0.78//103//26//P48884
F-NT2RP2003101//ATPASE INHIBITOR, MITOCHONDRIAL HOMOLOG.//0.40//28//46//P37209
F-NT2RP2003799//HYPOTHETICAL PROTEIN MJ0116.1.//0.80//55//32//P81303
F-NT2RP2004095
F-NT2RP2004732
F-NT2RP2004920//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//0.18//18//55//Q48251
F-NT2RP2005454

BNSDOCID: <EP___1074617A2_I_>

F-NT2RP2005776//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE) (FRAGMENT).//7.4e-38//136//41//P51003
F-NT2RP2005806//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//4.0e-08//180//28//P32323
F-NT2RP2005882
F-NT2RP3001282//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB.//0.0022//69//39//P39217
F-NT2RP3001723//TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3).//0.00035//127//31//P15276
F-NT2RP3002099//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.97//71//28//P05204
F-NT2RP3003155//CCAAT DISPLACEMENT PROTEIN (HOMEOBOX PROTEIN CLOX) (CLOX-1) (FRAGMENT).//0.064//110//34//P39881
F-NT2RP3004028//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.020//95//29//P15583
F-OVARC1000008//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//2.8e-05//165//29//P17437
F-OVARC1000724//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.035//152//30//P10162
F-OVARC1000751//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (VMW118 PROTEIN).//0.38//124//31//P28284
F-OVARC1001029
F-PLACE1000814//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.45//61//24//Q42377
F-PLACE1003030//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29).//0.70//121//32//P47845
F-PLACE1005549//RHO1 GDP-GTP EXCHANGE PROTEIN 1 (PROTEIN KINASE C SUPPRESSOR SKC1).//3.2e-08//205//24//P53046
F-PLACE1007218//IG KAPPA CHAIN V-III REGION (PC 7210).//0.99//52//38//P01668

Homology Search Result Data 8.

[0318] The result of the homology search of the GenBank using the clone sequence of 5'-end (54 clones selected in EXAMPLE 16.) except EST and STS.

[0319] Data include

the name of clone,
definition of the top hit data,
the P-value: the length of the compared sequence: identity (%), and
the Accession No. of the top hit data, as in the order separated by //.

[0320] Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000497
F-HEMBA1001750//Human mitochondrial genes for several tRNAs (Phe, Val, Leu) and 12S and 16S ribosomal RNAs.//6.6e-101//473//99//V00710
F-HEMBA1003854//Homo sapiens clone RG270D13, *** SEQUENCING IN PROGRESS ***, 18 unordered pieces.//1.7e-05//412//61//AC005081
F-HEMBA1004193//Human BAC clone RG343H22 from 7q31, complete sequence.//0.77//466//59//AC002386
F-HEMBA1004860//Human pigment epithelium-derived factor gene, complete cds.//6.7e-07//492//57//U29953
F-HEMBA1005572//HZF-16=Kruppel-related zinc finger gene homolog {alternatively spliced} [human, hepatoblastoma cell line, HEP-G2, mRNA, 2080 nt].//2.9e-47//341//77//S54641
F-HEMBA1006038//Human DNA sequence from clone 989H11 on chromosome 22q13.1-13.2, complete sequence.//0.28//436//59//Z83851
F-HEMBA1006092//Human chromosome 16pl3.11 BAC clone CIT987SK-29B12 complete sequence.//0.28//309//60//U95738
F-HEMBA1006406//HS_2268_B2_C07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=14 Row=F, genomic survey sequence.//3.7e-69//340//99//AQ070566
F-HEMBA1006650//H.sapiens CpG island DNA genomic Mse1 fragment, clone 5h5, forward read cpg5h5.f1a.//9.4e-24//143//96//Z55730
F-HEMBA1006812//X.laevis xUBFalphal mRNA for upstream binding factor 2.//0.96//234//64//X59863

BNSDOCID: <EP___1074617A2_I_>

F-HEMBB1000672//CIT-HSP-2350H6.TF CIT-HSP Homo sapiens genomic clone 2350H6, genomic survey sequence.//1.1e-68//375//94//AQ059158
F-HEMBB1001197//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//2.8e-10//229//66//U95760
F-HEMBB1001871//Equus caballus dermatan sulfate proteoglycan II mRNA, complete cds.//1.2e-27//619//62//AF038127
F-MAMMA1001252
F-MAMMA1002094//H.sapiens CpG island DNA genomic Mse1 fragment, clone 184g7, forward read cpg184g7.ft1a.//3.4e-29//167//97//Z59993
F-NT2RM4000634//Chionoecetes opilio (clone COP41) DNA microsatellite repeat regions.//1.4e-21//230//73//L49136
F-NT2RM4000657//Human mRNA for phospholipase C, complete cds.//0.029//245//61//D42108
F-NT2RM4000783//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence.//3.7e-36//324//70//AC005199
F-NT2RM4000857//RPCI11-49P19.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-49P19, genomic survey sequence.//1.5e-62//322//97//AQ051961
F-NT2RM4001178//Streptomyces coelicolor cosmid 7H1.//0.0025//296//62//AL021411
F-NT2RM4002420//Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.//0.00013//121//76//AC005670
F-NT2RP2000198//Human platelet glycoprotein IX mRNA, 3' end.//0.016//246//62//M25827
F-NT2RP2000551//Rattus norvegicus microsatellite sequence clone 82G9.//2.0e-08//223//69//AJ233812
F-NT2RP2000660//Homo sapiens chromosome 19, cosmid R30953, complete sequence.//0.0073//209//66//AC005622
F-NT2RP2001214
F-NT2RP2001460//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.0//80//76//AC005189
F-NT2RP2001756//CIT-HSP-2373P1.TR CIT-HSP Homo sapiens genomic clone 2373P1, genomic survey sequence.//3.0e-38//220//94//AQ110589
F-NT2RP2002056//Genomic sequence from Human 17, complete sequence.//1.2e-80//317//91//AC002094
F-NT2RP2002677//Homo sapiens chromosome 10 clone CIT987SK-1031G15 map 10q25, *** SEQUENCING IN PROGRESS ***, 1 ordered pieces.//0.032//141//70//AC006097
F-NT2RP2002755//Homo sapiens genomic DNA of 21q22.2 Down Syndrome region, segment 9/13.7/1.8e-22//377//69//AP000018
F-NT2RP2002843//Homo sapiens BAC clone RG030L05 from 7q22, complete sequence.//6.5e-16//311//63//AC005050
F-NT2RP2003101//Human FMR1 gene, 5' end.//0.32//105//67//L19476
F-NT2RP2003799//Human DNA for 5' terminal region of LINE-1 transposable element clone CGL1-4.//1.6e-33//119//96//X52233
F-NT2RP2004095//HS_3083_A1_A02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3083 Col=3 Row=A, genomic survey sequence.//1.0e-14//154//79//AQ106698
F-NT2RP2004732//CIT-HSP-631P16.TP CIT-HSP Homo sapiens genomic clone 631P16, genomic survey sequence.//2.3e-20//120//99//B79035
F-NT2RP2004920//Plasmodium falciparum MAL3P4, complete sequence.//0.030//397//59//AL008970
F-NT2RP2005454//Plasmodium falciparum chromosome 2, section 47 of 73 of the complete sequence.//0.97//455//56//AE001410
F-NT2RP2005776//H.sapiens PAP mRNA.//1.0e-33//451//68//X76770
F-NT2RP2005806//Mus musculus musculus sex determining protein (Sry) gene, complete cds.//0.029//412//60//U70652
F-NT2RP2005882//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//9.4e-25//155//90//Z93242
F-NT2RP3001282//RPCI11-52L16.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-52L16, genomic survey sequence.//3.2e-21//122//100//AQ052775
F-NT2RP3001723//H.sapiens CpG island DNA genomic Mse1 fragment, clone 13g5, reverse read cpg13g5.rt1a.//2.2e-18//163//85//Z56771
F-NT2RP3002099//Homo sapiens chromosome 17, clone hCIT.296_K_1, complete sequence.//1.3e-76//351//86//AC005180
F-NT2RP3003155
F-NT2RP3004028//Sequence 1 from patent US 5618695.//3.3e-13//217//70//I40055

BNSDOCID: <EP___1074617A2_I_>

F-OVARC1000008////0.0040//674//57//M82836
F-OVARC1000724//Herpes simplex virus type I immediate early (IE) gene 3 for transcriptional activator IE175 (= ICP 4)//1.1e-07//519//59//X06461
F-OVARC1000751//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//7.2e-11//509//62//AC004221
F-OVARC1001029//Human DNA sequence from clone 19408 on chromosome 6q24.1-25.3 Contains STS and GSSs, complete sequence.//1.1e-05//388//61//AL031769
F-PLACE1000814//Homo sapiens BAC clone GS011E15 from 5q31, complete sequence.//1.4e-84//717//78//AC002427
F-PLACE1003030
F-PLACE1005549//Human guanine nucleotide regulatory protein (NET1) mRNA, complete cds.//4.9e-56//709//68//U02081
F-PLACE1007218//Homo sapiens chromosome 20 clone RP3-387E22, *** SEQUENCING IN PROGRESS ***, in unordered pieces.//3.1e-39//214//98//AL031660

Homology Search Result Data 9.

[0321] The result of the homology search of the GenBank using the clone sequence of 3'-end (54 clones selected in EXAMPLE 16.) except EST and STS.

[0322] Data include

the name of clone,
definition of the top hit data,
the P-value: the length of the compared sequence: identity (%), and
the Accession No. of the top hit data, as in the order separated by //.

[0323] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

[0324] Data are not shown for the clones in which the P-value was higher than 1.

R-HEMBA1000497//***ALU WARNING: Human Alu-J subfamily consensus sequence.//1.4e-38//185//84//U14567
R-HEMBA1001750//Hansenula wingei mitochondrial DNA, complete sequence.//1.7e-07//399//59//D31785
R-HEMBA1003854//Human DNA sequence from clone 224A6 on chromosome 1p35.1-36.23 Contains part of a gene similar to Mouse Wnt-4 protein, the gene for CDC42 (cell division cycle 42 (GTP-binding protein, 25kD)), ESTs, STSs, GSSs and a CpG Island, complete sequence.//1.4e-75//309//85//AL031281
R-HEMBA1004193//***ALU WARNING: Human Alu-J subfamily consensus sequence.//1.1e-34//188//81//U14567
R-HEMBA1004860//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-06//239//66//AC004241
R-HEMBA1005572//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2, complete sequence.//3.1e-21//341//67//AJ010598
R-HEMBA1006038//Homo sapiens chromosome 19, cosmid R34094, complete sequence.//1.7e-24//307//71//AC004678
R-HEMBA1006092//H.Sapiens mRNA for alpha2-subunit of soluble guanylyl cyclase.//0.76//246//62//X63282
R-HEMBA1006406//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4 Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//1.3e-31//297//77//AL023574
R-HEMBA1006650//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.8e-15//350//65//AC003071
R-HEMBA1006812//Homo sapiens chromosome X clone RP3-424J12, *** SEQUENCING IN PROGRESS ***, in unordered pieces.//1.8e-55//430//81//Z82207
R-HEMBB1000672//Homo sapiens clone UWGC:y54c283 from 6p21, complete sequence.//9.1e-39//437//71//AC006166
R-HEMBB1001197//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.//1.5e-37//275//85//AC004593
R-HEMBB1001871//Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.//0.00097//410//59//AC004688
R-MAMMA1001252//Homo sapiens clone 201104, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.//2.9e-13//364//64//AC004529
R-MAMMA1002094//HS_3163_A1_A09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=17 Row=A, genomic survey sequence.//5.9e-41//256//91//AQ141441

BNSDOCID: <EP___1074617A2_I_>

R-NT2RM4000634//Homo sapiens chromosome 19, cosmid R30783, complete sequence.//1-6e-21//283//73//AC005258
R-NT2RM4000657
R-NT2RM4000783
R-NT2RM4000857//RPCI11-63K2.TK RPCI-11 Homo sapiens genomic clone RPCI-11-63K2, genomic survey sequence.//4.0e-07//62//98//AQ203073
R-NT2RM4001178
R-NT2RM4002420
R-NT2RP2000198//Homo sapiens Chromosome 16 BAC clone CIT987-SK37914 -complete genomic sequence, complete sequence.//0.58//108//67//AC002307
R-NT2RP2000551//Homo sapiens DNA, pseudoautosomal boundary-like sequence PABL2.//6.2e-72//391//87//D30043
R-NT2RP2000660//Homo sapiens chromosome 17, clone hRPK.640_I_15, complete sequence.//0.0058//166//69//AC005324
R-NT2RF2001214//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//0.93//117//65//U49822
R-NT2RP2001460
R-NT2RP2001756//CIT-HSP-2382021.TR CIT-HSP Homo sapiens genomic clone 2382021, genomic survey sequence.//3.4e-91//507//92//AQ114228
R-NT2RP2002056//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//0.00022//225//69//Z97181
R-NT2RP2002677//CIT-HSP-2349K20.TF CIT-HSP Homo sapiens genomic clone 2349K20, genomic survey sequence.//3.1e-29//178//94//AQ062168
R-NT2RP2002755//Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X *.//5.3e-39//449//72//Z81014
R-NT2RP2002843//Homo sapiens chromosome 17, clone hRPK.22_N_12, complete sequence.//0.0097//498//59//AC005412
R-NT2RP2003101//CIT-HSP-238301.TR CIT-HSP Homo sapiens genomic clone 238301, genomic survey sequence.//1.2e-32//344//75//AQ196754
R-NT2RP2003799////3.6e-05//408//60//AL010237
R-NT2RP2004095//Plasmodium falciparum chromosome 4 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.//2.1e-10//455//61//AL034557
R-NT2RP2004732//Human DNA sequence from clone 703H14 on chromosome 1q23.2-24.3 Contains 3' end of a novel gene, ESTs, CA repeat(D1S445), STS, GSSs, complete sequence.//5.1e-51//383//74//AL031287
R-NT2RP2004920//Homo sapiens chromosome 5, P1 clone 878H11 (LBNL H45), complete sequence.//0.062//315//61//AC005219
R-NT2RP2005454//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindDIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//0.75//246//63//Z86062
R-NT2RP2005776//Homo sapiens PAC clone DJ1189D06 from 7p15.3-p14, complete sequence.//0.91//232//61//AC005232
R-NT2RP2005806//Human neurofibromatosis type 1 (NF1) gene, intron 19a, complete sequence.//1.3e-19//405//66//U37368
R-NT2RP2005882//Plasmodium falciparum MAL3P1, complete sequence.//1.1e-09//533//60//Z97348
R-NT2RP3001282//Plasmodium falciparum MAL3P8, complete sequence.//0.00026//499//58//AL034560
R-NT2RP3001723//Human BAC clone RG354L07 from 7q31, complete sequence.//0.00035//337//61//AC002466
R-NT2RP3002099//Homo sapiens chromosome 17, clone hCIT.296_K_1, complete sequence.//1.8e-44//307//86//AC005180
R-NT2RP3003155
R-NT2RP3004028//F14A6-Sp6 IGF Arabidopsis thaliana genomic clone F14A6, genomic survey sequence.//0.95//95//65//B21351
R-OVARC1000008
R-OVARC1000724//Homo sapiens BAC clone RG017K18 from 7q31, complete sequence.//0.91//83//71//AC005161
R-OVARC1000751//HS_2222_A2_C09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=18 Row=E, genomic survey sequence.//2.8e-12//176//72//AQ033143
R-OVARC1001029//Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore X library) and PAC RPCI1-93D11 (from Roswell Park Cancer Center) complete sequence.//1.2e-09//165//75//AC002357

BNSDOCID: <EP___1074617A2_I_>

R-PLACE1000814//Homo sapiens BAC clone GS465N13 from 7p15-p21, complete sequence.//6.2e-52//514//75//AC004744
R-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//9.6e-33//225//90//AF032387
R-PLACE10e5549//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17, complete sequence.//0.097//323//61//AB007644
R-PLACE1007218//Homo sapiens chromosome 20 clone RP3-387E22, *** SEQUENCING IN PROGRESS ***, in unordered pieces.//1.1e-88//497//91//AL031660

Homology Search Result Data 10.

[0325] The result of the homology search of the Human Unigene using the clone sequence of 5'-end (54 clones selected in EXAMPLE 16.) .

[0326] Data include

the name of clone,
title of the top hit data,
the P-value: the length of the compared sequence: identity (%), and
the Accession No. of the top hit data, as in the order separated by //.

[0327] Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000497//ou15a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1626332 3', mRNA sequence.//1.0//186//65//AI018130
F-HEMBA1001750//Human mRNA for TI-227H.//2.5e-101//473//99//D50525
F-HEMBA1003854//Homo sapiens mRNA for KIAA1031 protein, partial cds.//7.2e-06//103//80//AB028954
F-HEMBA1004193//Homo sapiens mRNA for TL132.//0.75//334//59//AJ012755
F-HEMBA1004860//ny07e01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1271064 3' similar to contains Alu repetitive element;, mRNA sequence.//3.7e-06//140//70//AA749151
F-HEMBA1005572//HZF-16=Kruppel-related zinc finger gene homolog {alternatively spliced} [human, hepatoblastoma cell line, HEP-G2, mRNA, 2080 nt].//1.1e-48//341//77//S54641
F-HEMBA1006038//Homo sapiens gene for insulin receptor substrate-2, complete cds.//0.036//297//60//AB000732
F-HEMBA1006092//ab80f12.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853295 3' similar to contains Alu repetitive element;, mRNA sequence.//0.65//150//63//AA663266
F-HEMBA1006406//ws26e11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2498348 3' similar to TR:002710 002710 GAG POLYPROTEIN ; mRNA sequence.//1.4e-32//518//67//AI989639
F-HEMBA1006650//Homo sapiens Arp2/3 protein complex subunit p20-Arc (ARC20) mRNA, complete cds.//1.3e-19//136//90//AF006087
F-HEMBA1006812//zh49f01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415417 3', mRNA sequence.//1.3e-120//579//98//W80404
F-HEMBB1000672//Homo sapiens mRNA for KIAA1040 protein, partial cds.//0.00047//706//57//AB028963
F-HEMBB1001197//tq45e03.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2211772 3' similar to TR:001940 001940 STRAWBERRY NOTCH ;, mRNA sequence.//1.2e-16//117//92//AI580023
F-HEMBB1001871//Human chondroitin/dermatan sulfate proteoglycan (PG40) core protein mRNA, complete cds.//4.6e-26//527//62//M14219
F-MAMMA1001252
F-MAMMA1002094
F-NT2RM4000634//DKFZp434D1813_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1813 5', mRNA sequence.//9.7e-16//226//69//AL040136
F-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//7.6e-179//817//99//AB028992
F-NT2RM4000783//wd82f06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338115 3', mRNA sequence.//1.8e-20//470//65//AI703299
F-NT2RM4000857//Homo sapiens KIAA0416 mRNA, partial cds.//1.9e-46//749//65//AB007876
F-NT2RM4001178//Homo sapiens protein tyrosine phosphatase (PAC-1) mRNA, complete cds.//0.0024//254//63//L11329
F-NT2RM4002420//wg39f11.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367501 3' similar to contains element L1 L1 repetitive element ; mRNA sequence.//1.4e-13//127//84//AI742251

BNSDOCID: <EP___1074617A2_I_>

F-NT2RP2000198//Human mRNA for platelet glycoprotein IX.//0.0033//241//62//X52997
F-NT2RP2000551//ze37d12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361175 3', mRNA sequence.//5.0e-07//116//71//AA017066
F-NT2RP2000660//qx01g11.x1 NCI_CGAP_Br14 Homo sapiens cDNA clone IMAGE:1999364 3', mRNA sequence.//0.027//120//65//AI225283
F-NT2RP2001214
F-NT2RP2001460//wb50h10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309155 3', mRNA sequence.//0.0013//89//78//AI651878
F-NT2RP2001756//zw54e12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773902 3' similar to TR:G456660 G456660 ZINC FINGER PROTEIN ZFP-1 ; mRNA sequence.//2.3e-18//120//93//AA427992
F-NT2RP2002056//tw44g09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2262592 3' similar to contains Alu repetitive element; mRNA sequence.//2.4e-07//99//79//AI811687
F-NT2RP2002677
F-NT2RP2002755//zj83d10.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:461491 3' similar to contains element TAR1 repetitive element ; mRNA sequence.//1.9e-19//229//76//AA705059
F-NT2RP2002843//wt88dl2.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2514551 3' similar to TR: P79522 P79522 MHC CLASS I REGION PROLINE RICH PROTEIN.; mRNA sequence.//8.2e-15//314//67//AI964055
F-NT2RP2003101//wi65a03.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398156 3', mRNA sequence.//0.38//106//68//AI763133
F-NT2RP2003799//Homo sapiens mRNA; cDNA DKFZp564C142 (from clone DKFZp564C142).//2.5e-29//124//91//AL049979
F-NT2RP2004095
F-NT2RP2004732//Homo sapiens mRNA for KIAA0884 protein, partial cds.//2.6e-109//533//96//AB020691
F-NT2RP2004920//wz68d10.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2563219 3' similar to TR: 000172 000172 LINE-1 REVERSE TRANSCRIPTASE ;, mRNA sequence.//0.0020//220//61//AI969546
F-NT2RP2005454//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0.058//143//69//AB023194
F-NT2RP2005776//H.sapiens PAP mRNA.//4.3e-35//451//68//X76770
F-NT2RP2005806//HSZ78328 Human fetal brain S. Meier-Ewert Homo sapiens cDNA clone 2.48 (CEPH) 3', mRNA sequence.//2.0e-05//385//62//Z78328
F-NT2RP2005882//Human mRNA for KIAA0364 gene, complete cds.//7.3e-23//141//94//AB002362
F-NT2RP3001282
F-NT2RP3001723//ws73d05.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2503593 3' similar to contains MSR1.t1 TAR1 TAR1 repetitive element ; mRNA sequence.//2.6e-07//245//66//AW008782
F-NT2RP3002099//yg49d01.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:36239 3', mRNA sequence.//0.58//164//64//R46086
F-NT2RP3003155
F-NT2RP3004028//Homo sapiens mRNA for KIAA1074 protein, complete cds.//1.3e-29//488//66//AB028997
F-OVARC1000008//Homo sapiens mRNA for KIAA0665 protein, complete cds.//0.00032//430//59//AB014565
F-OVARC1000724//Homo sapiens mRNA for KIAA0641 protein, complete cds.//0.0054//426//58//AB014541
F-OVARC1000751//Human Tis11d gene, complete cds.//4.6e-12//527//62//U07802
F-OVARC1001029//qv29c05.x1 NCI_CGAP_Ov31 Homo sapiens cDNA clone IMAGE:1982984 3' similar to contains element L1 repetitive element ; mRNA sequence.//0.0012//145//68//AI252422
F-PLACE1000814//ak42f05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408641 3', mRNA sequence.//7.1e-31//275//76//AA868469
F-PLACE1003030
F-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A.//1.2e-57//737//67//AJ010046
F-PLACE1007218//yo34a08.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:179798 3', mRNA sequence.//2.2e-21//216//76//H52716

Homology Search Result Data 11.

[0328] The result of the homology search of the Human Unigene using the clone sequence of 3'-end (54 clones selected in EXAMPLE 16.).

[0329] Data include

the name of clone,

BNSDOCID: <EP___1074617A2_I_>

title of the top hit data,
the P-value: the length of the compared sequence: identity (%), and
the Accession No. of the top hit data, as in the order separated by //.

[0330] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

[0331] Data are not shown for the clones in which the P-value was higher than 1.

R-HEMBA1000497//np09h02.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1115859 similar to contains Alu repetitive element;contains element MER22 repetitive element ; mRNA sequence.//6.2e-38//185//83// AA614254
R-HEMBA1001750//yy71b10.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE: 278971 3', mRNA sequence.//0.004511193//63//N63303
R-HEMBA1003854//Homo sapiens mRNA; cDNA DKFZp564F133 (from clone DKFZp564F133).//3.4e-72//310// 80//AL049263
R-HEMBA1004193//tr01e08.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2217062 3' similar to contains Alu repetitive element;contains element MER4 repetitive element ; mRNA sequence.//1.5e-33//186//81// AI914747
R-HEMBA1004860//qh16b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844819 3', mRNA sequence.//0.017//118//69//AI218308
R-HEMBA1005572//wj16h05.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2403033 3', mRNA sequence.//4.6e-111//522//99//AI861830
R-HEMBA1006038//DKFZp434E1117_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E1117 5', mRNA sequence.//1.2e-22//295//72//AL041450
R-HEMBA1006092//qt30d09.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE: 1949489 3' similar to contains element PTR5 repetitive element ; mRNA sequence.//1.4e-87//422//98//AI337963
R-HEMBA1006406//Homo sapiens mRNA for KIAA0752 protein, partial cds.//4.1e-30//291-//76//AB018295
R-HEMBA1006650//H.sapiens mRNA for serine/threonine protein kinase EMK.//3.6e-09//319//62//X97630
R-HEMBA1006812//Human mRNA for KIAA0118 gene, partial cds.//3.1e-52//337//87//D42087
R-HEMBB1000672//Homo sapiens mRNA; cDNA DKFZp434M011 (from clone DKFZp434M011).//3.2e-48//276// 74//AL096734
R-HEMBB1001197//zt35b11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724317 5' similar to contains Alu repetitive element; mRNA sequence.//9.9e-44//275//88//AA410788
R-HEMBB1001871//wg20c02.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 2365634 3', mRNA sequence.//6.3e-104//501//98//AI741321
R-MAMMA1001252//aa61h04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825463 3' similar to contains Alu repetitive element;contains element XTR repetitive element ; mRNA sequence.//9.0e-19//127//91// AA504355
R-MAMMA1002094//wd28h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2329511 3', mRNA sequence.//2.5e-68//328//99//AI936520
R-NT2RM4000634//DKFZp434F2016_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434F2016 3', mRNA sequence.//8.2e-20//185//81//AL041146
R-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//5.7e-62//335//94//AB028992
R-NT2RM4000783
R-NT2RM4000857//Human megakaryocyte stimulating factor mRNA, complete cds.//0.00074//360//61//U70136
R-NT2RM4001178//tk08e03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2150428 3', mRNA sequence.//0.77//96//62//AI457506
R-NT2RM4002420//wl58b04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2429071 3', mRNA sequence.//2.4e-85//438//94//AI857508
R-NT2RP2000198//nx19b11.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1256541 3', mRNA sequence.//1.9e-45//270//91//AA738352
R-NT2RP2000551//tg80h11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2115141 3', mRNA sequence.//3.3e-53//311//85//AI417680
R-NT2RP2000660//ns42a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1186258 3', mRNA sequence.//4.3e-26//142//97//AA805691
R-NT2RP2001214//tw65g08.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2264606 3' similar to contains element MSR1 repetitive element ; mRNA sequence.//1.5e-57//289//97//AI680174
R-NT2RP2001460
R-NT2RP2001756//zw54e12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773902 3'

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similar to TR:G456660 G456660 ZINC FINGER PROTEIN ZFP-1 ; mRNA sequence.//6.0e-13//85//96//AA427992
R-NT2RP2002056//yh26a12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130846 3', mRNA sequence.//0.0016//208//65//R22302
R-NT2RP2002677//Homo sapiens mRNA for KIAA0524 protein, partial cds.//3.4e-26//339//71//AB011096
R-NT2RP2002755//qd50d10.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1732915 3', mRNA sequence.//1.5e-26//419//66//AI190698
R-NT2RP2002843//at31f08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2373639 3' similar to contains L1.t1 L1 repetitive element;, mRNA sequence.//1.8e-45//463//74//AI749673
R-NT2RP2003101//ty24h05.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2280057 3', mRNA sequence.//7.5e-73//347//99//AI758824
R-NT2RP2003799//Homo sapiens mRNA for KIAA0751 protein, complete cds.//0.0026//247//65//AB018294
R-NT2RP2004095//zv08c02.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:753026 3' similar to contains element MER32 repetitive element ; mRNA sequence.//9.6e-07//188//66//AA436455
R-NT2RP2004732//tu60a07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2255412 3' similar to contains Alu repetitive element;contains element L1 repetitive element ; mRNA sequence.//4.3e-25//414//68//AI678956
R-NT2RP2004920//wd13h02.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2328051 3', mRNA sequence.//6.8e-91//483//93//AI694022
R-NT2RP2005454//yy77g09.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:279616 3', mRNA sequence.//0.0070//325//59//N48302
R-NT2RP2005776//qq97d06.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1939307 3', mRNA sequence.//7.5e-08//89//82//AI338419
R-NT2RP2005806//wc29h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2316625 3' similar to contains MER2.b3 MER2 repetitive element ; mRNA sequence.//3.2e-16//235//71//AI671398
R-NT2RP2005882//wo31f09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2456969 3', mRNA sequence.//0.00095//352//59//AI925528
R-NT2RP3001282//wg35b03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367053 3', mRNA sequence.//1.7e-113//555//97//AI769199
R-NT2RP3001723//wo48e06.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2458594 3', mRNA sequence.//4.2e-98//471//98//AI926617
R-NT2RP3002099//DKFZp564L227_s1 564 (synonym: hfbr2) Homo sapiens cDNA clone DKFZp564L227 3', mRNA sequence.//9.2e-50//329//87//AL037910
R-NT2RP3003155//zp07a07.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595668 3', mRNA sequence.//1.4e-30//159//99//AA173172
R-NT2RP3004028//Homo sapiens protein kinase C-alpha mRNA, partial 3' UTR.//0.43//66//75//AF035594
R-OVARC1000008//wa69e12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2301454 3', mRNA sequence.//1.0e-77//376//98//AI699393
R-OVARC1000724//tf94b10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2106907 3', mRNA sequence.//0.71//27//100//AI380236
R-OVARC1000751//og93d04.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455847 3', mRNA sequence.//3.5e-13//274//63//AA863306
R-OVARC1001029//yz96e02.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:290906 5' similar to contains Alu repetitive element;contains element PTR5 repetitive element ; mRNA sequence//3.5e-13//175//74//N99464
R-PLACE1000814//tg49a08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112086 3' similar to contains Ll.t2 L1 L1 repetitive element; mRNA sequence.//2.2e-18//285//69//AI424789
R-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//4.0e-34//225//90//AF032387
R-PLACE1005549//tm26b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157693 3', mRNA sequence.//0.91//127//66//AI480253
R-PLACE1007218//yq06e01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:196152 5' similar to contains Alu repetitive element;contains LTR4 repetitive element; mRNA sequence.//2.4e-36//245//87//R92256

Homology Search Result Data 12.

[0332] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences. Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology,

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and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.

C-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS)//6.4E-99//457aa//45%//Q09996
C-HEMBA1000020//Homo sapiens beta 2 gene.//7.5E-264//1194bp//95%//X02344
C-HEMBA1000129//HYTOTHETICAL HELICASE C8A4.08C IN CHROMOSOME I.//3.8E-25//166aa//36%//Q09884
C-HEMBA1000201//Homo sapiensimRNA for integrase interactor 1b protein (INI1B).//0//1612bp//99%//AJ011738
C-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//1E-86//146aa//56%//Q61221
C-HEMBA1000231
C-HEMBA1000264
C-HEMBA1000280
C-HEMBA1000282
C-HEMBA1000303//"Mus musculus Plenty of SH3s (POSH) mRNA, complete cds."//7.1E-254//1440bp//87%//AF030131
C-HEMBA1000333//"Homo sapiens mRNA for KIAA0874 protein, partial cds."//4.8E-253//1148bp//99%//AB020681
C-HEMBA1000351
C-HEMBA1000356//Homo sapiens mRNA; cDNA DKFZp566C243 (from clone DKFZp566C243).//3.3E-287//815bp//98%//AL050274
C-HEMBA1000396
C-HEMBA1000411//ANKYRIN.//5.7E-12//127aa//38%//Q02357
C-HEMBA1000442
C-HEMBA1000456
C-HEMBA1000504
C-HEMBA1000518//PECANEX PROTEIN.//2.1E-19//227aa//38%//P18490
C-HEMBA1000519
C-HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.//2.4E-44//292aa//36%//Q01755
C-HEMBA1000542//"Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds."//2.2E-194//663bp//83%//D89340
C-HEMBA1000545
C-HEMBA1000557
C-HEMBA1000592//"Homo sapiens sorting nexin 6 (SNX6) mRNA, complete cds."//0//1465bp//99%//AF121856
C-HEMBA1000594
C-HEMBA1000604
C-HEMBA1000622
C-HEMBA1000637
C-HEMBA1000655
C-HEMBA1000657//"Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds."//7.2E-156//1366bp//76%//U35776
C-HEMBA1000749
C-HEMBA1000769
C-HEMBA1000773
C-HEMBA1000774
C-HEMBA1000822
C-HEMBA1000843
C-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD).//1E-78//119aa//87%//P51689
C-HEMBA1000870
C-HEMBA1000908
C-HEMBA1000934
C-HEMBA1000972
C-HEMBA1000986
C-HEMBA1000991
C-HEMBA1001008
C-HEMBA1001059//"Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 14."//4.8E-169//786bp//99%//U06088

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C-HEMBA1001094
C-HEMBA1001302//"Homo sapiens calcium binding protein precursor, mRNA, complete cds."//9.6E-258//682bp//94%//AF153686
C-HEMBA1001330
C-HEMBA1001497
C-HEMBA1001569//SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2).//2.3E-53//110aa//100%//P19065
C-HEMBA1001570
C-HEMBA1001620//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.6E-166//506aa//60%//P42803
C-HEMBA1001640
C-HEMBA1001655
C-HEMBA1001672//"Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds."//0//1707bp//98%//AF072247
C-HEMBA1001711
C-HEMBA1001723//"Rattus norvegicus G beta-like protein GBL mRNA, complete cds."//4.7E-172//1240bp//81%//AF051155
C-HEMBA1001746//"Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds."//7.6E-59//998bp//64%//AF098066
C-HEMBA1001781
C-HEMBA1001804//"Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds."//0//1637bp//99%//AF125158
C-HEMBA1001822//"Mus musculus Ese2L protein mRNA, complete cds."//1.9E-235//1329bp//89%//AF132479
C-HEMBA1001824
C-HEMBA1001866//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//5.7E-51//234aa//41%//Q09332
C-HEMBA1001910
C-HEMBA1001913//GCN20 PROTEIN.//2.3E-81//158aa//50%//P43535
C-HEMBA1001921//"Homo sapiens germinal center kinase related protein kinase mRNA, complete cds."//0//1850bp//99%//AF000145
C-HEMBA1001939
C-HEMBA1001950//"Homo sapiens mRNA for KIAA0971 protein, complete cds."//0//1974bp//99%//AB023188
C-HEMBA1001967//"Homo sapiens NY-REN-57 antigen mRNA, partial cds."//0//1721bp//99%//AF155114
C-HEMBA1002035//Homo sapiens mRNA; cDNA DKFZp586E0518 (from clone DKFZp586E0518).//0//2149bp//99%//AL050089
C-HEMBA1002092//"Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds."//1.3E-271//1583bp//88%//U92703
C-HEMBA1002102//ANKYRIN.//4.40E-10//106aa//35%//Q02357
C-HEMBA1002150
C-HEMBA1002151//"Rattus norvegicus p34 mRNA, complete cds."//1.1E-153//1059bp//82%//AF178669
C-HEMBA1002189
C-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//2.2E-199//392aa//89%//P47226
C-HEMBA1002229
C-HEMBA1002241//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//3.70E-06//95aa//33%//P46087
C-HEMBA1002341//"Homo sapiens mRNA for KIAA0771 protein, partial cds."//0//1514bp//99%//AB018314
C-HEMBA1002417//"Homo sapiens chromosome 19, cosmid R28784, complete sequence."//1.4E-299//294bp//100%//AC005954
C-HEMBA1002547//"Homo sapiens agrin precursor mRNA, partial cds."//0//1605bp//97%//AF016903
C-HEMBA1002703
C-HEMBA1002779
C-HEMBA1002816
C-HEMBA1002970

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C-HEMBA1002999//"Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds. "//1.4E-171//1552bp//75%//U20286
C-HEMBA1003021
C-HEMBA1003077//SLIT PROTEIN PRECURSOR.//2.6E-15//199aa//31%//P24014
C-HEMBA1003079
C-HEMBA1003273
C-HEMBA1003304
C-HEMBA1003309
C-HEMBA1003376
C-HEMBA1003384
C-HEMBA1003531
C-HEMBA1003548
C-HEMBA1003556
C-HEMBA1003571
C-HEMBA1003579
C-HEMBA1003684//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//2E-73//526aa//32%//Q13105
C-HEMBA1003692
C-HEMBA1003720
C-HEMBA1003725
C-HEMBA1003729
C-HEMBA1003758
C-HEMBA1003773//"Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds. "//5.8E-81//511bp//86%//U17343
C-HEMBA1003783//"Mus musculus bromodomain-containing protein BP75 mRNA, complete cds."// 1.1E-190//1204bp//84%//AF084259
C-HEMBA1003799
C-HEMBA1003804
C-HEMBA1003805//"Mus musculus KH domain RNA binding protein QKI-5A mRNA, complete cds."// 0//988bp//95%//AF090402
C-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).//8.10E-31//134aa//52%//P40484
C-HEMBA1003856
C-HEMBA1003866//"Mus musculus semaphorin VIa mRNA, complete cds."//1.2E-105//1192bp//70%// AF030430
C-HEMBA1003879
C-HEMBA1003880
C-HEMBA1003893
C-HEMBA1003908
C-HEMBA1003937
C-HEMBA1003942
C-HEMBA1003958
C-HEMBA1003976
C-HEMBA1003978//"Homo sapiens mRNA for KIAA0840 protein, partial cds."//0//1530bp//100%// AB020647
C-HEMBA1003985
C-HEMBA1004011
C-HEMBA1004024
C-HEMBA1004038
C-HEMBA1004045
C-HEMBA1004048
C-HEMBA1004111//"Homo sapiens mRNA for KIAA1276 protein, partial cds."//1.00E-163//751bp// 99%//AB033102
C-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT).//1.6E-166//416aa//72%//Q14141
C-HEMBA1004138
C-HEMBA1004143
C-HEMBA1004150
C-HEMBA1004168//"Homo sapiens geminin mRNA, complete cds."//3.9E-208//951 bp//99%// AF067855
C-HEMBA1004200

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C-HEMBA1004202//RAS-RELATED PROTEIN RAB-13.//6.2E-30//208aa//37%//P51153
C-HEMBA1004203//NUCLEOLAR PROTEIN NOP2.//1.5E-12//258aa//29%//P40991
C-HEMBA1004238
C-HEMBA1004248//"Homo sapiens insulin induced protein 2 mRNA, complete cds."//8.20E-175//552bp//97%//AF125392
C-HEMBA1004272
C-HEMBA1004274
C-HEMBA1004275//"Homo sapiens mRNA for KIAA1111 protein, partial cds."//0//1341bp//99%//AB029034
C-HEMBA1004286//"Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds."//0//1982bp//99%//AF022795
C-HEMBA1004312
C-HEMBA1004321//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.3E-93//357aa//42%//Q99676
C-HEMBA1004323
C-HEMBA1004327
C-HEMBA1004330
C-HEMBA1004341
C-HEMBA1004366
C-HEMBA1004372
C-HEMBA1004389//"Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds."//0//1437bp//99%//AF125158
C-HEMBA1004394
C-HEMBA1004408//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN-10).//3.2E-32//148aa//52%//P52017
C-HEMBA1004429
C-HEMBA1004460
C-HEMBA1004461
C-HEMBA1004502
C-HEMBA1004554
C-HEMBA1004560
C-HEMBA1004610
C-HEMBA1004629
C-HEMBA1004632
C-HEMBA1004637
C-HEMBA1004670
C-HEMBA1004672
C-HEMBA1004697
C-HEMBA1004711
C-HEMBA1004725
C-HEMBA1004730
C-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.9E-39//143aa//52%//P42743
C-HEMBA1004751
C-HEMBA1004752
C-HEMBA1004889//"Human C3f mRNA, complete cds."//6.70E-24//341aa//26%//U72515
C-HEMBA1004934
C-HEMBA1004944
C-HEMBA1004973
C-HEMBA1004977
C-HEMBA1005009//"Homo sapiens BAF53a (BAF53a) mRNA, complete cds."//0//1813bp//99%//AF041474
C-HEMBA1005083
C-HEMBA1005113
C-HEMBA1005133
C-HEMBA1005185
C-HEMBA1005219//NUCLEAR PROTEIN SNF7.//5.3E-10//189aa//25%//P39929
C-HEMBA1005252//"Homo sapiens mRNA for KIAA0585 protein, partial cds."//1.2E-268//1215bp//99%//AB011157

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C-HEMBA1005296
C-HEMBA1005314
C-HEMBA1005331
C-HEMBA1005394
C-HEMBA1005403
C-HEMBA1005423//"Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds. "//2E-213//537bp//99%//AF041248
C-HEMBA1005468
C-HEMBA1005469
C-HEMBA1005474
C-HEMBA1005517
C-HEMBA1005518
C-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1).//3.1E-154//285aa//99%//Q60809
C-HEMBA1005558//NUCLEAR PROTEIN SNF7.//6.40E-16//170aa//31%//P39929
C-HEMBA1005576//"Homo sapiens mRNA for KIAA0463 protein, partial cds."//1.1E-181//835bp// 99%//AB007932
C-HEMBA1005582//"TROPOMYOSIN 1, NON-MUSCLE ISOFORM (TROPOMYOSIN II) (CYTOSKELETAL TROPOMYOSIN)."//0.00000009//213aa//27%//P09492
C-HEMBA1005583
C-HEMBA1005595//"DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC)."//2.3E-54//562aa//29%//P34036
C-HEMBA1005609//Homo sapiens mRNA; cDNA DKFZp564K133 (from clone DKFZp564K133).//2.2e-315// 1448bp//99%//AL050012
C-HEMBA1005621//"Homo sapiens Mad2B protein (MAD2B) mRNA, complete cds."//2.9E-224// 1031bp//99%//AF139365
C-HEMBA1005666
C-HEMBA1005680
C-HEMBA1005685
C-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT).// 4.4E-17//167aa//34%//P25296
C-HEMBA1005746
C-HEMBA1005755
C-HEMBA1005813
C-HEMBA1005822
C-HEMBA1005834
C-HEMBA1005884
C-HEMBA1005891
C-HEMBA1005909
C-HEMBA1005911
C-HEMBA1005931
C-HEMBA1005963
C-HEMBA1005991
C-HEMBA1006005
C-HEMBA1006031//"Homo sapiens mRNA for putative phospholipase, complete cds."//0//1413bp// 99%//AB019435
C-HEMBA1006067
C-HEMBA1006081
C-HEMBA1006091
C-HEMBA1006100
C-HEMBA1006108//"Homo sapiens mRNA for KIAA0943 protein, partial cds."//4.8E-245//764bp// 99%//AB023160
C-HEMBA1006121
C-HEMBA1006130//SEL-10 PROTEIN.//0.000000043//219aa//25%//Q93794
C-HEMBA1006155
C-HEMBA1006158//"Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds." //0//1551bp//99%//AF048693
C-HEMBA1006182
C-HEMBA1006198//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//1.9E-19//215aa//39%//P05142
C-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//0//1615bp//99%//AF070557

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C-HEMBA1006253//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR.//0.00000002//62aa//53%//P42698
C-HEMBA1006259
C-HEMBA1006272//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.3E-123//200aa//73%//P10265
C-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//1E-210//490aa//77%//P25500
C-HEMBA1006283//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2.//0.000000012//176aa//30%//P32505
C-HEMBA1006284
C-HEMBA1006291//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-).//4.2E-12//215aa//23%//P70473
C-HEMBA1006293
C-HEMBA1006309//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION.//1.4E-48//248aa//43%//P38821
C-HEMBA1006349
C-HEMBA1006364
C-HEMBA1006381
C-HEMBA1006398//"Human L1 element L1.6 putative p150 gene, complete cds."//2E-277//1729bp//85%//U93563
C-HEMBA1006445//"Homo sapiens putative tumor supressor NOEY2 mRNA, complete cds."//1.4E-270//1224bp//100%//U96750
C-HEMBA1006483
C-HEMBA1006492
C-HEMBA1006497
C-HEMBA1006502
C-HEMBA1006507//"Homo sapiens mRNA for KIAA0666 protein, partial cds."//0//2334bp//99%//AB014566
C-HEMBA1006535
C-HEMBA1006559//"Mus musculus PRAJA1 (Praja1) mRNA, complete cds."//2.8E-206//1107bp//83%//U06944
C-HEMBA1006566
C-HEMBA1006579
C-HEMBA1006583
C-HEMBA1006612
C-HEMBA1006624//DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG.//0.00000069//109aa//38%//Q58323
C-HEMBA1006643
C-HEMBA1006674
C-HEMBA1006682
C-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMC1-TFG2 INTERGENIC REGION.//3.3E-22//241aa//31%//P53196
C-HEMBA1006717
C-HEMBA1006744
C-HEMBA1006754
C-HEMBA1006767
C-HEMBA1006789
C-HEMBA1006832
C-HEMBA1006885//"Homo sapiens gene for Proline synthetase associated, complete cds."//0//1467bp//96%//AB018566
C-HEMBA1006900
C-HEMBA1006926
C-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.//1.8E-226//1039bp//99%//AJ010841
C-HEMBA1006973//"Homo sapiens rab3-GAP regulatory domain mRNA, complete cds."//5.6E-143//740bp//94%//AF004828
C-HEMBA1006993
C-HEMBA1007002
C-HEMBA1007062
C-HEMBA1007080

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C-HEMBA1007087//HYPOTHETICAL PROTEIN MJ0162.//2E-45//304aa//32%//Q57626
C-HEMBA1007112//Homo sapiens mRNA; cDNA DKFZp586C1817 (from clone DKFZp586C1817).//0//1619bp//99%//AL117450
C-HEMBA1007194//"Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds."//0//1588bp//99%//AF139658
C-HEMBA1007206
C-HEMBA1007256
C-HEMBA1007267
C-HEMBA1007281
C-HEMBA1007300//"Homo sapiens 3',5'-cyclic nucleotide phosphodiesterase 10A1 (PDE10A) mRNA, splice variant 1, complete cds."//0//1519bp//99%//AF127479
C-HEMBA1007301
C-HEMBA1007319
C-HEMBA1007320
C-HEMBA1007327
C-HEMBA1007347
C-HEMBB1000005
C-HEMBB1000030
C-HEMBB1000048
C-HEMBB1000099
C-HEMBB1000141
C-HEMBB1000198
C-HEMBB1000217//"Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds."//0//1038bp//99%//AF090385
C-HEMBB1000218
C-HEMBB1000274
C-HEMBB1000312
C-HEMBB1000402
C-HEMBB1000420
C-HEMBB1000480
C-HEMBB1000530
C-HEMBB1000550
C-HEMBB10000556//"Homo sapiens mRNA for KIAA0750 protein, complete cds."//6.3E-74//1213bp//64%//AB018293
C-HEMBB1000586
C-HEMBB1000592
C-HEMBB1000593//"Homo sapiens transferrin receptor 2 alpha (TFR2) mRNA, complete cds."//1.3E-107//503bp//99%//AF067864
C-HEMBB1000649
C-HEMBB1000693//"Homo sapiens neuroan1 mRNA, complete cds."//0//2952bp//94%//AF040723
C-HEMBB1000822
C-HEMBB1000826
C-HEMBB1000890
C-HEMBB1000915//SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (EC 3.4.21.-).//1.10E-08//129aa//31%//P29122
C-HEMBB1001008
C-HEMBB1001020//"Homo sapiens mRNA for KIAA0889 protein, complete cds."//0//1812bp//98%//AB020696
C-HEMBB1001051
C-HEMBB1001112//"Homo sapiens sec61 homolog mRNA, complete cds."//6E-145//961bp//83%//AF077032
C-HEMBB1001221
C-HEMBB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).//5.4E-93//196aa//54%//P46938
C-HEMBB1001282//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//7E-43//394aa//34%//P16157
C-HEMBB1001302
C-HEMBB1001335
C-HEMBB1001337

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C-HEMBB1001356
C-HEMBB1001364
C-HEMBB1001366
C-HEMBB1001367
C-HEMBB1001527
C-HEMBB1001537
C-HEMBB1002359
C-HEMBB1002415
C-HEMBB1002457
C-HEMBB1002492
C-HEMBB1002495
C-HEMBB1002502
C-HEMBB1002550//HYPOTHETICAL UOG-1 PROTEIN.//5E-28//266aa//33%//P27544
C-HEMBB1002600//"Homo sapiens tetraspan NET-5 mRNA, complete cds."//0//1417bp//99%// AF089749
C-HEMBB1002607//"Homo sapiens vitamin D3 receptor interacting protein (DRIP80) mRNA, complete cds. "//2E-136//660bp//98%//AF105421
C-HEMBB1002684
C-HEMBB1002692
C-HEMBB1002697
C-HEMBB1002705//"Homo sapiens CGI-27 protein mRNA, complete cds."//7.80E-285//841bp//96%// AF132961
C-MAMMA1000019
C-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FM05).//8.2E-198//868bp//99%// Z47553
C-MAMMA1000025
C-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//1.5E-90//323aa//48%//P47226
C-MAMMA1000069
C-MAMMA1000084
C-MAMMA1000139
C-MAMMA1000163
C-MAMMA1000171
C-MAMMA1000173//"Homo sapiens src homology 3 domain-containing protein HIP-55 mRNA, complete cds."//2.6E-164//1044bp//87%//AF197060
C-MAMMA1000277
C-MAMMA1000278
C-MAMMA1000284//P.walti mRNA for mp associated protein 55.//2.2E-109//864bp//76%//X99836
C-MAMMA1000309
C-MAMMA1000312
C-MAMMA1000313
C-MAMMA1000361
C-MAMMA1000388//"Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds."// 0//1466bp//99%//AB015132
C-MAMMA1000395
C-MAMMA1000410
C-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//2.00E-30//119aa// 53%//Q09232
C-MAMMA1000421
C-MAMMA1000422
C-MAMMA1000468
C-MAMMA1000472
C-MAMMA1000490
C-MAMMA1000524
C-MAMMA1000567
C-MAMMA1000612//"Rattus norvegicus G beta-like protein GBL mRNA, complete cds."//1E-95// 1115bp//72%//AF051155
C-MAMMA1000623
C-MAMMA1000625//GYP7 PROTEIN.//2.1E-41//198aa//40%//P48365

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C-MAMMA1000664
C-MAMMA1000670
C-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.-).//4.4E-33//250aa//33%//P42660
C-MAMMA1000713//L-RIBULOKINASE (EC 2.7.1.16).//7.70E-17//246aa//29%//P94524
C-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//1E-77//395aa//45%//014646
C-MAMMA1000734//Homo sapiens mRNA for SEC63 protein.//0//1587bp//99%//AJ011779
C-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//9E-299//1033aa//55%//P87115
C-MAMMA1000746
C-MAMMA1000775
C-MAMMA1000824//ACTIN.//6.2E-20//284aa//28%//P53500
C-MAMMA1000831
C-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4).//7.8E-40//101aa//54%//027540
C-MAMMA1000842
C-MAMMA1000843
C-MAMMA1000856
C-MAMMA1000865
C-MAMMA1000875
C-MAMMA1000906
C-MAMMA1000908
C-MAMMA1000914
C-MAMMA1000956//Homo sapiens CLDN8 gene for claudin-8.//0//1767bp//99%//AJ250711
C-MAMMA1000968
C-MAMMA1000979
C-MAMMA1001008//"Homo sapiens aspartic-like protease mRNA, complete cds."//2.50E-276//1263bp//99%//AF117892
C-MAMMA1001021
C-MAMMA1001041//"SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1)."//1.6E-16//113aa//41%//Q01082
C-MAMMA1001059//Homo sapiens mRNA for DEAD Box Protein 5.//0//1440bp//99%//AJ237946
C-MAMMA1001075//"Homo sapiens CGI-72 protein mRNA, complete cds."//1.3E-181//397bp//98%//AF151830
C-MAMMA1001078
C-MAMMA1001091
C-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN).//4E-49//125aa//68%//P51521
C-MAMMA1001110
C-MAMMA1001126
C-MAMMA1001139//SRE-2 PROTEIN.//5.80E-35//239aa//38%//Q09273
C-MAMMA1001143
C-MAMMA1001154
C-MAMMA1001181//ABC1 PROTEIN HOMOLOG PRECURSOR.//1.30E-07//81aa//45%//Q92338
C-MAMMA1001215
C-MAMMA1001244
C-MAMMA1001259//"Mus musculus F-box protein FBX18 mRNA, partial cds."//2.3E-271//1414bp//89%//AF184275
C-MAMMA1001260//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//2.1E-52//630aa//30%//P34537
C-MAMMA1001343
C-MAMMA1001411//Homo sapiens mRNA; cDNA DKFZp56400823 (from clone DKFZp56400823).//0//2131bp//99%//AL080121
C-MAMMA1001419
C-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) (FRAGMENT).//6.5E-129//260aa//92%//P52623
C-MAMMA1001510
C-MAMMA1001522
C-MAMMA1001576//"Human gamma-tubulin mRNA, complete cds."//7.5E-276//1561bp//90%//

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M61764
C-MAMMA1001604
C-MAMMA1001620
C-MAMMA1001635
C-MAMMA1001649
C-MAMMA1001686
C-MAMMA1001692
C-MAMMA1001743//Y BOX BINDING PROTEIN-1 (Y-BOX TRANSCRIPTION FACTOR).//8.5E-32//171aa//36%//P21573
C-MAMMA1001754//"Homo sapiens CGI-11 protein mRNA, complete cds."//0//1837bp//98%//AF132945
C-MAMMA1001757
C-MAMMA1001764
C-MAMMA1001768//CELL DIVISION CYCLE PROTEIN 48 HOMOLOG MJ1156.//3.8E-45//351aa//38%//Q58556
C-MAMMA1001771//M.musculus mRNA for semaphorin B.//2.60E-200//1272bp//79%//X85991
C-MAMMA1001790
C-MAMMA1001837//ZINC FINGER PROTEIN 29 (ZFP-29).//2.6E-77//507aa//38%//Q07230
C-MAMMA1001858
C-MAMMA1001868//TRICHOHYALIN.//2.7E-19//359aa//25%//P22793
C-MAMMA1001970
C-MAMMA1002042
C-MAMMA1002068
C-MAMMA1002153
C-MAMMA1002156
C-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN).//6E-66//157aa//70%//P15880
C-MAMMA1002174
C-MAMMA1002209
C-MAMMA1002219//"Homo sapiens mRNA for KIAA1067 protein, partial cds."//1.1E-181//861bp//98%//AB028990
C-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR).//8.8E-217//310aa//86%//P70541
C-MAMMA1002243
C-MAMMA1002268//"Mus musculus sphingosine kinase (SPHKIa) mRNA, partial cds."//1E-190//1624bp//76%//AF068748
C-MAMMA1002269
C-MAMMA1002292
C-MAMMA1002294
C-MAMMA1002297//Homo sapiens mRNA for Rab6 GTPase activating protein.//1.1E-214//881bp//97%//AJ011679
C-MAMMA1002312
C-MAMMA1002329//M.musculus mRNA for semaphorin B.//3.80E-45//332bp//84%//X85991
C-MAMMA1002333
C-MAMMA1002351//FERRIPYOCHELIN BINDING PROTEIN.//0.000078//127aa//26%//P40882
C-MAMMA1002353
C-MAMMA1002355
C-MAMMA1002356
C-MAMMA1002362
C-MAMMA1002380
C-MAMMA1002384
C-MAMMA1002427
C-MAMMA1002470//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1E-11//128aa//36%//P47623
C-MAMMA1002485//"Homo sapiens stanniocalcin-related protein mRNA, complete cds."//0//1822bp//99%//AF098462
C-MAMMA1002494
C-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION.//1.2E-34//337aa//31%//P43571
C-MAMMA1002530//"Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete

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cds."//0//1910bp//99%//AF065214
C-MAMMA1002554
C-MAMMA1002585//"Homo sapiens mRNA for KIAA0860 protein, complete cds."//0//1405bp//99%//AB020667
C-MAMMA1002598
C-MAMMA1002619//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//9.5E-16//159aa//37%//Q09931
C-MAMMA1002655//"Homo sapiens mRNA for ganglioside sialidase, complete cds."//0//1515bp//99%//AB008185
C-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.1E-45//618aa//26%//P27550
C-MAMMA1002673
C-MAMMA1002684//"Homo sapiens mRNA for KIAA0214 protein, complete cds."//0//3174bp//99%//D86987
C-MAMMA1002711
C-MAMMA1002769//"Homo sapiens cell cycle progression restoration 8 protein (CPR8) mRNA, complete cds."//2.2E-25//330bp//77%//AF011794
C-MAMMA1002775
C-MAMMA1002782
C-MAMMA1002796
C-MAMMA1002807
C-MAMMA1002838
C-MAMMA1002842//"Mus musculus c-Cb1 associated protein CAP mRNA, complete cds."//2.6E-58//373bp//81%//U58883
C-MAMMA1002869//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//1.4E-160//305aa//85%//P48059
C-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN).//5.7E-30//214aa//35%//P48060
C-MAMMA1002886
C-MAMMA1002890
C-MAMMA1002938//"Homo sapiens mRNA for KIAA0698 protein, complete cds."//8.4E-252//1139bp//100%//AB014598
C-MAMMA1002964
C-MAMMA1003011//HESTONE MACRO-H2A.1.//2.7E-123//370aa//66%//Q02874
C-MAMMA1003013//DNA POLYMERASE BETA (EC 2.7.7.7).//7.4E-46//332aa//36%//P06746
C-MAMMA1003015
C-MAMMA1003019
C-MAMMA1003035//RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//1.9E-13//108aa//33%//P23851
C-MAMMA1003039
C-MAMMA1003044
C-MAMMA1003049
C-MAMMA1003056
C-MAMMA1003057//MD6 PROTEIN.//3.1E-225//419aa//97%//Q60584
C-MAMMA1003066
C-MAMMA1003099
C-MAMMA1003104
C-MAMMA1003113//"Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds."//1.1E-234//1178bp//86%//AF071316
C-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA).//2.2E-105//217aa//89%//P46735
C-MAMMA1003135
C-MAMMA1003146//Homo sapiens mRNA for GalT3 protein.//4.3E-218//996bp//99%//Y15062
C-MAMMA1003150//"Homo sapiens mRNA for KIAA1096 protein, partial cds."/0//1342bp//99%//AB029019
C-MAMMA1003166//"Homo sapiens MLL septin-like fusion protein (MSF) mRNA, complete cds."//3.10E-158//592bp//97%//AF123052
C-NT2RM1000032

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C-NT2RM1000035//"Human mRNA for KIAA0199 gene, partial cds."//0//2948bp//99%//D83782
C-NT2RM1000039//HYPOTHETICAL 41.4 KD PROTEIN IN SRLQ-HYPF INTERGENIC REGION (EC 1.18.1.-) (ORF4) (ORF2).//2.90E-14//299aa//25%//P37596
C-NT2RM1000055//"Homo sapiens mRNA for KIAA0829 protein, partial cds."//0//3111bp//99%// AB020636
C-NT2RM1000059
C-NT2RM1000062
C-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//1.2E-10//150aa//28%//P87072
C-NT2RM1000119
C-NT2RM1000127
C-NT2RM1000131//"Homo sapiens mRNA for KIAA0792 protein, complete cds."//0//2980bp//99%// AB018335
C-NT2RM1000132//"Homo sapiens NADH:ubiquinone oxidoreductas NDUFS6 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds."//7.8E-110//516bp//99%//AF044959
C-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3.3E-3 8//469aa//27%//P49902
C-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//1.2E-10//150aa//28%//P87072
C-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//1.1E-10//94aa//47%//042643
C-NT2RM1000199//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2476bp//99%// AJ245820
C-NT2RM1000244//"Homo sapiens TRAF4 associated factor 1 mRNA, partial cds."//2E-126//592bp// 99%//U81002
C-NT2RM1000252//H.sapiens E-MAP-115 mRNA.//9.7E-35//569bp//64%//X73882
C-NT2RM1000256//"Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds."//0//3012bp//99%//AB016789
C-NT2RM1000260//"Human mRNA for KIAA0130 gene, complete cds."//0//3139bp//98%//D50920.
C-NT2RM1000271
C-NT2RM1000300
C-NT2RM1000314//"Human mRNA for KIAA0159 gene, complete cds."//0//4349bp//99%//D63880
C-NT2RM1000354//"Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds."//7.4E-245//2101bp//68%//AF111423
C-NT2RM1000355//"Homo sapiens transmembrane protein BRI (BRI) mRNA, complete cds."//0// 1599bp//99%//AF152462
C-NT2RM1000365
C-NT2RM1000377//"Homo sapiens dual specificity phosphatase MKP5 (MKP5) mRNA, complete cds." //3.2E-196//1016bp//94%//AF179212
C-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.// 0.000000019//67aa//31%//P53915
C-NT2RM1000399
C-NT2RM1000430//"Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds."// 1.4E-185//1486bp//81%//AF084928
C-NT2RM1000555//"Homo sapiens mRNA for KIAA0885 protein, complete cds."//0//2885bp//99%// AB020692
C-NT2RM1000563//TRANSMISSION-BLOCKING TARGET ANTIGEN S230 PRECURSOR.//0.0000068//199aa// 30%//Q08372
C-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.5E-75//301aa//39%//P43636
C-NT2RM1000661//"Homo sapiens translation initiation factor 4e mRNA, complete cds."//4.3E-210// 960bp//99%//AF038957
C-NT2RM1000666//DNA-BINDING PROTEIN A.//2.2E-09//165aa//34%//P16989
C-NT2RM1000672
C-NT2RM1000691//Homo sapiens mRNA for PLU-1 protein.//0//3104bp//99%//AJ132440
C-NT2RM1000699
C-NT2RM1000741//"Homo sapiens mRNA for KIAA0567 protein, partial cds."//1.1E-295//1338bp// 99%//AB011139
C-NT2RM1000742//"Homo sapiens AC133 antigen mRNA, complete cds."//0//3524bp//99%// AF027208

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C-NT2RM1000746//"Homo sapiens polyamine modulated factor-1 (PMF1) mRNA, complete cds."// 6.70E-227//1043bp//99%//AF141310
C-NT2RM1000770//DXS6673E PROTEIN.//1.4E-39//194aa//48%//Q14202
C-NT2RM1000772//VEGETATTOLE INCOMPATIBILITY PROTEIN HET-E-1.//7.3E-15//280aa//27%//Q00808
C-NT2RM1000780
C-NT2RM1000800//Mus musculus partial mRNA for B-IND1 protein (B-indl gene).//1.1E-98//571bp//89%//Z97207
C-NT2RM1000802
C-NT2RM1000811//"Homo sapiens AC133 antigen mRNA, complete cds."//0//3524bp//99%// AF027208
C-NT2RM1000826//"Homo sapiens mRNA for KIAA0885 protein, complete cds."//0//2885bp//99%// AB020692
C-NT2RM1000829
C-NT2RM1000850//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//9.7E-42//333aa//36%// P16157
C-NT2RM1000852//"Homo sapiens putative ATP-dependent RNA helicase ROK1 mRNA, complete cds. "//0//2206bp//99%//AF077033
C-NT2RM1000857//"Homo sapiens mRNA for KIAA0962 protein, partial cds."//0//3716bp//99%// AB023179
C-NT2RM1000874//"Homo sapiens death effector domain-containing testicular molecule mRNA, complete cds."//1.4E-244//1113bp//99%//AF043733
C-NT2RM1000882//"Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds."//4.30E-122// 1394bp//69%//AF126799
C-NT2RM1000885//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1.8E-56//630aa// 30%//P34537
C-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135)//0//1020aa//89%//P70700
C-NT2RM1000898//"ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR)."//8.9E-26//229aa//29%// P02583
C-NT2RM1000905//"Homo sapiens HSPC021 mRNA, complete cds."//0//1480bp//99%//AF077207
C-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//1E-15//266aa//26%// P46577
C-NT2RM1000927
C-NT2RM1000962
C-NT2RM1000978
C-NT2RM1001003//"Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds."//0// 2230bp//99%//AF030233
C-NT2RM1001043
C-NT2RM1001066
C-NT2RM1001072//"1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II) (PLC-148)."//8.3E-47// 259aa//35%//P08487
C-NT2RM1001085//"Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds. "//3.7E-32//460bp//64%//AF053768
C-NT2RM1001102//"Human HEM45 mRNA, complete cds."//2.3E-27//482bp//63%//U88964
C-NT2RM1001105
C-NT2RM1001139//Homo sapiens mRNA; cDNA DKFZp564F0522 (from clone DKFZp564F0522).//0//1756bp// 99%//AL049943
C-NT2RM2000420
C-NT2RM2000566//"Homo sapiens integrin alpha-7 mRNA, complete cds."//0//2519bp//96%// AF032108
C-NT2RM2000609
C-NT2RM2000612//"Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds."//2.6E-106//1069bp//74%//U35776
C-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//2.9E-103//249aa//73%//P28160
C-NT2RM2001588
C-NT2RM2001605//Homo sapiens mRNA for PLU-1 protein.//0//3114bp//99%//AJ132440
C-NT2RM2001613//"Homo sapiens sec61 homolog mRNA, complete cds."//0//2601bp//99%// AF084458

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C-NT2RM2001632//KES 1 PROTEIN.//1.40E-31//342aa//34%//P35844
C-NT2RM2001648//"Homo sapiens sec61 homolog mRNA, complete cds."//0//2421bp//99%//AF084458
C-NT2RM2001652//"Homo sapiens guanine nucleotide exchange factor mRNA, complete cds."//0//2608bp//99%//AF111162
C-NT2RM2001659//ZINC/CADMIUM RESISTANCE PROTEIN.//3.4E-39//161aa//34%//P20107
C-NT2RM2001664//"Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds."//0//2471bp//99%//AF044195
C-NT2RM2001668//"Homo sapiens putative WHSC1 protein (WHSC1) mRNA, alternative splice product ending in intron 11, complete cds."//6.2E-16//464bp//62%//AF083391
C-NT2RM2001671//"Oryctolagus cuniculus sarcolemmal associated protein (SLAP1) mRNA, complete cds."//0//1843bp//94%//U21155
C-NT2RM2001675
C-NT2RM2001681
C-NT2RM2001688//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I.//4.60E-20//253aa//30%//Q09674
C-NT2RM2001695//Homo sapiens clone H63 unknown mRNA.//0//2016bp//99%//AF103804
C-NT2RM2001696
C-NT2RM2001698//"Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds."//6.2E-253//1170bp//99%//AB028600
C-NT2RM2001700//"ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3.99.-) (VL-CAD) (FRAGMENT)."//5.7E-130//536aa//49%//P50544
C-NT2RM2001716
C-NT2RM2001723
C-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//7.2E-16//381aa//27%//Q09931
C-NT2RM2001743//"Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds."//0//1498bp//99%//AF011792
C-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210.//8.8E-11//119aa//36%//Q92609
C-NT2RM2001760//"Homo sapiens sec61 homolog mRNA, complete cds."//0//2379bp//99%//AF084458
C-NT2RM2001768
C-NT2RM2001771//ZINC FINGER PROTEIN 135.//6.4E-154//394aa//64%//P52742
C-NT2RM2001782//"Homo sapiens GDP-mannose pyrophosphorylase A (GMPPA) mRNA, complete cds."//0//1470bp//99%//AF135422
C-NT2RM2001784
C-NT2RM2001785//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2146bp//99%//AL050118
C-NT2RM2001813
C-NT2RM2001823//CHD1 PROTEIN.//1.8E-106//631aa//39%//P32657
C-NT2RM2001839//"Homo sapiens calumein (Calu) mRNA, complete cds."//0//2415bp//97%//AF013759
C-NT2RM2001840
C-NT2RM2001855
C-NT2RM2001867//"Homo sapiens mRNA for KIAA0943 protein, partial cds."//0//967bp//99%//AB023160
C-NT2RM2001879
C-NT2RM2001983//"Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds."//0//1658bp//98%//AF089816
C-NT2RM2002145//"Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds."//8.5E-191//1524bp//81%//AF084928
C-NT2RM4000027
C-NT2RM4000030//LAS1 PROTEIN.//5.6E-12//184aa//32%//P36146
C-NT2RM4000046//GOLIATH PROTEIN (G1 PROTEIN).//0.000008//112aa//31%//Q06003
C-NT2RM4000155//"THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE--TRNA LIGASE) (THRRS)."//1.2E-157//321aa//61%//P26639
C-NT2RM4000156//H.sapiens HPBRII-7 gene.//3.6E-21//785bp//60%//X67336

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C-NT2RM4000167//"Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds."//0//1946bp//99%//AF071592
C-NT2RM4000199
C-NT2RM4000200
C-NT2RM4000202//ZINC FINGER PROTEIN MOK-2 (HOK-2).//4.9E-32//170aa//41%//Q16600
C-NT2RM4000233//"Mus musculus semaphorin VIa mRNA, complete cds."//3.4E-231//1395bp//86%//AF030430
C-NT2RM4000244
C-NT2RM4000251
C-NT2RM4000265
C-NT2RM4000324
C-NT2RM4000327
C-NT2RM4000356//RAS-RELATED PROTEIN RAB-17.//5.9E-80//213aa//75%//P35292
C-NT2RM4000425
C-NT2RM4000433//"Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds."//4.1E-271//2085bp//77%//AF062476
C-NT2RM4000514
C-NT2RM4000531//ZINC FINGER PROTEIN 29 (ZFP-29).//2.4E-89//389aa//43%//007230
C-NT2RM4000532
C-NT2RM4000534
C-NT2RM4000603
C-NT2RM4000611//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//2.9E-09//108aa//31%//Q00808
C-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//2.7E-146//420aa//60%//P27550
C-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL1374.//1.2E-28//180aa//30%//P74168
C-NT2RM4000689
C-NT2RM4000698
C-NT2RM4000700
C-NT2RM4000712//"Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds."//1E-136//1104bp//77%//AF022789
C-NT2RM4000717
C-NT2RM4000733//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000041//207aa//29%//P52154
C-NT2RM4000734//"Homo sapiens mRNA for KIAA0760 protein, partial cds."//0//2273bp//99%//AB018303
C-NT2RM4000741//"Homo sapiens hSGT1 mRNA for hSgt1p, complete cds."//0//2184bp//99%//D88208
C-NT2RM4000751//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.9E-125//301aa//53%//Q99676
C-NT2RM4000764
C-NT2RM4000778
C-NT2RM4000787
C-NT2RM4000790
C-NT2RM4000795//"Homo sapiens mRNA for KIAA0951 protein, complete cds."//0//1847bp//96%//AB023168
C-NT2RM4000796
C-NT2RM4000798//"Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 mRNA, complete cds."//0//2603bp//99%//AF084521
C-NT2RM4000813
C-NT2RM4000820//VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45 SUBUNIT).//1.10E-24//138aa//44%//P40682
C-NT2RM4000833
C-NT2RM4000848
C-NT2RM4000852
C-NT2RM4000855
C-NT2RM4000887
C-NT2RM4000895
C-NT2RM4000950
C-NT2RM4000979
C-NT2RM4001002//Homo sapiens mRNA; cDNA DKFZp586G0518 (from clone DKFZp586G0518).//0//2259bp//

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100%//AL050092
C-NT2RM4001032
C-NT2RM4001047//M025 PROTEIN.//8E-140//333aa//80%//Q06138
C-NT2RM4001054//"Homo sapiens sec61 homolog mRNA, complete cds."//3.1E-190//1315bp//81%//AF077032
C-NT2RM4001084//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I.//0.000000032//165aa//33%//Q09820
C-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME II.//5.9E-86//292aa//48%//Q09417
C-NT2RM4001140//HOMEOBOX PROTEIN MSH-D.//1E-11//103aa//38%//Q01704
C-NT2RM4001151
C-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN.//4.1E-197//445aa//78%//Q27969
C-NT2RM4001160
C-NT2RM4001187
C-NT2RM4001191//"Homo sapiens clone 24963 mRNA sequence, complete cds."//0//1950bp//99%//AF131737
C-NT2RM4001200//ZINC FINGER PROTEIN 135.//9.5E-135//375aa//60%//P52742
C-NT2RM4001203//"Homo sapiens mRNA for KIAA0839 protein, partial cds."//0//3047bp//99%//AB020646
C-NT2RM4001204//"Homo sapiens mRNA for KIAA1089 protein, partial cds."//0//2349bp//99%//AB029012
C-NT2RM4001217//"Homo sapiens nuclear matrix protein NRP/B (NRPB) mRNA, complete cds."//7.3E-148//1409bp//72%//AF059611
C-NT2RM4001256//"Xenopus laevis putative Zic3 binding protein mRNA, complete cds."//4.30E-55//289bp//77%//AF129131
C-NT2RM4001258
C-NT2RM4001309
C-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-LIKE (EC 2.7.1.137) (PI3-KINASE) (PTDINS-3-KINASE) (PI3K).//3.50E-35//124aa//65%//P54676
C-NT2RM4001316//"ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.3) (MCAD)."//2.3E-31//334aa//30%//P08503
C-NT2RM4001320//"Homo sapiens mRNA for Neuroblastoma, complete cds."//1.8E-39//728bp//64%//D89016
C-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).//1E-28//171aa//37%//P32626
C-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HOL1 INTERGENIC REGION.//8.1E-30//265aa//33%//P53742
C-NT2RM4001347//"Homo sapiens NY-REN-25 antigen mRNA, partial cds."//0//2300bp//99%//AF155103
C-NT2RM4001371//"Homo sapiens IDN3 mRNA, partial cds."//0//2524bp//99%//AB019494
C-NT2RM4001382//"Homo sapiens RanBP7/importin 7 mRNA, complete cds."//2.2E-237//1079bp//99%//AF098799
C-NT2RM4001384
C-NT2RM4001410
C-NT2RM4001411//"Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA, complete cds."//0//1962bp//87%//AF020526
C-NT2RM4001412//"Homo sapiens nGAP mRNA, complete cds."//0//1918bp//99%//AF047711
C-NT2RM4001414
C-NT2RM4001437
C-NT2RM4001444//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS).//1.4E-118//444aa//46%//P73505
C-NT2RM4001454
C-NT2RM4001455
C-NT2RM4001483//ZINC FINGER PROTEIN 136.//5.1E-106//357aa//55%//P52737
C-NT2RM4001489//"Homo sapiens mRNA for KIAA0685 protein, complete cds."//0//1810bp//99%//AB014585
C-NT2RM4001522
C-NT2RM4001557//"Homo sapiens mRNA for KIAA1040 protein, partial cds."//0//1547bp//97%//AB028963

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C-NT2RM4001565
C-NT2RM4001566//"Homo sapiens mRNA for KIAA1114 protein, complete cds."//0//1900bp//99%//AB029037
C-NT2RM4001582//"Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds."//1.5E-284//1082bp//90%//AF071317
C-NT2RM4001592//"Homo sapiens mRNA for KIAA1122 protein, partial cds."//0//2170bp//99%//AB032948
C-NT2RM4001594
C-NT2RM4001597//M.musculus red-1 gene.//2.1E-171//1414bp//78%//X92750
C-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).//2.6E-32//203aa//39%//Q12600
C-NT2RM4001629//"MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LARGE HOMOLOG 3)."//1.5E-93//278aa//38%//Q13368
C-NT2RM4001650
C-NT2RM4001662
C-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REGION.//2.7E-84//410aa//42%//P37339
C-NT2RM4001682
C-NT2RM4001710
C-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT).//8.9E-141//354aa//72%//Q14141
C-NT2RM4001715
C-NT2RM4001731//"Homo sapiens mRNA for KIAA1004 protein, partial cds."//0//1922bp//100%//AB023221
C-NT2RM4001746
C-NT2RM4001754
C-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.1.-).//4.1E-186//639aa//58%//Q05512
C-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1).//7.9E-66//311aa//35%//Q03164
C-NT2RM4001810//"Homo sapiens mRNA for KIAA0863 protein, complete cds."//0//2377bp//99%//AB020670
C-NT2RM4001813//LECTIN BRA-2.//0.00000048//114aa//30%//P17346
C-NT2RM4001823//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).///2.9E-55//325aa//37%//P28160
C-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.9E-161//481aa//56%//P51523
C-NT2RM4001836
C-NT2RM4001841//"Homo sapiens mRNA for KIAA0920 protein, complete cds."//0//1861bp//98%//AB023137
C-NT2RM4001842
C-NT2RM4001856
C-NT2RM4001858//T-BOX CONTAINING PROTEIN TBX6L (FRAGMENT).//6.5E-22//126aa//46%//P79779
C-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//4.3E-244//1248bp//94%//Y17711
C-NT2RM4001876//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//6.5E-23//184aa//36%//Q15404
C-NT2RM4001880//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-).//5.9E-09//268aa//26%//P47486
C-NT2RM4001922//"Homo-sapiens mRNA for KIAA0957 protein, complete cds."//0//2165bp//99%//AB023174
C-NT2RM4001930//"Homo sapiens dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl glucosyltransferase (ALG6) mRNA, complete cds."//0//1930bp//99%//AF102851
C-NT2RM4001940//"Homo sapiens timeless homolog mRNA, complete cds."//0//2087bp//99%//AF098162
C-NT2RM4001953
C-NT2RM4001965
C-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//2.6E-261//1563bp//84%//X99330
C-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.8E-112//457aa//47%//P51523
C-NT2RM4001984
C-NT2RM4001987//"NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM 180) [CONTAINS: N-CAM 140]."//3.2E-17//281aa//30%//P16170
C-NT2RM4002013//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1

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INTERGENIC REGION.//6.9E-94//589aa//35%//P42935
C-NT2RM4002018
C-NT2RM4002034//"Homo sapiens hiwi mRNA, partial cds."//1.9E-53//1585bp//60%//AF104260
C-NT2RM4002044
C-NT2RM4002054
C-NT2RM4002063//"Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds."//0//1865bp//99%//U82267
C-NT2RM4002066//"Homo sapiens thyroid hormone receptor-associated protein complex component TRAP230 mRNA, complete cds."//1.50E-211//1123bp//71%//AF117755
C-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//2.8E-105//556aa//41%//Q04652
C-NT2RM4002128
C-NT2RM4002140
C-NT2RM4002145//SLIT PROTEIN PRECURSOR.//1.40E-09//127aa//33%//P24014
C-NT2RM4002161//"Homo sapiens laforin (EPM2A) mRNA, complete cds."//0//2671bp//99%//AF084535
C-NT2RM4002174//MRP PROTEIN.//9.1E-68//264aa//51%//P21590
C-NT2RM4002189//"GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)."//6.2E-33//688aa//27%//P08640
C-NT2RM4002205//"ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)."//3E-37//122aa//72%//Q07803
C-NT2RM4002213//"Homo sapiens protein phosphatase methylesterase-1 (PME-1) mRNA, complete cds."//0//2452bp//100%//AF157028
C-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//3.7E-19//147aa//41%//P40809
C-NT2RM4002251//"ALPHA-1,3-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.101) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE I) (GNT-I) (GLCNAC-TI)."//2.2E-36//320aa//38%//P27808
C-NT2RM4002256
C-NT2RM4002266
C-NT2RM4002281
C-NT2RM4002287
C-NT2RM4002294
C-NT2RM4002301
C-NT2RM4002323//ANTIGEN GOR (FRAGMENT).//0.000000001//154aa//33 %//P48778
C-NT2RM4002339
C-NT2RM4002344
C-NT2RM4002373//"Homo sapiens mRNA for KIAA0649 protein, complete cds."//0//2666bp//99%//AB014549
C-NT2RM4002374
C-NT2RM4002383
C-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.3E-29//275aa//30%//P27095
C-NT2RM4002438//"Xenopus laevis putative Zic3 binding protein mRNA, complete cds."//1.1E-49//611bp//70%//AF129131
C-NT2RM4002446
C-NT2RM4002452
C-NT2RM4002457
C-NT2RM4002460//"ENV POLYPROTEIN (COAT POLYPROTEIN) [CONTAINS: COAT PROTEINS GP70, GP20]."//0.0000016//226aa//24%//P51515
C-NT2RM4002493
C-NT2RM4002527//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.9E-15//366aa//27%//Q00808
C-NT2RM4002532//PROTEIN HOM1.//2E-16//276aa//28%//P55137
C-NT2RM4002558//"Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds."//0//1797bp//99%//AF055899
C-NT2RM4002567
C-NT2RM4002593
C-NT2RM4002594//MSP1 PROTEIN HOMOLOG.//2.7E-68//236aa//58%//P54815
C-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//2.3E-101//488aa//45%//032038

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C-NT2RP1000324
C-NT2RP1000363//"Homo sapiens mRNA for KIAA0638 protein, partial cds."//0//1345bp//99%//AB014538
C-NT2RP1000418
C-NT2RP1000513//"Human NifU-like protein (hNifU) mRNA, partial cds."//6.50E-171//516bp//99%//U47101
C-NT2RP1000721
C-NT2RP1000730
C-NT2RP1000767
C-NT2RP1000836
C-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//5.2E-20//306aa//33%//Q09531
C-NT2RP1000943
C-NT2RP1001033//"Homo sapiens delta-tubulin mRNA, complete cds."//2.10E-285//1290bp//100%//AF201333
C-NT2RP1001073//"Homo sapiens U6 snRNA-associated Sm-like protein LSm5 mRNA, complete cds."//8.1E-107//504bp//99%//AF182291
C-NT2RP1001199
C-NT2RP1001248
C-NT2RP1001253//"Homo sapiens oscillin (hLn) mRNA, complete cds."//0//2020bp//99%//AF029914
C-NT2RP1001286
C-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//32%//Q12024
C-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//32%//Q12024
C-NT2RP1001310//"Homo sapiens mitochondrial carrier homolog 1 isoform a mRNA, partial cds; nuclear gene for mitochondrial product."//0//1732bp//99%//AF176006
C-NT2RP1001361//"Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA, complete cds."//6.5E-116//541bp//100%//AF070652
C-NT2RP1001385//HYPOTHETICAL 48.8 KD PROTEIN IN SSU81-SCS2 INTERGENIC REGION.//2.7E-22//284aa//25%//P40074
C-NT2RP1001432
C-NT2RP2000040//"Homo sapiens mRNA for KIAA0747 protein, partial cds."//0//2648bp//99%//AB013290
C-NT2RP2000076//Homo sapiens partial mRNA for polyhomeotic 2 protein (PH2 gene).//7.9E-20//265bp//73%//AJ242730
C-NT2RP2000098
C-NT2RP2000108
C-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//9.7E-41//278aa//36%//P40556
C-NT2RP2000258//ACTIVATOR 1 140 KD SUBUNIT (REPLICATION FACTOR C LARGE SUBUNIT) (A1 140 KD SUBUNIT) (RF-C 140 KD SUBUNIT) (ACTIVATOR 1 LARGE SUBUNIT) (DNA-BINDING PROTEIN PO-GA).//7.1E-12//213aa//23%//P35251
C-NT2RP2000289
C-NT2RP2000327
C-NT2RP2000337
C-NT2RP2000420//ZINC FINGER PROTEIN 165.//8.5E-33//155aa//52%//P49910
C-NT2RP2000459
C-NT2RP2000498
C-NT2RP2000758
C-NT2RP2001137
C-NT2RP2001149
C-NT2RP2001168//VERPROLIN.//1.5E-09//143aa//33%//P37370
C-NT2RP2001173//"Homo sapiens mRNA for KIAA0480 protein, complete cds."//0//1780bp//99%//AB007949
C-NT2RP2001174//GASTRULA ZINC FINGER PROTEIN XLCGF46.1 (FRAGMENT).//6E-10//88aa//38%//P18722
C-NT2RP2001196
C-NT2RP2001226
C-NT2RP2001268//"Homo sapiens mRNA for KIAA0810 protein, partial cds."//0//3301bp//98%//AB018353

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C-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-ALPHA HOMOLOG) (BRAIN PROTEIN 147) (FRAGMENT).//4.4E-91//179aa//99%//P28663
C-NT2RP2001295//ZINC/CADMIUM RESISTANCE PROTEIN.//8.3E-39//161aa//34%//P20107
C-NT2RP2001312
C-NT2RP2001327//"TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN)."//5.5E-116//311aa//71%//Q13829
C-NT2RP2001328
C-NT2RP2001366
C-NT2RP2001378//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//2E-11//403aa//25%//Q02817
C-NT2RP2001392//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//8.4E-192//581aa//54%//P93647
C-NT2RP2001394//Homo sapiens mRNA for SCML2 protein.//0//2068bp//99%//Y18004
C-NT2RP2001420//"Mus musculus nuclear protein NIP45 mRNA, complete cds."//9E-112//742bp//82%//U76759
C-NT2RP2001450
C-NT2RP2001467
C-NT2RP2001506
C-NT2RP2001511//"Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds."//3.2E-297//2206bp//75 %//AF093097
C-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1.//0//2502bp//99%//Y14494
C-NT2RP2001536//"Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds."//0//2326bp//99%//AF035586
C-NT2RP2001560//VAV2 PROTEIN.//0.00000015//219aa//27%//Q60992
C-NT2RP2001576//HYPOTHETICAL 62.2 KD PROTEIN C4G8.12C IN CHROMOSOME I.//8.2E-29//294aa//31%//Q09837
C-NT2RP2001581
C-NT2RP2001597//"RYANODINE RECEPTOR, CARDIAC MUSCLE."//0.000000036//127aa//36%//P30957
C-NT2RP2001628
C-NT2RP2001663//ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).//1.1E-47//126aa//53%//P42897
C-NT2RP2001748//FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS) (FARNESYL DIPHOSPHATE SYNTHETASE) (DIMETHYLALLYLTRANSFERASE (EC 2.5.1.1) / GERANYLTRANSTRANSFERASE (EC 2.5.1.10)) (KIAA0032).//5.40E-47//96aa//97%//P14324
C-NT2RP2001813
C-NT2RP2001883//"Homo sapiens CGI-01 protein mRNA, complete cds."//0//2306bp//99%//AF132936
C-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5.//2.3E-38//395aa//30%//P53946
C-NT2RP2001947
C-NT2RP2001985//"Homo sapiens high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha mRNA, complete cds."//2.00E-38//435bp//67%//AF090989
C-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//6.5E-129//279aa//85%//Q08469
C-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//1.7E-47//247aa//52%//P35331
C-NT2RP2002058//"Homo sapiens WD repeat protein WDR3 (WDR3) mRNA, complete cds."//0//2510bp//99%//AF083217
C-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.7/1.5E-294//1334bp//99%//AF052183
C-NT2RP2002078//PECANEX PROTEIN.//1.8E-09//195aa//32%//P18490
C-NT2RP2002079//"HISTONE H1, GONADAL."//4.4E-11//214aa//34%//P02256
C-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//3389bp//99%//AJ007509
C-NT2RP2002185//"Homo sapiens ubiquilin mRNA, complete cds."//0//1789bp//99%//AF176069
C-NT2RP2002193//"Homo sapiens PIAS3 mRNA for protein inhibitor of activatied STAT3, complete cds."//0//2809bp//99%//AB021868
C-NT2RP2002231
C-NT2RP2002235
C-NT2RP2002252//"Mus musculus (clone pVZmSin3A9) mSin3A9 mRNA, complete cds."//0//3118bp//91%//L38621

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C-NT2RP2002292
C-NT2RP2002408
C-NT2RP2002442//HESA PROTEIN.//2.8E-14//163aa//30%//P46037
C-NT2RP2002464//DNA CROSS-LINK REPAIR PROTEIN PS02/SNM1.//6.50E-07//171aa//27%//P30620
C-NT2RP2002498
C-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC1744).//4.6E-144//537aa//49%//Q02386
C-NT2RP2002520//"Homo sapiens transcription factor RFX-B (RFXB) mRNA, complete cds."//3.70E-34//668bp//61%//AF105427
C-NT2RP2002549
C-NT2RP2002609//2-HYDROXYMUCONIC SEMIALDEHYDE HYDROLASE (EC 3.1.1.-) (HMSH).//2.80E-08//109aa//37%//P19076
C-NT2RP2002706
C-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1.//4.9E-85//489aa//43%//P55194
C-NT2RP2002800
C-NT2RP2002880//GLUCOSE REPRESSION MEDIATOR PROTEIN.//0.000039//206aa//23%//P14922
C-NT2RP2002891
C-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II.//4.1E-87//395aa//40%//Q18964
C-NT2RP2002939//ZINC FINGER PROTEIN 136.//5.4E-70//282aa//42%//P52737
C-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//716aa//91%//P70700
C-NT2RP2003034
C-NT2RP2003099
C-NT2RP2003137//UBIQUITIN.//0.000026//70aa//30%//P13117
C-NT2RP2003157//"Homo sapiens CGI-74 protein mRNA, complete cds."//0//2037bp//99%//AF151832
C-NT2RP2003158//"Homo sapiens mRNA for proteasome subunit p58, complete cds."//0//2091bp//99%//D67025
C-NT2RP2003165
C-NT2RP2003243//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//99%//AJ242978
C-NT2RP2003277//"Homo sapiens mRNA for KIAA0625 protein, partial cds."//0//3788bp//99%//AB014525
C-NT2RP2003286//PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4) (RNA-3'- PHOSPHATE CYCLASE) (RNA CYCLASE).//4.1E-88//374aa//47%//Q23400
C-NT2RP2003297
C-NT2RP2003307//KINESIN LIGHT CHAIN (KLC).//2.2E-199//550aa//70%//Q07866
C-NT2RP2003308//CROOKED NECK PROTEIN.//5.4E-244//622aa//67%//P17886
C-NT2RP2003347//BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN HOMOLOG.//0.000022//261aa//24%//P48754
C-NT2RP2003391//Homo sapiens mRNA for nuclear transport receptor.//0//1509bp//99%//AJ133769
C-NT2RP2003393
C-NT2RP2003445
C-NT2RP2003466//"Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds."7/0//2194bp//99%//AF126799
C-NT2RP2003480//"Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds."//0//3012bp//99%//AF125158
C-NT2RP2003506//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//5.4E-14//106aa//46%//P04175
C-NT2RP2003511
C-NT2RP2003513//"Human mRNA for KIAA0270 gene, partial cds."//0//2137bp//97%//D87460
C-NT2RP2003567//"Homo sapiens mRNA for KIAA0462 protein, partial cds."//0//2343bp//99%//AB007931
C-NT2RP2003604//"Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds."//0//2442bp//99%//AF030233
C-NT2RP2003691
C-NT2RP2003713//"Homo sapiens ubiquitin-specific protease 3 (USP3) mRNA, complete cds."//0//2018bp//99%//AF073344

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C-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//0//869aa//80%//P53620
C-NT2RP2003764
C-NT2RP2003769
C-NT2RP2003777
C-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//3.7E-21//137aa//43%//Q11076
C-NT2RP2003857//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).//0.00000016//117aa//29%//Q91955
C-NT2RP2003981//"Homo sapiens mRNA for KIAA0804 protein, partial cds."//0//3046bp//99%//AB018347
C-NT2RP2003984//Homo sapiens mRNA; cDNA DKFZp564A026 (from clone DKFZp564A026).//0//2514bp//99%//AL050367
C-NT2RP2004041//SYNAPSINS IA AND IB.//0.00000074//159aa//32%//P17599
C-NT2RP2004066//"Human DNA sequence from clone 134019 on chromosome 1p36.11-36.33, complete sequence."//0//2410bp//99%//AL034555
C-NT2RP2004081
C-NT2RP2004124
C-NT2RP2004152
C-NT2RP2004165
C-NT2RP2004187//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).//5.6E-31//424aa//28%//007231
C-NT2RP2004239//"Homo sapiens lok mRNA for protein kinase, complete cds."//0//3044bp//99%//AB015718
C-NT2RP2004245
C-NT2RP2004364
C-NT2RP2004365
C-NT2RP2004366//"Homo sapiens mRNA for KIAA0986 protein, partial cds."//0//2790bp//97%//AB023203
C-NT2RP2004373
C-NT2RP2004476//"Homo sapiens cyclin L ania-6a mRNA, complete cds."//0//2075bp//99%//AF180920
C-NT2RP2004551
C-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03.//3E-117//625aa//40%//Q09903
C-NT2RP2004600
C-NT2RP2004664//"Homo sapiens mRNA for KIAA0460 protein, partial cds."//0//2368bp//99%//AB007929
C-NT2RP2004743
C-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).//1.3E-26//190aa//41-%//P38692
C-NT2RP2004816//"Homo sapiens H beta 58 homolog mRNA, complete cds."//0//2144bp//96%//AF054179
C-NT2RP2004861
C-NT2RP2004897
C-NT2RP2004933//"Homo sapiens mRNA for ZIP-kinase, complete cds."//0//2103bp//99%//AB007144
C-NT2RP2004978//ACTIN-LIKE PROTEIN ARP8.//3.3E-47//353aa//30%//Q12386
C-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL ADDITION ENZYME) (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFERASE).//4E-91//218aa//44%//Q92089
C-NT2RP2005162//"Homo sapiens aspartyl aminopeptidase mRNA, complete cds."//0//1615bp//99%//AF005050
C-NT2RP2005204//"Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds."//0//1262bp//99%//AF090385
C-NT2RP2005227
C-NT2RP2005287
C-NT2RP2005288//"Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds."//0//2992bp//99%//AF060219
C-NT2RP2005490//"Mus musculus D3Mm3e (D3Mm3e) mRNA, complete cds."//1.8E-175//1102bp//

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83%//AF053628
C-NT2RP2005539//"Homo sapiens mRNA for KIAA0850 protein, complete cds."//0//1560bp//99%//AB020657
C-NT2RP2005605//QUEUINE TRNA-RIBOSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME).//8.2E-23//164aa//28%//032053
C-NT2RP2005722//"Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds."//0//2545bp//99%//AB011414
C-NT2RP2005732
C-NT2RP2005784//"Homo sapiens ubiquitin-conjugating enzyme variant Kua (UBE2V) mRNA, complete cds."//0//2191bp//92%//AF155120
C-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//2.3E-39//318aa//31%//P40004
C-NT2RP2005859//"Homo sapiens mRNA for KIAA0863 protein, complete cds."//0//1649bp//99%//AB020670
C-NT2RP2006023
C-NT2RP2006334//Homo sapiens mRNA; cDNA DKFZp434J154 (from clone DKFZp434J154).//0//2318bp//99%//AL080155
C-NT2RP2006441
C-NT2RP3000002
C-NT2RP3000050//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.2E-150//490aa//53%//Q05481
C-NT2RP3000055
C-NT2RP3000068
C-NT2RP3000080
C-NT2RP3000085//ACETYL-/PROPIONYL-COENZYME A CARBOXYLASE ALPHA CHAIN [CONTAINS: BIOTIN CARBOXYLASE (EC 6.3.4.14); BIOTIN CARBOXYL CARRIER PROTEIN (BCCP)].//1.9E-123//436aa//50%//P46401
C-NT2RP3000092
C-NT2RP3000109//P54 PROTEIN PRECURSOR.//0.0000065//358aa//22%//P13692
C-NT2RP3000134
C-NT2RP3000149
C-NT2RP3000197
C-NT2RP3000207//"GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)."//2.9E-11//721aa//23%//P08640
C-NT2RP3000233//"Human DNA sequence from clone 22D12 on chromosome Xq21.1-21.33. Contains a novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogenous set of other types of proteins. Contains ESTs and GSSs, complete sequence."//0//1462bp//99%//AL035424
C-NT2RP3000235
C-NT2RP3000247
C-NT2RP3000267
C-NT2RP3000299//"Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds."//0//2730bp//82%//D29766
C-NT2RP3000324
C-NT2RP3000341//"Homo sapiens mitochondrial inner membrane preprotein translocase Timl7a mRNA, nuclear gene encoding mitochondrial protein, complete cds."//1.5E-246//1124bp//99%//AF106622
C-NT2RP3000393//"Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds."//5.8E-266//1373bp//86%//AF061817
C-NT2RP3000441//"Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds."//3.40E-42//645bp//67%//AF098066
C-NT2RP3000449
C-NT2RP3000451
C-NT2RP3000456
C-NT2RP3000542
C-NT2RP3000561
C-NT2RP3000562//"Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds."//0//2165bp//99%//AF093097
C-NT2RP3000578//HES1 PROTEIN.//1-3E-22//229aa//27%//P35843
C-NT2RP3000590//UVS-2 PROTEIN.//1.3E-22//458aa//24%//P33288

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C-NT2RP3000592
C-NT2RP3000622
C-NT2RP3000624
C-NT2RP3000685
C-NT2RP3000736//HYPOTHETICAL PROTEIN KIAA0140.//1.2E-166//305aa//99%//014153
C-NT2RP3000742//"1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT)."//4.1E-165//371aa//49%//P10895
C-NT2RP3000753
C-NT2RP3000826
C-NT2RP3000865
C-NT2RP3000875//MEVALONATE KINASE (EC 2.7.1.36) (MK).//7.7E-87//175aa//98%//Q03426
C-NT2RP3001007
C-NT2RP3001055
C-NT2RP300111//"Homo sapiens TRF-proximal protein mRNA, complete cds."//1.50E-149//731bp//97%//AF097725
C-NT2RP3001120//ZINC FINGER PROTEIN 136.//7.8E-170//512aa//58%//P52737
C-NT2RP3001126
C-NT2RP3001150//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000031//207aa//29%//P52154
C-NT2RP3001232
C-NT2RP3001268//"Homo sapiens zinc finger protein ZNF228 (ZNF228) mRNA, complete cds."//0//3606bp//99%//AF198358
C-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein.//1.3E-99//669bp//83%//Y18101
C-NT2RP3001274//"Homo sapiens mRNA for KIAA1037 protein, partial cds."//0//2254bp//99%//AB028960
C-NT2RP3001281
C-NT2RP3001297
C-NT2RP3001318
C-NT2RP3001338//ZINC FINGER PROTEIN 81 (FRAGMENT).//2.4E-16//175aa//28%//P51508
C-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN).//3.6E-25//129aa//34%//P32089
C-NT2RP3001374
C-NT2RP3001428//NUCLEOPROTEIN TPR.//1.4E-128//152aa//99%//P12270
C-NT2RP3001432
C-NT2RP3001447
C-NT2RP3001449//"Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae) bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs, complete sequence."//0//1827bp//99%//AL031282
C-NT2RP3001453//ANTIGEN PEPTIDE TRANSPORTER 2 (APT2) (HISTOCOMPATIBILITY ANTIGEN MODIFIER 2).//3.2E-90//157aa//59%//P36371
C-NT2RP3001459
C-NT2RP3001527//"Human Spl40 protein (Spl40) mRNA, complete cds."//4.3E-290//793bp//93%//U63420
C-NT2RP3001538//HYPOTHETICAL 39.0 KD PROTEIN T2.8D9.3 IN CHROMOSOME II.//9.10E-10//158aa//31%//Q10022
C-NT2RP3001580//"Mus musculus strain C57BL/J germ cell-less protein (Gcl) mRNA, complete cds."//0//1730bp//85%//AF163665
C-NT2RP3001587//"Human anthracycline-associated resistance ARX mRNA, complete cds."//0//2617bp//99%//U35832
C-NT2RP3001589
C-NT2RP3001607
C-NT2RP3001608

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C-NT2RP3001671//"Homo sapiens mRNA for KIAA0850 protein, complete cds."//0//2310bp//99%//AB020657
C-NT2RP3001672//"Homo sapiens Sex comb on midleg homolog 1 isoform 2 (SCMH1) mRNA, complete cds."//0//2836bp//99%//AF149046
C-NT2RP3001678
C-NT2RP3001688//"Homo sapiens glucocorticoid modulatory element binding protein-1 (GMEB1) mRNA, complete cds."//0//1695bp//99%//AF099013
C-NT2RP3001690//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.00000024//481aa//21%//P25386
C-NT2RP3001698
C-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR.//3.4E-33//161aa//32%//P54356
C-NT2RP3001716
C-NT2RP3001752
C-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.8E-117//462aa//55%//P52272
C-NT2RP3001844
C-NT2RP3001854//Homo sapiens mRNA; cDNA DKFZp564G013 (from clone DKFZp564G013).//0//1528bp//99%//AL050011
C-NT2RP3001855//HOMEOBOX PROTEIN PKNOX1 (HOMEOBOX PROTEIN PREP-1).//8.1E-125//302aa//60%//P55347
C-NT2RP3001898//"Homo sapiens mRNA for UDP-N-acetylglucosamine: alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV, complete cds."//0//1587bp//100%//AB000624
C-NT2RP3001931
C-NT2RP3001969//TRICHOHYALIN.//2.7E-11//442aa//23%//P37709
C-NT2RP3002002
C-NT2RP3002004//H.sapiens mRNA for FAST kinase.//1.50E-19211475bp//94%//X86779
C-NT2RP3002007//SAP1 PROTEIN.//1.1E-68//474aa//32%//P39955
C-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//5.30E-25//139aa//48%//Q09232
C-NT2RP3002045//"Homo sapiens mRNA for KIAA0899 protein, partial cds."//0//33 85bp//99%//AB020706
C-NT2RP3002056//"Homo sapiens Rb binding protein homolog mRNA, partial cds."//0//2374bp//99%//AF083249
C-NT2RP3002062//"Homo sapiens mRNA for KIAA0873 protein, partial cds."//0//3764bp//99%//AB020680
C-NT2RP3002081//"Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds."//4.1E-233//1896bp//69%//AF111423
C-NT2RP3002097
C-NT2RP3002108//DEC1 PROTEIN (MDM20 PROTEIN).//7.90E-09//181aa//22%//Q12387
C-NT2RP3002142
C-NT2RP3002146
C-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING PROTEIN GST1-HS).//2.8E-253//474aa//93%//P15170
C-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP7//1.9E-151//223aa//91%//Q02614
C-NT2RP3002166
C-NT2RP3002181
C-NT2RP3002244
C-NT2RP3002248
C-NT2RP3002273//SCD6 PROTEIN.//1.30E-09//295aa//28%//P45978
C-NT2RP3002276
C-NT2RP3002304
C-NT2RP3002501//THREONINE DEHYDRATASE CATABOLIC (EC 4.2.1.16) (THREONINE DEAMINASE).//3.70E-43//318aa//37%//P05792
C-NT2RP3002529//Homo sapiens mRNA for leucocyte vacuolar protein sorting.//0//2276bp//99%//AJ133421
C-NT2RP3002566
C-NT2RP3002587
C-NT2RP3002590
C-NT2RP3002631

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C-NT2RP3002650//"Mus musculus growth suppressor 1L (Gros1) mRNA, complete cds."//0//2109bp//87%//AF165163
C-NT2RP3002663//"Homo sapiens putative glycolipid transfer protein mRNA, complete cds."//8.10E-263//1243bp//97%//AF103731
C-NT2RP3002671//ELONGATION FACTOR 2 (EF-2).//2.50E-73//179aa//36%//P13060
C-NT2RP3002763
C-NT2RP3002861
C-NT2RP3002911
C-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).//2E-111//551aa//42%//Q04652
C-NT2RP3002953//"Homo sapiens protocadherin beta 5 (PCDH-beta5) mRNA, complete cds."//0//2388bp//99%//AF152498
C-NT2RP3002988//"Homo sapiens IkB kinase-b (IKK-beta) mRNA, complete cds."//1.8E-292//1325bp//99%//AF080158
C-NT2RP3003008
C-NT2RP3003101//"Mouse mRNA for tetracycline transporter-like protein, complete cds."//3.6E-83//807bp//72%//D88315
C-NT2RP3003204
C-NT2RP3003278
C-NT2RP3003282//"Homo sapiens dynamin (DNM) mRNA, complete cds."//0//2596bp//98%//L36983
C-NT2RP3003290//"Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds."//1.5e-310//1468bp//82%//AB033922
C-NT2RP3003302
C-NT2RP3003313//"Homo sapiens thyroid hormone receptor-associated protein complex component TRAP80 mRNA, complete cds."//0//2476bp//99%//AF117657
C-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (R052).//1.3E-35//178aa//44%//Q62191
C-NT2RP3003344
C-NT2RP3003353//HYPOTHETICAL 26.2 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.//2.80E-07//161aa//28%//P40084
C-NT2RP3003377
C-NT2RP3003385//"Mus musculus SKD3 mRNA, complete cds."//0//2133bp//85%//U09874
C-NT2RP3003433
C-NT2RP3003490//"Homo sapiens mRNA for KIAA0725 protein, partial cds."//0//2437bp//99%//AB018268
C-NT2RP3003491//"Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds."//5.6E-36//842bp//62%//AF091624
C-NT2RP3004206//CROOKED NECK PROTEIN.//1.4E-220//567aa//67%//P17886
C-NT2RP3004207//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2445bp//100%//AJ245820
C-NT2RP3004209//"Homo sapiens ubiquitin processing protease (Ubp-M) mRNA, complete cds."//0//2320bp//99%//AF126736
C-NT2RP3004242//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//4.7E-13//118aa//33%//P52734
C-NT2RP3004246
C-NT2RP3004258//"Homo sapiens ZIS1 mRNA, complete cds."//0//1861bp//99%//AF065391
C-NT2RP3004262//"Homo sapiens heat shock protein hsp40-3 mRNA, complete cds."//2.4E-248//1126bp//100%//AF088982
C-NT2RP3004341
C-NT2RP3004378
C-NT2RP3004424//Homo sapiens mRNA for stromal antigen 3 (STAG3 gene).//1E-66//364bp//93%//AJ007798
C-NT2RP3004428
C-NT2RP3004451
C-NT2RP3004454//"Homo sapiens mRNA for KIAA0448 protein, complete cds."//0//2875bp//99%//AB007917
C-NT2RP3004472//GERM CELL-LESS PROTEIN.//1.6E-61//170aa//40%//Q01820
C-NT2RP3004498//"Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds."//2E-249//1777bp//80%//U83176
C-NT2RP3004504//M.musculus mRNA for CPEB protein.//1.9E-295//893bp//92%//Y08260

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C-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).//3.7E-37//190aa//39%//P40484
C-NT2RP3004534//"Mouse oncogene (ect2) mRNA, complete cds."//0//2075bp//87%//L11316
C-NT2RP4000528//NPL4 PROTEIN.//9.8E-86//515aa//37%//P33755
C-NT2RP4000907//"Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds."//0//2127bp//86%//D45913
C-NT2RP4001029//"Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds."//0//1711bp//90%//U20086
C-NT2RP4001336//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN.//0.000016//186aa//29%//024076
C-NT2RP4001389//KES1 PROTEIN.//1.70E-31//342aa//34%//P35844
C-NT2RP4001442
C-NT2RP4001529//"Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds."/1.70E-255//1148bp//90%//U20086
C-NT2RP4001656//VACUOLAR BIOGENESIS PROTEIN END1 (PEP5 PROTEIN).//1.10E-45//310aa//27%//P12868
C-OVARC1000106//"TROPOMYOSIN 1, FUSION PROTEIN 33."//0.000032//165aa//27%//P49455
C-OVARC1000198
C-OVARC1000682//"PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B)."//1.1E-209//293aa//95%//P39098
C-OVARC1000703
C-OVARC1000722//"Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds."//0//759bp//98%//AF038661
C-OVARC1000730
C-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN.//0.000000017//78aa//48%//P25159
C-OVARC1000781
C-OVARC1000787
C-OVARC10008347/Homo sapiens mRNA for atopy related autoantigen CALCJ/2.8E-258//1183bp//99%//Y17711
C-OVARC1000846//NUCLEOLIN (PROTEIN C23).//0.0000097//109aa//30%//P08199
C-OVARC1000850//"Homo sapiens PB39 mRNA, complete cds."//0//2095bp//99%//AF045584
C-OVARC1000862//M.musculus mRNA for FT1.//5.9E-226//1498bp//81%//Z67963
C-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).//2.2E-50//206aa//52%//P40484
C-OVA-RC1000883
C-OVARC1000886
C-OVARC1000912
C-OVARC1000915//"Homo sapiens histone deacetylase 5 mRNA, complete cds."//1.60E-121//591bp//97%//AF132608
C-OVARC1000924
C-OVARC1000964
C-OVARC1000984
C-OVARC1001004
C-OVARC1001010
C-OVARC1001011
C-OVARC1001032
C-OVARC1001044
C-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSOR.//1.9E-35//76aa//98%//P43490
C-OVARC1001068//"Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds."//0//1819bp//99%//AF082657
C-OVARC1001074
C-OVARC1001092//"Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F185707 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))."//2E-214//769bp//97%//AJ005897
C-OVARC1001107//"Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds."//6.1E-276//594bp//98%//AF167572
C-OVARC1001154//"Homo sapiens clone 24720 epithelin 1 and 2 mRNA, complete cds."//2.3E-296//1561bp//93%//AF055008
C-OVARC1001161
C-OVARC1001167
C-OVARC1001170

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C-OVARC1001171//"Homo sapiens translation initiation factor 3 47 kDa subunit mRNA, complete cds."//5.7E-151//436bp//92%//U94855
C-OVARC1001173
C-OVARC1001176
C-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2.//1.1E-11//221aa//25%//P48510
C-OVARC1001188
C-OVARC1001232//"CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT)."//5.10E-22//83aa//37%//Q10568
C-OVARC1001270
C-OVARC1001271//NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1).//0.0000014//224aa//26%//P25976
C-OVARC1001306//N-MYC PROTO-ONCOGENE PROTEIN.//0.00000073//247aa//27%//P18444
C-OVARC1001344
C-OVARC1001369
C-OVARC1001372//"Homo sapiens mRNA for KIAA0897 protein, partial cds."//0//840bp//97%//AB020704
C-OVARC1001391
C-OVARC1001399
C-OVARC1001417//"Homo sapiens thyroid hormone receptor-associated protein complex component TRAP170 mRNA, complete cds."//0//1715bp//99%//AF135802
C-OVARC1001419//"Homo sapiens GOK (STIM1) mRNA, complete cds."//4.9E-48//586bp//69%//U52426
C-OVARC1001436//ENL PROTEIN.//0.00000009//81aa//39%//Q03111
C-OVARC1001453
C-OVARC1001476//"Mus musculus YGR163w mRNA homologue, complete cds."//1.80E-187//510bp//89%//AB017616
C-OVARC1001480
C-OVARC1001489
C-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE PROTEIN 1).//0//777aa//91%//P98161
C-OVARC1001525
C-OVARC1001555//NGG1-INTERACTING FACTOR 3.//4.4E-19//130aa//40%//P53081
C-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//0//1167bp//100%//AF031165
C-OVARC1001600
C-OVARC1001610//"Homo sapiens choline/ethanolaminephosphotransferase (CEPT1) mRNA, complete cds."//0//1870bp//99%//AF068302
C-OVARC1001702
C-OVARC1001703//"Mus musculus ARL-6 interacting protein-2 (Aip-2) mRNA, complete cds."//3.5E-16//399bp//61%//AF133670
C-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).//2.80E-10//106aa//38%//Q62267
C-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).//4.4E-40//195aa//41%//P07106
C-OVARC1001726//APICAL-LIKE PROTEIN (APXL PROTEIN).//4.3E-16//116aa//43%//Q13796
C-OVARC1001731//"TROPOMYOSIN ALPHA CHAIN, FIBROBLAST ISOFORM F2."//4E-122//282aa//85%//P08942
C-OVARC1001745
C-OVARC1001762//"N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA-AMINO, ACETYLTRANSFERASE 1)."//6.4E-85//514aa//34%//P12945
C-OVARC1001766//"Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds."//0//963bp//99%//U97670
C-OVARC1001767//"Homo sapiens mRNA for KIAA0675 protein, complete cds."//0//2083bp//99%//AB014575
C-OVARC1001768
C-OVARC1001791
C-OVARC1001795
C-OVARC1001802

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C-OVARC1001809//"Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds."//2.7E-190//1624bp//76%//AF068748
C-OVARC1001828
C-OVARC1001846
C-OVARC1001861
C-OVARC1001879
C-OVARC1001880
C-OVARC1001883
C-OVARC1001916
C-OVARC1001928
C-OVARC1001942//"N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA-AMINO, ACETYLTRANSFERASE 1)."//3.1E-81//497aa//35%//P12945
C-OVARC1001943//"Mus musculus DEBT-91 mRNA, complete cds."//0//2035bp//87%//AF143859
C-OVARC1001950
C-OVARC1001987//"Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds."//2.3E-220//652bp//84%//AF061817
C-OVARC1002050//"Homo sapiens mRNA for actin binding protein ABP620, complete cds."//0//1019bp//99%//AB029290
C-OVARC1002082
C-OVARC1002107
C-OVARC1002127//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER 2 (BRAIN DIGOXIN CARRIER PROTEIN) (BRAIN-SPECIFIC ORGANIC ANION TRANSPORTER) (OATP-B1).//5.4E-52//306aa//35%//035913
C-OVARC1002138//SAP1 PROTEIN.//7.6E-60//128aa//59%//P39955
C-OVARC1002156
C-OVARC1002158
C-PLACE1000004//"Homo sapiens IDN3-B mRNA, complete cds."//0//2365bp//99%//AB019602
C-PLACE1000040//TRANSFORMING PROTEIN P21/K-RAS 2B.//1.4E-17//185aa//32%//P08643
C-PLACE1000048
C-PLACE1000050
C-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//7.9E-54//190bp//94%//L22154
C-PLACE1000081//"Human SEC7 homolog Tic (TIC) mRNA, complete cds."//0//2077bp//99%//U63127
C-PLACE1000094
C-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//1.8E-62//158aa//81%//P20290
C-PLACE1000214
C-PLACE1000236
C-PLACE1000246
C-PLACE1000292
C-PLACE1000308
C-PLACE1000332
C-PLACE1000453
C-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.60E-47//207aa//46%//P51522
C-PLACE1000599
C-PLACE1000610//MSN5 PROTEIN.//0.0000026//136aa//26%//P52918
C-PLACE1000653//"Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds."//0//1992bp//99%//AF180371
C-PLACE1000656//"Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin))."//2.1E-277//1260bp//99%//AJ005896
C-PLACE1000706//"Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds."//0//1366bp//99%//AF119043
C-PLACE1000712
C-PLACE1000749
C-PLACE1000769//"Homo sapiens CGI-18 protein mRNA, complete cds."//0//1985bp//98%//AF132952
C-PLACE1000786//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-

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CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//7.10E-09//59aa//47%//P52734
C-PLACE1000849
C-PLACE1000856//"Homo sapiens mRNA for KIAA0974 protein, partial cds."//0//1310bp//100%//AB023191
C-PLACE1000931
C-PLACE1000987//"Homo sapiens mRNA for KIAA0724 protein, complete cds."//0//1749bp//99%//AB018267
C-PLACE1001010
C-PLACE1001015
C-PLACE1001024
C-PLACE1001062//"Homo sapiens PAC clone DJ1049N15 from 7q31.2-7q32, complete sequence."//2.7E-32//470bp//71%//AC006020
C-PLACE1001104
C-PLACE1001168
C-PLACE1001171//MYOTUBULARIN.//7.1E-84//198aa//73%//Q13496
C-PLACE1001185//"Homo sapiens mRNA for KIAA0943 protein, partial cds."//0//1668bp//99%//AB023160
C-PLACE1001238//"Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds."//2E-202//1333bp//80%//D14336
C-PLACE1001280
C-PLACE1001294//M.musculus GEG-154 mRNA.//4.3E-221//1057bp//78%//X7I642
C-PLACE1001304//"Homo sapiens zinc finger protein dp mRNA, complete cds."//0//2421bp//99%//AF153201
C-PLACE1001311
C-PLACE1001323
C-PLACE1001351
C-PLACE1001414
C-PLACE1001440
C-PLACE1001456
C-PLACE1001517//"Homo sapiens gene for glycosylphosphatidylinositol anchor attachment 1 (GPAA1), complete cds."//4.60E-112//392bp//87%//AB002137
C-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1).//5.7E-130//244aa//99%//Q60809
C-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.4E-118//429aa//48%//P51523
C-PLACE1001634
C-PLACE1001640
C-PLACE1001672//PROBABLE AMINOTRANSFERASE T01B11.2 (EC 2.6.1.-).//4.3E-66//174aa//45%//P91408
C-PLACE1001705
C-PLACE1001716
C-PLACE1001720
C-PLACE1001745
C-PLACE1001748//"Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds."//0//2602bp//99%//AF061243
C-PLACE1001771//Homo sapiens mRNA for transient receptor potential protein
TRP6.//0//2900bp//99%//AJ006276
C-PLACE1001799
C-PLACE1001845//"Mus musculus cyclin ania-6a mRNA, complete cds."//3.30E-31//925bp//62%//AF159159
C-PLACE1001897
C-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).//6.5E-58//112aa//100%//076094
C-PLACE1002157
C-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX COMPONENT SWI3) (TRANSCRIPTION FACTOR TYE2).//0.00005//179aa//23%//P32591
C-PLACE1002227
C-PLACE1002259
C-PLACE1002319
C-PLACE1002395//"Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds."//7.9E-

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100//966bp//75%//AB030505
C-PLACE1002477
C-PLACE1002493//"Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds. "//1.7E-113//545bp//98%//AF042273
C-PLACE1002500
C-PLACE1002514
C-PLACE1002532//HOMEOBOX PROTEIN DLX-5.//1.2E-152//289aa//96%//P70396
C-PLACE1002537
C-PLACE1002571//ACTIN-LIKE PROTEIN 13E.//5E-99//386aa//48%//P45890
C-PLACE10025 83//"GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2 PRECURSOR (GLUTAMATE RECEPTOR 6) (GLUR-6) (GLUTAMATE RECEPTOR BETA-2) (GLUR BETA-2) (FRAGMENT)."//5.6E-34// 76aa//98%//P39087
C-PLACE1002598//OLIGORIBONUCLEASE (EC 3.1.-.-).//5.5E-17//76aa//56%//P45340
C-PLACE1002625
C-PLACE1002655//ADSEVERIN (SCINDERIN)(SC).//2.5E-278//543aa//92%//Q28046
C-PLACE1002768
C-PLACE1002782//"Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds."//3.8E-43// 385bp//77%//U50927
C-PLACE1002816//HISTONE DEACETYLASE HDA1.//2.20E-48//217aa//46%//P53973
C-PLACE1002853
C-PLACE1002908//"Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds."//0// 1654bp//99%//AB028600
C-PLACE1002962
C-PLACE1002968
C-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4).//1.4E-78//496aa//37%//Q49091
C-PLACE1003025
C-PLACE1003027//"Homo sapiens mRNA for KIAA0516 protein, partial cds."//2.1e-314//1417bp// 100%//AB011088
C-PLACE1003044//"Homo sapiens mRNA for KIAA0829 protein, partial cds."//0//1382bp//96%// AB020636
C-PLACE1003176
C-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//4.9E-76//309aa//47%// Q15391
C-PLACE1003256
C-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN.//7.9E-22//70aa7/47%//P21541
C-PLACE1003343
C-PLACE1003361
C-PLACE1003366//"Homo sapiens otoferlin (OTOF) mRNA, complete cds."//1.4E-78//542bp//67%// AF107403
C-PLACE1003373
C-PLACE1003375
C-PLACE1003394//"Sprague-Dawley (clone LRB13) RAB14 mRNA, complete cds."//2.30E-150// 774bp//94%//M83680
C-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//1.3E-40//278aa//36%//P40556
C-PLACE1003454
C-PLACE1003478
C-PLACE1003516
C-PLACE1003519//H.sapiens hnRNP-E2 mRNA.//5.1E-218//905bp//99%//X78136
C-PLACE1003521//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//0.0000011//101aa//32%// Q09475
C-PLACE1003528
C-PLACE1003537//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).//7.7E-68//404aa//33%//P32802
C-PLACE1003566
C-PLACE1003584
C-PLACE1003593
C-PLACE1003605//HAP5 TRANSCRIPTIONAL

BNSDOCID: <EP___1074617A2_I_>

ACTIVATOR.//0.00000023//82aa//35%//Q02516
C-PLACE1003618
C-PLACE1003638
C-PLACE1003738//ZINC FINGER PROTEIN 135.//9.6E-118//350aa//46%//P52742
C-PLACE1003760//"Homo sapiens tetraspanin TM4-A mRNA, complete cds."//5.2E-289//1313bp//97%//AF133423
C-PLACE1003768
C-PLACE1003795
C-PLACE1003886
C-PLACE1003888//"Homo sapiens mRNA for KIAA1092 protein, partial cds."//0//2057bp//99%//AB029015
C-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE).//1.4E-243//584aa//74%//P17812
C-PLACE1003915//"PROBABLE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19) (ARGININE- -TRNA LIGASE) (ARGRS)."//2.4E-108//581aa//40%//Q05506
C-PLACE1004118
C-PLACE1004256//"Mus musculus short coiled coil protein SCOCO (Scoc) mRNA, complete cds."//2E-93//960bp//76%//AF115778
C-PLACE1004274
C-PLACE1004284
C-PLACE1005331
C-PLACE1005739//Homo sapiens mRNA; cDNA DKFZp564A032 (from clone DKFZp564A032).//0//2190bp//99%//AL050267
C-PLACE1005828
C-PLACE1005876//"CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT)."//0//730aa//99%//Q10568
C-PLACE1005890//BEM46 PROTEIN (FRAGMENT).//9.9E-42//224aa//43%//P54069
C-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).//2E-28//236aa//30%//P98110
C-PLACE1007053
C-PLACE1007068
C-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).//5.3E-26//309aa//30%//Q04652
C-PLACE1009921
C-PLACE1010401
C-PLACE1010856
C-PLACE1010857
C-PLACE1010917
C-PLACE1010925
C-PLACE1010926//"Homo sapiens mRNA for KIAA0554 protein, partial cds."//0//1160bp//100%//AB011126
C-PLACE1010942//"Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds."//0//1440bp//99%//AF114487
C-PLACE1010944
C-PLACE1010954
C-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//5.3E-98//297aa//48%//P45890
C-PLACE1011026
C-PLACE1011046//"1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1 (EC 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PLC-154)."//0//646aa//97%//P10894
C-PLACE1011054
C-PLACE1011057
C-PLACE1011109//"ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)."//1.50E-22//63aa//88%//Q07803
C-PLACE1011114//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//2.9E-71//190aa//44%//Q03532
C-PLACE1011133
C-PLACE1011143
C-PLACE1011165
C-PLACE1011185//INSERTION ELEMENT IS1 PROTEIN INSB.//1.3E-89//167aa//100%//P03830

BNSDOCID: <EP___1074617A2_I_>

C-PLACE1011219//PROBABLEOXIDOREDUCTASE (EC 1.-.-.-).//3.2E-12//212aa//29%//Q03326
C-PLACE1011221
C-PLACE1011263//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp564O043).//0//2487bp//99%//AL050390
C-PLACE1011325
C-PLACE1011332//"Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds."//7.2E-151//697bp//99%//AF102265
C-PLACE1011340//"Homo sapiens IDN3-B mRNA, complete cds."//1.20E-74//380bp//97%//AB019602
C-PLACE1011399//"Homo sapiens CGI-72 protein mRNA, complete cds."//3.2E-90//427bp//99%//AF151830
C-PLACE1011433//"Homo sapiens mRNA for KIAA0530 protein, partial cds."//0//1946bp//99%//AB011102
C-PLACE1011452
C-PLACE1011465
C-PLACE1011472//"Homo sapiens mRNA for KIAA0712 protein, complete cds."//0//2022bp//99%//AB018255
C-PLACE1011477//"Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds."//0//2040bp//99%//AF065482
C-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//4.90E-11//147aa//32%//P52178
C-PLACE1011520
C-PLACE1011563
C-PLACE1011567
C-PLACE1011576//"Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds."//0//1791bp//82%//L11672
C-PLACE1011586
C-PLACE1011643
C-PLACE1011649
C-PLACE1011664//CROOKED NECK PROTEIN.//1.6E-187//505aa//64%//P17886
C-PLACE1011682
C-PLACE1011719
C-PLACE1011729
C-PLACE1011858//Homo sapiens mRNA; cDNA DKFZp586C021 (from clone DKFZp586C021).//0//1490bp//99%//AL050287
C-PLACE1011874
C-PLACE1011875//"Homo sapiens mRNA for KIAA0580 protein, partial cds."//4.1E-112//524bp//100%//AB011152
C-PLACE1011923//"Homo sapiens serum-inducible kinase mRNA, complete cds."//0//2782bp//99%//AF059617
C-PLACE1011982
C-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//2.6E-42//104aa//49%//Q09475
C-PLACE2000015//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN).//1.1E-116//364aa//45%//P42566
C-PLACE2000017
C-PLACE2000021//"Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, complete cds."//2.7E-107//981bp//74%//AF082556
C-PLACE2000047
C-PLACE2000062//"Homo sapiens mRNA for type II membrane protein similar to HIV gp120-binding C-type lectin, complete cds, clone:HP01347."//6.3E-166//656bp//94%//AB015629
C-PLACE2000100
C-PLACE2000111
C-PLACE2000172
C-PLACE2000187
C-PLACE2000216//"Dog nonerythroid beta-spectrin mRNA, 3' end.&quot,//3.2E-253//1799bp//83%//L02897
C-PLACE2000246//"Homo sapiens mRNA for KIAA0795 protein, partial cds."//4.60E-172//796bp//99%//AB018338

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C-PLACE2000317
C-PLACE2000341//"Homo sapiens sodium-dependent multivitamin transporter (SMVT) mRNA, complete cds."/0//1554bp//99%//AF069307
C-PLACE2000366
C-PLACE2000373//F-SPONDIN PRECURSOR.//8.6E-16//371aa//28%//P35446
C-PLACE2000394
C-PLACE2000398//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//6.3E-37//90aa//98%//P10586
C-PLACE2000411//"Homo sapiens mRNA for KIAA1037 protein, partial cds."//0//2515bp//99%//AB028960
C-PLACE2000425
C-PLACE2000427//PROBABLE HELICASE MOT1.//1.2E-26//200aa//27%//P32333
C-PLACE2000433
C-PLACE2000438//"POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN- UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYLGALACTOSAMINYLTRANSFERASE)(GALNAC-T1)."//2.1E-86//348aa//41%//Q10472
C-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//2.5E-25//165aa//40%//P33450
C-PLACE2000477//"Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds."//6.7E-127//671bp//94%//AF072733
C-PLACE3000009
C-PLACE3000020//"Homo sapiens type III adenylyl cyclase (AC-III) mRNA, complete cds."//0//2253bp//99%//AF033861
C-PLACE3000103
C-PLACE3000142
C-PLACE3000145//TENSIN.//1E-108//277aa//75%//Q04205
C-PLACE3000156
C-PLACE3000157
C-PLACE3000197
C-PLACE3000208
C-PLACE3000226//"Homo sapiens mRNA for KIAA0962 protein, partial cds."//0//4805bp//99%//AB023179
C-PLACE3000242//"Homo sapiens mRNA for KIAA1114 protein, complete cds."//0//2786bp//96%//AB029037
C-PLACE3000363
C-PLACE3000405
C-PLACE3000416//"Homo sapiens mRNA for actin binding protein ABP620, complete cds."//1.80E-141//565bp//98%//AB029290
C-PLACE3000477
C-PLACE4000106//"Homo sapiens mRNA for KIAA0462 protein, partial cds."//0//6702bp//99%//AB007931
C-PLACE4000323
C-PLACE4000326//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1).//8.10E-24//319aa//31%//P30771
C-PLACE4000369//"Homo sapiens mRNA for KIAA1025 protein, partial cds."//0//4830bp//99%//AB028948
C-PLACE4000445//Homo sapiens mRNA; cDNA DKFZp434C212 (from clone DKFZp434C212).//0//2565bp//99%//AL080196
C-PLACE4000558//"Homo sapiens mRNA for KIAA0729 protein, partial cds."//0//1051bp//97%//AB018272
C-PLACE4000581//FIBROPELLIN I PRECURSOR (EPIDERMAL GROWTH FACTOR-RELATED PROTEIN 1) (UEGF-1).//9.3E-70//226aa//52%//P10079
C-PLACE4000593
C-PLACE4000612//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//7.1E-154//340aa//40%//P21414
C-PLACE4000670
C-THYRO1000026
C-THYRO1000085//"PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B."//2E-72//155aa//92%//

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Q06710
C-THYRO1000107
C-THYRO1000111
C-THYRO1000132//"Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds."//1.1E-159//824bp//95%//U97018
C-THYRO1000156
C-THYRO1000173//"Homo sapiens AP-mu chain family member mu1B (HSMU1B) mRNA, complete cds."//0//1713bp//99%//AF020797
C-THYRO1000186
C-THYRO1000187
C-THYRO1000241
C-THYRO1000279
C-THYRO1000327//"Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds."//0//1567bp//99%//AF124145
C-THYRO1000452
C-THYRO1000471
C-THYRO1000484
C-THYRO1000502
C-THYRO1000505
C-THYRO1000585//"Homo sapiens protein associated with Myc mRNA, complete cds."//0//1901bp//99%//AF075587
C-THYRO1000596
C-THYRO1000662//"Homo sapiens XPV mRNA for DNA polymerase eta, complete cds."//0//2341 bp//99%//AB024313
C-THYRO1000666//Mus musculus mRNA for kinesin like protein 9.//0//2001bp//86%//AJ132889
C-THYRO1000715
C-THYRO1000734
C-THYRO1000748//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//3.30E-96//335aa//52%//P98171
C-THYRO1000756//"ALPHA-N-ACETYLGALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (EC 2.4.99.-) (ST6GALNACIII) (STY)."//1.8E-55//243aa//42%//Q64686
C-THYRO1000777
C-THYRO1000783//"Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds."//2.4E-157//1656bp//70%//U37373
C-THYRO1000787
C-THYRO1000793
C-THYRO1000796
C-THYRO1000843
C-THYRO1000852//"Human branched chain aminotransferase precursor (BCATm) mRNA, nuclear gene encoding mitochondrial protein, complete cds."//3.3E-147//790bp//93%//U68418
C-THYRO1000865
C-THYRO1000895
C-THYRO1000926//"Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds."//0//2387bp//99%//AF079529
C-THYRO1000951//DIHYDROXYACETONE KINASE 2 (EC 2.7.1.29) (GLYCERONE KINASE).//5E-83//566aa//37%//P43550
C-THYRO1000952
C-THYRO1000983//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//6.30E-17//143aa//39%//P35132
C-THYRO1001003//UBIQUITIN-CONJUGATING ENZYME E2-21.2 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).//5.90E-14//84aa//41%//P52491
C-THYRO1001031
C-THYRO1001062
C-THYRO1001100//ZINC FINGER X-LINKED PROTEIN ZXDA (FRAGMENT).//1.2E-67//245aa//62%//P98168
C-THYRO1001133
C-THYRO1001134//"Homo sapiens CGI-78 protein mRNA, complete cds."//0//1898bp//99%//AF151835
C-THYRO1001173

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C-THYRO1001213
C-THYRO1001321
C-THYRO1001322
C-THYRO1001365
C-THYRO1001401
C-THYRO1001411
C-THYRO1001434
C-THYRO1001534
C-THYRO1001541
C-THYRO1001559
C-THYRO1001570
C-THYRO1001595
C-THYRO1001605
C-THYRO1001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//0//1784bp//99%//AJ002190
C-THYRO1001656//"Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds."//4.1E-273//1947bp//82%//AF175968
C-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//0//1820bp//99%//AJ225089
C-THYRO1001673
C-THYRO1001703//NIFR3-LIKE PROTEIN.//2.90E-32//282aa//32%//P45672
C-THYRO1001706
C-THYRO1001738//TUBULIN-TYROSINE LIGASE (EC 6.3.2.25) (TTL).//2.4E-20//217aa//30%//P38584
C-THYRO1001745
C-THYRO1001793
C-THYRO1001809//MYOCYTE NUCLEAR FACTOR (MNF).//1.4E-74//158aa//89%//P42128
C-THYRO1001895
C-THYRO1001907
C-VESEN1000122
C-Y79AA1000037//DNA-BINDING PROTEIN BMI-1.//2.4E-30//80aa//60%//P25916
C-Y79AA1000059//"Homo sapiens immunophilin homolog ARA9 mRNA, complete cds."//2.9E-70//1040bp//65%//U78521
C-Y79AA1000065
C-Y79AA1000131
C-Y79AA1000181//"Homo sapiens CGI-01 protein mRNA, complete cds."//0//1858bp//99%//AF132936
C-Y79AA1000202
C-Y79AA1000214//"Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds."//7.1E-71//345bp//100%//AF081192
C-Y79AA1000230
C-Y79AA1000258
C-Y79AA1000268//"Mus musculus Nip21 mRNA, complete cds."//2.10E-50//648bp//64%//AF035207
C-Y79AA1000313//CALPHOTIN.//0.000011//336aa//23%//Q02910
C-Y79AA1000328//SEL-10 PROTEIN.//0.000000067//219aa//25 %//Q93794
C-Y79AA1000355
C-Y79AA1000368//REDUCED VIABILTTY UPON STARVATION PROTEIN 161.//4E-20//261 aa//27%//P25343
C-Y79AA1000420
C-Y79AA1000469//"Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete cds."//8.30E-252//1207bp//85%//U41736
C-Y79AA1000480
C-Y79AA1000540
C-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//0//652aa//98%//P17427
C-Y79AA1000574//Homo sapiens clone H17 unknown mRNA.//0//1932bp//99%//AF103801
C-Y79AA1000627//"Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds."//2E-287//203 lbp//82%//AF060503
C-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1.//5.80E-254//1477bp//84%//X69942

BNSDOCID: <EP___1074617A2_I_>

C-Y79AA1000734//"Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds."//0//1594bp//99%//AF093670
C-Y79AA1000748//"Homo sapiens CGI-05 protein mRNA, complete cds."//1.9E-239//1367bp//91%//AF152097
C-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//4.9E-91//200aa//64%//Q61990
C-Y79AA1000774
C-Y79AA1000782//CYTOSOLIC PURINE 5'-NUCLEOTEDASE (EC 3.1.3.5).//3E-37//469aa//27%//P49902
C-Y79AA1000784//"Homo sapiens RanBP7/importin 7 mRNA, complete cds."//1.10E-236//1076bp//99%//AF098799
C-Y79AA1000794//"Homo sapiens actin-associated protein 2E4/kaptin (2E4) mRNA, 2E4-1 allele, complete cds."//0//1610bp//99%//AF105369
C-Y79AA1000800//"Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds."//1.6E-284//1288bp//99%//AF072733
C-Y79AA1000805
C-Y79AA1000824
C-Y79AA1000833//TUBULIN ALPHA-1 CHAIN.//5E-173//220aa//79%//P05209
C-Y79AA1000850
C-Y79AA1000962//"MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II)."//4.2E-17//430aa//27%//Q99323
C-Y79AA1000968//"Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds."//3.9E-248//1468bp//87%//U38253
C-Y79AA1000976
C-Y79AA1001023
C-Y79AA1001041
C-Y79AA1001048//"ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD)."//3.1E-138//583aa//47%//P45953
C-Y79AA1001077
C-Y79AA1001078
C-Y79AA1001145
C-Y79AA1001177
C-Y79AA1001185
C-Y79AA1001211//"Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds."//0//1435bp//99%//AF139658
C-Y79AA1001228
C-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HYDROXYSTEROID DEHYDROGENASE 1).//7.7E-50//228aa//42%//P51657
C-Y79AA1001236//"Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin))."//0//1653bp//99%//AJ005892
C-Y79AA1001281
C-Y79AA1001312//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46).//0.000000023//193aa//30%//Q03309
C-Y79AA1001323//"Mus musculus mRNA for GSG1, complete cds."//3.3E-172//1171bp//83%//D87325
C-Y79AA1001391//HOMEOBOX PROTEIN HOX-A13 (HOX-1J).//1.2E-58//178aa//66%//P31271
C-Y79AA1001394//CELL DIVISION PROTEIN FTSH HOMOLOG (EC 3.4.24.-).//1.2E-13//230aa//32%//O83746
C-Y79AA1001402//"Homo sapiens paraneoplastic cancer-testis-brain antigen (MA4) mRNA, partial cds."//8.50E-65//784bp//62%//AF083115
C-Y79AA1001493//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//3.80E-18//151aa//38%//P35132
C-Y79AA1001533//"Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds."//4.5E-193//1333bp//80%//D14336
C-Y79AA1001541
C-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//7.5E-76//85aa//90%//P42356
C-Y79AA1001555
C-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.9E-40//482aa//27%//P27550

BNSDOCID: <EP___1074617A2_I_>

C-Y79AA1001585
C-Y79AA1001603//"POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN- UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1)."//1.7E-84//313aa//48%//Q07537
C-Y79AA1001613//ZINC FINGER PROTEIN 132.//3.8E-91//209aa//41%//P52740
C-Y79AA1001665
C-Y79AA1001679//"Homo sapiens lambda-crystallin mRNA, complete cds."//3.4e-310//1430bp//98%//AF077049
C-Y79AA1001696//"Homo sapiens mRNA for KIAA1109 protein, partial cds."//0//1669bp//100%//AB029032
C-Y79AA1001705//"Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds."//3.4E-47//626bp//68%//AF033120
C-Y79AA1001711//"Human 60-kdal ribonucleoprotein (Ro) mRNA, complete cds."//1.2E-258//1185bp//99%//J04137
C-Y79AA1001781
C-Y79AA1001805
C-Y79AA1001827//"Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA, complete cds."//0//1689bp//98%//AF177145
C-Y79AA1001846
C-Y79AA1001923
C-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//1E-10//94aa//47%//O42643
C-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.9E-39//143aa//52%//P42743
C-Y79AA1002083//H.sapiens mRNA for MUF1 protein.//5E-163//752bp//99%//X86018
C-Y79AA1002089
C-Y79AA1002115
C-Y79AA1002125
C-Y79AA1002204
C-Y79AA1002208//ANKYRIN.//8.1E-34//188aa//38%//Q02357
C-Y79AA1002209//"Homo sapiens CGI-04 protein mRNA, complete cds."//0//1617bp//99%//AF132939
C-Y79AA1002229//DNA CROSS-LINK REPAIR PROTEIN PSO2/SNM1.//7.10E-17//213aa//31%//P30620
C-Y79AA1002246//SYNAPTOTAGMIN V.//1.6E-28//286aa//32%//000445
C-Y79AA1002298
C-Y79AA1002307//"Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds."//0//1209bp//99%//AF116574
C-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.9E-186//1130bp//82%//X67877
C-Y79AA1002351
C-Y79AA1002407
C-Y79AA1002433//"Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit mRNA, complete cds."//0//1545bp//96%//AF152961
C-Y79AA1002472//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.5E-136//472aa//49%//Q05481

Homology Search Result Data 13.

[0333] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences. Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.

C-HEMBA1000042
C-HEMBA1000141//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1135bp//100%//AF196304
C-HEMBA1000150//H.sapiens gene for U5 snRNP-specific 200kD protein.//2.50E-153//525bp//91%//Z70200
C-HEMBA1000213
C-HEMBA1000243

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C-HEMBA1000244
C-HEMBA1000251
C-HEMBA1000338
C-HEMBA1000357
C-HEMBA1000376
C-HEMBA1000428
C-HEMBA1000469
C-HEMBA1000497
C-HEMBA1000561//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.40E-37//674aa//25%//Q05481
C-HEMBA1000569//GPI-ANCHORED PROTEIN P137.//6.50E-19//265aa//32%//Q60865
C-HEMBA1000575
C-HEMBA1000591//PTB-ASSOCIATED SPLICING FACTOR (PSF).//2.20E-17//198aa//40%//P23246
C-HEMBA1000673
C-HEMBA1000702
C-HEMBA1000722
C-HEMBA1000726
C-HEMBA1000876
C-HEMBA1000942
C-HEMBA1000943
C-HEMBA1000960
C-HEMBA1000985
C-HEMBA1001019//CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.-) (P34 PROTEIN KINASE) (CYCLIN-DEPENDENT KINASE 1) (CDK1).//3.10E-10//70aa//58%//P06493
C-HEMBA1001020
C-HEMBA1001024
C-HEMBA1001026
C-HEMBA1001051
C-HEMBA1001060
C-HEMBA1001071//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSORS.//1.50E-92//82aa//100%//P02461
C-HEMBA1001077//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.//2.00E-80//432bp//94%//AF119043
C-HEMBA1001099
C-HEMBA1001121
C-HEMBA1001123
C-HEMBA1001208
C-HEMBA1001213
C-HEMBA1001226
C-HEMBA1001247
C-HEMBA1001299
C-HEMBA1001319
C-HEMBA1001323
C-HEMBA1001327
C-HEMBA1001361
C-HEMBA1001375
C-HEMBA1001377
C-HEMBA1001383
C-HEMBA1001391
C-HEMBA1001411
C-HEMBA1001432
C-HEMBA1001433
C-HEMBA1001435
C-HEMBA1001442
C-HEMBA1001463
C-HEMBA1001515
C-HEMBA1001522
C-HEMBA1001557
C-HEMBA1001566

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C-HEMBA1001589
C-HEMBA1001608
C-HEMBA1001636
C-HEMBA1001647
C-HEMBA1001651
C-HEMBA1001658
C-HEMBA1001675//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.//5.40E-09//101aa//35%//P54787
C-HEMBA1001712
C-HEMBA1001734//CADHERIN-11 PRECURSOR (OSTEOBLAST-CADHERIN) (OB-CADHERIN) (OSF-4).//1.10E-38//87aa//96%//P55288
C-HEMBA1001745
C-HEMBA1001750
C-HEMBA1001784
C-HEMBA1001791
C-HEMBA1001803
C-HEMBA1001820
C-HEMBA1001835
C-HEMBA1001888
C-HEMBA1001912
C-HEMBA1001915
C-HEMBA1001918
C-HEMBA1001940
C-HEMBA1001942
C-HEMBA1001964
C-HEMBA1002022
C-HEMBA1002039
C-HEMBA1002100
C-HEMBA1002113
C-HEMBA1002119
C-HEMBA1002139//LIM AND SH3 DOMAIN PROTEIN LASP-1 (MLN 50).//7.10E-05//51aa//49%//Q14847
C-HEMBA1002160
C-HEMBA1002162
C-HEMBA1002166
C-HEMBA1002185
C-HEMBA1002204
C-HEMBA1002328
C-HEMBA1002337
C-HEMBA1002348
C-HEMBA1002381
C-HEMBA1002486
C-HEMBA1002498
C-HEMBA1002538
C-HEMBA1002552
C-HEMBA1002555//Homo sapiens mSin3A associated polypeptide p30 mRNA, complete cds.//5.30E-51//768bp//68%//AF055993
C-HEMBA1002558
C-HEMBA1002621
C-HEMBA1002629
C-HEMBA1002645
C-HEMBA1002659
C-HEMBA1002661
C-HEMBA1002666
C-HEMBA1002678
C-HEMBA1002679
C-HEMBA1002712
C-HEMBA1002716
C-HEMBA1002742

BNSDOCID: <EP___1074617A2_I_>

C-HEMBA1002746//DNA POLYMERASE BETA (EC 2.7.7.7).//5.00E-37//268aa//34%//P06746
C-HEMBA1002748
C-HEMBA1002780
C-HEMBA1002801
C-HEMBA1002826
C-HEMBA1002833
C-HEMBA1002921
C-HEMBA1002934
C-HEMBA1002944
C-HEMBA1002968
C-HEMBA1003034
C-HEMBA1003037
C-HEMBA1003071//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR (ALS).//1.30E-09//121aa//40%//P35858
C-HEMBA1003078
C-HEMBA1003083
C-HEMBA1003086
C-HEMBA1003098//Homo sapiens NY-REN-6 antigen mRNA, partial cds.//6.20E-273//1253bp//99%//AF155096
C-HEMBA1003133
C-HEMBA1003142
C-HEMBA1003166
C-HEMBA1003197
C-HEMBA1003202
C-HEMBA1003220
C-HEMBA1003229
C-HEMBA1003276
C-HEMBA1003278
C-HEMBA1003328
C-HEMBA1003373
C-HEMBA1003597
C-HEMBA1003598
C-HEMBA1003656
C-HEMBA1003680//PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-).//2.40E-92//423aa//47%//P34629
C-HEMBA1003733
C-HEMBA1003742
C-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//3.70E-124//347aa//55%//Q16665
C-HEMBA1003803
C-HEMBA1003854
C-HEMBA1003926
C-HEMBA1003939
C-HEMBA1003987
C-HEMBA1004012
C-HEMBA1004015
C-HEMBA1004193
C-HEMBA1004225
C-HEMBA1004241
C-HEMBA1004267
C-HEMBA1004295//Homo sapiens NY-REN-25 antigen mRNA, partial cds.//9.40E-31//381bp//65%//AF155103
C-HEMBA1004354//CHL1 PROTEIN.//9.90E-26//130aa//42%//P22516
C-HEMBA1004356//H.sapiens MSSP-2 mRNA.//3.00E-243//573bp//98%//X77494
C-HEMBA1004396
C-HEMBA1004405
C-HEMBA1004433
C-HEMBA1004538
C-HEMBA1004542
C-HEMBA1004573

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C-HEMBA1004577
C-HEMBA1004604//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.//0//1612bp//99%//AF193844
C-HEMBA1004617
C-HEMBA1004631
C-HEMBA1004705
C-HEMBA1004733
C-HEMBA1004748
C-HEMBA1004778
C-HEMBA1004803
C-HEMBA1004807
C-HEMBA1004820
C-HEMBA1004865
C-HEMBA1004880
C-HEMBA1004900
C-HEMBA1004909
C-HEMBA1004960
C-HEMBA1004978
C-HEMBA1004980
C-HEMBA1004983
C-HEMBA1004995
C-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0//2212bp//99%//AB014548
C-HEMBA1005029//Homo sapiens CGI-13 protein mRNA, complete cds.//0//1487bp//99%//AF132947
C-HEMBA1005035
C-HEMBA1005039
C-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16).//3.40E-101//106aa//98%//P35290
C-HEMBA1005050
C-HEMBA1005062
C-HEMBA1005066
C-HEMBA1005075
C-HEMBA1005079
C-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//0//2762bp//99%//AF080561
C-HEMBA1005123
C-HEMBA1005149
C-HEMBA1005152
C-HEMBA1005201//Homo sapiens CGI-07 protein mRNA, complete cds.//0//1608bp//99%//AF132941
C-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.90E-179//361aa//95%//Q00004
C-HEMBA1005223
C-HEMBA1005232
C-HEMBA1005241
C-HEMBA1005275
C-HEMBA1005293
C-HEMBA1005311
C-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial.//3.90E-241//1095bp//99%//AJ007581
C-HEMBA1005359//ZINC FINGER PROTEIN 137.//3.90E-85//206aa//69%//P52743
C-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds.//9.00E-77//620bp//74%//AF071787
C-HEMBA1005374
C-HEMBA1005382
C-HEMBA1005411
C-HEMBA1005426
C-HEMBA1005443
C-HEMBA1005447
C-HEMBA1005497
C-HEMBA1005500
C-HEMBA1005506
C-HEMBA1005508

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C-HEMBA1005526
C-HEMBA1005530//Homo sapiens anaphase-promoting complex subunit 7 (APC7) mRNA, complete cds.//0//1578bp//98%//AF191340
C-HEMBA1005548//Homo sapiens MAFB/Kreisler basic region/leucine zipper transcription factor (MAFB) mRNA, complete cds.//1.00E-220//1014bp//99%//AF134157
C-HEMBA1005552
C-HEMBA1005568
C-HEMBA1005588
C-HEMBA1005593
C-HEMBA1005606
C-HEMBA1005616
C-HEMBA1005627
C-HEMBA1005670
C-HEMBA1005679
C-HEMBA1005699
C-HEMBA1005705
C-HEMBA1005732//Human mRNA for KIAA1293 gene, complete cds.//5.50E-102//317bp//98%//D14697
C-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU/M-TYPE).//2.00E-36//342aa//33%//P00789
C-HEMBA1005852
C-HEMBA1005894
C-HEMBA1005921
C-HEMBA1006035
C-HEMBA1006036
C-HEMBA1006090
C-HEMBA1006138
C-HEMBA1006173
C-HEMBA1006252
C-HEMBA1006268//Homo sapiens HQ0024c mRNA, complete cds.//3.50E-157//845bp//92%//AF073836
C-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.60E-130//332aa//62%//002193
C-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//3.50E-105//381aa//54%//P28160
C-HEMBA1006380
C-HEMBA1006416
C-HEMBA1006421
C-HEMBA1006424
C-HEMBA1006426
C-HEMBA1006446
C-HEMBA1006485//PUROMYCIN-SENSITIVE AMINOPEPTIDASE (EC 3.4.11.-) (PSA).//1.90E-81//153aa//97%//P55786
C-HEMBA1006486
C-HEMBA1006494
C-HEMBA1006546
C-HEMBA1006562
C-HEMBA1006595
C-HEMBA1006597
C-HEMBA1006631
C-HEMBA1006639
C-HEMBA1006652//60S RIBOSOMAL PROTEIN L7.//2.40E-44//206aa//47%//P14148
C-HEMBA1006659
C-HEMBA1006665
C-HEMBA1006676
C-HEMBA1006695
C-HEMBA1006709
C-HEMBA1006758//Homo sapiens protocadherin beta 13 (PCDH-beta13) mRNA, complete cds.//0//1832bp//91%//AF152492
C-HEMBA1006780
C-HEMBA1006807//Homo sapiens mRNA for SPOP.//5.70E-125//1109bp//75%//AJ000644
C-HEMBA1006824

BNSDOCID: <EP___1074617A2_I_>

C-HEMBA1006865
C-HEMBA1006921
C-HEMBA1006949
C-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2.3-sialyltransferase.//1.90E-80//447bp//89%//X74570
C-HEMBA1007051
C-HEMBA1007052
C-HEMBA1007066
C-HEMBA1007073
C-HEMBA1007078
C-HEMBA1007085
C-HEMBA1007113
C-HEMBA1007121//Homo sapiens bisphosphate 3'-nucleotidase mRNA, complete cds.//1.70E-252//1118bp//92%//AF125042
C-HEMBA1007129
C-HEMBA1007147
C-HEMBA1007151//Homo sapiens synphilin 1 mRNA, complete cds.//0//1900bp//99%//AF076929
C-HEMBA1007178
C-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds.//0//1212bp//98%//D86987
C-HEMBA1007224//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1590bp//99%//AF196304
C-HEMBA1007243//Chinese hamster hprt mRNA, complete cds.//2.00E-58//650bp//70%//J00060
C-HEMBA1007251
C-HEMBA1007288
C-HEMBA1007322
C-HEMBA1007341
C-HEMBB1000050
C-HEMBB1000054
C-HEMBB1000059
C-HEMBB1000089
C-HEMBB1000113
C-HEMBB1000144//GUANYLATE CYCLASE ACTIVATING PROTEIN 2 (GCAP 2) (RETINAL GUANYLYL CYCLASE ACTIVATOR PROTEIN P24).//1.40E-24//71aa//77%//P51177
C-HEMBB1000173
C-HEMBB1000175
C-HEMBB1000272
C-HEMBB1000317//FIBULIN-1, ISOFORM D PRECURSOR.//7.10E-62//458aa//35%//P37888
C-HEMBB1000318
C-HEMBB1000336
C-HEMBB1000341
C-HEMBB1000343
C-HEMBB1000354
C-HEMBB1000374
C-HEMBB1000434
C-HEMBB1000441
C-HEMBB1000491
C-HEMBB1000493
C-HEMBB1000510
C-HEMBB1000652
C-HEMBB1000672
C-HEMBB1000684
C-HEMBB1000709
C-HEMBB1000726
C-HEMBB1000770
C-HEMBB1000827
C-HEMBB1000831
C-HEMBB1000883
C-HEMBB1000888

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C-HEMBB1000893
C-HEMBB1000913
C-HEMBB1000996
C-HEMBB1001004
C-HEMBB1001047
C-HEMBB1001060
C-HEMBB1001114
C-HEMBB1001119
C-HEMBB1001133
C-HEMBB1001142
C-HEMBB1001177
C-HEMBB1001208
C-HEMBB1001209
C-HEMBB1001249
C-HEMBB1001253
C-HEMBB1001254
C-HEMBB1001271
C-HEMBB1001304
C-HEMBB1001317
C-HEMBB1001348
C-HEMBB1001394
C-HEMBB1001410
C-HEMBB1001424
C-HEMBB1001426
C-HEMBB1001429//Homo sapiens leucine aminopeptidase mRNA, complete cds.//0//1933bp//99%//AF061738
C-HEMBB1001436
C-HEMBB10014437/Rattus norvegicus pyruvate dehydrogenase phosphatase isoenzyme 1 mRNA, complete cds.//3.00E-130//553bp//86%//AF062740
C-HEMBB1001449
C-HEMBB1001458
C-HEMBB1001521
C-HEMBB1001531
C-HEMBB1001535
C-HEMBB1001536
C-HEMBB1001564
C-HEMBB1001565
C-HEMBB1001585
C-HEMBB1001588
C-HEMBB1001603
C-HEMBB1001618
C-HEMBB1001635
C-HEMBB1001653
C-HEMBB1001668
C-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//0//2035bp//99%//AB014546
C-HEMBB1001685
C-HEMBB1001695
C-HEMBB1001707
C-HEMBB1001735
C-HEMBB1001736//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 (EIF3 P116) (EIF3 P110).//4.60E-15//391aa//25%//P55884
C-HEMBB1001747
C-HEMBB1001749//TRANSCRIPTIONAL ACTIVATOR GCN5.//1.70E-16//84aa//47%//Q03330
C-HEMBB1001753
C-HEMBB1001756
C-HEMBB1001760
C-HEMBB1001785
C-HEMBB1001797
C-HEMBB1001802//Human desmin mRNA, complete cds.//0//1523bp//98%//U59167

BNSDOCID: <EP___1074617A2_I_>

C-HEMBB1001816
C-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA complete cds.//0//1514bp//99%//AF056209
C-HEMBB1001839//GASTRULA ZINC FINGER PROTEIN XLCGF42.1 (FRAGMENT).//6.90E-11//87aa//35%//P18720
C-HEMBB1001850
C-HEMBB1001863
C-HEMBB1001868
C-HEMBB1001874
C-HEMBB1001880
C-HEMBB1001899
C-HEMBB1001906
C-HEMBB1001910
C-HEMBB1001911
C-HEMBB1001921
C-HEMBB1001922
C-HEMBB1001930
C-HEMBB1001944
C-HEMBB1001945
C-HEMBB1001947
C-HEMBB1001950//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.-) (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1.60E-41//370aa//31%//P54304
C-HEMBB1001952
C-HEMBB1001957
C-HEMBB1001962
C-HEMBB1001983
C-HEMBB1001990
C-HEMBB1001996
C-HEMBB1002002
C-HEMBB1002005
C-HEMBB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYPIVC1).//2.70E-49//139aa//55%//P29981
C-HEMBB1002043
C-HEMBB1002045
C-HEMBB1002049
C-HEMBB1002050
C-HEMBB1002068
C-HEMBB1002092
C-HEMBB1002139
C-HEMBB1002142
C-HEMBB1002190
C-HEMBB1002193
C-HEMBB1002217//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-132//399aa//44%//Q05481
C-HEMBB1002218
C-HEMBB1002232
C-HEMBB1002247
C-HEMBB1002249
C-HEMBB1002266//NEURONAL PROTEIN.//2.10E-46//121aa//76%//P41737
C-HEMBB1002327
C-HEMBB1002329
C-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.//1.10E-274//1249bp//99%//AJ010841
C-HEMBB1002358
C-HEMBB1002371
C-HEMBB1002387
C-HEMBB1002409
C-HEMBB1002425
C-HEMBB1002442//LIN-10 PROTEIN.//9.70E-14//121aa//31%//P34692

BNSDOCID: <EP___1074617A2_I_>

C-HEMBB1002453
C-HEMBB1002458
C-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds.//7.70E-258//774bp//99%//U43885
C-HEMBB1002489
C-HEMBB1002510//GYP7 PROTEIN.//3.10E-50//192aa//42%//P48365
C-HEMBB1002520
C-HEMBB1002522
C-HEMBB1002545
C-HEMBB1002579
C-HEMBB1002582
C-HEMBB1002596
C-HEMBB1002603
C-HEMBB1002610
C-HEMBB1002613
C-HEMBB1002617
C-HEMBB1002623
C-HEMBB1002635
C-HEMBB1002677
C-HEMBB1002683
C-HEMBB1002699
C-HEMBB1002702
C-MAMMA1000009
C-MAMMA1000043
C-MAMMA1000045//ENV POLYPROTEIN [CONTAINS: SURFACE PROTEIN GP85; MEMBRANE PROTEIN GP37].//1.90E-07//249aa//27%//P03396
C-MAMMA1000057
C-MAMMA1000085//PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.16) (CYSTEINE--TRNA LIGASE) (CYSRS).//2.10E-90//427aa//39%//Q09860
C-MAMMA1000092
C-MAMMA1000103
C-MAMMA1000117
C-MAMMA1000129
C-MAMMA1000133
C-MAMMA1000155
C-MAMMA1000175
C-MAMMA1000198
C-MAMMA1000241
C-MAMMA1000251
C-MAMMA1000254
C-MAMMA1000287
C-MAMMA1000307
C-MAMMA1000331
C-MAMMA1000339
C-MAMMA1000340
C-MAMMA1000348
C-MAMMA1000356
C-MAMMA1000360
C-MAMMA1000402
C-MAMMA1000414
C-MAMMA1000431
C-MAMMA1000444
C-MAMMA1000458
C-MAMMA1000500
C-MAMMA1000522
C-MAMMA1000576
C-MAMMA1000583
C-MAMMA1000594
C-MAMMA1000605

BNSDOCID: <EP___1074617A2_I_>

C-MAMMA1000616
C-MAMMA1000643
C-MAMMA1000684//Homo sapiens 7-60 mRNA, complete cds.//0//2402bp//99%//AF109134
C-MAMMA1000696
C-MAMMA1000707
C-MAMMA1000714
C-MAMMA1000720
C-MAMMA1000744
C-MAMMA1000761
C-MAMMA1000776
C-MAMMA1000798
C-MAMMA1000839
C-MAMMA1000851
C-MAMMA1000863
C-MAMMA1000867
C-MAMMA1000876
C-MAMMA1000880
C-MAMMA1000883
C-MAMMA1000921
C-MAMMA1000931
C-MAMMA1000941
C-MAMMA1000957
C-MAMMA1000962
C-MAMMA1000975
C-MAMMA1000987
C-MAMMA1001003
C-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CG-R) (LSH-R) (LUTEINIZING HOROMINE RECEPTOR) (FRAGMENT).//1.20E-26//276aa//28%//Q90674
C-MAMMA1001038//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//2.60E-107//190aa//95%//Q15746
C-MAMMA1001082
C-MAMMA1001162
C-MAMMA1001186
C-MAMMA1001191
C-MAMMA1001206
C-MAMMA1001220
C-MAMMA1001243
C-MAMMA1001249
C-MAMMA1001256
C-MAMMA1001268
C-MAMMA1001271
C-MAMMA1001274
C-MAMMA1001292
C-MAMMA1001305//RHO-GTPASE-ACTIVATING PROTEIN 1 (GTPASE-ACTIVATING PROTEIN RHOGAP) (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//2.20E-98//283aa//63%//Q07960
C-MAMMA1001324
C-MAMMA1001341
C-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//1.40E-165//312aa//99%//P02750
C-MAMMA1001397
C-MAMMA1001408
C-MAMMA1001420
C-MAMMA1001442
C-MAMMA1001452
C-MAMMA1001465
C-MAMMA1001487
C-MAMMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU-TYPE).//5.70E-55//86aa//97%//P07384

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C-MAMMA1001547
C-MAMMA1001551
C-MAMMA1001575
C-MAMMA1001590
C-MAMMA1001600
C-MAMMA1001606
C-MAMMA1001627//Homo sapiens mRNA for transcription factor TBX6.//5.20E-189//871bp//99%//AJ007989
C-MAMMA1001663
C-MAMMA1001670
C-MAMMA1001671
C-MAMMA1001679//F-ACTIN CAPPING PROTEIN BETA SUBUNIT (CAPZ).//0.00000058//29aa//100%//P47756
C-MAMMA1001711
C-MAMMA1001735//TUBULIN BETA-5 CHAIN (BETA-TUBULIN CLASS-V).//5.90E-240//445aa//97%//P09653
C-MAMMA1001744
C-MAMMA1001745
C-MAMMA1001751//Homo sapiens tandem pore domain potassium channel TWIK-2 (KCNK6) mRNA, complete cds.//0//2332bp//99%//AF117708
C-MAMMA1001783
C-MAMMA1001788
C-MAMMA1001806
C-MAMMA1001812
C-MAMMA1001815
C-MAMMA1001817
C-MAMMA1001818
C-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene.//1.30E-198//1157bp//80%//Y13148
C-MAMMA1001824
C-MAMMA1001851
C-MAMMA1001854
C-MAMMA1001864
C-MAMMA1001878
C-MAMMA1001890
C-MAMMA1001907
C-MAMMA1001908
C-MAMMA1001931
C-MAMMA1001969
C-MAMMA1002011
C-MAMMA1002032
C-MAMMA1002041
C-MAMMA1002047
C-MAMMA1002056
C-MAMMA1002058
C-MAMMA1002078
C-MAMMA1002082
C-MAMMA1002084
C-MAMMA1002093
C-MAMMA1002094
C-MAMMA1002118
C-MAMMA1002125
C-MAMMA1002132
C-MAMMA1002140
C-MAMMA1002143//Homo sapiens Cdc42 effector protein 4 mRNA, complete cds7/1.70E-252//1170bp//99%//AF099664
C-MAMMA1002145
C-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE 1) (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) (TSA) (PRP) (NATURAL KILLER CELL ENHANCING FACTOR B) (NKEF-B).//5.20E-61//60aa//90%//P32119
C-MAMMA1002230
C-MAMMA1002250

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C-MAMMA1002282
C-MAMMA1002293
C-MAMMA1002298
C-MAMMA1002299
C-MAMMA1002308
C-MAMMA1002310
C-MAMMA1002311
C-MAMMA1002322
C-MAMMA1002339
C-MAMMA1002352
C-MAMMA1002359
C-MAMMA1002360
C-MAMMA1002392
C-MAMMA1002411
C-MAMMA1002413
C-MAMMA1002417
C-MAMMA1002428//LYSOSOME MEMBRANE PROTEIN II (LIMP II) (85 KD LYSOSOMAL MEMBRANE SIALOGLYCOPROTEIN) (LGP85) (CD36 ANTIGEN-LIKE 2).//1.10E-24//96aa//68%//Q14108
C-MAMMA1002434
C-MAMMA1002446
C-MAMMA1002454
C-MAMMA1002461
C-MAMMA1002475
C-MAMMA1002556
C-MAMMA1002566
C-MAMMA1002612
C-MAMMA1002622//VILLIN.//7.20E-35//53aa//64%//P02640
C-MAMMA1002637//KINESIN LIGHT CHAIN (KLC).//1.30E-198//550aa//70%//Q07866
C-MAMMA1002650//Mus musculus ODA-8S protein mRNA, complete cds.//5.40E-57//480bp//68%//AF194030
C-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//4.3e-317//1942bp//85%//AF018261
C-MAMMA1002727
C-MAMMA1002748
C-MAMMA1002758
C-MAMMA1002780
C-MAMMA1002820
C-MAMMA1002833
C-MAMMA1002843
C-MAMMA1002895
C-MAMMA1002937//ZINC FINGER PROTEIN 135.//8.30E-99//393aa//43%//P52742
C-MAMMA1003004
C-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds.//0//1533bp//99%//AF077952
C-NT2RM1000001//D.melanogaster sap47-2 mRNA.//1.50E-10//417bp//62%//X80110
C-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds.//0//3376bp//99%//D31886
C-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds.//0//3551bp//99%//AB014590
C-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds.//0//3035bp//96%//AB014561
C-NT2RM1000421//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775 C-NT2RM1000499
C-NT2RM1001059//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB4.//3.60E-11//180aa//28%//Q99383
C-NT2RM1001092//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.60E-115//332aa//52%//Q05481
C-NT2RM2001592//Homo sapiens mRNA for KIAA1067 protein, partial cds.//0//3471bp//99%//AB028990
C-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds.//0//1632bp//99%//AB014518
C-NT2RM2001637
C-NT2RM2001641
C-NT2RM2001670//ZINC FINGER PROTEIN 29 (ZFP-29).//6.50E-104//407aa//43%//Q07230
C-NT2RM2001699

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C-NT2RM2001706
C-NT2RM2001718
C-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds.//0//2892bp//99%//AB007931
C-NT2RM2001805
C-NT2RM4000086
C-NT2RM4000215//MAK16 PROTEIN.//1.30E-68//295aa//49%//P10962
C-NT2RM4000414
C-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).//1.00E-59//595aa//28%//Q04652
C-NT2RM4000634
C-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//0//1412bp//100%//AB028992
C-NT2RM4000783
C-NT2RM4000857//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//6.70E-22//250aa//29%//P02750
C-NT2RM4000971
C-NT2RM4000996//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//8.00E-211//738aa//50%//Q05481
C-NT2RM4001092//ZINC FINGER PROTEIN GLO3.//3.10E-24//265aa//33%//P38682
C-NT2RM4001178//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//1.10E-48//218aa//43%//Q03532
C-NT2RM4001569
C-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds.//8.10E-300//1395bp//98%//M37712
C-NT2RM4001905
C-NT2RM4001938//Homo sapiens mRNA for KIAA0898 protein, partial cds.//0//2234bp//99%//AB020705
C-NT2RM4002062//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//1.90E-31//80aa//52%//P36419
C-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//9.30E-293//1751bp//83%//AF072758
C-NT2RM4002093//Homo sapiens neural polypyrimidine tract binding protein (PTB) mRNA, complete cds.//0//2550bp//99%//AF176085
C-NT2RM4002109//Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.//0//2572bp//99%//AF071592
C-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.90E-70//454bp//85%//AF035940
C-NT2RM4002194//Mus musculus semaphorin VIa mRNA, complete cds.//5.20E-297//1753bp//87%//AF030430
C-NT2RM4002390
C-NT2RM4002398
C-NT2RM4002420
C-NT2RM4002534
C-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//0//1915bp//87%//AF022962
C-NT2RM4002571//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T2).//4.60E-78//921bp//69%//X85019
C-NT2RP1000358//Homo sapiens mRNA; cDNA DKFZp564C186 (from clone DKFZp564C186).//0//1938bp//88%//AL050019
C-NT2RP1000522//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//8.20E-83//345aa//47%//Q61068
C-NT2RP1000609//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2165bp//99%//AL050118
C-NT2RP1000677//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER (ORGANIC ANION TRANSPORTING POLYPEPTIDE).//1.20E-78//483aa//31%//P46721
C-NT2RP1000701//Homo sapiens phospholipase A2 activating protein (PLA2P) mRNA, complete cds.//0//1687bp//99%//AF145020
C-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.80E-176//829bp//98%//AF047020
C-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds.//0//1555bp//99%//AF064094
C-NT2RP1000916
C-NT2RP1000944
C-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//0//2085bp//99%//U82267
C-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9.//2.30E-116//319aa//46%//Q06218

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C-NT2RP1001113
C-NT2RP1001173//Homo sapiens mRNA; cDNA DKFZp566D1146 (from clone DKFZp566D1146).//0//2333bp//99%//AL080222
C-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//5.20E-108//1278bp//69%//U79139
C-NT2RP1001185//Human isovaleryl-coA dehydrogenase (IVD) mRNA, complete cds.//1.90E-158//729bp//99%//M34192
C-NT2RP1001247//Homo sapiens TGF-beta type secreted signaling protein LEFTYA mRNA, complete cds.//0//2006bp//100%//AF081513
C-NT2RP1001311
C-NT2RP1001313//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//7.50E-121//1394bp//69%//AF126799
C-NT2RP2000001//Homo sapiens mRNA for KIAA1111 protein, partial cds.//0//3188bp//99%//AB029034
C-NT2RP2000027
C-NT2RP2000183//DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL SPECIFIC PROTEIN NSP60).//3.30E-16//114aa//44%//002675
C-NT2RP2000198
C-NT2RP2000523//APOLIPOPROTEIN B MRNA EDITING PROTEIN (HEPR) (APOBEC-1).//6.00E-16//124aa//34%//P41238
C-NT2RP2000551
C-NT2RP2000644
C-NT2RP2000660//SAP1 PROTEIN.//5.20E-68//474aa//32%//P39955
C-NT2RP2000678
C-NT2RP2000715
C-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds.//0//1562bp//99%//U80811
C-NT2RP2000970
C-NT2RP2001347
C-NT2RP2001460//TRICHOHYALIN.//1.00E-14//521aa//24%//P37709
C-NT2RP2001613//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNTD.//6.10E-12//184aa//31%//P24391
C-NT2RP2001634//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//0//2445bp//99%//U97067
C-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds.//0//1287bp//99%//AF058718
C-NT2RP2001677
C-NT2RP2001678
C-NT2RP2001720
C-NT2RP2001740//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//7.90E-52//220aa//44%//Q61068
C-NT2RP2001756//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.70E-49//411aa//32%//P51523
C-NT2RP2001839//SCY1 PROTEIN.//5.40E-32//621aa//24%//P53009
C-NT2RP2001861
C-NT2RP2001869//ZINC FINGER PROTEIN 191.//7.10E-26//126aa//52%//014754
C-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AIF-1) (IONIZED CALCIUM BINDING ADAPTER MOLECULE 1).//1.20E-45//141aa//65%//P55008
C-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end.//0//2518bp//98%//M74161
C-NT2RP2001936
C-NT2RP2001943
C-NT2RP2001946
C-NT2RP2002032
C-NT2RP2002033
C-NT2RP2002041
C-NT2RP2002047
C-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//1.60E-226//1301bp//88%//U87306

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C-NT2RP2002124//Homo sapiens mRNA for KIAA1097 protein, partial cds.//0//1772bp//95%//AB029020
C-NT2RP2002172
C-NT2RP2002219
C-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//0//1528bp//98%//AF005418
C-NT2RP2002316
C-NT2RP2002373
C-NT2RP2002439
C-NT2RP2002475
C-NT2RP2002546
C-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-155//562aa//50%//P51523
C-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds.//9.20E-147//874bp//87%//U19181
C-NT2RP2002643
C-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.//3.50E-74//727bp//72%//AF041107
C-NT2RP2002736
C-NT2RP2002740
C-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.//9.90E-54//964bp//64%//D89016
C-NT2RP2002752
C-NT2RP2002753
C-NT2RP2002857
C-NT2RP2003000//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//1.90E-11//132aa//38%//Q13829
C-NT2RP2003073
C-NT2RP2003164//Homo sapiens mRNA for protein kinase.//0//2313bp//99%//AJ132545
C-NT2RP2003206
C-NT2RP2003228//H.sapiens P1-Cdc21 mRNA.//0//2870bp//98%//X74794
C-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.60E-186//1551bp//77%//AF023657
C-NT2RP2003237
C-NT2RP2003272//Homo sapiens ubiquilin mRNA, complete cds.//0//1789bp//99%//AF176069
C-NT2RP2003280
C-NT2RP2003293
C-NT2RP2003394//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//5.50E-13//302aa//26%//P25386
C-NT2RP2003401//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//9.60E-78//346aa//43%//061068
C-NT2RP2003456
C-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/PDGF2) mRNA, complete cds.//0//1746bp//95%//M12783
C-NT2RP2003522//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//1764bp//99%//AF125158
C-NT2RP2003559
C-NT2RP2003564//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//2.10E-59//270aa//46%//P19474
C-NT2RP2003581
C-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.//9.40E-243//1624bp//82%//AJ006215
C-NT2RP2003702//Homo sapiens 17 beta-hydroxysteroid dehydrogenase type VII (HSD17B7) mRNA, complete cds.//2.1e-313//978bp//99%//AF098786
C-NT2RP2003704//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//1.80E-72//350bp//100%//AJ132637
C-NT2RP2003727
C-NT2RP2003751
C-NT2RP2003781//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.//5.50E-63//253aa//50%//Q09201
C-NT2RP2003825
C-NT2RP2003871

BNSDOCID: <EP___1074617A2_I_>

C-NT2RP2003885
C-NT2RP2003912//SERINE/THREONINE-PROTEIN KINASE NEK1 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 1).//6.10E-183//387aa//87%//P51954
C-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds.//0//2866bp//98%//AB007916
C-NT2RP2003988
C-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//2.30E-53//141aa//78%//P20290
C-NT2RP2004098//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//5.40E-30//319aa//31%//Q01513
C-NT2RP2004142
C-NT2RP2004170//Homo sapiens mRNA for transducin (beta) like 1 protein.//1.10E-138//1236bp//74%//Y12781
C-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds.//3.80E-52//397bp//82%//AF003998
C-NT2RP2004207
C-NT2RP2004226
C-NT2RP2004232//Homo sapiens EPK2 mRNA for serine/threonine kinase, complete cds.//0//2272bp//99%//AB015982
C-NT2RP2004242//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//9.90E-12//427aa//26%//P19246
C-NT2RP2004270//PROTEIN PTM1 PRECURSOR.//1.40E-16//334aa//24%//P32857
C-NT2RP2004321
C-NT2RP2004339
C-NT2RP2004347
C-NT2RP2004396//Homo sapiens mRNA for activator of S phase Kinase, complete cds.//5.40E-243//1108bp//99%//AB028069
C-NT2RP2004399
C-NT2RP2004400
C-NT2RP2004412
C-NT2RP2004425//Mus musculus axotrophin mRNA, complete cds.//0//2321bp//86%//AF155739
C-NT2RP2004490
C-NT2RP2004523
C-NT2RP2004538//Mus musculus kinesin-like protein KIF1B (Kif1b) mRNA, complete cds.//0//1387bp//86%//AF090190
C-NT2RP2004580
C-NT2RP2004587//Homo sapiens mRNA for KIAA0888 protein, partial cds.//0//2886bp//100%//AB020695
C-NT2RP2004594
C-NT2RP2004681
C-NT2RP2004709
C-NT2RP2004710//Homo sapiens mRNA for KIAA1014 protein, partial cds.//0//2587bp//100%//AB023231
C-NT2RP2004732//Homo sapiens mRNA for KIAA0884 protein, partial cds.//0//1774bp//99%//AB020691
C-NT2RP2004767
C-NT2RP2004775
C-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1 (KS1) mRNA, complete cds.//1.00E-228//1666bp//75%//U56732
C-NT2RP2004962
C-NT2RP2004982
C-NT2RP2005003//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//1.80E-99//376aa//43%//P19474
C-NT2RP2005018
C-NT2RP2005020
C-NT2RP2005022
C-NT2RP2005031
C-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds.//0//4069bp//99%//AB014564
C-NT2RP2005139//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).//0.000000022//139aa//35%//Q05921
C-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//2769bp//98%//AJ007509
C-NT2RP2005254
C-NT2RP2005325//Homo sapiens LIM-homeodomain protein HLHX2 (LHX2) mRNA, complete cds.//0//1643bp//

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99%//AF124735
C-NT2RP2005336//TRICHOHYALIN.//5.40E-10//545aa//22%//P37709
C-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPASE 5 (EC 3.6.1.38).//2.10E-124//636aa//38%//P32660
C-NT2RP2005360
C-NT2RP2005407//OXYSTEROL-BINDING PROTEIN.//5.30E-63//410aa//40%//P22059
C-NT2RP2005454
C-NT2RP2005457//Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA, complete cds.//1.20E-130//608bp//99%//AF070652
C-NT2RP2005476//Human p190-B (p190-B) mRNA, complete cds.//3.40E-108//668bp//88%//U17032
C-NT2RP2005491//PARAMYOSIN (PMY) (ANTIGEN B).//0.00000015//279aa//26%//P35418
C-NT2RP2005496//ZINC FINGER PROTEIN 135.//2.90E-146//398aa//59%//P52742
C-NT2RP2005501
C-NT2RP2005531//PROTEIN 4.1 (BAND 4.1) (P4.1).//5.50E-70//393aa//39%//P11171
C-NT2RP2005600//Homo sapiens mRNA for KIAA1020 protein, partial cds.//0//2554bp//99%//AB028943
C-NT2RP2005645
C-NT2RP2005694//X-LINKED RETINITIS PIGMENTOSA GTPASE REGULATOR.//2.60E-10//175aa//27%//Q92834
C-NT2RP2005701//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//3.00E-63//323aa//39%//Q62158
C-NT2RP2005741
C-NT2RP2005806
C-NT2RP2005815
C-NT2RP2005841
C-NT2RP2005882
C-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//1.50E-67//388aa//44%//P25500
C-NT2RP2006103
C-NT2RP2006166
C-NT2RP2006258
C-NT2RP2006261
C-NT2RP2006321
C-NT2RP2006454
C-NT2RP2006598//Homo sapiens retinoid x receptor interacting protein mRNA, complete cds.//3.10E-295//1193bp//99%//AF113538
C-NT2RP3000046//MITOCHONDRIAL GTPASE MSS1 PRECURSOR.//4.60E-78//421aa//37%//P32559
C-NT2RP3000047//NPL4 PROTEIN.//1.10E-85//526aa//36%//P33755
C-NT2RP3000418
C-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//2.90E-1511319aa//26%//P37908
C-NT2RP3000487
C-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//0//1934bp//99%//X16667
C-NT2RP3000526
C-NT2RP3000603//NEUROGENIC DIFFERENTIATION FACTOR 1.//3.70E-11//90aa//42%//Q13562
C-NT2RP3000605//Mus musculus mRNA for wizL, complete cds.//0//2232bp//82%//AB012265
C-NT2RP3000628
C-NT2RP3000739//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//1.40E-24//155aa//37%//Q10149
C-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.).//8.30E-108//331aa//50%//P27448
C-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A.//1.90E-46//73aa//98%//P39027
C-NT2RP3001057//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//9.00E-201//584aa//54%//Q05481
C-NT2RP3001113//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//2.90E-11//631aa//23%//P25386
C-NT2RP3001245//Homo sapiens mRNA for KIAA0923 protein, complete cds.//0//2659bp//99%//AB023140
C-NT2RP3001253//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//1.70E-10//540aa//23%//P32380
C-NT2RP3001356

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C-NT2RP3001383
C-NT2RP3001399//SSU72 PROTEIN.//1.30E-16//84aa//52%//P53538
C-NT2RP3001554//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//1.40E-76//388aa//32%//P46821
C-NT2RP3001712//Homo sapiens HP1-BP74 protein mRNA, complete cds.//0//1788bp//99%//AF113534
C-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//1.10E-240//902bp//99%//AF054177
C-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds.//6.90E-132//774bp//88%//AF008554
C-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT).//7.10E-132//294aa//84%//Q14141
C-NT2RP3001739
C-NT2RP3001777
C-NT2RP3001857//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.20E-14//242aa//24%//Q00808
C-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds.//0//3747bp//99%//AB014575
C-NT2RP3001944
C-NT2RP3002033
C-NT2RP3002054
C-NT2RP3002063//Homo sapiens mRNA for KIAA1033 protein, partial cds.//0//2830bp//99%//AB028956
C-NT2RP3002099
C-NT2RP3002102
C-NT2RP3002147
C-NT2RP3002163
C-NT2RP3002173
C-NT2RP3002255
C-NT2RP3002303//PROBABLE UNDECAPRENYL PYROPHOSPHATE SYNTHETASE (EC 2.5.1.31) (UPP SYNTHETASE) (DI-TRANS-POLY-CIS-DECAPRENYLCISTRANSFERASE).//8.60E-49//243aa//43%//Q58767
C-NT2RP3002343
C-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15).//4.20E-70//590bp//76%//X16396
C-NT2RP3002399//DNA REPLICATION LICENSING FACTOR MCM4 (CDC21 HOMOLOG)(P1-CDC21).//8.60E-79//416aa//34%//P33991
C-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds.//0//3811bp//99%//AB014578
C-NT2RP3002545//Homo sapiens mRNA; cDNA DKFZp586G0518 (from clone DKFZp586G0518).//0//2499bp//99%//AL050092
C-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III.//5.80E-40//161aa//52%//Q10010
C-NT2RP3002602//PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (EC 5.3.4.1) (ERP60) (58 KD MICROSOMAL PROTEIN) (P58) (HIP-70) (Q-2).//2.90E-19/173aa//28%//P11598
C-NT2RP3002603
C-NT2RP3002628//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//2.50E-26//90aa//42%//P38660
C-NT2RP3002659
C-NT2RP3002660
C-NT2RP3002682//Homo sapiens CGI-145 protein mRNA, complete cds.//0//1596bp//98%//AF151903
C-NT2RP3002687
C-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kifib), complete cds.//1.10E-93//1205bp//69%//D17577
C-NT2RP3002701
C-NT2RP3002785//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//2.50E-55//187aa//39%//Q24371
C-NT2RP3002869//Mus musculus semaphorin VIa mRNA, complete cds.//2.50E-232//1282bp//85%//AF030430
C-NT2RP3002876
C-NT2RP3002877
C-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//0//2085bp//94%//AB018314
C-NT2RP3002969//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2722bp//99%//D89053
C-NT2RP3002972//Halocynthia roretzi mRNA for HrPET-1, complete cds.//3.90E-52//899bp//64%//AB029333
C-NT2RP3003032//Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds.//0//2656bp//99%//AF084555
C-NT2RP3003061//ANKYRIN.//1.40E-20//200aa//37%//Q02357
C-NT2RP3003071//NEUROGENIC PROTEIN BIG BRAIN.//1.10E-05//258aa//24%//P23645

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C-NT2RP3003078
C-NT2RP3003139
C-NT2RP3003145//Mus musculus metallocarboxypeptidase CPX-1 mRNA, complete cds.//0//2251bp//81%// AF07773 8
C-NT2RP3003150
C-NT2RP3003197//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I.//5.70E-09//169aa// 31%//Q09674
C-NT2RP3003203//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//2.00E-210//1851bp//76%//AF110267
C-NT2RP3003210
C-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//4.30E-187//1750bp//75%//U20286
C-NT2RP3003230//Homo sapiens mRNA for hCRNN4, complete cds.//0//2350bp//99%//AB030656
C-NT2RP3003242//Homo sapiens stanniocalcin-related protein mRNA, complete cds.//0//2366bp//99%// AF098462
C-NT2RP3003251//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A))// 4.20E-86//366aa//48%//P19474
C-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//1.10E-170// 585aa//54%//O64948
C-NT2RP3003311
C-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds.//9.20E-45// 782bp//65%//U90653
C-NT2RP3003427
C-NT2RP3003543
C-NT2RP3003552
C-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC REGION.//4.50E-30// 191aa//40%//P40529
C-NT2RP3003564
C-NT2RP3003589//Homo sapiens ras-related GTP-binding protein mRNA, complete cds.//0//3131bp//94%// AF106681
C-NT2RP3003621
C-NT2RP3003625
C-NT2RP3003656
C-NT2RP3003659//HES1 PROTEIN.//5.90E-22//229aa//27%//P35843
C-NT2RP3003686
C-NT2RP3003701//F-SPONDIN PRECURSOR.//1.80E-17//324aa//26%//P35446
C-NT2RP3003716//SLIT PROTEIN PRECURSOR.//6.60E-10//150aa//34%//P24014
C-NT2RP3003726//Homo sapiens spermatogenesis associated PD1 mRNA, complete cds.//0//2568bp//99%// U28164
C-NT2RP3003795
C-NT2RP3003805
C-NT2RP3003809//SAV PROTEIN.//1.10E-131//576aa//41%//Q07590
C-NT2RP3003819
C-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP).//9.60E-19//174aa//31%// P02720
C-NT2RP3003831//Homo sapiens ENDOGL-1 (alias ENGL-a) mRNA for endonuclease G-like protein-1, complete cds.//2.2e-316//1436bp//99%//AB020523
C-NT2RP3003833
C-NT2RP3003842
C-NT2RP3003846//Homo sapiens mRNA for putative phospholipase, complete cds.//4.80E-277//1255bp//99%// AB019435
C-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds.//0//2557bp//99%//AB018343
C-NT2RP3003876
C-NT2RP3003914//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//2.20E-20//76aa//64%//Q09332
C-NT2RP3003918//Homo sapiens VAMP-associated protein B (VAP-B) mRNA, complete cds.//0//2191bp//99%// AF086628
C-NT2RP3003989

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C-NT2RP3004016//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1).//1.50E-17//226aa//26%//Q13263
C-NT2RP3004070
C-NT2RP3004145
C-NT2RP3004215
C-NT2RP3004253
C-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds.//5.10E-24//597bp//61 %//AF007871
C-NT2RP3004348//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.10E-185//1130bp//82%//X67877
C-NT2RP3004490//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//0//1778bp//99%//AC003982
C-NT2RP3004503
C-NT2RP3004566//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-95//434aa//43%//P51523
C-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acetylglucosamine-6-O-sulfotransferas e (GlcNAc6ST), complete cds.//0//2393bp//99%//AB014679
C-NT2RP4000023
C-NT2RP4000218
C-NT2RP4000424
C-NT2RP4001213//ZINC FINGER PROTEIN 184 (FRAGMENT).//5.70E-141//511aa//43%//Q99676
C-NT2RP4001447
C-NT2RP4001841
C-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1.//1.40E-85//489aa//43%//P55194
C-NT2RP4002047//GTP-BINDING PROTEIN LEPA.//1.50E-168//601aa//52%//067618
C-NT2RP4002075
C-NT2RP4002083
C-OVARC1000001/Homo sapiens mRNA for actin binding protein ABP620, complete cds.//7.00E-217//683bp//99%//AB029290
C-OVARC1000008
C-OVARC1000017
C-OVARC1000058
C-OVARC1000068
C-OVARC1000071//Homo sapiens NTF2-related export protein NXT1 (NXT1) mRNA, complete cds.//1.50E-47//727bp//67%//AF156957
C-OVARC1000085//Human mRNA for proteasome subunit HC5.//1.00E-151//699bp//100%//D00761
C-OVARC1000109
C-OVARC1000114
C-OVARC1000145
C-OVARC1000240
C-OVARC1000302
C-OVARC1000408
C-OVARC1000414
C-OVARC1000440
C-OVARC1000442
C-OVARC1000496
C-OVARC1000556//RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1.-) (S6KII-ALPHA 2) (P90-RSK 2) (RIBOSOMAL S6 KINASE 3) (RSK3) (PP90RSK3).//3.30E-67//132aa//95%//015349
C-OVARC1000557
C-OVARC1000578
C-OVARC1000622
C-OVARC1000679//Homo sapiens myosin-IXa mRNA, complete cds.//0//808bp//99%//AF117888
C-OVARC1000681
C-OVARC1000700
C-OVARC1000724
C-OVARC1000751//PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16) (PP2C).//5.60E-11//74aa//37%//P49596
C-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR (75 KD GLUCOSE REGULATED PROTEIN) (GRP 75).//3.90E-46//78aa//98%//035501
C-OVARC1000885//OXIDOREDUCTASE UCPA (EC 1.-.-.-).//1.30E-32//170aa//34%//P37440

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C-OVARC1000936//COAT PROTEIN GP37 (ENV PROTEIN GP37).//0.0000054//135aa//28%//P03398
C-OVARC1000937//S-PHASE ENTRY CYCLIN 6.//4.90E-10//61aaaa//49%//P32943
C-OVARC1000960
C-OVARC1000971
C-OVARC1000999//ANKYRIN HOMOLOG PRECURSOR.//4.10E-11//189aa//32%//Q06527
C-OVARC1001000
C-OVARC1001029
C-OVARC1001040
C-OVARC1001051//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN).//1.10E-08//216aa//23%//P42566
C-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//5.1e-310//1588bp//93%//AF051782
C-OVARC1001118
C-OVARC1001129
C-OVARC1001169
C-OVARC1001240
C-OVARC1001261
C-OVARC1001339
C-OVARC1001342//40S RIBOSOMAL PROTEIN S8.//1.40E-110//207aa//99%//P09058
C-OVARC1001357
C-OVARC1001442
C-OVARC1001611
C-OVARC1001813
C-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//0//1760bp//99%//AF054174
C-OVARC1002143
C-OVARC1002165//3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 2 (EC 1.3.99.5) (STEROID 5-ALPHA-REDUCTASE 2) (SR TYPE 2).//7.60E-08//114aa//37%//P31213
C-OVARC1002182//BETA-TRCP (BETA-TRANSDUCIN REPEAT-CONTAINING PROTEIN) (BTRCP).//1.70E-09//207aa//30%//Q91854
C-PLACE1000014
C-PLACE1000078
C-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//0//2041bp//87%//U35245
C-PLACE1000793//NEUROGENIC PROTEIN BIG BRAIN.//1.70E-07//251aa//24%//P23645
C-PLACE1000814
C-PLACE1000979//ZINC FINGER PROTEIN 135.//2.50E-153//326aa//64%//P52742
C-PLACE1001007
C-PLACE1001054//Homo sapiens mRNA for RuvB-like DNA helicase TIP49b, complete cds.//4.00E-300//1355bp//100%//AB024301
C-PLACE1001088
C-PLACE1001136
C-PLACE1001241
C-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds.//5.90E-228//827bp//99%//AF009615
C-PLACE1001395
C-PLACE1001740
C-PLACE1001746
C-PLACE1001983//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//7.50E-16//319aa//26%//P37908
C-PLACE1002066
C-PLACE1002115
C-PLACE1002213
C-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds.//0//1657bp//98%//AB018271
C-PLACE1002450//Human zinc finger protein mRNA, complete cds.//0//2565bp//99%//U69274
C-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//0//2092bp//84%//U69262
C-PLACE1002499
C-PLACE1002578
C-PLACE1002714

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C-PLACE1002772
C-PLACE1002775//PEREGRIN (BR140 PROTEIN).//3.80E-13//272aa//28%//P55201
C-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//5.50E-203//396aa//86%//P51522
C-PLACE1002993
C-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//8.50E-44//225bp//100%//AF032387
C-PLACE1003205
C-PLACE1003249
C-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSORS.//1.70E-23//594aa//33%//P28481
C-PLACE1003553
C-PLACE1003592
C-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.//2.60E-93//270aa//66%//P46975
C-PLACE1003669//TRICHOHYALIN.//5.60E-09//219aa//30%//P22793
C-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA, complete cds.//6.20E-282//1316bp//98%//AF053305
C-PLACE1003870
C-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//3.70E-222//651aa//66%//P25500
C-PLACE1003892
C-PLACE1003900
C-PLACE1004336
C-PLACE1004384
C-PLACE1004425
C-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//2.90E-56//276aa//41%//P51522
C-PLACE1004506//Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds.//2.10E-16//402bp//62%//U90878
C-PLACE1004518
C-PLACE1004550//Homo sapiens CGI-20 protein mRNA, complete cds.//3.50E-274//1305bp//97%//AF132954
C-PLACE1004681
C-PLACE1004693
C-PLACE1004716//Homo sapiens HSPC038 protein mRNA, complete cds.//2.70E-103//586bp//91%//AF125099
C-PLACE1004815
C-PLACE1004836
C-PLACE1004838
C-PLACE1004840
C-PLACE1004900
C-PLACE1004985
C-PLACE1005085
C-PLACE1005086
C-PLACE1005108
C-PLACE1005146
C-PLACE1005409
C-PLACE1005453
C-PLACE1005477
C-PLACE1005557//60S RIBOSOMAL PROTEIN L27.//1.90E-11//60aa//48%//P46288
C-PLACE1005595
C-PLACE1005603
C-PLACE1005639
C-PLACE1005727//Homo sapiens STRIN protein (STRIN) mRNA, complete cds.//2.00E-118//378bp//98%//AF162680
C-PLACE1005799
C-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2040bp//99%//AF065482
C-PLACE1005884
C-PLACE1005968
C-PLACE1006002

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C-PLACE1006003//Homo sapiens CGI-94 protein mRNA, complete cds.//2.40E-177//829bp//99%//AF151852
C-PLACE1006017
C-PLACE1006037
C-PLACE1006076
C-PLACE1006143
C-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0//1489bp//100%//AB014548
C-PLACE1006288//VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 1 (VDAC1) (PLASMALEMMAL PORIN) (OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN) (PORIN 31HL) (PORIN 31HM).//4.60E-117//147aa//80%//P21796
C-PLACE1006318//Mus musculus skm-BOP2 (Bop) mRNA, complete cds.//3.00E-07//376bp//59%//U76374
C-PLACE1006368//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//1.30E-18//460aa//24%//Q00547
C-PLACE1006371
C-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.20E-83//313aa//49%//P27550
C-PLACE1006506//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.//0//2170bp//99%//AF191338
C-PLACE1006521
C-PLACE1006534//Homo sapiens mRNA; cDNA DKFZp564G1964 (from clone DKFZp564G1964).//1.70E-192//883bp//99%//AL110144
C-PLACE1006617
C-PLACE1006640
C-PLACE1006754//BILIARY GLYCOPROTEIN 1 PRECURSOR (BGP-1) (ANTIGEN CD66) (CD66A ANTIGEN).//6.20E-63//191aa//43%//P13688
C-PLACE1006760
C-PLACE1006779
C-PLACE1006805
C-PLACE1006815
C-PLACE1006867
C-PLACE1007045
C-PLACE1007097
C-PLACE1007111
C-PLACE1007112
C-PLACE1007140//Homo sapiens mRNA for KIAA1009 protein, complete cds.//0//3492bp//99%//AB023226
C-PLACE1007218
C-PLACE1007454
C-PLACE1007478
C-PLACE1007677
C-PLACE10077057/Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.//1.10E-184//1096bp//82%//AB033922
C-PLACE1007737
C-PLACE1007743
C-PLACE1007852//Homo sapiens mRNA for KIAA0878 protein, complete cds.//1.00E-232//1174bp//94%//AB020685
C-PLACE1007877
C-PLACE1008045
C-PLACE1008080//Homo sapiens mRNA for HEXIM1 protein, complete cds.//0//2152bp//99%//AB021179
C-PLACE1008111//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).//3.00E-25//208aa//37%//Q03326
C-PLACE1008201//Rattus rattus zinc finger protein, complete cds.//0//2265bp//83%//L23077
C-PLACE1008231
C-PLACE1008244//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//9.50E-21//148aa//38%//Q00808
C-PLACE1008330//EOSINOPHIL LYSOPHOSPHOLIPASE (EC 3.1.1.5) (CHARCOT-LEYDEN CRYSTAL PROTEIN) (LYSOLECITHIN ACYLHYDROLASE) (CLC) (GALACTIN- 10).//2.20E-23//94aa//47%//Q05315
C-PLACE1008331
C-PLACE1008369
C-PLACE1008392
C-PLACE1008405
C-PLACE1008424

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C-PLACE1008584
C-PLACE1008625
C-PLACE1008630
C-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2).//5.20E-90//483aa//38%//002668
C-PLACE1008715
C-PLACE1008748
C-PLACE1008757
C-PLACE1008798
C-PLACE1008851
C-PLACE1008947
C-PLACE1009039
C-PLACE1009048
C-PLACE1009050
C-PLACE10091137/Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//0//2529bp//99%//AF035586
C-PLACE1009150
C-PLACE1009200
C-PLACE1009246//POLLEN SPECIFIC PROTEIN SF3.//4.40E-16//82aa//43%//P29675
C-PLACE1009298//Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds.//0//2262bp//99%//AF191298
C-PLACE1009308//GLUCOSE REPRESSION MEDIATOR PROTEIN.//4.00E-06//439aa//23%//P14922
C-PLACE1009398//ZINC FINGER PROTEIN 135.//6.20E-97//361aa//51%//P52742
C-PLACE1009410
C-PLACE1009477//Homo sapiens mRNA for KIAA0684 protein, partial cds.//6.50E-148//592bp//99%//AB014584
C-PLACE1009493
C-PLACE1009539
C-PLACE1009595
C-PLACE1009637
C-PLACE1009639
C-PLACE1009798//RLR1 PROTEIN.//1.60E-18//270aa//23%//P53552
C-PLACE1009861//CATHEPSIN B-LIKE CYSTEINE PROTEINASE 6 PRECURSOR (EC 3.4.22.-).//6.50E-28//209aa//38%//P43510
C-PLACE1009888
C-PLACE1009925//Homo sapiens RNA helicase (RIG-I) mRNA, complete cds.//0//1730bp//99%//AF038963
C-PLACE1009947
C-PLACE1010069
C-PLACE1010089//Homo sapiens mRNA for KIAA1097 protein, partial cds.//0//1554bp//100%//AB029020
C-PLACE1010231//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR).//5.10E-27//371aa//28%//Q14246
C-PLACE1010270
C-PLACE1010562
C-PLACE1010579//Homo sapiens PTB domain adaptor protein CED-6 mRNA, complete cds.//9.30E-299//1362bp//99%//AF200715
C-PLACE1010624
C-PLACE1010628//Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds.//7.50E-08//324bp//64%//AF109907
C-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//1.80E-222//808aa//52%//Q09332
C-PLAC.E1010702//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//5.20E-151//427aa//55%//P28160
C-PLACE1010761
C-PLACE1010802 C-PLACE1010833//CALTRACTIN (CENTRIN).//0.0000001//154aa//28%//P41209
C-PLACE1010896//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//1.50E-25//583aa//23%//P35580
C-PLACE1010916
C-PLACE1010947
C-PLACE1010965
C-PLACE1011032

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C-PLACE1011041//Homo sapiens mRNA for BAP2-alpha protein, complete cds.//0//1701bp//97%//AB015019
C-PLACE1011056//HISTONE H1, GONADAL.//6.80E-13//154aa//37%//P02256
C-PLACE1011090//Homo sapiens mRNA; cDNA DKFZp586A0522 (from clone DKFZp586A0522).//0//880bp//99%//AL050159
C-PLACE1011160//Homo sapiens HFB30 mRNA, complete cds.//0//1691bp//99%//AB022663
C-PLACE1011214
C-PLACE1011229//Homo sapiens ubiquitin-specific protease homolog (UPH) mRNA, complete cds.//2.30E-152//701bp//99%//AF153604
C-PLACE1011273
C-PLACE1011291
C-PLACE1011310//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE.//3.50E-20//496aa//25%//P10587
C-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2).//1.70E-78//383aa//39%//Q61703
C-PLACE1011503
C-PLACE1011635//Homo sapiens heparan sulfate D-glucosaminyl 3-O-sulfotransferase-3B (30ST3B1) mRNA, complete cds.//0//1559bp//99%//AF105377
C-PLACE1011646//Homo sapiens clone 25059 mRNA sequence.//5.00E-223//1035bp//99%//AF131752
C-PLACE1011650
C-PLACE1011675
C-PLACE1011725
C-PLACE1011749
C-PLACE1011922//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//1.30E-15//409aa//27%//P35580
C-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//0//1163bp//100%//AB018256
C-PLACE2000006
C-PLACE2000007//Homo sapiens mRNA for KIAA0913 protein, partial cds.//0//1968bp//97%//AB020720
C-PLACE2000034//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//2.20E-29//212aa//35%//P10586
C-PLACE2000039//Rattus norvegicus cytoplasmic dynein heavy chain (MAP 1C), mRNA, complete cds.//4.60E-291//1167bp//89%//L08505
C-PLACE2000061
C-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0//3174bp//99%//AF027219
C-PLACE2000097
C-PLACE2000103
C-PLACE2000115
C-PLACE2000124
C-PLACE2000140
C-PLACE2000164//TIPD PROTEIN.//2.10E-59//481aa//33%//O15736
C-PLACE2000176
C-PLACE2000223
C-PLACE2000235
C-PLACE2000274//DYNEIN BETA CHAIN, CILIARY.//2.20E-167//880aa//37%//P23098
C-PLACE2000302
C-PLACE2000347
C-PLACE2000359
C-PLACE2000371//TENSIN.//2.90E-78//561aa//37%//Q04205
C-PLACE2000379
C-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//1.60E-14//180aa//39%//P14209
C-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//9.90E-229//821aa//54%//Q09996
C-PLACE2000450
C-PLACE2000455
C-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//0//1979bp//90%//Y17267
C-PLACE3000070
C-PLACE3000119
C-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC15.//1.90E-08//281 aa//22%//P22224
C-PLACE3000136

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C-PLACE3000147//Homo sapiens metalloproteinase with thrombospondin type 1 motifs ADAMTS1 (ADAMTS1) mRNA, complete cds.//0//2043bp//99%//AF170084
C-PLACE3000148
C-PLACE3000155//Homo sapiens mRNA for KIAA0672 protein, complete cds.//2.10E-75//382bp//99%//AB014572
C-PLACE3000160
C-PLACE3000169//ZINC FINGER PROTEIN 135.//2.50E-90//358aa//47%//P52742
C-PLACE3000194
C-PLACE3000199
C-PLACE3000218//Homo sapiens putative protein O-mannosyltransferase (POMT2) mRNA, complete cds.//0//1862bp//98%//AF105020
C-PLACE3000230
C-PLACE3000244//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//0//1435aay/92%//P53995
C-PLACE3000254//Homo sapiens transcriptional activator SRCAP (SRCAP) mRNA, complete cds.//0//4583bp//83%//AF143946
C-PLACE3000276
C-PLACE3000310
C-PLACE3000320
C-PLACE3000331
C-PLACE3000339//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.60E-08//359aa//23 %//P08640
C-PLACE3000352
C-PLACE3000353//Homo sapiens mRNA; cDNA DKFZp586H0623 (from clone DKFZp586H0623).//0//2456bp//99%//AL096739
C-PLACE3000362
C-PLACE3000365
C-PLACE3000388
C-PLACE3000413
C-PLACE3000425
C-PLACE4000009//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//2.90E-54//626aa//29%//P35580
C-PLACE4000014//X-LINKED HELICASE II (X-LINKED NUCLEAR PROTEIN) (XNP).//3.10E-111//348aa//41%//P46100
C-PLACE4000052//Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA, complete cds.//0//4661bp//99%//AF165281
C-PLACE4000089
C-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds.//1.60E-86//190aa//88%//AF091234
C-PLACE4000129
C-PLACE4000147
C-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//7.00E-22//369aa//25%//P52746
C-PLACE4000211//Homo sapiens TTF-I interacting peptide 5 mRNA, partial cds.//1.70E-262//1217bp//98%//AF000422
C-PLACE4000222
C-PLACE4000269//Homo sapiens mRNA for KIAA1067 protein, partial cds.//0//3787bp//99%//AB028990
C-PLACE4000270
C-PLACE4000300
C-PLACE4000387
C-PLACE4000392
C-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//0//5142bp//90%//Z70200
C-PLACE4000450//Homo sapiens TTF-I interacting peptide 5 mRNA, partial cds.//2.70E-261//1217b.p//98%//AF000422
C-PLACE4000465
C-PLACE4000489//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//5.70E-60//254aa//44%//P13002
C-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//0//6340bp//87%//Y17267
C-SKNMC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//5.50E-35//431aa//29%//O60100

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C-SKNMC1000046//Homo sapiens liprin-alpha3 mRNA, partial cds.//1.90E-162//749bp//99%//AF034800
C-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (M-TYPE).//3.20E-41//87aa//98%//P17655
C-THYRO1000034//TRICHOHYALIN.//9.40E-10//176aa//30%//P37709
C-THYRO1000070
C-THYRO1000072//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//3.40E-16//201aa//29%//P11799
C-THYRO1000092
C-THYRO1000121//Homo sapiens mRNA for KIAA1116 protein, complete cds.//0//2159bp//99%//AB029039
C-THYRO1000124
C-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//0//2362bp//99%//AJ005698
C-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//0//1409bp//98%//AB014552
C-THYRO1000206
C-THYRO1000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.00E-118//239aa//66%//P51523
C-THYRO1000253
C-THYRO1000270
C-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//0//2161bp//99%//AB016068
C-THYRO1000320
C-THYRO1000358//SELENIUM-BINDING LIVER PROTEIN.//2.30E-229//237aa//79%//P17563
C-THYRO1000368
C-THYRO1000381
C-THYRO1000387
C-THYRO1000394//Homo sapiens peroxisomal membrane protein PMP 24 mRNA, complete cds.//1.20E-299//1325bp//99%//AF072864
C-THYRO10003957/Homo sapiens actin-binding protein (IPP) mRNA, complete cds.//0//2092bp//99%//AF156857
C-THYRO1000401
C-THYRO1000488//Homo sapiens HFB30 mRNA, complete cds.//0//2254bp//100%//AB022663
C-THYRO1000501//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//4.20E-98//408aa//42%//P19474
C-THYRO1000558
C-THYRO1000570
C-THYRO1000605//Homo sapiens histone acetyltransferase (HBOa) mRNA, complete cds.//0//3080bp//99%//AF140360
C-THYRO1000625
C-THYRO1000637
C-THYRO1000676
C-THYRO1000684//Homo sapiens mRNA for KIAA0872 protein, complete cds.//0//2131bp//99%//AB020679
C-THYRO1000712
C-THYRO1000805
C-THYRO1000815
C-THYRO1000855
C-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//7.50E-57//315aa//43%//P32322
C-THYRO1000988
C-THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//8.40E-12//167aa//29%//P31948
C-THYRO1001120//Mus musculus FX-induced thymoma transcript (FXI-T1) mRNA, complete cds.//1.90E-92//1479bp//66%//U38252
C-THYRO1001204//Homo sapiens cathepsin Z precursor (CTSZ) gene, exons 4, 5, and 6 and complete cds; and TH1 gene partial sequence.//3.80E-100//478bp//99%//AF136276
C-THYRO1001262
C-THYRO1001271
C-THYRO1001287//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE) (FRAGMENT).//3.40E-51//429aa//33%//P45701
C-THYRO1001313//Homo sapiens sorting nexin 11 (SNX11) mRNA, complete cds.//0//2330bp//94%//AF121861
C-THYRO1001347
C-THYRO1001363//Homo sapiens mRNA; cDNA DKFZp56400423 (from clone DKFZp56400423).//0//2173bp//99%//AL080120

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C-THYRO1001374//Homo sapiens mRNA forKIAA0707 protein, partial cds.//0//1700bp//99%//AB014607
C-THYRO1001403
C-THYRO1001405//PLECTIN.//6.90E-19//450aa//27%//P30427
C-THYRO1001406//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//1676bp//98%//AF078850
C-THYRO1001426
C-THYRO1001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//2.70E-171//559aa//59%//P35580
C-THYRO1001480
C-THYRO1001487
C-THYRO1001584
C-THYRO1001661
C-THYRO1001746
C-THYRO1001772
C-THYRO1001854
C-Y79AA1000013//Mus musculus RING finger protein A07 mRNA, complete cds.//8.90E-205//1435bp//81 %//AF171060
C-Y79AA1000033//Homo sapiens CARD4 mRNA, complete cds.//0//2929bp//96%//AF126484
C-Y79AA1000231//Homo sapiens nucleolar protein NOP5/NOP58 mRNA, complete cds.//0//1515bp//99%//AF123534
C-Y79AA1000342//Homo sapiens Ciz1 mRNA, complete cds.//0//2644bp//81%//AB030835
C-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//0//2048bp//93%//X84692
C-Y79AA1000410
C-Y79AA1000539
C-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence.//1.00E-302//1375bp//99%//AF091080
C-Y79AA1000802
C-Y79AA1000827
C-Y79AA1000966//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%//AF100757
C-Y79AA1000969
C-Y79AA1000985//Human centrosomal protein kendrin mRNA, complete cds.//4.70E-151//985bp//87%//U52962
C-Y79AA1001061
C-Y79AA1001068
C-Y79AA1001216
C-Y79AA1001299//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//996bp//99%//AJ011738
C-Y79AA1001511
C-Y79AA1001594//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//2.50E-14//410aa//24%//Q00547
C-Y79AA1001692//Mus musculus strain C57BL/J germ cell-less protein (Gcl) mRNA, complete cds.//1.40E-78//227aa//40%//Q01820
C-Y79AA1001866//Homo sapiens zinc finger protein ZNF180 (ZNF180) mRNA, complete cds.//0//2927bp//97%//AF192913
C-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//4.50E-08//135aa//31%//P43489
C-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1).//9.00E-17//120aa//45%//Q24133
C-Y79AA1002210/YTUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//0.0000018//140aa7/25%//Q13829
C-Y79AA1002211//PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN HOMOLOG F40A3.3.//1.70E-17//146aa//35%//016264
C-Y79AA1002220
C-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//0//3168bp//99%//AB014592
C-Y79AA1002258//Homo sapiens mRNA for HIP1R, complete cds.//0//2106bp//99%//AB013384
C-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//6.90E-140//966bp//82%//Y18208
C-Y79AA1002399//Homo sapiens mRNA for sperm protein.//0//1163bp//95%//X91879
C-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds.//3.9e-317//1902bp//86%//U49385
C-Y79AA1002431//TRANSDUCIN-LIKE ENHANCER PROTEIN 2 (ESG2).//9.80E-62//318aa//35%//Q04725

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C-Y79AA1002482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.70E-137//340aa//51%//Q05481
C-Y79AA1002487//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.//7.3e-310//1444bp//98%//AF129534
C-HEMBA1000290
C-HEMBA1000459
C-HEMBA1000505
C-HEMBA1001196//Human DNA topoisomerase II (top2) mRNA, complete cds.//1.60E-268//1213bp//100%//J04088
C-HEMBA1002503
C-HEMBA1002508
C-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//0//2432bp//99%//AJ011972
C-HEMBA1003480
C-HEMBA1003538//COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41).//2.40E-110//242aa//58%//P00736
C-HEMBA10036451/TTPD PROTEIN.//2.40E-10//289aa//23%//015736
C-HEMBA1003646//Homo sapiens mRNA for KIAA1013 protein, partial cds.//0//3049bp//99%//AB023230
C-HEMBA1003667
C-HEMBA1003679//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN).//1.00E-09//611aa//22%//P23253
C-HEMBA1003827
C-HEMBA1003838
C-HEMBA1004055
C-HEMBA1004056
C-HEMBA1004086
C-HEMBA1004335
C-HEMBA1004353//C-MYC BINDING PROTEIN MM-1.//3.00E-71//89aa//96%//Q99471
C-HEMBA1004479//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//3.10E-51//152aa//40%//Q61221
C-HEMBA1004499//Homo sapiens delta-tubulin mRNA, complete cds.//3.40E-92//483bp//95%//AF201333
C-HEMBA1004507
C-HEMBA1004638
C-HEMBA1004669//SON PROTEIN (SON3).//7.30E-17//288aa//36%//P18583
C-HEMBA1004709
C-HEMBA1004860
C-HEMBA1005206//Drosophila simulans anon73B1 gene and Su(P) gene.//1.90E-11//376bp//63%//AJ250308
C-HEMBA1005472
C-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.90E-129//332aa//61%//002193
C-HEMBA1005572
C-HEMBA1005780
C-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//2371bp//100%//AF082516
C-HEMBA1006038//LAMININ ALPHA-5 CHAIN (FRAGMENT).//3.10E-33//81aa//64%//Q61001
C-HEMBA1006124
C-HEMBA1006461
C-HEMBA1006521//3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE).//4.00E-33//177aa//42%//P25716
C-HEMBA1006617
C-HEMBA1006650//ARP2/3 COMPLEX 20 KD SUBUNIT (P20-ARC).//9.00E-40//113aa//82%//015509
C-HEMBA1006779
C-HEMBA1006796
C-HEMBA1006812
C-HEMBA1006914//Human anthracycline-associated resistance ARX mRNA, complete cds.//0//1837bp//99%//U35832
C-HEMBA1007174//Homo sapiens mRNA for KIAA1065 protein, complete cds.//0//1079bp//97%//AB028988
C-HEMBB1000240
C-HEMBB1000264//CHL1 PROTEIN.//9.50E-19//104aa//45%//P22516

BNSDOCID: <EP___1074617A2_I_>

C-HEMBB1000335
C-HEMBB1000337
C-HEMBB1000554
C-HEMBB1000573
C-HEMBB1000749
C-HEMBB1000774
C-HEMBB1000835
C-HEMBB1001197
C-HEMBB1001315
C-HEMBB1001482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-57//941aa//27%//Q05481
C-HEMBB1001500
C-HEMBB1001562//CYLICIN II (MULTIPLE-BAND POLYPEPTIDE II).//1.40E-06//373aa//21%//Q28092
C-HEMBB1001619
C-HEMBB1001630
C-HEMBB1001665
C-HEMBB1001684//Homo sapiens mRNA for KIAA1108 protein, partial cds.//0//2348bp//99%//AB029031
C-HEMBB1001812
C-HEMBB1001834
C-HEMBB1001869
C-HEMBB1001871//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S 1).//5.40E-75//241aa//48%//P47853
C-HEMBB1001872//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR) (CELL SURFACE GLYCOPROTEIN F4/80).//1.90E-22//210aa//27%//Q61549
C-HEMBB1001905//TRICHOHYALIN.//2.10E-10//268aa//27%//P37709
C-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds.//1.60E-131//874bp//86%//U47742
C-HEMBB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E).//6.90E-132//561aa//50%//Q24574
C-HEMBB1001925
C-HEMBB1002044//Mus musculus mRNA for vascular cadherin-2.//0//3562bp//81%//Y08715
C-HEMBB1002134//ZINC-FINGER PROTEIN NEURO-D4.//8.10E-56//176aa//67%//P56163
C-HEMBB1002152
C-HEMBB1002300
C-HEMBB1002381
C-HEMBB1002383
C-HEMBB1002534
C-MAMMA1000143
C-MAMMA1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.40E-134//359aa//63%//P51523
C-MAMMA1000227
C-MAMMA1000257
C-MAMMA1000264
C-MAMMA1000270
C-MAMMA1000279
C-MAMMA1000372
C-MAMMA1000559
C-MAMMA1000752
C-MAMMA1000760
C-MAMMA1000778
C-MAMMA1000855
C-MAMMA1000859
C-MAMMA1000897//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3) (SERUM-DERIVED HYALURONAN-ASSOCIATED PROTEIN) (SHAP).//1.00E-141//576aa//37%//Q06033
C-MAMMA1000940
C-MAMMA1001073
C-MAMMA1001080//Homo sapiens SNC73 protein (SNC73) mRNA, complete cds.//1.6e-312//1596bp//94%//

BNSDOCID: <EP___1074617A2_I_>

AF067420
C-MAMMA10011987/Homo sapiens eps15RmRNA, partial cds.//0//2253bp//99%//AB015346
C-MAMMA1001202
C-MAMMA1001222//EBNA-2 NUCLEAR PROTEIN.//6.60E-09//255aa//29%//P12978
C-MAMMA1001252
C-MAMMA1001296
C-MAMMA1001502
C-MAMMA1001630
C-MAMMA1001633//ZINC FINGER PROTEIN 165.//6.30E-39//160aa//55%//P49910
C-MAMMA1001683
C-MAMMA1001715
C-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.//0//1603bp//99%//AF095687
C-MAMMA1001760
C-MAMMA1001769
C-MAMMA1001785
C-MAMMA1001848
C-MAMMA1001874
C-MAMMA1001956
C-MAMMA1002009
C-MAMMA1002033
C-MAMMA1002155
C-MAMMA1002498
C-MAMMA1002545
C-MAMMA1002571
C-MAMMA1002573//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3)(GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//2.60E-19//666aa//23%//P08640
C-MAMMA1002590
C-MAMMA1002617//ZINC FINGER PROTEIN 135.//7.60E-89//252aa//57%//P52742
C-MAMMA1002618
C-MAMMA1002636
C-MAMMA1002646
C-MAMMA1002665
C-MAMMA1002708
C-MAMMA1002728
C-MAMMA1002744
C-MAMMA1002764
C-MAMMA1002765
C-MAMMA1002830
C-MAMMA1002844//TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT).//4.90E-10//334aa//22%//P52178
C-MAMMA100285 8//Rat cMG1 mRNA.//3.70E-238//1147bp//92%//X52590
C-MAMMA1002880
C-MAMMA1002892
C-MAMMA1002909
C-MAMMA1002941
C-MAMMA1002947
C-MAMMA1002972//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27.//1.10E-05//69aa//42%//P40343
C-MAMMA1002973
C-MAMMA1002987
C-MAMMA1003003
C-MAMMA1003026//Homo sapiens HSPC057 mRNA, complete cds.//0//1773bp//98%//AF161542
C-MAMMA1003031
C-MAMMA1003089
C-NT2RM1000092//MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2).//1.00E-07//362aa//23%//P39843
C-NT2RM1000272

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C-NT2RM1000341
C-NT2RM1000539//Homo sapiens mRNA for Lsm5 protein.//3.00E-158//733bp//99%//AJ238097
C-NT2RM1000553//Homo sapiens putative glycolipid transfer protein mRNA, complete cds.//3.40E-177//814bp//99%//AF103731
C-NT2RM1000623//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775
C-NT2RM1000702//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//5.60E-08//187aa//27%//P49695
C-NT2RM1000833//Homo sapiens sec61 homolog mRNA, complete cds.//0//3541bp//99%//AF084458
C-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//5107bp//99%//AF082516
C-NT2RM1001082
C-NT2RM1001112
C-NT2RM2001105//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//1.20E-28//805bp//61%//AF053091
C-NT2RM2001360//Homo sapiens clone C40 unknown mRNA.//1.00E-250//1136bp//100%//AF103798
C-NT2RM2001797//Homo sapiens mRNA; cDNA DKFZp572C163 (from clone DKFZp572C163); partial cds.//0//2300bp//100%//AL110217
C-NT2RM2001803//Homo sapiens IkappaB kinase cbmplex associated protein (IKAP) mRNA, complete cds.//0//2249bp//99%//AF044195
C-NT2RM4002504
C-NT2RP1000409
C-NT2RP1000460//Homo sapiens mRNA for KIAA1068 protein, partial cds.//0//3199bp//99%//AB028991
C-NT2RP1000746//Homo sapiens 60S acidic ribosomal protein PO mRNA, complete cds.//9.70E-196//901bp//99%//AF173378
C-NT2RP1000796
C-NT2RP1001013//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.70E-253//425aa//98%//P51522
C-NT2RP2001214
C-NT2RP2001233//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.00E-128//409aa//45%//Q05481
C-NT2RP2001440//Homo sapiens mRNA for 14-3-3gamma, complete cds.//0//3712bp//99%//AB024334
C-NT2RP2002056
C-NT2RP2002105//H.sapiens MSH-R gene for melanocyte stimulating hormone receptor.//0//1644bp//98%//X65634
C-NT2RP2002333
C-NT2RP2002677
C-NT2RP2002755
C-NT2RP2002843
C-NT2RP2003101
C-NT2RP2003668
C-NT2RP2003799
C-NT2RP2004095
C-NT2RP2004300
C-NT2RP2004675
C-NT2RP2004920//TRANSCRIPTIONAL REGULATOR ATRX (X-LINKED NUCLEAR PROTEIN) (HETEROCHROMATIN PROTEIN 2) (HP1 ALPHA-INTERACTING PROTEIN) (HP1-BP38 PROTEIN).//4.20E-09//804aa//22%//Q61687
C-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//2.10E-308//1437bp//98%//AF045583
C-NT2RP2005719//GPI-ANCHORED PROTEIN P137.//4.00E-14//99aa//43%//Q14444
C-NT2RP2005726
C-NT2RP2005776//POLY(A) POLYMERASE TYPE 2 (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//4.40E-55//358aa//42%//P51005
C-NT2RP2005980
C-NT2RP2006184//Homo sapiens mRNA for KIAA0918 protein, partial cds.//0//4235bp//99%//AB020725
C-NT2RP2006534//5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-1 CHAIN (EC 2.7.1.-) (AMPK ALPHA-1 CHAIN) (FRAGMENT).//3.20E-11//32aa//96%//Q13131
C-NT2RP2006554

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C-NT2RP3000584
C-NT2RP3001115
C-NT2RP3001723//Homo sapiens cell recognition molecule Caspr2 (CASPR2) mRNA, complete cds.//1.40E-58//1138bp//63%//AF193613
C-NT2RP3001938//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//1.30E- 22//227aa//33%//P08458
C-NT2RP3002330//Homo sapiens eRFS mRNA, complete cds.//0//2443bp//99%//U87791
C-NT2RP3002402
C-NT2RP3002484//Homo sapiens mRNA for KIAA0998 protein, partial cds.//1.20E-124//597bp//98%//AB023215
C-NT2RP3002512
C-NT2RP3002713
C-NT2RP3002770//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//1.00E-07//70aa//41%//P17564
C-NT2RP3002799
C-NT2RP3002810//HISTIDINE-RICH PROTEIN KE4.//2.20E-10//260aa//26%//Q31125
C-NT2RP3002818//INSERTION ELEMENT IS2A HYPOTHETICAL 48.2 KD PROTEIN.//5.70E-226//303aa//97%//P51026
C-NT2RP3002955
C-NT2RP3002985
C-NT2RP3003059//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//3.80E-152//1007bp//82%//U78090
C-NT2RP3003121
C-NT2RP3003133//Homo sapiens ZK1 mRNA for Kruppel-type zinc fmger protein, complete cds.//0//1998bp//91%//AB011414
C-NT2RP3003138//Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.//0//2159bp//98%//AF071592
C-NT2RP3003155
C-NT2RP3003157
C-NT2RP3003185//TROPOMYOSIN 1, FUSION PROTEIN 33.//2.80E-06//402aa//23%//P49455
C-NT2RP3003264
C-NT2RP3003346
C-NT2RP3003403
C-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//6.30E-270//743bp//90%//AF071317
C-NT2RP3003500//SCY1 PROTEIN.//9.20E-27//601aa//23%//P53009
C-NT2RP3003572
C-NT2RP3003576
C-NT2RP3003665//Homo sapiens mRNA for beta-ureidopropionase, complete cds.//0//1690bp//99%//AB013885
C-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//2.20E-13//146aa//42%//P14209
C-NT2RP3003680//Homo sapiens mRNA; cDNA DKFZp434J154 (from clone DKFZp434J154); complete cds.//0//2047bp//95%//AL080155
C-NT2RP3003799//Rattus norvegicus Srg1 (Sytr1) mRNA, complete cds.//9.00E-238//1529bp//84%//U71294
C-NT2RP3003800//Rattus norvegicus tyrosine protein kinase pp60-c-src mRNA, complete cds.//1.90E-163//924bp//89%//AF130457
C-NT2RP3003828
C-NT2RP3003932
C-NT2RP3003992//Homo sapiens mRNA; cDNA DKFZp564C186 (from clone DKFZp564CI 86).//0//2739bp//99%//AL050019
C-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein.//6.50E-240//1215bp//94%//X84692
C-NT2RP3004028
C-NT2RP3004041
C-NT2RP3004051
C-NT2RP3004078//H.sapiens HRFX2 mRNA.//0//1806bp//99%//X76091
C-NT2RP3004093
C-NT2RP3004095
C-NT2RP3004125//Mus musculus zinc finger protein splice variant FIZ1-B (Fiz1) mRNA, complete cds.//4.60E-229//1560bp//78%//AF126747
C-NT2RP3004148//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-

BNSDOCID: <EP___1074617A2_I_>

DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//7.90E-05//271aa//22%//P08640
C-NT2RP3004155//Homo sapiens COQ7 protein mRNA, complete cds.//1.10E-179//823bp//100%//AF098948
C-NT2RP3004189//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1J/1.30E-14//242aa//24%//Q00808
C-NT2RP3004332
C-NT2RP3004349
C-NT2RP3004470
C-NT2RP4000035
C-NT2RP4000049
C-NT2RP4000102
C-NT2RP4000167
C-NT2RP4000515
C-NT2RP4000517
C-NT2RP4000519
C-NT2RP5003512//Homo sapiens mRNA for KIAA1291 protein, partial cds.//0//1980bp//99%//AB033117
C-OVARC1000092
C-OVARC1000533
C-OVARC1000678
C-OVARC1000689//Homo sapiens mRNA; cDNA DKFZp434C1415 (from clone DKFZp434C1415); partial cds.//0//2032bp//99%//AL133014
C-OVARC1000802
C-OVARC1000890
C-OVARC1000891
C-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//0//1961bp//82%//AB005549
C-OVARC1001072
C-OVARC1001117
C-OVARC1001200//Mus musculus mRNA for HS1 binding protein 3.//5.80E-88//658bp//80%//AJ132192
C-OVARC1001244//H.sapiens mRNA for Drosophila female sterile homeotic (FSH) homologue.//0//1467bp//99%//X62083
C-OVARC1001329
C-OVARC1001341
C-OVARC1001376
C-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//0//1876bp//98%//AF016507
C-OVARC1001873
C-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//1.60E-81//212aa//70%//P34547
C-PLACE1000547//Homo sapiens GDP-mannose pyrophosphorylase B (GMPPB) mRNA, complete cds.//3.70E-241//1124bp//98%//AF135421
C-PLACE1001036//Homo sapiens mRNA for KIAA1017 protein, complete cds.//0//2117bp//99%//AB023234
C-PLACE1001076
C-PLACE1001118//ZINC FINGER PROTEIN 135.//5.40E-147//443aa//57%//P52742
C-PLACE1001366
C-PLACE1001545
C-PLACE1001608
C-PLACE1002004
C-PLACE1002256
C-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1.//4.50E-76//180aa//83%//P41233
C-PLACE1002591//CORONIN-LIKE PROTEIN P57.//4.40E-70//208aa//66%//P31146
C-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//0//2462bp//89%//AF079765
C-PLACE1003383
C-PLACE1003864
C-PLACE1004793//RETROVIRUS-RELATED ENV POLYPROTEIN.//5.20E-47//577aa//25%//P10267
C-PLACE1004913
C-PLACE1004979
C-PLACE1005052//Homo sapiens CGI-16 protein mRNA, complete cds.//6.6e-313//1413bp//99%//AF132950

BNSDOCID: <EP___1074617A2_I_>

C-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//2431bp//99%//AB011148
C-PLACE1005128
C-PLACE1005162
C-PLACE1005176//Homo sapiens hypothalamus protein HT001 mRNA, complete cds.//3.90E-212//1040bp//96%//AF113539
C-PLACE1005467//PENICILLIN-BINDING PROTEIN 4* (PBP 4*) (PBP 4A).//1.10E-09//93aa//31%//P32959
C-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A.//7.60E-97//1287bp//67%//AJ010046
C-PLACE1005584//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).//6.80E-09//267aa//30%//P29128
C-PLACE1005611//Mus musculus mRNA for mDjlO, complete cds.//2.00E-33//379bp//66%//AB028860
C-PLACE1005802
C-PLACE1005850
C-PLACE1005898
C-PLACE1005932
C-PLACE1006129//Homo sapiens HSPC057 mRNA, complete cds.//0//2849bp//98%//AF161542
C-PLACE1006360
C-PLACE1006795
C-PLACE1006878//TRNA-SPUCING ENDONUCLEASE SUBUNIT SEN2 (EC 3.1.27.9) (TRNA-INTRON ENDONUCLEASE).//1.90E-08//122aa//36%//P16658
C-PLACE1007557
C-PLACE1007807
C-PLACE1008181
C-PLACE1008426//Homo sapiens mRNA for KIAA1288 protein, partial cds.//0//3311bp//99%//AB033114
C-PLACE1008455
C-PLACE1008941
C-PLACE1009935
C-PLACE1010310//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//1.20E-18//467aa//30%//P46804
C-PLACE1011891
C-PLACE10118967/Mus musculus Wnt10a mRNA, complete cds.//2.60E-287//1820bp//85%//U61969
C-PLACE2000003
C-PLACE2000132
C-PLACE2000170
C-PLACE2000335
C-PLACE3000124
C-PLACE3000158
C-PLACE3000207
C-PLACE3000221
C-PLACE3000271
C-PLACE3000304
C-PLACE3000322
C-PLACE3000341
C-PLACE3000373
C-PLACE3000399
C-PLACE3000401
C-PLACE3000402
C-PLACE3000406
C-PLACE3000475
C-PLACE4000063//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//1.70E-15//740aa//23%//P08640
C-PLACE4000093
C-PLACE4000100//Homo sapiens hydroxypyruvate reductase (GRHPR) gene, complete cds.//0//4199bp//97%//AF146689
C-PLACE4000131//Homo sapiens mRNA; cDNA DKFZp586J0917 (from clone DKFZp586J0917); partial cds.//0//1612bp//97%//AL117455
C-PLACE4000247
C-PLACE4000250
C-PLACE4000252

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C-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD protein.//0//5143bp//90%//Z70200
C-PLACE4000261//PEREGRIN (BR140 PROTEIN).//9.50E-10//128aa//34%//P55201
C-PLACE4000320
C-PLACE4000344
C-PLACE4000367
C-PLACE4000401//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//7.20E-22//54aa//62%//Q01576
C-PLACE4000411//Homo sapiens mRNA; cDNA DKFZp586D0624 (from clone DKFZp586D0624); partial cds.//0//2159bp//98%//AL117654
C-PLACE4000487
C-PLACE4000494
C-PLACE4000521
C-PLACE4000548//Homo sapiens mRNA for KIAA0947 protein, partial cds.//0//4864bp//99%//AB023164
C-SKNMC1000013//Homo sapiens ATP-binding cassette protein M-ABC1 mRNA, nuclear gene encoding mitochondrial protein, complete cds.//0//2384bp//99%//AF047690
C-SKNMC1000091//Homo sapiens mRNA for leucine-zipper protein, complete cds.//6.10E-190//872bp//99%//AB021663
C-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//0//3711bp//99%//AB018333
C-THYRO1000569//Mus musculus hematopoietic zinc finger protein mRNA, complete cds.//0//1557bp//91%//AF118566
C-THYRO1001142
C-THYRO1001189//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-200//546aa//62%//005481
C-THYRO1001320
C-THYRO1001537//Homo sapiens mRNA; cDNA DKFZp586A0522 (from clone DKFZp586A0522); partial cds.//0//1010bp//98%//AL050159
C-THYRO1001602
C-THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).//9.30E-34//220aa//38%//Q04652
C-THYRO1001828
C-Y79AA1000346//Homo sapiens nonclathrin coat protein gamma2-COP mRNA, complete cds.//0//2520bp//99%//AF157833
C-Y79AA1001167
C-Y79AA1001384//Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds.//0//4708bp//99%//AF055084
C-Y79AA1001875//RAS-RELATED PROTEIN RAB-7.//9.40E-12//34aa//97%//P51149
C-Y79AA1002103//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.00E-257//549aa//76%//P16415
C-HEMBA1006092
C-HEMBA1006406
C-HEMBB1000790
C-HEMBB1000917
C-HEMBB1002280
C-MAMMA1000802
C-MAMMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.000000017//46aa//60%//P20931
C-MAMMA1002597
C-MAMMA1002868
C-NT2RP2003161
C-NT2RP2003339
C-NT2RP3001282
C-PLACE1001761
C-PLACE1004491
C-PLACE1004686
C-PLACE1005574
C-PLACE1006382
C-PLACE1006792
C-PLACE3000455
C-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds.//0//2567bp//88%//AF030430
C-THYRO1000916

BNSDOCID: <EP___1074617A2_I_>

C-HEMBA1000327
C-HEMBB1000637
C-HEMBB1001967
C-MAMMA1000266
C-NT2RP2002979
C-PLACE1007866
C-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE PAK-GAMMA (EC 2.7.1.-) (GAMMA-PAK) (P21-ACTIVATED KINASE 2) (PAK-2) (PAK65) (S6/H4 KINASE).//9.80E-25//155aa//45%//Q13177
C-PLACE4000156//ZINC FINGER PROTEIN 132.//7.10E-151//476aa//46%//P52740
C-THYRO1001637
C-MAMMA1002215
C-MAMMA1002721
C-NT2RP2002070

Homology search result 14.

[0334] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences. In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be compared. Each data includes Clone name, Definition in matching data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of matching data. These items are shown in this order, separated by a double-slash mark, //.

C-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.90E-250//554aa//85%//061712
C-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//6.40E-99//457aa//45%//Q09996
C-HEMBA1000020//Homo sapiens beta 2 gene.//7.50E-264//1194bp//95%//X02344
C-HEMBA1000030//Homo sapiens ARF GTPase-activating protein GITI mRNA, complete cds.//0//1759bp//99%//AF124490
C-HEMBA1000129//HYPOTHETICAL HEUCASE C8A4.08C IN CHROMOSOME I.//3.80E-25//166aa//36%//Q09884
C-HEMBA1000141//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0/1135bp//100%//AF196304
C-HEMBA1000150//Homo sapiens putative RNA helicase mRNA, complete cds.//5.20E-213//525bp//99%//AF085356
C-HEMBA1000156//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//1.90E-12//368aa//24%//P08553
C-HEMBA1000158//HEPATOCYTE NUCLEAR FACTOR 3-GAMMA (HNF-3G).//5.00E-16//166aa//36%//P35584
C-HEMBA1000168//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE D.//2.90E-14//303aa//25%//P35662
C-HEMBA1000185//RAS-RELATED PROTEIN RAL-A.//3.40E-12//125aa//31 %//P48555
C-HEMBA1000201//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//1612bp//99%//AJ011738
C-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//1.00E-86//146aa//56%//Q61221
C-HEMBA1000303//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//7.10E-254//1440bp//87%//AF030131
C-HEMBA1000304//Rattus norvegicus Ca^{2+}-dependent activator protein (CAPS) mRNA, complete cds.//5.10E-131//712bp//91%//U16802
C-HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1//5.20E-49//107aa//91%//035594
C-HEMBA1000333//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.//0//1866bp//100%//AF174601
C-HEMBA1000369//Homo sapiens mRNA for PICK1, complete cds.//0//1949bp//98%//AB026491
C-HEMBA1000411//ANKYRIN.//5.70E-12//127aa//38%//Q02357
C-HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).//3.30E-45//481aa//29%//Q04652
C-HEMBA1000491//RAS-LIKE PROTEIN 2.//2.00E-22//188aa//31%//P22279
C-HEMBA1000518//PECANEX PROTEIN.//2.10E-19//227aa//38%//P18490
C-HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.//2.40E-44//292aa//36%//Q01755
C-HEMBA1000531//HEAT SHOCK 70 KD PROTEIN COGNATE 1 (HEAT SHOCK 70 KD PROTEIN 70C) (FRAGMENTS).//2.60E-12//73aa//41%//P02826

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C-HEMBA1000542//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//2.20E-194//663bp//83%//D89340
C-HEMBA1000555//Mus musculus Msx2 interacting nuclear target protein mRNA, complete cds.//7.90E-226//1501bp//83%//AF156529
C-HEMBA1000561//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.40E-37//674aa//25 %//Q05481
C-HEMBA1000569//GPI-ANCHORED PROTEIN P137.//6.50E-19//265aabp//32%//Q60865
C-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//2.10E-144//602bp//77%//AF045573
C-HEMBA1000591//PTB-ASSOCIATED SPLICING FACTOR (PSF).//2.20E-17//198aa//40%//P23246
C-HEMBA1000592//Homo sapiens sorting nexin 6 (SNX6) mRNA, complete cds.//0//1465bp//99%//AF121856
C-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.80E-55//179aa//61%//O43295
C-HEMBA1000657//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//7.20E-156//1366bp//76%//U35776
C-HEMBA1000851//Homo sapiens DNA binding protein p96PIF mRNA, complete cds.//0//1862bp//99%//AF173868
C-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD).//1.00E-78//119aa//87%//P51689
C-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN)//1.60E-30//127aa//40%//P43366
C-HEMBA1000919//HYPOTHETICAL 65.5 KD TRP-ASP REPEATS CONTAINING PROTEIN F02E8.5 IN CHROMOSOME X.//1.00E-10//288aa//23%//Q19124
C-HEMBA1001019//CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.-) (P34 PROTEIN KINASE) (CYCLIN-DEPENDENT KINASE 1) (CDK1).//3.10E-10//70aa//58%//P06493
C-HEMBA1001043//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)(FRAGMENT).//1.40E-12//131aa//38%//Q01485
C-HEMBA1001059//Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 14.//4.80E-169//786bp//99%//U06088
C-HEMBA1001071//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//1.50E-92//82aa//100%//P02461
C-HEMBA1001077//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.//2.00E-80//432bp//94%//AF119043
C-HEMBA1001088//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//3.50E-50//176aa//57%//P48059
C-HEMBA1001137//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065)(HA0946) (FRAGMENT).//1.50E-116//197aa//58%//Q06730
C-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//6.80E-79//179aa//80%//P51646
C-HEMBA1001197//Homo sapiens rap2 interacting protein x mRNA, complete cds.//0//1511bp//99%//AF112221
C-HEMBA1001257//Homo sapiens mRNA 2-methylacyl-CoA racemase.//0//1672bp//99%//AJ130733
C-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//0.00000002//198aa//29%//Q60401
C-HEMBA1001302//Homo sapiens calcium binding protein precursor, mRNA, complete cds.//9.60E-258//682bp//94%//AF153686
C-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//1.40E-133//614bp//99%//AF057358
C-HEMBA1001387//GTP-BINDING PROTEIN TC10.//2.90E-64//104aa//82%//P17081
C-HEMBA1001405//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//5.60E-25//863bp//60%//AF053091
C-HEMBA1001446//Homo sapiens rap2 interacting protein x mRNA, complete cds.//9.20E-55//719bp//68%//AF112221
C-HEMBA1001455//Mus musculus transposon-derived Buster2 transposase-like protein gene, partial cds.//4.20E-290//2008bp//81%//AF205599
C-HEMBA1001476//Human DNA topoisomerase II (top2) mRNA, complete cds.//1.60E-268//1213bp//100%//J04088
C-HEMBA1001510//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).//1.70E-16//63aa//61%//P18850
C-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//4.90E-37//399aa//29%//P29166
C-HEMBA1001569//SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2).//2.30E-53//110aa//100%//P19065
C-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//808bp//97%//AJ012449

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C-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//4.90E-156//348aa//83%//Q14141
C-HEMBA1001620//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.60E-166//506aa//60%//P42803
C-HEMBA1001635//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA).//1.60E-10//155aa//28%//Q63679
C-HEMBA1001651//CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 1 (CYTADHERENCE ACCESSORY PROTEIN 1).//6.20E-07//362aa//24%//Q50365
C-HEMBA1001661//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//4.60E-36//365aa//33%//P33450
C-HEMBA1001672//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds.//0//1707bp//98%//AF072247
C-HEMBA1001675//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.//5.40E-09//101aa//35%//P54787
C-HEMBA1001714//Homo sapiens mRNA for ATPase inhibitor precursor, complete cds.//3.70E-78//200bp//100%//AB029042
C-HEMBA1001723//Homo sapiens G protein beta subunit mRNA, partial cds.//3.10E-267//1212bp//99%//AF195883
C-HEMBA1001734//CADHERIN-11 PRECURSOR (OSTEOBLAST-CADHERIN) (OBCADHERIN) (OSF-4).//1.10E-38//87aa//96%//P55288
C-HEMBA1001744//SCY1 PROTEIN.//9.90E-32//481aa//25%//P53009
C-HEMBA1001746//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.//7.60E-59//998bp//64%//AF098066
C-HEMBA1001804//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//1637bp//99%//AF125158
C-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//3.80E-11//206aa//36%//P11675
C-HEMBA1001819//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.90E-135//459aa//52%//Q99676
C-HEMBA1001822//Mus musculus Ese2L protein mRNA, complete cds.//1.90E-235//1329bp//89%//AF132479
C-HEMBA1001824//Homo sapiens nuclear protein NP94 mRNA, complete cds.//1.40E-199//1180bp//89%//AF159025
C-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//7.60E-64//221aa//55%//Q07230
C-HEMBA1001866//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//5.70E-51//234aa//41%//Q09332
C-HEMBA1001869//TRITHORAX PROTEIN.//9.60E-05//166aa//27%//P20659
C-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (ME2GLYDH).//9.30E-36//395aa//26%//Q63342
C-HEMBA1001913//GCN20 PROTEIN.//2.30E-81//158aa//50%//P43535
C-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//0//1850bp//99%//AF000145
C-HEMBA1001967//Homo sapiens NY-REN-57 antigen mRNA, partial cds.//0//1721bp//99%//AF155114
C-HEMBA1002035//Homo sapiens BAZ1A mRNA for bromodomain adjacent to zinc finger domain 1A, complete cds.//0//2149bp//99%//AB032252
C-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.30E-271//1583bp//88%//U92703
C-HEMBA1002102//ANKYRIN.//4.40E-10//106aa//35%//Q02357
C-HEMBA1002139//LIM AND SH3 DOMAIN PROTEIN LASP-1 (MLN 50).//7.10E-05//51aa//49%//Q14847
C-HEMBA1002151//Rattus norvegicus p34 mRNA, complete cds.//1.10E-153//1059bp//82%//AF178669
C-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.40E-51//180aa//56%//P79293
C-HEMBA1002177//TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).//6.00E-13//190aa//36%//P43694
C-HEMBA1002212//TYROSINE-PROTEIN KINASE-2 (EC 2.7.1.112) (FRAGMENT).//3.00E-17//267aa//29%//P18161
C-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//2.20E-199//392aa//89%//P47226
C-HEMBA1002241//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//3.70E-06//95aa//33%//P46087
C-HEMBA1002267//Sus scrofa decorin mRNA, complete cds.//1.10E-46//302bp//90%//AF125537
C-HEMBA1002341//P53-BINDING PROTEIN 2 (53BP2) (FRAGMENT).//3.80E-55//109aa//96%//Q62415
C-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//

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1847bp//99%//AF092563
C-HEMBA1002417/mGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1).//1.00E-121//489aa//52%//P39447
C-HEMBA1002419//TRICHOHYALIN.//1.90E-09//299aa//24%//P22793
C-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.//4.20E-24//109aa//55%//Q00994
C-HEMBA1002469//DXS8237E PROTEIN (FRAGMENT).//3.50E-50//199aa//61%//P98175
C-HEMBA1002475//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.10E-12//285aa//31%//P17437
C-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1.//6.80E-53//257aa//36%//P48732
C-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//0//2432bp//99%//AJ011972
C-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds.//0//1605bp//97%//AF016903
C-HEMBA1002555//Homo sapiens mSin3A associated polypeptide p30 mRNA, complete cds.//5.30E-51//768bp//68%//AF055993
C-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds.//6.80E-305//951bp//99%//AF075587
C-HEMBA1002746//DNA POLYMERASE BETA (EC 2.7.7.7).//5.00E-37//268aa//34%//P06746
C-HEMBA1002768//Mus musculus formin binding protein 17 mRNA, partial cds.//7.80E-237//1522bp//85%//AB011126
C-HEMBA1002770//Rattus norvegicus mRNA for TIP120, complete cds.//2.90E-176//1024bp//88%//D87671
C-HEMBA1002777//Fugu rubripes BAW (BAW) mRNA, complete cdsJ/3.40E-54//319bp//76%//AF153879
C-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//8.2e-314//1437bp//99%//AF071185
C-HEMBA1002818//Homo sapiens mRNA for fibulin-4.//2.00E-304//1383bp//99%//AJ132819
C-HEMBA1002876//HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME n.//1.50E-44//188aa//52%//Q09297
C-HEMBA1002935//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.30E-15//371aa//25%//Q05481
C-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//2.00E-34//300aa//34%//P16157
C-HEMBA1002951//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//4.40E-06//324aa//24%//P32380
C-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17) (DPDE4).//1.20E-27//63aa//100%//P14646
C-HEMBA1002997//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//3.80E-25//534aa//24%//Q02224
C-HEMBA1002999//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//1.40E-171//1552bp//75%//U20286
C-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA,//0//1558bp//99%//AF054182
C-HEMBA1003071//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR (ALS).//1.30E-09//121aa//40%//P35858
C-HEMBA1003077//SLIT PROTEIN PRECURSOR.//2.60E-15//199aa//31%//P24014
C-HEMBA1003096//Mouse 19.5 mRNA, complete cds.//5.60E-117//1139bp//72%//M32486
C-HEMBA1003098//Homo sapiens NY-REN-6 antigen mRNA, partial cds.//6.20E-273//1253bp//99%//AF155096
C-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//8.50E-51//221aa//33%//P41940
C-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//0//1583bp//99%//AJ005670
C-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE (EC 2.1.1.61).//5.90E-74//134aa//53%//P44551
C-HEMBA1003199//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.//8.50E-87//285bp//90%//AF129534
C-HEMBA1003235//TROPOMYOSIN.//2.30E-06//109aa//33%//Q02088
C-HEMBA1003250//PROTEIN KINASE APK1A (EC 2.7.1.-).//7.20E-41//245aa//42%//Q06548
C-HEMBA1003281//POLIOVIRUS RECEPTOR PRECURSOR.//6.00E-11//239aa//32%//P32506
C-HEMBA1003286//Homo sapiens mRNA for beta-1,4-galactosyltransferase IV, complete cds.//5.40E-229//1043bp//99%//AB024436
C-HEMBA1003291//SNF1-RELATED PROTEIN KINASE KIN10 (EC 2.7.1.-) (AKIN10)7/6.20E-28//126aa//51%//

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Q38997
C-HEMBA1003369//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//2.00E-08//248aa//23%//Q02224
C-HEMBA1003408//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (VERSION 1).//7.80E-13//297aa//30%//P18616
C-HEMBA1003417//Homo sapiens BAG-family molecular chaperone regulator-2 mRNA, complete cds.//1.50E-255//1179bp//99%//AF095192
C-HEMBA1003418//TRICHOHYALIN.//8.70E-19//281aa//31%//P37709
C-HEMBA1003433//Homo sapiens gene for NBS1, complete cds.//0//511bp//94%//AB013139
C-HEMBA1003538//COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41).//2.40E-110//242aa//58%//P00736
C-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (TSLET-2).//8.80E-189//360aa//96%//P50480
C-HEMBA1003555//NUCLEOTIDE-BINDING PROTEIN (NBP).//2.10E-68//251aa//52%//P53384
C-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAMMA-I).//1.20E-31//71aa//100%//P16874
C-HEMBA1003568//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//7.90E-49//279aa//32%//P19474
C-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1.//6.90E-206//445aa//74%//Q13330
C-HEMBA1003581//TALIN.//4.40E-45//52aa//98%//P26039
C-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP).//4.40E-10//118aa//35%//P19682
C-HEMBA1003615//Homo sapiens ART-4 mRNA, complete cds.//0//1713bp//99%//AB026125
C-HEMBA1003617//Homo sapiens ubiquitin-like product Chap1/Dsk2 mRNA, complete cds.//6.90E-178//501bp//97%//AB015344
C-HEMBA1003645//TIPD PROTEIN.//2.40E-10//289aa//23%//O15736
C-HEMBA1003662//TBX2 PROTEIN (T-BOX PROTEIN 2).//1.20E-75//151aa//99%//Q13207
C-HEMBA1003679//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN).//1.00E-09//611aa//22%//P23253
C-HEMBA1003680//PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-).//2.40E-92//423aa//47%//P34629
C-HEMBA1003684//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//2.00E-73//526aa//32%//Q13105
C-HEMBA1003690//HISTONE DEACETYLASE HDA1.//2.10E-59//249aa//47%//P53973
C-HEMBA1003742//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//1.70E-44//501bp//67%//AF037339
C-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//3.70E-124//347aa//55%//Q16665
C-HEMBA1003773//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//5.80E-81//511bp//86%//U17343
C-HEMBA1003783//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//1.10E-190//1204bp//84%//AF084259
C-HEMBA1003805//Mus musculus KH domain RNA binding protein QKI-5A mRNA, complete cds.//0//988bp//95%//AF090402
C-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).//8.10E-31//134aa//52%//P40484
C-HEMBA1003866//Mus musculus semaphorin VIa mRNA, complete cds.//1.20E-105//1192bp//70%//AF030430
C-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//3.80E-16//89aa//46%//P16372
C-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//8.50E-221//1188bp//78%//AF091234
C-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT).//1.60E-166//416aa//72%//Q14141
C-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//3.90E-208//951 bp//99%//AF067855
C-HEMBA1004199//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//8.40E-60//243aa//39%//P34529
C-HEMBA1004202//RAS-RELATED PROTEIN RAB-13.//6.20E-30//208aa//37%//P51153
C-HEMBA1004203//NUCLEOLAR PROTEIN NOP2.//1.50E-12//258aa//29%//P40991
C-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//0//1892bp//99%//U50748
C-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//5.70E-217//1217bp//88%//AF095927
C-HEMBA1004248//INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 (IMMEDIATE-EARLY PROTEIN CL-6).//2.00E-43//98aa//84%//Q08755

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C-HEMBA1004275//Homo sapiens PHD-finger protein (GRC5) mRNA, complete cds.//1.10E-152//1403bp//69%// AF043725
C-HEMBA1004276//Homo sapiens AP-4 adaptor complex beta4 subunit mRNA, complete cds.//4.80E-257// 738bp//99%//AF092094
C-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.//0//1982bp// 99%//AF022795
C-HEMBA1004295//Homo sapiens NY-REN-25 antigen mRNA, partial cds.//9.40E-31//381bp//65%//AF155103
C-HEMBA1004321//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.30E-93//357aa//42%//Q99676
C-HEMBA1004353//C-MYC BINDING PROTEIN MM-1.//3.00E-71//89aa//96%//Q99471
C-HEMBA1004354//CHL1 PROTEIN.//9.90E-26//130aa//42%//P22516
C-HEMBA1004356//H.sapiens MSSP-2 mRNA.//3.00E-243//573bp//98%//X77494
C-HEMBA1004389//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0// 1437bp//99%//AF125158
C-HEMBA1004408//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN-10).//3.20E-32//148aa//52%//P52017
C-HEMBA1004479//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//3.10E-51//152aa//40%//Q61221
C-HEMBA1004499//Homo sapiens delta-tubulin mRNA, complete cds.//3.40E-92//483bp//95%//AF201333
C-HEMBA1004509//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME ,4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//2.70E-12//200aa//28%//Q13107
C-HEMBA1004534//Homo sapiens gamma-filamin (ABPL) mRNA, complete cds.//1.2e-316//1445bp//99%// AF089841
C-HEMBA1004573//Homo sapiens mRNA for HELG protein.//2.00E-59//483bp//68%//AJ277291
C-HEMBA1004604//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.//0//1612bp//99%//AF193844
C-HEMBA1004669//SON PROTEIN (SON3).//7.30E-17//288aa//36%//P18583
C-HEMBA1004697//MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) (FRAGMENT).//2.90E-05//303aa//21%//P35749
C-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUTTIN CARRIER PROTEIN) (PM42).//9.90E-39//143aa//52%//P42743
C-HEMBA1004752//Homo sapiens mRNA for LAK-4p, complete cds.//4.60E-109//650bp//89%//AB002405
C-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds.//9.10E-34//515bp//66%//U49082
C-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds.//2.60E-246//1249bp//94%// L39060
C-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.40E-111//314aa//58%//P08547
C-HEMBA1004795//CDC4-UKE PROTEIN (FRAGMENT).//3.80E-69//198aa//66%//P50851
C-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//8.20E-154//317aa//94%// Q00004
C-HEMBA1004889//Human C3f mRNA, complete cds.//6.70E-24//341aabp//26%//U72515
C-HEMBA1004929//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//2.50E-05//148aa//24%// P25386
C-HEMBA1004930//26S PROTEASOME SUBUNIT S5B (KIAA0072) (HA1357).//3.30E-27//65aa//100%//Q16401
C-HEMBA1004972//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEURO FILAMENT PROTEIN) (NF-H).// 0.00000096//286aa//23%//P12036
C-HEMBA1004973//ZINC-BINDING PROTEIN A337/4.10E-08//121aa//33%//Q02084
C-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//0//1813bp//99%//AF041474
C-HEMBA1005029//Homo sapiens CGI-13 protein mRNA, complete cds.//0//1487bp//99%//AF132947
C-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16).//3.40E-101//106aa//98%//P35290
C-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//0//2762bp//99%// AF080561
C-HEMBA1005201//Homo sapiens CGI-07 protein mRNA, complete cds.//0//1608bp//99%//AF132941
C-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.90E-179//361aa//95%// Q00004
C-HEMBA1005206//Drosophila simulans anon73Bl gene and Su(P) gene.//1.90E-11//376bp//63%//AJ250308
C-HEMBA1005219//NUCLEAR PROTEIN SNF7.//5.30E-10//189aa//25%//P39929
C-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial.//3.90E-241//1095bp//99%//AJ007581
C-HEMBA1005359//ZINC FINGER PROTEIN 137.//3.90E-85//206aa//69%//P52743
C-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds.//9.00E-77//620bp//74%//

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AF071787
C-HEMBA1005394//Mus musculus pantothenate kinase 1 beta (panKIbeta) mRNA, complete cds.//3.90E-126//1097bp//75%//AF200357
C-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.//2.00E-213//537bp//99%//AF041248
C-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.90E-129//332aa//61%//O02193
C-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1).//3.10E-154//285aa//99%//Q60809
C-HEMBA1005530//Homo sapiens anaphase-promoting complex subunit 7 (APC7) mRNA, complete cds.//0//1578bp//98%//AF191340
C-HEMBA1005548//Homo sapiens MAFB/Kreisler basic region/leucine zipper transcription factor (MAFB) mRNA, complete cds.//1.00E-220//1014bp//99%//AF134157
C-HEMBA1005558//NUCLEAR PROTEIN SNF7.//6.40E-16//170aa//31%//P39929
C-HEMBA1005576//Mus musculus mRNA for plexin 2, complete cds.//1.20E-122//870bp//82%//D86949
C-HEMBA1005581//Homo sapiens SLIT2 (SLIL2) mRNA, complete cds.//0//1721bp//100%//AF133270
C-HEMBA1005582//TROPOMYOSIN 1, NON-MUSCLE ISOFORM (TROPOMYOSIN II) (CYTOSKELETAL TROPOMYOSIN).//0.00000009//213aa//27%//P09492
C-HEMBA1005595//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).//2.30E-54//562aa//29%//P34036
C-HEMBA1005621//Homo sapiens Mad2-like protein mRNA, complete cds.//8.00E-211//962bp//99%//AF072933
C-HEMBA1005666//Homo sapiens mRNA for DIPB protein.//8.60E-147//685bp//99%//AJ249128
C-HEMBA1005699//EPHRIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 8) (LERK-8) (EPH-RELATED RECEPTOR TRANSMEMBRANE LIGAND ELK-L3).//2.10E-37//98aa//81 %//Q15768
C-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT).//4.40E-17//167aa//34%//P25296
C-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU/M-TYPE).//2.00E-36//342aa//33%//P00789
C-HEMBA1005931//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//5.60E-15//76aa//51%//P51522
C-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//2371bp//100%//AF082516
C-HEMBA1006031//Homo sapiens mRNA for putative phospholipase, complete cds.//0//1413bp//99%//AB019435
C-HEMBA1006038//LAMININ ALPHA-5 CHAIN (FRAGMENT).//3.10E-33//81aa//64%//Q61001
C-HEMBA1006067//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.//8.20E-12//297bp//64%//AF098066
C-HEMBA1006130//SEL-10 PROTEIN.//0.000000043//219aa//25 %//Q93794
C-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//0//155 lbp//99%//AF048693
C-HEMBA1006198//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//1.90E-19//215aa//39%//P05142
C-HEMBA1006248//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//8.60E-23//151aa//37%//P16372
C-HEMBA1006253//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR.//0.00000002//62aa//53%//P42698
C-HEMBA1006268//Homo sapiens HQ0024c mRNA, complete cds.//3.50E-157//845bp//92%//AF073836
C-HEMBA1006272//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.30E-123//200aa//73%//P10265
C-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//1.00E-210//490aa//77%//P25500
C-HEMBA1006283//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2.//0.000000012//176aa//30%//P32505
C-HEMBA1006291//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-).//4.20E-12//215aa//23%//P70473
C-HEMBA1006309//Homo sapiens aspartyl aminopeptidase mRNA, complete cds.//5.30E-169//774bp//100%//AF005050
C-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//3.70E-225//1189bp//88%//AF076183
C-HEMBA1006344//RADIXIN.//1.50E-31//333aa//28%//P26043
C-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.60E-130//332aa//62%//O02193
C-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//3.50E-105//381aa//54%//P28160
C-HEMBA1006398//Human L1 element L1.6 putative pi 50 gene, complete cds.//2.00E-277//1729bp//85%//U93563
C-HEMBA1006445//Homo sapiens putative tumor supressor NOEY2 mRNA, complete cds.//1.40E-270//1224bp//

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100%//U96750
C-HEMBA1006474//40 KD PROTEIN.//1.40E-39//292aa//34%//Q01552
C-HEMBA1006485//PUROMYCIN-SENSITIVE AMINOPEPTIDASE (EC 3.4.11.-) (PSA).//1.90E-81//153aa//97%//P55786
C-HEMBA1006507//DIAPHANOUS PROTEIN HOMOLOG 2.//1.40E-46//316aa//32%//O60879
C-HEMBA1006521//3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE).//4.00E-33//177aa//42%//P25716
C-HEMBA1006559//Mus musculus PRAJA1 (Praja1) mRNA, complete cds.//2.80E-206//1107bp//83%//U06944
C-HEMBA1006583//Drosophila melanogaster Scribble (scrib) mRNA, complete cds.//1.70E-63//1002bp//65%//AF190774
C-HEMBA1006624//DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG.//0.00000069//109aa//38%//Q58323
C-HEMBA1006650//ARP2/3 COMPLEX 20 KD SUBUNIT (P20-ARC).//9.00E-40//113aa//82%//O15509
C-HEMBA1006652//60S RIBOSOMAL PROTEIN L7.//2.40E-44//206aa//47%//P14148
C-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMC1-TFG2 INTERGENIC REGION.//3.30E-22//241aa//31%//P53196
C-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//0.000000043//111aa//40%//Q01485
C-HEMBA1006758//Homo sapiens protocadherin beta 13 (PCDH-beta13) mRNA, complete cds.//0//1832bp//91%//AF152492
C-HEMBA1006807//Homo sapiens mRNA for SPOP.//5.70E-125//1109bp//75%//AJ000644
C-HEMBA1006877//OXYSTEROL-BINDINGPROTEIN.//2.00E-59//378aa//39%//P16258
C-HEMBA1006885//Homo sapiens gene for Proline synthetase associated, complete cds.//0//1467bp//96%//AB018566
C-HEMBA1006914//Human anthracycline-associated resistance ARX mRNA, complete cds.//0//1837bp//99%//U35832
C-HEMBA1006941//Homo sapiens PKCq-interacting protein PICOT (PICOT) mRNA, complete cds.//2.10E-271//1234bp//99%//AF118649
C-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.60E-143//740bp//94%//AF004828
C-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/I-4)GlcNAc alpha-2.3-sialyltransferase.//1.90E-80//447bp//89%//X74570
C-HEMBA1007018//DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (UC57/59) (DYNEIN LIGHT CHAIN A) (DLC-A).//2.40E-188//391aa//89%//Q90828
C-HEMBA1007087//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//8.30E-27//253aa//30%//Q10568
C-HEMBA1007121//Homo sapiens bisphosphate 3'-nucleotidase mRNA, complete cds.//1.70E-252//1118bp//92%//AF125042
C-HEMBA1007151//Homo sapiens synphilin 1 mRNA, complete cds.//0//1900bp//99%//AF076929
C-HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds.//3.80E-271//642bp//99%//AF062085
C-HEMBA1007194//Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds.//0//1588bp//99%//AF139658
C-HEMBA1007224//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1590bp//99%//AF196304
C-HEMBA1007243//Chinese hamster hprt mRNA, complete cds.//2.00E-58//650bp//70%//J00060
C-HEMBA1007251//Homo sapiens F-box protein FBX29 (FBX29) mRNA, partial cds.//5.00E-58//330bp//95%//AF176707
C-HEMBA1007300//Homo sapiens 3',5'-cyclic nucleotide phosphodiesterase 10A1 (PDE10A) mRNA, splice variant 1, complete cds.//0//1519bp//99%//AF127479
C-HEMBA1007301//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//6.20E-18//115aa//33%//P13941
C-HEMBB1000036//Homo sapiens CGI-51 protein mRNA, complete cds.//0//1665bp//99%//AF151809
C-HEMBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//2.80E-187//1582bp//80%//AF084928
C-HEMBB1000083//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//1.90E-22//426aa//25%//P11799
C-HEMBB1000119//Homo sapiens ASMTL gene.//0//1891bp//99%//Y15521
C-HEMBB1000144//GUANYLATE CYCLASE ACTIVATING PROTEIN 2 (GCAP 2) (RETINAL GUANYLYL CYCLASE ACTIVATOR PROTEIN P24).//1.40E-24//71aa//77%//P51177

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C-HEMBB1000217//Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds.//0//1038bp//99%//AF090385
C-HEMBB1000226//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE EEEDB.5.//2.70E-12//112aa//47%//Q09530
C-HEMBB1000264//CHL1 PROTEIN.//9.50E-19//104aa//45%//P22516
C-HEMBB1000266//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHROMOSOME V.//6.10E-09//242aa//26%//Q23256
C-HEMBB1000317//FIBULIN-1, ISOFORM D PRECURSOR.//7.10E-62//458aa//35%//P37888
C-HEMBB1000593//Homo sapiens transfemn receptor 2 alpha (TFR2) mRNA, complete cds.//1.30E-107//503bp//99%//AF067864
C-HEMBB1000631//LONGEVITY-ASSURANCE PROTEIN 1 (LONGEVITY ASSURANCE FACTOR 1).//4.10E-19//232aa//28%//P78970
C-HEMBB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//2.20E-28//273aa//31%//P27671
C-HEMBB1000693//Homo sapiens neuroan1 mRNA, complete cds.//0//2952bp//94%//AF040723
C-HEMBB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//6.20E-130//692bp//93%//U53475
C-HEMBB1000763//Homo sapiens CGI-89 protein mRNA, complete cds.//0//1676bp//96%//AF151847
C-HEMBB1000781//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.//1.20E-126//613bp//97%//AF111105
C-HEMBB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//5.10E-54//232aa//43%//P39956
C-HEMBB1000831//Homo sapiens breast cancer nuclear receptor-binding auxiliary protein (BRX) mRNA, complete cds.//5.80E-60//301bp//99%//AF126008
C-HEMBB1000915//SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (EC 3.4.21.-).//1.10E-08//129aa//31%//P29122
C-HEMBB1000927//Homo sapiens A-type potassium channel modulatory protein 2 (KCHIP2) mRNA, complete cds.//1.30E-126//592bp//99%//AF199598
C-HEMBB1000947//Homo sapiens clone HAW100 putative ribonuclease III mRNA, complete cds.//0//2292bp//99%//AF116910
C-HEMBB1000973//Mus musculus schlafen3 (Slfn3) mRNA, complete cds.//3.40E-120//580bp//67%//AF099974
C-HEMBB1000985//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//8.60E-18//178aa//30%//P28575
C-HEMBB1001011//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.40E-73//230aa//45%//P51523
C-HEMBB1001056//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//2.90E-19//264aa//34%//P46087
C-HEMBB1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//3.60E-52//331bp//80%//AF010144
C-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.40E-307//1447bp//97%//AF034803
C-HEMBB1001112//Homo sapiens sec61 homolog mRNA, complete cds.//6.00E-145//961 bp//83 %//AF077032
C-HEMBB1001137//Homo sapiens mRNA for putative phospholipase, complete cds.//0//3069bp//99%//AB019435
C-HEMBB1001151//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//4.20E-210//1835bp//76%//AF110267
C-HEMBB1001175//ANKYRIN.//7.00E-11//169aa//31%//Q02357
C-HEMBB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).//5.40E-93//196aa//54%//P46938
C-HEMBB1001242//Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds.//1.80E-284//713bp//100%//AF089897
C-HEMBB1001282//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//7.00E-43//394aa//34%//P16157
C-HEMBB1001288//COPPER HOMEOSTASIS PROTEIN CUTC.//7.80E-46//163aa//51%//P46719
C-HEMBB1001294//GTP-BINDING PROTEIN TC10.//1.20E-79//196aa//80%//P17081
C-HEMBB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.30E-129//724bp//86%//U92703
C-HEMBB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//2.10E-65//458bp//79%//D63850
C-HEMBB1001339//DXS8237E PROTEIN (FRAGMENT).//4.60E-06//124aa//37%//P98175
C-HEMBB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.10E-58//292bp//99%//AF097441

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C-HEMBB1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%//AF100757
C-HEMBB1001429//Homo sapiens leucine aminopeptidase mRNA, complete cds.//0//1933bp//99%//AF061738
C-HEMBB1001443//Rattus norvegicus pyruvate dehydrogenase phosphatase isoenzyme 1 mRNA, complete cds.//3.00E-130//553bp//86%//AF062740
C-HEMBB1001482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-57//941aa//27%//Q05481
C-HEMBB1001562//CYLICIN II (MULTIPLE-BAND POLYPEPTIDE II).//1.40E-06//373aa//21%//Q28092
C-HEMBB1001564//VACUOLAR ATP SYNTHASE SUBUNIT H (EC 3.6.1.34) (V-ATPASE H SUBUNIT) (V-ATPASE M9.2 SUBUNIT) (9.2 KD MEMBRANE ACCESSORY PROTEIN).//9.60E-32//80aa//78%//O15342
C-HEMBB1001673//Homo sapiens gene for new zinc finger protein, complete cds.//0//1919bp//99%//AB012770
C-HEMBB1001736//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 (EIF3 P116) (EIF3 P110).//4.60E-15//391aa//25%//P55884
C-HEMBB1001749//TRANSCRIPTIONAL ACTIVATOR GCN5.//1.70E-16//84aa//47%//Q03330
C-HEMBB1001802//Human desmin mRNA, complete cds.//0//1523bp//98%//U59167
C-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//0//1514bp//99%//AF056209
C-HEMBB1001839//GASTRULA ZINC FINGER PROTEIN XLCGF42.1 (FRAGMENT).//6.90E-11//87aa//35%//P18720
C-HEMBB1001871//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S1).//5.40E-75//241aa//48%//P47853
C-HEMBB1001872//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR) (CELL SURFACE GLYCOPROTEIN F4/80).//1.90E-22//210aa//27%//Q61549
C-HEMBB1001905//TRICHOHYALIN.//2.10E-10//268aa//27%//P37709
C-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds.//1.60E-131//874bp//86%//U47742
C-HEMBB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E).//6.90E-132//561aa//50%//Q24574
C-HEMBB1001950//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.-) (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1.60E-41//370aa//31%//P54304
C-HEMBB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYPIVC1).//2.70E-49//139aa//55%//P29981
C-HEMBB1002044//Mus musculus mRNA for vascular cadherin-2.//0//3562bp//81%//Y08715
C-HEMBB1002134//ZINC-FINGER PROTEIN NEURO-D4.//8.10E-56//176aa//67%//P56163
C-HEMBB1002193//TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE DTK) (TK19-2).//8.70E-61//77aa//74%//P55144
C-HEMBB1002217//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-132//399aa//44%//Q05481
C-HEMBB1002266//NEURONAL PROTEIN.//2.10E-46//121aa//76%//P41737
C-HEMBB1002342//Homo sapiens PKCq-interacting protein PICOT (PICOT) mRNA, complete cds.//1.50E-229//1045bp//99%//AF118649
C-HEMBB1002442//LIN-10 PROTEIN.//9.70E-14//121aa//31%//P34692
C-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds.//7.70E-258//774bp//99%//U43885
C-HEMBB1002510//GYP7 PROTEIN.//3.10E-50//192aa//42%//P48365
C-HEMBB1002550//HYPOTHETICAL UOG-1 PROTEIN.//5.00E-28//266aa//33%//P27544
C-HEMBB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds.//0//1417bp//99%//AF089749
C-HEMBB1002607//Homo sapiens vitamin D3 receptor interacting protein (DRIP80) mRNA, complete cds.//2.00E-136//660bp//98%//AF105421
C-HEMBB1002705//Homo sapiens CGI-27 protein mRNA, complete cds.//7.80E-285//841bp//96%//AF132961
C-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FMO5).//8.20E-198//868bp//99%//Z47553
C-MAMMA1000045//ENV POLYPROTEIN [CONTAINS: SURFACE PROTEIN GP85; MEMBRANE PROTEIN GP37].//1.90E-07//249aa//27%//P03396
C-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//1.50E-90//323aa//48%//P47226
C-MAMMA1000085//PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.16) (CYSTEINE--TRNA LIGASE) (CYSRS).//2.10E-90//427aa//39%//Q09860
C-MAMMA1000173//Homo sapiens src homology 3 domain-containing protein HIP-55 mRNA, complete cds.//2.60E-164//1044bp//87%//AF197060
C-MAMMA1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.40E-134//359aa//63%//

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P51523
C-MAMMA1000284//P.walti mRNA for rnp associated protein 55.//2.20E-109//864bp//76%//X99836
C-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds.//0//1466bp//99%//AB015132
C-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//2.00E-30//119aa//53%//Q09232
C-MAMMA1000612//Homo sapiens G protein beta subunit mRNA, partial cds.//8.30E-178//1992bp//84%//AF195883
C-MAMMA1000625//GYP7 PROTEIN.//2.10E-41//198aa//40%//P48365
C-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.).//4.40E-33//250aa//33%//P42660
C-MAMMA1000684//Homo sapiens opioid growth factor receptor mRNA, complete cds.//0//2391bp//99%//AF172451
C-MAMMA1000713//L-RBULOKINASE (EC 2.7.1.16).//7.70E-17//246aa//29%//P94524
C-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//1.00E-77//395aa//45%//O14646
C-MAMMA1000734//Homo sapiens mRNA for SEC63 protein.//0//1587bp//99%//AJ011779
C-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//9.00E-299//1033aa//55%//P87115
C-MAMMA1000824//ACTIN.//6.20E-20//284aa//28%//P53500
C-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4).//7.80E-40//101aa//54%//O27540
C-MAMMA1000897//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (TTI HEAVY CHAIN H3) (SERUM-DERIVED HYALURONAN-ASSOCIATED PROTEIN) (SHAP).//1.00E-141//576aa//37%//Q06033
C-MAMMA1000956//Homo sapiens CLDN8 gene for claudin-8.//0//1767bp//99%//AJ250711
C-MAMMA1001008//Homo sapiens aspartic-like protease mRNA, complete cds.//2.50E-276//1263bp//99%//AF117892
C-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CG-R) (LSH-R) (LUTEINIZING HOROMINE RECEPTOR) (FRAGMENT).//1.20E-26//276aa//28%//Q90674
C-MAMMA1001038//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN]//2.60E-107//190aa//95%//Q15746
C-MAMMA1001041//SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1).//1.60E-16//113aa//41%//Q01082
C-MAMMA1001059//Homo sapiens mRNA for DEAD Box Protein 5.//0//1440bp//99%//AJ237946
C-MAMMA1001075//Homo sapiens CGI-72 protein mRNA, complete cds.//1.30E-181//397bp//98%//AF151830
C-MAMMA1001080//Homo sapiens SNC73 protein (SNC73) mRNA, complete cds.//1.6e-312//1596bp//94%//AF067420
C-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN).//4.00E-49//125aa//68%//P51521
C-MAMMA1001139//SRE-2 PROTEIN.//5.80E-35//239aa//38%//Q09273
C-MAMMA1001181//ABC1 PROTEIN HOMOLOG PRECURSOR.//1.30E-07//81aa//45%//Q92338
C-MAMMA1001198//Homo sapiens eps15R mRNA, partial cds.//0//2253bp//99%//AB015346
C-MAMMA1001222//EBNA-2 NUCLEAR PROTEIN.//6.60E-09//255aa//29%//P12978
C-MAMMA1001259//Mus musculus F-box protein FBX18 mRNA, partial cds.//2.30E-271//1414bp//89%//AF184275
C-MAMMA1001260//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//2.10E-52//630aa//30%//P34537
C-MAMMA1001305//RHO-GTPASE-ACTIVATING PROTEIN 1 (GTPASE-ACTIVATING PROTEIN RHOGAP) (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//2.20E-98//283aa//63%//Q07960
C-MAMMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.000000017//46aa//60%//P20931
C-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//1.40E-165//312aa//99%//P02750
C-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) (FRAGMENT).//6.50E-129//260aa//92%//P52623
C-MAMMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU-TYPE).//5.70E-55//86aa//97%//P07384
C-MAMMA1001576//Human gamma-tubulin mRNA, complete cds.//7.50E-276//1561bp//90%//M61764
C-MAMMA1001627//Homo sapiens mRNA for transcription factor TBX6.//5.20E-189//871bp//99%//AJ007989
C-MAMMA1001633//ZINC FINGER PROTEIN 165.//6.30E-39//160aa//55%//P49910

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C-MAMMA1001679//F-ACTIN CAPPING PROTEIN BETA SUBUNIT (CAPZ).//0.00000058//29aa//100%//P47756
C-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.//0//1603bp//99%//AF095687
C-MAMMA1001735/TUBULIN BETA-5 CHAIN (BETA-TUBULIN CLASS-V).//5.90E-240//445aa//97%//P09653
C-MAMMA1001743//Y BOX BINDING PROTEIN-1 (Y-BOX TRANSCRIPTION FACTOR).//8.50E-32//171aa//36%//P21573
C-MAMMA1001751//Homo sapiens tandem pore domain potassium channel TWIK-2 (KCNK6) mRNA, complete cds.//0//2332bp//99%//AF117708
C-MAMMA1001754//Homo sapiens Vacuolar proton pump subunit SFD alpha isoform mRNA complete cds.//0//1987bp//99%//AF112204
C-MAMMA1001768//CELL DIVISION CYCLE PROTEIN 48 HOMOLOG MJ1156.//3.80E-45//351aa//38%//Q58556
C-MAMMA1001771//M.musculus mRNA for semaphorin B.//2.60E-200//1272bp//79%//X85991
C-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene.//1.30E-198//1157bp//80%//Y13148
C-MAMMA1001837//ZINC FINGER PROTEIN 29 (ZFP-29).//2.60E-77//507aa//38%//Q07230
C-MAMMA1001868//TRICHOHYALIN.//2.70E-19//359aa//25%//P22793
C-MAMMA1002143//Homo sapiens Cdc42 effector protein 4 mRNA, complete cds.//1.70E-252//1170bp//99%//AF099664
C-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN).//6.00E-66//157aa//70%//P15880
C-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE 1) (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) (TSA) (PRP) (NATURAL KILLER CELL ENHANCING FACTOR B) (NKEF-B).//5.20E-61//60aa//90%//P32119
C-MAMMA1002219//Rattus norvegicus rexo70 mRNA, complete cds.//1.30E-181//861bp//98%//AF032667
C-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR).//8.80E-217//310aa//86%//PP70541
C-MAMMA1002268//Mus musculus sphingosine kinase (SPHKIa) mRNA, partial cds.//1.00E-190//1624bp//76%//AF068748
C-MAMMA1002297//Homo sapiens mRNA for Rab6 GTPase activating protein.//1.10E-214//881bp//97%//AJ011679
C-MAMMA1002329//M.musculus mRNA for semaphorin B.//3.80E-45//332bp//84%//X85991
C-MAMMA1002351//Mus musculus dynactin subunit p25 (p25) mRNA, complete cds.//4.30E-119//773bp//86%//AF190795
C-MAMMA1002385//RIBONUCLEOPROTEIN RB97D.//1.50E-07//206aa//29%//Q02926
C-MAMMA1002428//LYSOSOME MEMBRANE PROTEIN II (LIMP II) (85 KD LYSOSOMAL MEMBRANE SIALOGLYCOPROTEIN) (LGP85) (CD36 ANTIGEN-LIKE 2).//1.10E-24//96aa//68%//Q14108
C-MAMMA1002470//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1.00E-11//128aa//36%//P47623
C-MAMMA1002485//Homo sapiens stanniocalcin-related protein mRNA, complete cds.//0//1822bp//99%//AF098462
C-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION.//1.20E-34//337aa//31%//P43571
C-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.//0//1910bp//99%//AF065214
C-MAMMA1002573//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//2.60E-19//666aa//23%//P08640
C-MAMMA1002617//ZINC FINGER PROTEIN 135.//7.60E-89//252aa7/57%//P52742
C-MAMMA1002619//PROBABLE UBIQUTTIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUTTIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUTTINATING ENZYME).//9.50E-16//159aa//37%//Q09931
C-MAMMA1002622//VILLIN.//7.20E-35//53aa//64%//P02640
C-MAMMA1002637//KINESIN LIGHT CHAIN (KLC).//1.30E-198//550aa//70%//Q07866
C-MAMMA1002650//Mus musculus ODA-8S protein mRNA, complete cds.//5.40E-57//480bp//68%//AF194030
C-MAMMA1002655//Homo sapiens mRNA for ganglioside sialidase, complete cds.//0//1515bp//99%//AB008185
C-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.10E-45//618aa//26%//P27550
C-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//4.3e-317//1942bp//85%//AF018261
C-MAMMA1002769//Homo sapiens cell cycle progression restoration 8 protein (CPR8) mRNA, complete cds.//

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2.20E-25//330bp//77%//AF011794
C-MAMMA1002842//Mus musculus c-Cbl associated protein CAP mRNA, complete cds.//2.60E-58//373bp//81%//U58883
C-MAMMA1002844//TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT).//4.90E-10//334aa//22%//P52178
C-MAMMA1002858//Rat cMG1 mRNA.//3.70E-238//1147bp//92%//X52590
C-MAMMA1002869//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//1.40E-160//305aa//85%//P48059
C-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN).//5.70E-30//214aa//35%//P48060
C-MAMMA1002937//ZINC FINGER PROTEIN 135.//8.30E-99//393aa//43%//P52742
C-MAMMA1002972//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27.//1.10E-05//69aa//42%//P40343
C-MAMMA1003011//HISTONE MACRO-H2A.1.//2.70E-123//370aa//66%//Q02874
C-MAMMA1003013//DNA POLYMERASE BETA (EC 2.7.7.7).//7.40E-46//332aa//36%//P06746
C-MAMMA1003035//RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//1.90E-13//108aa//33%//P23851
C-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds.//0//1533bp//99%//AF077952
C-MAMMA1003057//MD6 PROTEIN.//3.10E-225//419aa//97%//Q60584
C-MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//1.10E-234//1178bp//86%//AF071316
C-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA).//2.20E-105//217aa//89%//P46735
C-MAMMA1003146//Homo sapiens mRNA for GalT3 protein.//4.30E-218//996bp//99%//Y15062
C-MAMMA1003150//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.//5.00E-13//592aa//24%//P47179
C-MAMMA1003166//Homo sapiens MLL septin-like fusion protein (MSF) mRNA, complete cds.//3.10E-158//592bp//97%//AF123052
C-NT2RM1000001//D.melanogaster sap47-2 mRNA.//1.50E-10//417bp//62%//X80110
C-NT2RM1000039//HYPOTHETICAL 41.4 KD PROTEIN IN SRLQ-HYPF INTERGENIC REGION (EC 1.18.1.-) (ORF4) (ORF2).//2.90E-14//299aa//25%//P37596
C-NT2RM1000055//Rattus norvegicus mRNA for TIP120, complete cds.//0//3106bp//89%//D87671
C-NT2RM1000080//UNC-1 PROTEIN.//5.90E-25//211aa//31%//Q21190
C-NT2RM1000086//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//8.40E-52//364aa//32%//P34537
C-NT2RM1000092//MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2).//1.00E-07//362aa//23%//P39843
C-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//1.20E-10//150aa//28%//P87072
C-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUFS6 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds.//7.80E-110//516bp//99%//AF044959
C-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3.30E-38//469aa//27%//P49902
C-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//1.20E-10//150aa//28%//P87072
C-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//1.10E-10//94aa//47%//O42643
C-NT2RM1000199//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2476bp//99%//AJ245820
C-NT2RM1000244//Homo sapiens TRAF4 associated factor 1 mRNA, partial cds.//2.00E-126//592bp//99%//U81002
C-NT2RM1000252//H.sapiens E-MAP-115 mRNA.//9.70E-35//569bp//64%//X73882
C-NT2RM1000256//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.//0//3012bp//99%//AB016789
C-NT2RM1000257//MAGO NASHI PROTEIN.//7.90E-69//143aa//91%//P49028
C-NT2RM1000260//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP100 mRNA, complete cds.//0//2766bp//99%//AF055995
C-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V- ATPASE 28 KD ACCESSORY PROTEIN).//1.50E-106//118aa//97%//P39942

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C-NT2RM1000354//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//7.40E-245//2101bp//68%//AF111423
C-NT2RM1000355//Homo sapiens transmembrane protein BRI (BRI) mRNA, complete cds.7/0//1599bp//99%//AF152462
C-NT2RM1000377//Homo sapiens dual specificity phosphatase MKP5 (MKP5) mRNA, complete cds.//3.20E-196//1016bp//94%//AF179212
C-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.000000019//67aa//31%//P53915
C-NT2RM1000421//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775
C-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//1.40E-185//1486bp//81%//AF084928
C-NT2RM1000499//Caenorhabditis elegans mRNA for centaurin gamma 1A.//3.00E-17//927bp//58%//AJ132700
C-NT2RM1000539//Homo sapiens mRNA for Lsm5 protein.//3.00E-158//733bp//99%//AJ238097
C-NT2RM1000553//Homo sapiens putative glycolipid transfer protein mRNA, complete cds.//3.40E-177//814bp//99%//AF103731
C-NT2RM1000555//UNR PROTEIN.//0//678aa//98%//P18395
C-NT2RM1000563//TRANSMISSION-BLOCKING TARGET ANTIGEN S230 PRECURSOR.//0.0000068//199aa//30%//Q08372
C-NT2RM1000623//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775
C-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.50E-75//301aa//39%//P43636
C-NT2RM1000661//Homo sapiens translation initiation factor 4e mRNA, complete cds.//5.70E-210//960bp//99%//AF038957
C-NT2RM1000666//DNA-BINDING PROTEIN A.//2.20E-09//165aa//34%//P16989
C-NT2RM1000691//Homo sapiens mRNA for PLU-1 protein.//0//3104bp//99%//AJ132440
C-NT2RM1000702//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//5.60E-08//187aa//27%//P49695
C-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds.//0//3524bp//99%//AF027208
C-NT2RM1000746//Homo sapiens polyamine modulated factor-1 (PMF1) mRNA, complete cds.//6.70E-227//1043bp//99%//AF141310
C-NT2RM1000770//DXS6673E PROTEIN.//1.40E-39//194aa//48%//Q14202
C-NT2RM1000772//VEGETATABLE INCOMPATIBILITY PROTEIN HET-E-1.//7.30E-15//280aa//27%//Q00808
C-NT2RM1000800//Mus musculus partial mRNA for B-IND1 protein (B-indl gene).//1.10E-98//571bp//89%//Z97207
C-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds.//0//3524bp//99%//AF027208
C-NT2RM1000826//UNR PROTEIN.//0//678aa//98%//P18395
C-NT2RM1000833//Homo sapiens sec61 homolog mRNA, complete cds.//0//3541 bp//99%//AF08445 8
C-NT2RM1000850//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//9.70E-42//333aa//36%//P16157
C-NT2RM1000852//Homo sapiens putative ATP-dependent RNA helicase ROK1 mRNA, complete cds.//0//2206bp//99%//AF077033
C-NT2RM1000874//Homo sapiens death effector domain-containing testicular molecule mRNA, complete cds.//1.40E-244//1113bp//99%//AF043733
C-NT2RM1000882//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//4.30E-122//1394bp//69%//AF126799
C-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//5107bp//99%//AF082516
C-NT2RM1000885//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1.80E-56//630aa//30%//P34537
C-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//1020aa//89%//P70700
C-NT2RM1000898//ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR).//8.90E-26//229aa//29%//P02583
C-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//1.00E-15//266aa//26%//P46577
C-NT2RM1001003//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.//0//2230bp//99%//AF030233
C-NT2RM1001008//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//1.60E-13//119aa//36%//Q09701
C-NT2RM1001059//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB4.//3.60E-11//180aa//28%//

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Q99383
C-NT2RM1001072//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODEESTERASE GAMMA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II) (PLC-148).//8.30E-47//259aa//35%//P08487
C-NT2RM1001092//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.60E-115//332aa//52%//Q05481
C-NT2RM1001102//Human HEM45 mRNA, complete cds.//2.30E-27//482bp//63%//U88964
C-NT2RM1001115//ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14).//5.60E-06//239aa//27%//P54197
C-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//2.20E-144//362aa//71%//P25167
C-NT2RM2000030//DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DH IC) (CYTOPLASMIC DYNEIN INTERMEDIATE CHAIN).//0.00000043//136aa//31%//P54703
C-NT2RM2000092//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUTTIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//1.30E-36//160aa//40%//P50102
C-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1574bp//99%//AF067223
C-NT2RM2000260//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//3.60E-19//181aa//34%//P14918
C-NT2RM2000322//SPERMIDINE SYNTHASE (EC 2.5.1.16) (PUTRESCINE AMINOPROPYLTRANSFERASE) (AMINOPROPYLTRANSFERASE).//8.10E-06//167aa//29%//O48660
C-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN.//1.80E-14//245aa//29%//P11274
C-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//0//1506bp//99%//U48251
C-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLEOTIDE//1.70E-68//419aa//36%//P50849
C-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).//1.60E-54//344aa//33 %//P32802
C-NT2RM2000407//Mus musculus semaphorin VIa mRNA, complete cds.//9.70E-201//826bp//84%//AF030430
C-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//1.00E-222//237aa//89%//Q08469
C-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION.//1.00E-07//157aa//28%//P36113
C-NT2RM2000469//NITROGEN PERMEASE REACTIVATOR PROTEIN (EC 2.7.1.-).//8.90E-06//377aa//24%//P22211
C-NT2RM2000490//SYNAPTOTAGMIN (P65).//1.80E-13//166aa//34%//P41823
C-NT2RM2000502//Rattus norvegicus W307 mRNA, complete cds.//1.70E-58//381bp//86%//U78304
C-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//1673bp//99%//AF061243
C-NT2RM2000522//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.30E-12//282aa//32%//P17437
C-NT2RM2000566//Homo sapiens integrin alpha-7 mRNA, complete cds.//0//2519bp//96%//AF032108
C-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS).//1.70E-187//741aa//46%//P73505
C-NT2RM2000588//HISTONE DEACETYLASE HDA1.//2.80E-60//384aa//40%//P53973
C-NT2RM2000594//Homo sapiens DNA cytosine-5 methyltransferase 3 beta 3 (DNMT3B) mRNA, complete cds.//0//2712bp//99%//AF156487
C-NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.//4.90E-70//838bp//69%//AF179221
C-NT2RM2000609//Homo sapiens CTL1 gene.//0//1559bp//99%//AJ245620
C-NT2RM2000612//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//2.60E-106//1069bp//74%//U35776
C-NT2RM2000624//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//4.40E-32//319aa//35%//Q08170
C-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//3.70E-142//285aa//90%//P32391
C-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//3.80E-23//184aa//36%//Q15404
C-NT2RM2000718//Homo sapiens endocrine regulator mRNA, complete cds.//0//1731bp//99%//AF121141

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C-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//2.90E-103//249aa//73%//P28160
C-NT2RM2000740//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//5.70E-53//266aa//43%//P41877
C-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP).//9.50E-279//545aa//98%//P23514
C-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//1.70E-200//927bp//99%//AB015046
C-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//8.20E-154//285aa//99%//Q60809
C-NT2RM2001065//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1554bp//99%//AF100757
C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//2.40E-15//266aa//26%//P46577
C-NT2RM2001105//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//1.20E-28//805bp//61%//AF053091
C-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.30E-20//267aa//35%//P05143
C-NT2RM2001201//EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5).//1.50E-07//95aa//35%//P48724
C-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10).//3.60E-10//177aa//32%//P97924
C-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMIDOHYDROLASE).//1.30E-180//328aa//99%//P13264
C-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.60E-166//312aa//98%//P53995
C-NT2RM2001324//ZYXIN.//6.80E-55//200aa//41%//Q04584
C-NT2RM2001345//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//2.90E-08//334aa//22%//Q00808
C-NT2RM2001424//Homo sapiens mRNA for EIB-55kDa-associated protein.//0//1621bp//99%//AJ007509
C-NT2RM2001499//LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2).//7.40E-121//437aa//57%//P52569
C-NT2RM2001547//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.90E-27//90aa//42%//P38660
C-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//4.30E-61//312aa//44%//P19474
C-NT2RM2001592//Rattus norvegicus rexo70 mRNA, complete cds.//3.10E-156//909bp//88%//AF032667
C-NT2RM2001605//Homo sapiens mRNA for PLU-1 protein.//0//3114bp//99%//AJ132440
C-NT2RM2001613//Homo sapiens sec61 homolog mRNA, complete cds.//0//2601 bp//99%//AF084458
C-NT2RM2001632//KES1 PROTEIN.//1.40E-31//342aa//34%//P35844
C-NT2RM2001635//NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145).//1.20E-142//566aa//56%//P52591
C-NT2RM2001648//Homo sapiens sec61 homolog mRNA, complete cds.//0//2421 bp//99%//AF084458
C-NT2RM2001652//Homo sapiens guanine nucleotide exchange factor mRNA, complete cds.//0//2608bp//99%//AF111162
C-NT2RM2001659//ZINC/CADMIUM RESISTANCE PROTEIN.//3.40E-39//161aa//34%//P20107
C-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA complete cds.//0//2471bp//99%//AF044195
C-NT2RM2001668//Homo sapiens putative WHSC1 protein (WHSC1) mRNA, alternative splice product ending in intron 11, complete cds.//6.20E-16//464bp//62%//AFQ83391
C-NT2RM2001670//ZINC FINGER PROTEIN 29 (ZFP-29).//6.50E-104//407aa//43%//Q07230
C-NT2RM2001671//Oryctolagus cuniculus sarcolemmal associated protein (SLAP1) mRNA, complete cds.//0//1843bp//94%//U21155
C-NT2RM2001688//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I.//4.60E-20//253aa//30%//Q09674
C-NT2RM2001698//Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds.//6.20E-253//1170bp//99%//AB028600
C-NT2RM2001700//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3.99.-) (VLCAD) (FRAGMENT).//5.70E-130//536aa//49%//P50544
C-NT2RM2001716//Homo sapiens BPTF mRNA for bromodomain PHD finger transcription factor, complete cds.//0//1774bp//98%//AB032251
C-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-

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ZYME).//7.20E-16//381aa//27%//Q09931
C-NT2RM2001743//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//0//1498bp//99%//AF011792
C-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210.//8.80E-11//119aa//36%//Q92609
C-NT2RM2001760//Homo sapiens sec61 homolog mRNA, complete cds.//0//2379bp//99%//AF084458
C-NT2RM2001771//ZINC FINGER PROTEIN 135.//6.40E-154//394aa//64%//P52742
C-NT2RM2001782//Homo sapiens GDP-mannose pyrophosphorylase A (GMPPA) mRNA, complete cds.//0//1470bp//99%//AF135422
C-NT2RM2001785//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//0//2150bp//99%//AF126799
C-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//0//2249bp//99%//AF044195
C-NT2RM2001823//CHD1 PROTEIN.//1.80E-106//631aa7/39%//P32657
C-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds.//0//2415bp//97%//AF013759
C-NT2RM2001886//PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN2 (EC 3.1.13.4) (PAB1P-DEPENDENT POLY(A)-NUCLEASE).//3.00E-54//337aa//39%//P53010
C-NT2RM2001896//CELL DIVISION PROTEIN FTSJ.//5.10E-26//204aa//34%//P28692
C-NT2RM2001930//M.musculus mRNA for semaphorin G.//5.20E-135//894bp//83%//X97818
C-NT2RM2001935//Homo sapiens single-strand selective monofunctional uracil DNA glycosylase mRNA, complete cds.//0//1454bp//99%//AF125182
C-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//2.70E-27//216aa//34%//P28320
C-NT2RM2001950//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION.//0.0000001//212aa//23%//P38250
C-NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.//0//1658bp//98%//AF089816
C-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//1.90E-39//253aa//35%//P37838
C-NT2RM2001997//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//1.30E-10//232aa//28%//Q12730
C-NT2RM2001998//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//3.10E-12//206aa//30%//Q09782
C-NT2RM2002004//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//2.90E-08//83aa//44%//P40796
C-NT2RM2002014//HYPOTHETICAL 81.4 KD PROTEIN IN GREB-FEOA INTERGENIC REGION.//1.10E-89//425aa//41%//P46837
C-NT2RM2002030//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.//0//1959bp//99%//AB016789
C-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.00000099//338aa//24%//Q07878
C-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//5.00E-62//104aa//57%//Q61990
C-NT2RM2002091//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//7.10E-29//805bp//61 %//AF053091
C-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//0//1807bp//99%//AJ010840
C-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//0//1868bp//99%//AF030435
C-NT2RM2002128//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//4.90E-13//487aa7/26%//P49695
C-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//8.00E-31//105aa//47%//P47805
C-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//8.50E-191//1524bp//81%//AF084928
C-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//7.10E-155//381aa//72%//P25167
C-NT2RM4000030//LAS1 PROTEIN.//5.60E-12//184aa//32%//P36146
C-NT2RM4000046//GOLIATH PROTEIN (G1 PROTEIN).//0.000008//112aa//31%//Q06003
C-NT2RM4000104//ZINC FINGER PROTEIN 135.//1.50E-81//251aa//53%//P52742
C-NT2RM4000139//R.norvegicus trg mRNA.//2.30E-114//1161bp//72%//X68101

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C-NT2RM4000155//THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE--TRNA LIGASE) (THRRS).//1.20E-157//321aa//61%//P26639
C-NT2RM4000156//H.sapiens HPBRII-7 gene.//3.60E-21//785bp//60%//X67336
C-NT2RM4000167//Homo sapiens mRNA for Chromokinesin (KIF 4 gene).//0//1946bp//99%//AJ271784
C-NT2RM4000169//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//4.80E-13//686aa//23%//P25386
C-NT2RM4000191//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.//9.20E-75//439aa//41%//P16381
C-NT2RM4000202//ZINC FINGER PROTEIN MOK-2 (HOK-2).//4.90E-32//170aa//41%//Q16600
C-NT2RM4000215//MAK16 PROTEIN.//1.30E-68//295aa//49%//P10962
C-NT2RM4000229//Gallus gallus actin filament-associated protein (AFAP-110) mRNA, complete cds.//1.10E-27//633bp//64%//L20303
C-NT2RM4000233//Mus musculus semaphorin Via mRNA, complete cds.//3.40E-231//1395bp//86%//AF030430
C-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//2.20E-276//1124bp//97%//M99438
C-NT2RM4000344//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//0//2030bp//99%//AJ132637
C-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//1.50E-21//208aa//35%//Q24371
C-NT2RM4000356//RAS-RELATED PROTEIN RAB-17.//5.90E-80//213aa//75%//P35292
C-NT2RM4000386//Mus musculus ODZ3 (Odz3) mRNA, partial cds.//0//2156bp//87%//AF195418
C-NT2RM4000421//Homo sapiens mRNA for nuclear transport receptor.//0//1730bp//99%//AJ133769
C-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.//4.10E-271//2085bp//77%//AF062476
C-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//8.00E-20//393aa//24%//Q10297
C-NT2RM4000471//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2092bp//99%//AF097025
C-NT2RM4000486//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.80E-11//242aa//31%//P04280
C-NT2RM4000496//SAP1 PROTEIN.//8.30E-53//434aa//29%//P39955
C-NT2RM4000515//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H) (FRAGMENT).//1.10E-11//394aa//24%//P16884
C-NT2RM4000531//ZINC FINGER PROTEIN 29 (ZFP-29).//2.40E-89//389aa//43%//Q07230
C-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).//1.00E-59//595aa//28%//Q04652
C-NT2RM4000595//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//8.70E-15//403aa//30%//P26337
C-NT2RM4000611//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//2.90E-09//108aa//31%//Q00808
C-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//2.70E-146//420aa//60%//P27550
C-NT2RM4000657//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III).//3.00E-68//297aa//40%//P51178
C-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL13747/1.20E-28//180aa//30%//P74168
C-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.//1.00E-136//1104bp//77%//AF022789
C-NT2RM4000733//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000041//207aa//29%//P52154
C-NT2RM4000734//Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds.//0//2071bp//99%//AF221712
C-NT2RM4000741//Homo sapiens hSGT1 mRNA for hSgt1p, complete cds.//0//2184bp//99%//D88208
C-NT2RM4000751//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.90E-125//301aa//53%//Q99676
C-NT2RM4000798//Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 mRNA, complete cds.//0//2603bp//99%//AF084521
C-NT2RM4000820//VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45 SUBUNIT).//1.10E-24//138aa//44%//P40682
C-NT2RM4000857//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//6.70E-22//250aa//29%//P02750
C-NT2RM4000996//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//8.00E-211//738aa//50%//Q05481
C-NT2RM4001047//MO25 PROTEIN.//8.00E-140//333aa//80%//Q06138
C-NT2RM4001054//Homo sapiens sec61 homolog mRNA, complete cds.//3.10E-190//1315bp//81%//AF077032
C-NT2RM4001084//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I.//0.000000032//165aa//33%//Q09820

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C-NT2RM4001092//ZINC FINGER PROTEIN GLO37/3.10E-24//265aa//33%//P38682
C-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME II.//5.90E-86//292aa//48%//Q09417
C-NT2RM4001140//HOMEOBOX PROTEIN MSH-D.//1.00E-11//103aa//38%//Q01704
C-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN.//4.10E-197//445aa//78%//Q27969
C-NT2RM4001178//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//1.10E-48//218aa//43%//Q03532
C-NT2RM4001200//ZINC FINGER PROTEIN 135.//9.50E-135//375aa//60%//P52742
C-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//0//2310bp//99%//AF004828
C-NT2RM4001217//Mus musculus actin-binding protein (ENC-1) mRNA, complete cds.//3.10E-148//1445bp//72%//U65079
C-NT2RM4001256//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//4.30E-55//289bp//77%//AF129131
C-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-UKE (EC 2.7.1.137) (PI3-KINASE) (PTDINS-3-KINASE) (PI3K).//3.50E-35//124aa//65%//P54676
C-NT2RM4001316//ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.3) (MCAD).//2.30E-31//334aa//30%//P08503
C-NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds.//1.80E-39//728bp//64%//D89016
C-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).//1.00E-28//171aa//37%//P32626
C-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HOL1 INTERGENIC REGION.//8.10E-30//265aa//33%//P53742
C-NT2RM4001347//Homo sapiens NY-REN-25 antigen mRNA, partial cds.//0//2300bp//99%//AF155103
C-NT2RM4001371//Homo sapiens IDN3 mRNA, partial cds.//0//2524bp//99%//AB019494
C-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//2.20E-237//1079bp//99%//AF098799
C-NT2RM4001411//Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA, complete cds.//0//1962bp//87%//AF020526
C-NT2RM4001412//Homo sapiens nGAP mRNA, complete cds.//0//1918bp//99%//AF047711
C-NT2RM4001444//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS).//1.40E-118//444aa//46%//P73505
C-NT2RM4001483//ZINC FINGER PROTEIN 136.//5.10E-106//357aa//55%//P52737
C-NT2RM4001566//NECDIN.//9.80E-44//227aa//41%//P25233
C-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//1.50E-284//1082bp//90%//AF071317
C-NT2RM4001592//HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC REGION.//7.60E-56//213aa//49%//P31380
C-NT2RM4001597//M.musculus red-1 gene./12.10E-171//1414bp//78%//X92750
C-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3)J/2.60E-32//203aa//39%//Q12600
C-NT2RM4001629//MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LARGE HOMOLOG 3).//1.50E-93//278aa//38%//Q13368
C-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REGION.//2.70E-84//410aa//42%//P37339
C-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT).//8.90E-141//354aa//72%//Q14141
C-NT2RM4001731//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.//0//1922bp//100%//AF179221
C-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.).//4.10E-186//639aa//58%//Q05512
C-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1).//7.90E-66//311aa//35%//Q03164
C-NT2RM4001810//AGGRECAN CORE PROTEIN PRECURSOR (CARTILAGE-SPECIFIC PROTEOGLYCAN CORE PROTEIN) (CSPCP) (CHONDROITIN SULFATE PROTEOGLYCAN CORE PROTEIN 1).//5.10E-07//263aa//30%//P16112
C-NT2RM4001813//LECTIN BRA-2.//0.00000048//114aa//30%//P17346
C-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds.//8.10E-300//1395bp//98%//M37712
C-NT2RM4001823//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)7/2.90E-55//325aa//37%//P28160
C-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.90E-161//481aa//56%//P51523
C-NT2RM4001858//T-BOX CONTAINING PROTEIN TBX6L (FRAGMENT).//6.50E-22//126aa//46%//P79779

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C-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//4.30E-244//1248bp//94%// Y17711
C-NT2RM4001876//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//6.50E-23//184aa// 36%//Q15404
C-NT2RM4001880//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-).//5.90E-09//268aa//26%//P47486
C-NT2RM4001930//Homo sapiens dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl glucosyltransferase (ALG6) mRNA, complete cds.//0//1930bp//99%//AF102851
C-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//0//2087bp//99%//AF098162
C-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//2.60E-261//1563bp//84%//X99330
C-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.80E-112//457aa//47%// P51523
C-NT2RM4001987//NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM 180) [CONTAINS: N-CAM 140].//3.20E-17//281aa//30%//P16170
C-NT2RM4002013//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1 INTERGENIC REGION.//6.90E-94//589aa//35%//P42935
C-NT2RM4002034//Homo sapiens hiwi mRNA, partial cds.//1.90E-53//1585bp//60%//AF104260
C-NT2RM4002062//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).// 1.90E-31//80aa//52%//P36419
C-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//0//1865bp//99%// U82267
C-NT2RM4002066//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP230 mRNA, complete cds.//1.50E-211//1123bp//71 %//AF117755
C-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//9.30E-293//1751bp//83%// AF072758
C-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//2.80E-105//556aa//41 %//Q04652
C-NT2RM4002093//Homo sapiens neural polypyrimidine tract binding protein (PTB) mRNA, complete cds.//0// 2550bp//99%//AF176085
C-NT2RM4002109//Homo sapiens mRNA for Chromokinesin (KIF 4 gene).//0//2572bp//99%//AJ271784
C-NT2RM4002145//SLIT PROTEIN PRECURSOR.//1.40E-09//127aa//33%//P24014
C-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.90E-70//454bp//85%//AF035940
C-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, complete cds.//0//2671bp//99%//AF084535
C-NT2RM4002174//MRPPROTEIN.//9.10E-68//264aa//51%//P21590
C-NT2RM4002189//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//6.20E-33//688aa//27%//P08640
C-NT2RM4002194//Mus musculus semaphorin VIa mRNA, complete cds.//5.20E-297//1753bp//87%//AF030430
C-NT2RM4002205//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//3.00E-37//122aa// 72%//Q07803
C-NT2RM4002213//Homo sapiens protein phosphatase methylesterase-1 (PME-1) mRNA, complete cds.//0// 2452bp//100%//AF157028
C-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//3.70E-19//147aa//41%//P40809
C-NT2RM4002251//ALPHA-1,3-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.101) (N-GLYCOSYLOLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE I) (GNT- I) (GLCNAC-T I).//2.20E-36//320aa//38%//P27808
C-NT2RM4002323//ANTIGEN GOR (FRAGMENT).//0.000000001//154aa//33%//P48778
C-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.30E-29//275aa//30%//P27095
C-NT2RM4002438//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//1.10E-49//611 bp//70%// AF129131
C-NT2RM4002460//ENV POLYPROTEIN (COAT POLYPROTEIN) [CONTAINS: COAT PROTEINS GP70, GP20].//0.0000016//226aa//24%//P51515
C-NT2RM4002527//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.90E-15//366aa//27%//Q00808
C-NT2RM4002532//PROTEIN HOM1.//2.00E-16//276aa//28%//P55137
C-NT2RM4002558//Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds.//0//1797bp//99%// AF055899
C-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//0//1915bp//87%//AF022962
C-NT2RM4002571//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T2).// 4.60E-78//921bp//69%//X85019
C-NT2RM4002594//MSP1 PROTEIN HOMOLOG.//2.70E-68//236aa//58%//P54815

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C-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA UGASE) (ASPRS).// 2.30E-101//488aa//45%//O32038
C-NT2RP1000018//Homo sapiens mRNA for NIK, partial cds.//0//1747bp//99%//AB013385
C-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1652bp//99%//AJ012449
C-NT2RP1000040//Mus musculus donson protein (Donson) mRNA, partial cds.//5.90E-150//1025bp//82%// AF193608
C-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsa12.//0//1162bp//99%//X98834
C-NT2RP1000111//COP1 REGULATORY PROTEIN.//4.00E-116//296aa//51%//P93471
C-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//4.50E-50//181aa//60%//P51859
C-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//3.40E-270// 951bp//98%//AF011792
C-NT2RP1000202//ANKYRIN.//1.00E-25//302aa//34%//Q02357
C-NT2RP1000272//Mus musculus mRNA for neural specific sr protein NSSR 2, complete cds.//1.40E-267// 1155bp//87%//AB015895
C-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.30E-275//1249bp//99%//AF053551
C-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//8.70E-47//155aa//58%//P32447
C-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.70E-15//162aa//30%//P25343
C-NT2RP1000363//R.norvegicus LL5 mRNA7/7.90E-262//1175bp//83%//X74226
C-NT2RP1000376//Homo sapiens Ca^{2+}-independent phospholipase A2 long isoform (iPLA2) mRNA, complete cds.//0//2252bp//96%//AF102989
C-NT2RP1000413//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN).//1.90E-153//230aa//99%// P55161
C-NT2RP1000439//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//1.80E-94//1019bp//63%//AF111423
C-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN).//2.40E-10//227aa//25%//Q08257
C-NT2RP1000460//NUCLEAR MOVEMENT PROTEIN NUDC.//3.80E-19//149aa//36%//P17624
C-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//2.60E-94// 254aa//47%//P34580
C-NT2RP1000478//TUBULIN BETA-5 CHAIN (CLASS-V).//4.50E-240//445aa//97%//P09653
C-NT2RP1000481//Homo sapiens antigen NY-CO-3 (NY-CO-3) mRNA, partial cds.//7.5e-315//1445bp//99%// AF039688
C-NT2RP1000493//POSSIBLE DNA-REPAIR PROTEIN XP-E (POSSIBLE XERODERMA PIGMENTOSUM GROUP E PROTEIN) (UV-DAMAGED DNA-BINDING PROTEIN) (UV-DDB).//3.60E-30//534aa//23%//P33194
C-NT2RP1000513//Human NifU-like protein (hNifU) mRNA, partial cds.//6.50E-171//516bp//99%//U47101
C-NT2RP1000522//UBIQUTIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//8.20E-83//345aa//47%//Q61068
C-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.10E-27//193aa//35%//P49020
C-NT2RP1000574//HOMEOBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//3.50E-75//151aa//94%// P97367
C-NT2RP1000630//NECDIN.//2.40E-44//227aa//41%//P25233
C-NT2RP1000677//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER (ORGANIC ANION TRANSPORTING POLYPEPTIDE).//1.20E-78//483aa//31%//P46721
C-NT2RP1000701//Homo sapiens phospholipase A2 activating protein (PLA2P) mRNA, complete cds.//0// 1687bp//99%//AF145020
C-NT2RP1000733//Human mRNA for GSPT1-TK protein,complete cds.//0//2057bp//99%//E14379
C-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds.//0//2186bp//99%//AF101434
C-NT2RP1000746//Homo sapiens 60S acidic ribosomal protein PO mRNA, complete cds.//9.70E-196//901bp// 99%//AF173378
C-NT2RP1000782//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.20E-30//232aa//30%//O35566
C-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//8.20E-83//334aa//50%//Q07960
C-NT2RP1000833//Homo sapiens cGMP phosphodiesterase AI (PDE9A) mRNA, complete cds.//0//1494bp//99%//

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AF067223
C-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.80E-176//829bp//98%//AF047020
C-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.20E-30//232aa//30%//O35566
C-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds.//0//1555bp//99%//AF064094
C-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//5.20E-20//306aa//33%//Q09531
C-NT2RP1000915//AUTOANTIGEN NGP-1.//1.70E-19//343aa//25%//Q13823
C-NT2RP1000947//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds.//4.60E-105//504bp//99%//U39317
C-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//1.40E-23//370aa//28%//Q04652
C-NT2RP1000958//AUTOANTIGEN NGP-1.//1.40E-19//343aa//25%//Q13823
C-NT2RP1000959//Human acidic ribosomal phosphoprotein P0 mRNA, complete cds.//2.50E-236//966bp//99%//M17885
C-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//8.90E-299//554aa//99%//P19338
C-NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds.//2.20E-78//1529bp//61%//L01790
C-NT2RP1001013//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.70E-253//425aa//98%//P51522
C-NT2RP1001033//Homo sapiens delta-tubulin mRNA, complete cds.//2.10E-285//1290bp//100%//AF201333
C-NT2RP1001073//Homo sapiens U6 snRNA-associated Sm-like protein LSm5 mRNA, complete cds.//8.10E-107//504bp//99%//AF182291
C-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//0//2085bp//99%//U82267
C-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9.//2.30E-116//319aa//46%//Q06218
C-NT2RP1001113//Homo sapiens CTL2 gene.//0//2790bp//98%//AJ245621
C-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//5.20E-108//1278bp//69%//U79139
C-NT2RP1001185//Human isovaleryl-coA dehydrogenase (IVD) mRNA, complete cds.//1.90E-158//729bp//99%//M34192
C-NT2RP1001247//Homo sapiens TGF-beta type secreted signaling protein LEFTYA mRNA, complete cds.//0//2006bp//100%//AF081513
C-NT2RP1001253//Homo sapiens oscillin (hLn) mRNA, complete cds.//0//2020bp//99%//AF029914
C-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//32%//Q12024
C-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//32%//Q12024
C-NT2RP1001310//Homo sapiens mitochondrial carrier homolog 1 isoform a mRNA, partial cds; nuclear gene for mitochondrial product.//0//1732bp//99%//AF176006
C-NT2RP1001313//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//7.50E-121//1394bp//69%//AF126799
C-NT2RP1001361//Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA, complete cds.//6.50E-116//541bp//100%//AF070652
C-NT2RP1001385//HYPOTHETICAL 48.8 KD PROTEIN IN SSU81-SCS2 INTERGENIC REGION.//2.70E-22//284aa//25%//P40074
C-NT2RP1001395//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.//0//1782bp//99%//AF210052
C-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//8.90E-141//396aa//67%//P91917
C-NT2RP1001449//Mus musculus Gng31g mRNA, complete cds.//7.20E-165//800bp//87%//AF069954
C-NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).//1.20E-137//629bp//100%//AJ005257
C-NT2RP1001482//Mouse oncogene (ect2) mRNA, complete cds.//2.10E-158//755bp//86%//L11316
C-NT2RP1001494//MALE STERILITY PROTEIN 2.//7.20E-40//261aa//27%//Q08891
C-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.60E-166//506aa//60%//P42803
C-NT2RP1001546//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.60E-30//232aa//30%//O35566
C-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//5.80E-121//271aa//89%//P47758
C-NT2RP1001665//CALMODUUN.//0.00000051//83aa//30%//P02594

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C-NT2RP2000006//DNAJ PROTEIN (40 KD HEAT SHOCK CHAPERONE PROTEIN) (HSP40).//9.80E-17//79aa//55%//O34136
C-NT2RP2000008//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.40E-177//726aa//47%//P51523
C-NT2RP2000032//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)7/1.80E-22//184aa//34%//Q01730
C-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//0//1390bp//98%//AF061749
C-NT2RP2000054//Homo sapiens putative ring zinc finger protein NY-REN-43 antigen mRNA, complete cds.//0//2245bp//99%//AF155109
C-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EPSILON).//9.40E-16//45aa//100%//P49446
C-NT2RP2000067//Mus musculus ODZ3 (Odz3) mRNA, partial cds.//0//3546bp//99%//AF195418
C-NT2RP2000070//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//3.40E-51//383aa//32%//P33450
C-NT2RP2000076//Homo sapiens partial mRNA for polyhomeotic 2 protein (PH2 gene).//7.90E-20//265bp//73%//AJ242730
C-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//0//2244bp//99%//AB018356
C-NT2RP2000126//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//2.50E-117//541aa//42%//P41877
C-NT2RP2000133//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.//0//1490bp//99%//AF175966
C-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//4.40E-226//423aa//99%//P35585
C-NT2RP2000153//GAR2 PROTEIN.//9.80E-23//311aa//28%//P41891
C-NT2RP2000157//MLO2 PROTEIN.//2.60E-11//62aa//40%//Q09329
C-NT2RP2000161//DIS3 PROTEIN HOMOLOG.//4.10E-35//184aa//44%//Q17632
C-NT2RP2000183//DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL SPECIFIC PROTEIN NSP60).//3.30E-16//114aa//44%//O02675
C-NT2RP2000195//Homo sapiens androgen induced protein (AIG-1) mRNA, complete cds.//7.80E-152//704bp//99%//AF153605
C-NT2RP2000224//INSULIN RECEPTOR SUBSTRATE-1 (IRS-1).//0.000043//103aa//28%//P35568
C-NT2RP2000248//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//3.40E-21//210aa//33%//P56558
C-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//9.70E-41//278aa//36%//P40556
C-NT2RP2000258//ACTIVATOR 1 140 KD SUBUNIT (REPLICATION FACTOR C LARGE SUBUNIT) (AI 140 KD SUBUNIT) (RF-C 140 KD SUBUNIT) (ACTIVATOR 1 LARGE SUBUNIT) (DNA-BINDING PROTEIN PO-GA).//7.10E-12//213aa//23%//P35251
C-NT2RP2000270//Human putative G-protein coupled receptor (SH120) mRNA, complete cds.//1.30E-242//1043bp//99%//U78723
C-NT2RP2000288//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//1.60E-27//576aa//25%//Q10297
C-NT2RP2000297//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.30E-186//256aa//60%//Q99676
C-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds.//4.30E-279//1193bp//99%//U82381
C-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2.00E-111//226aa//92%//P08760
C-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds.//0//2331bp//99%//U83981
C-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds.//0//1886bp//99%//L28010
C-NT2RP2000420//ZINC FINGER PROTEIN 165.//8.50E-33//155aa//52%//P49910
C-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//0//1757bp//99%//AF102265
C-NT2RP2000448//KES1 PROTEIN.//8.70E-54//392aa//38%//P35844
C-NT2RP2000523//APOLIPOPROTEIN B MRNA EDITING PROTEIN (HEPR) (APOBEC-1).//6.00E-16//124aa//34%//P41238
C-NT2RP2000660//SAP1 PROTEIN.//5.20E-68//474aa//32%//P39955

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C-NT2RP2000668//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.30E-27//349aa//32%//Q01577
C-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE)//2.70E-100//488aa//44%//O32038
C-NT2RP2000764//NIFS PROTEIN.//6.60E-36//252aa//42%//P12623
C-NT2RP2000809//Homo sapiens BAG-family molecular chaperone regulator-5 mRNA, complete cds.//0//3347bp//99%//AF095195
C-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//5-.60E-08//179aa//29%//Q99104
C-NT2RP2000814//GELATION FACTOR (ACTIN BINDING PROTEIN 120) (ABP-120).//1.10E-07//96aa//29%//P13466
C-NT2RP2000816//MAGNESIUM-CHELATASE 30 KD SUBUNIT.//7.90E-08//172aa//28%//P26174
C-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds.//0//1562bp//99%//U80811
C-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2.//0//694aa//99%//O60841
C-NT2RP2000892//Rattus norvegicus db83 mRNA, complete cds.//2.90E-191//1094bp//85%//AB006135
C-NT2RP2000931//MATRIN 3.//2.40E-289//467aa//95%//P43244
C-NT2RP2000943//Homo sapiens sec24D protein mRNA, complete cds.//0//2767bp//99%//AF130464
C-NT2RP2000965//Homo sapiens mRNA for fls353, complete cds.//0//1989bp//96%//AB024704
C-NT2RP2001070//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE).//5.80E-46//222aa//45%//Q20939
C-NT2RP2001081//SYNAPTOTAGMIN IV.//4.20E-118//430aa//54%//P50232
C-NT2RP2001127//Homo sapiens mRNA for PLU-1 protein.//0//2514bp//99%//AJ132440
C-NT2RP2001168//VERPROLIN.//1.50E-09//143aa//33%//P37370
C-NT2RP2001174//GASTRULA ZINC FINGER PROTEIN XLCGF46.1 (FRAGMENT).//6.00E-10//88aa//38%//P18722
C-NT2RP2001233//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.00E-128//409aa//45%//Q05481
C-NT2RP2001245//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHAIN) (NMMHC).//2.20E-10//366aa//28%//P14105
C-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-ALPHA HOMOLOG) (BRAIN PROTEIN 147) (FRAGMENT).//4.40E-91//179aa//99%//P28663
C-NT2RP2001295//ZINC/CADMIUM RESISTANCE PROTEIN.//8.30E-39//161aa//34%//P20107
C-NT2RP2001327//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//5.50E-116//311aa//71%//Q13829
C-NT2RP2001378//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//2.00E-11//403aa//25%//Q02817
C-NT2RP2001392//MTTOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//8.40E-192//581aa//54%//P93647
C-NT2RP2001394//Homo sapiens mRNA for SCML2 protein.//0//2068bp//99%//Y18004
C-NT2RP2001397//Homo sapiens mRNA for cyclin B2, complete cds.//1.9e-316//1428bp//100%//AB020981
C-NT2RP2001420//Mus musculus nuclear protein NIP45 mRNA, complete cds.//9.00E-112//742bp//82%//U76759
C-NT2RP2001440//Homo sapiens mRNA for 14-3-3gamma, complete cds.//0//3712bp//99%//AB024334
C-NT2RP2001460//TRICHOHYAUN.//1.00E-14//521aa//24%//P37709
C-NT2RP2001511//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//3.20E-297//2206bp//75%//AF093097
C-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1.//0//2502bp//99%//Y14494
C-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//0//2326bp//99%//AF035586
C-NT2RP2001560//VAV2 PROTEIN.//0.00000015//219aa//27%//Q60992
C-NT2RP2001576//HYPOTHETICAL 62.2 KD PROTEIN C4G8.12C IN CHROMOSOME I.//8.20E-29//294aa//31%//Q09837
C-NT2RP2001597//RYANODINE RECEPTOR, CARDIAC MUSCLE.//0.000000036//127aa//36%//P30957
C-NT2RP2001601//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1748bp//99%//AF196304
C-NT2RP2001613//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT).//6.10E-12//184aa//31%//P24391
C-NT2RP2001634//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//0//2445bp//99%//U97067
C-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mR-

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NA, complete cds.//0//1287bp//99%//AF058718
C-NT2RP2001663//ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE), (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).//1.10E-47//126aa//53%//P42897
C-NT2RP2001740//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//7.90E-52//220aa//44%//Q61068
C-NT2RP2001748//FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS) (FARNESYL DIPHOSPHATE SYNTHETASE) (DIMETHYLALLYLTRANSFERASE (EC 2.5.1.1) / GERANYLTRANSTRANSFERASE (EC 2.5.1.10)) (KIAA0032).//5.40E-47//96aa/797%//P14324
C-NT2RP2001756//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.70E-49//411aa//32%//P51523
C-NT2RP2001839//SCY1 PROTEIN.//5.40E-32//621aa//24%//P53009
C-NT2RP2001869//ZINC FINGER PROTEIN 191.//7.10E-26//126aa//52%//O14754
C-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AIF-1) (IONIZED CALCIUM BINDING ADAPTER MOLECULE 1).//1.20E-45//141aa//65%//P55008
C-NT2RP2001883//Homo sapiens CGI-01- protein mRNA, complete cds.//0//2306bp//99%//AF132936
C-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end.//0//2518bp//98%//M74161
C-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5.//2.30E-38//395aa//30%//P53946
C-NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA, complete cds.//4.70E-177//1538bp//74%//AF062378
C-NT2RP2001985//Homo sapiens high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha mRNA, complete cds.//2.00E-38//435bp//67%//AF090989
C-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//6.50E-129//279aa//85%//Q08469
C-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//1.70E-47//247aa//52%//P35331
C-NT2RP2002046//Homo sapiens mRNA for transcription factor.//0//1664bp//99%//AJ130894
C-NT2RP2002058//Homo sapiens WD repeat protein WDR3 (WDR3) mRNA, complete cds.//0//2510bp//99%//AF083217
C-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//1.60E-226//1301bp//88%//U87306
C-NT2RP2002078//PECANEX PROTEIN.//1.80E-09//195aa//32%//P18490
C-NT2RP2002079//HISTONE HI, GONADAL.//4.40E-11//214aa//34%//P02256
C-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//33 89bp//99%//AJ007509
C-NT2RP2002105//H.sapiens MSH-R gene for melanocyte stimulating hormone receptor.//0//1644bp//98%//X65634
C-NT2RP2002124//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//4.30E-44//155aa//37%//Q13107
C-NT2RP2002185//Homo sapiens ubiquilin mRNA, complete cds.//0//1789bp//99%//AF176069
C-NT2RP2002193//Homo sapiens PIAS3 mRNA for protein inhibitor of activatied STAT3, complete cds.//0//2809bp//99%//AB021868
C-NT2RP2002252//Mus musculus (clone pVZmSin3A9) mSin3A9 mRNA, complete cds.//0//3118bp//91%//L38621
C-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//0//1528bp//98%//AF005418
C-NT2RP2002270//AF-9 PROTEIN.//1.20E-07//74aa//36%//P42568
C-NT2RP2002312//Homo sapiens mRNA for CDS2 protein.//0//2333bp//99%//Y16521
C-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds.//8.40E-254//1158bp//99%//AB015594
C-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//4.30E-240//1105bp//99%//AF038958
C-NT2RP2002408//Homo sapiens mRNA for TOLLIP protein.//3.20E-210//1136bp//93%//AJ242972
C-NT2RP2002442//HESA PROTEIN.//2.80E-14//163aa//30%//P46037
C-NT2RP2002464//DNA CROSS-LINK REPAIR PROTEIN PSO2/SNM1.//6.50E-07//171aa//27%//P30620
C-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//0//2180bp//99%//AB005289
C-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC1744).//4.60E-144//537aa//49%//Q02386
C-NT2RP2002520//Homo sapiens transcription factor RFX-B (RFXB) mRNA, complete cds.//3.70E-34//668bp//61%//AF105427

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C-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//6.20E-19//288aa//26%//Q11073
C-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-155//562aa//50%//P51523
C-NT2RP2002595//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//7.50E-35//181aa//42%//P12815
C-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds.//9.20E-147//874bp//87%//U19181
C-NT2RP2002609//2-HYDROXYMUCONIC SEMIALDEHYDE HYDROLASE (EC 3.1.1.-) (HMSH).//2.80E-08//109aa//37%//P19076
C-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.).//1.70E-51//326aa//38%//P55345
C-NT2RP2002701//HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME II.//1.90E-14//210aa//30%//O14345
C-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1.//4.90E-85//489aa//43%//P55194
C-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.//3.50E-74//727bp//72%//AF041107
C-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.//9.90E-54//964bp//64%//D89016
C-NT2RP2002862//60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN).//8.80E-10//203aa//27%//P29764
C-NT2RP2002880//GLUCOSE REPRESSION MEDIATOR PROTEIN.//0.000039//206aa//23%//P14922
C-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//1.90E-136//623bp//100%//AF038392
C-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II.//4.10E-87//395aa//40%//Q18964
C-NT2RP2002939//ZINC FINGER PROTEIN 136.//5.40E-70//282aa//42%//P52737
C-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//4.60E-80//147aa//100%//P51669
C-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//1.00E-08//98aa//36%//P10129
C-NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds.//0//2209bp//99%//AB026190
C-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//716aa//91%//P70700
C-NT2RP2003000//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//L90E-11//132aa//38%//Q13829
C-NT2RP2003121//Mus musculus enhancer of polycbmb (Epc1) mRNA, complete cds.//2.30E-82//642bp//68%//AF079765
C-NT2RP2003125//RING CANAL PROTEIN (KELCH PROTEIN).//2.40E-38//539aa//25%//Q04652
C-NT2RP2003137//UBIQUITIN.//0.000026//70aa//30%//P13117
C-NT2RP2003157//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.30E-13//185aa//38%//Q08170
C-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds.//0//2091bp//99%//D67025
C-NT2RP2003164//Homo sapiens mRNA for protein kinase.//0//2313bp//99%//AJ132545
C-NT2RP2003177//Homo sapiens recombination and sister chromatid cohesion protein homolog (hrec8) mRNA, partial cds.//0//1641bp//99%//AF006264
C-NT2RP2003228//H.sapiens Pl-Cdc21 mRNA.//0//2870bp//98%//X74794
C-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.60E-186//1551bp//77%//AF023657
C-NT2RP2003243//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//99%//AJ242978
C-NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.//0//1580bp//99%//AF151811
C-NT2RP2003272//Homo sapiens ubiquilin mRNA, complete cds.//0//1789bp//99%//AF176069
C-NT2RP2003277//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1).//1.90E-16//145aa//43%//P30771
C-NT2RP2003286//PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4) (RNA-3'- PHOSPHATE CYCLASE) (RNA CYCLASE).//4.20E-88//374aa//47%//Q23400
C-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds.//0//1526bp//99%//AB006572
C-NT2RP2003307//KINESIN LIGHT CHAIN (KLC).//2.20E-199//550aa//70%//Q07866
C-NT2RP2003308//CROOKED NECK PROTEIN.//5.40E-244//622aa//67%//P17886

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C-NT2RP2003329//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//3.60E-14//332aa//32%//P26337
C-NT2RP2003347//BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN HOMOLOG.//0.000022//261aa//24%//P48754
C-NT2RP2003391//Homo sapiens mRNA for nuclear transport receptor.//0//1509bp//99%//AJ133769
C-NT2RP2003394//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//5.50E-13//302aa//26%//P25386
C-NT2RP2003401//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//9.60E-78//346aa//43%//Q61068
C-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//5.00E-131//269aa//91%//P38378
C-NT2RP2003466//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//0//2194bp//99%//AF126799
C-NT2RP2003480//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//3012bp//99%//AF125158
C-NT2RP2003506//NADPH-CYTQCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//5.40E-14//106aa//46%//P04175
C-NT2RP2003513//Homo sapiens mRNA for paralemmin.//0//2137bp//97%//Y14770
C-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/PDGF2) mRNA, complete cds.//0//1746bp//95%//M12783
C-NT2RP2003522//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//1764bp//99%//AF125158
C-NT2RP2003543//HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE SLR1673 (EC 2.1.1.-).//1.70E-17//148aa//34%//P74261
C-NT2RP2003564//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//2.10E-59//270aa//46%//P19474
C-NT2RP2003596//Mus musculus Fas-apoptosis inhibitory molecule (Faim) mRNA, complete cds.//4.80E-82//530bp//85%//AF130367
C-NT2RP2003604//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.//0//2442bp//99%//AF030233
C-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.//9.40E-243//1624bp//82%//AJ006215
C-NT2RP2003702//Homo sapiens 17 beta-hydroxysteroid dehydrogenase type VII (HSD17B7) mRNA, complete cds.//2.1e-313//978bp//99%//AF098786
C-NT2RP2003704//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//1.80E-72//350bp//100%//AJ132637
C-NT2RP2003713//Homo sapiens ubiquitin-specific protease 3 (USP3) mRNA, complete cds.//0//2018bp//99%//AF073344
C-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//5.40E-29//85aa//72%//Q05481
C-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//1.70E-75//147aa//93%//P51669
C-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//0//869aa//80%//P53620
C-NT2RP2003781//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.//5.50E-63//253aa//50%//Q09201
C-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//3.70E-21//137aa//43%//Q11076
C-NT2RP2003857//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).//0.00000016//117aa//29%//Q91955
C-NT2RP2003871//Homo sapiens transposon-derived Buster1 transposase-like protein gene, complete cds.//0//2807bp//99%//AF205601
C-NT2RP2003912//SERINE/THREONINE-PROTEIN KINASE NEK1 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 1).//6.10E-183//387aa//87%//P51954
C-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//1.50E-23//200aa//30%//O09175
C-NT2RP2003981//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS8.//1.40E-16//664aa7/20%//

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P39702
C-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).// 2.30E-53//141aa//78%//P20290
C-NT2RP2004041//SYNAPSINS IA AND B.//0.00000074//159aa//32%//P17599
C-NT2RP2004066//Mus musculus Msx2 interacting nuclear target protein mRNA, complete cds.//2.70E-288// 1994bp//81%//AF156529
C-NT2RP2004098//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//5.40E-30//319aa//31%//Q01513
C-NT2RP2004170//Homo sapiens mRNA for transducin (beta) like 1 protein.//1.10E-138//1236bp//74%//Y12781
C-NT2RP2004187//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).// 5.60E-31//424aa//28%//Q07231
C-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds.//3.80E-52//397bp//82%// AF003998
C-NT2RP2004232//Homo sapiens EPK2 mRNA for serine/threonine kinase, complete cds.//0//2272bp//99%// AB015982
C-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds.//0//3044bp//99%//AB015718
C-NT2RP2004242//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).// 9.90E-12//427aa//26%//P19246
C-NT2RP2004245//Mus musculus pantothenate kinase 1 beta (panKlbeta) mRNA, complete cds.//6.40E-117// 1122bp//72%//AF200357
C-NT2RP2004270//PROTEIN PTM1 PRECURSOR.//1.40E-16//334aa//24%//P32857
C-NT2RP2004366//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS 13.//1.30E-51//505aa// 29%//Q07878
C-NT2RP2004389//PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR.//9.30E-15// 126aa//39%//P38120
C-NT2RP2004392//MNN4 PROTEIN7/1.40E-11//143aa//27%//P36044
C-NT2RP2004396//Homo sapiens mRNA for activator of S phase Kinase, complete cds.//5.40E-243//1108bp// 99%//AB028069
C-NT2RP2004425//Mus musculus axotrophin mRNA, complete cds.//0//2321bp//86%//AF155739
C-NT2RP2004476//Homo sapiens cyclin L ania-6a mRNA, complete cds.//0//2075bp//99%//AF180920
C-NT2RP2004538//Mus musculus kinesin-like protein KIF1B (Kif1b) mRNA, complete cds.//0//1387bp//86%// AF090190
C-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03.//3.00E-117//625aa//40%// Q09903
C-NT2RP2004587//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).// 7.30E-07//352aa//23%//P07197
C-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//8.50E-233//1061bp//99%//AJ006291
C-NT2RP2004681//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).// 2.60E-07//426aa//23%//P19246
C-NT2RP2004689//HYPOTHETICAL 192.5 KD PROTEIN C6G9.10C IN CHROMOSOME I.//5.60E-64//616aa// 33%//Q92355
C-NT2RP2004710//Mus musculus formin binding protein 30 mRNA, complete cds.//1.50E-280//1464bp//85%// U40750
C-NT2RP2004732//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).// 7.30E-07//352aa//23%//P07197
C-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).//1.30E-26//190aa//41%//P38692
C-NT2RP2004791//PUTATIVE LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.4) (LEUCINE-- TRNA LIGASE) (LEURS).//9.50E-73//153aa//59%//Q10490
C-NT2RP2004799//PROBABLE SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//3.70E-135//414aa//62%//P53588
C-NT2RP2004816//H58 PROTEIN.//9.00E-173//327aa//98%//P40336
C-NT2RP2004920//TRANSCRIPTIONAL REGULATOR ATRX (X-LINKED NUCLEAR PROTEIN) (HETEROCHROMATIN PROTEIN 2) (HP1 ALPHA-INTERACTING PROTEIN) (HP1-BP38 PROTEIN).//4.20E-09//804aa// 22%//Q61687
C-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds.//0//2103bp//99%//AB007144
C-NT2RP2004959//P54 PROTEIN PRECURSOR.//0.00000095//297aa//20%//P13692
C-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1 (KS1) mRNA, complete cds.//1.00E-

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228//1666bp//75%//U56732
C-NT2RP2004978//ACTIN-LIKE PROTEIN ARP8.//3.30E-47//353aa//30%//Q12386
C-NT2RP2005003//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).// 1.80E-99//376aa//43%//P19474
C-NT2RP2005012//Homo sapiens mRNA for SEC63 protein.//0//1693bp//99%//AJ011779
C-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//3.30E-47//155aa//59%//P32447
C-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL ADDITION ENZYME) (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFERASE).//4.00E-91//218aa//44%// Q92089
C-NT2RP2005116//PUTATIVE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 ALPHA SUBUNIT (EIF-3 ALPHA).//2.00E-173//273aa//57%//P34466
C-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//0//2388bp//98%// X98743
C-NT2RP2005139//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).//0.000000022//139aa//35%//Q05921
C-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//0.00E-01//1437bp//98%// AF045583
C-NT2RP2005162//Homo sapiens aspartyl aminopeptidase mRNA, complete cds.//0//1615bp//99%//AF005050
C-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//2769bp//98%//AJ007509
C-NT2RP2005204//Homo sapiens SUMO-1-activating enzyme E1N subunit (SUA1) mRNA, complete cds.//0// 1262bp//99%//AF090385
C-NT2RP2005239//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2087bp//99%//AF097025
C-NT2RP2005276//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0/2122bp//99%//D89053
C-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//0//2992bp//99%// AF060219
C-NT2RP2005315//Homo sapiens meningioma-expressed antigen 5 (MEA5) mRNA, partial cds.//1.90E-170// 780bp//100%//AF036144
C-NT2RP2005325//Homo sapiens LIM-homeodomain protein HLHX2 (LHX2) mRNA, complete cds.//0//1643bp// 99%//AF124735
C-NT2RP2005336//TRICHOHYALIN.//5.40E-10//545aa//22%//P37709
C-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPASE 5 (EC 3.6.1.38).//2.10E-124//636aa// 38%//P32660
C-NT2RP2005358//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds.//0//2199bp//99%//AF072247
C-NT2RP2005360//Homo sapiens sentrin/SUMO-specific protease (SENP1) mRNA, complete cds.//1.30E-52// 753bp//67%//AF149770
C-NT2RP2005393//AUTOANTIGEN NGP-1.//7.20E-39//224aa//35%//Q13823
C-NT2RP2005407//OXYSTEROL-BINDING PROTEIN.//5.30E-63//410aa//40%//P22059
C-NT2RP2005436//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.20E-13//185aa//38%//Q08170
C-NT2RP2005441//Homo sapiens hypothalamus protein HT002 mRNA, complete cds.//4.10E-202//962bp//98%// AF113540
C-NT2RP2005457//Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA, complete cds.//1.20E-13 0//608bp//99%//AF070652
C-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2.//3.00E-44//252aa//41%//P38127
C-NT2RP2005476//Human pl90-B (pl90-B) mRNA, complete cds.//3.40E-108//668bp//88%//U17032
C-NT2RP2005490//Mus musculus D3Mm3e (D3Mm3e) mRNA, complete cds.//1.80E-175//1102bp//83%// AF053628
C-NT2RP2005491//PARAMYOSIN (PMY) (ANTIGEN B).//0.00000015//279aa//26%//P35418
C-NT2RP2005496//ZINC FINGER PROTEIN 135.//2.90E-146//398aa//59%//P52742
C-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55).//5.20E-81//166aa//88%//P36876
C-NT2RP2005509//Homo sapiens CGI-45 protein mRNA, complete cds.//0//1825bp//99%//AF151803
C-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0// 3994bp//99%//AF092563
C-NT2RP2005525//Mus musculus kanadaptin mRNA, complete cds.//2.40E-304//1687bp//85%//AF035526
C-NT2RP2005531//PROTEIN 4.1 (BAND 4.1) (P4.1).//5.50E-70//393aa//39%//P11171
C-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1560bp//98%//AJ012449

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C-NT2RP2005549//PUTATIVE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE).//2.00E-20//181aa//36%//Q39366
C-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds.//1.00E-46//576bp//70%//AF062529
C-NT2RP2005605//QUEUINE TRNA-RIBOSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME).//8.20E-23//164aa//28%//O32053
C-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//8.9e-313//1455bp//98%//AF062085
C-NT2RP2005635//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1.00E-11//128aa//36%//P47623
C-NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).//1.20E-13//74aa//45%//P56101
C-NT2RP2005669//Homo sapiens death effector domain-containing testicular molecule mRNA, complete cds.//1.60E-248//1129bp//99%//AF043733
C-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.40E-200//908bp//99%//AF089814
C-NT2RP2005694//X-LINKED RETINITIS PIGMENTOSA GTPASE REGULATOR.//2.60E-10//175aa//27%//Q92834
C-NT2RP2005701//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//3.00E-63//323aa//39%//Q62158
C-NT2RP2005712//Homo sapiens myosin X (MYO10) mRNA, partial cds.//0//2681 bp//99%//AF132022
C-NT2RP2005719//GPI-ANCHORED PROTEIN P137.//4.00E-14//99aa//43%//Q14444
C-NT2RP2005722//Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds.//0//2545bp//99%//AB011414
C-NT2RP2005723//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN).//3.00E-09//169aa//28%//P38074
C-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//0//1968bp//99%//AF068868
C-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//1966bp//99%//AF082516
C-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A (EIF-4A).//1.70E-61//374aa//38%//P47943
C-NT2RP2005767//G.gallus PB1 gene.//5.00E-163//1158bp//81%//X90849
C-NT2RP2005773//Homo sapiens pyrroline 5-carboxylate reductase isoform (P5CR2) mRNA, complete cds.//2.70E-180//656bp//99%//AF151351
C-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN-BINDING PROTEIN) (SABP).//2.10E-213//249aa//85%//Q02038
C-NT2RP2005776//POLY(A) POLYMERASE TYPE 2 (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//4.40E-55//358aa//42%//P51005
C-NT2RP2005784//Homo sapiens ubiquitin-conjugating enzyme variant Kua (UBE2V) mRNA, complete cds.//0//2191bp//92%//AF155120
C-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//2.30E-39//318aa//31%//P40004
C-NT2RP2005835//SHP1 PROTEIN.//1.80E-28//208aa//32%//P34223
C-NT2RP2005841//Homo sapiens mRNA for ALEX3, complete cds.//3.50E-52//1091bp//59%//AB039669
C-NT2RP2005933//NUCLEOPORIN NUP57 (NUCLEAR PORE PROTEIN NUP57).//5.00E-11//155aa//34%//P48837
C-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//1.50E-67//388aa//44%//P25500
C-NT2RP2006043//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.50E-13//185aa//38%//Q08170
C-NT2RP2006071//Homo sapiens adaptor protein APPL mRNA, complete cds.//5.80E-120//1257bp//64%//AF169797
C-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.10E-214//1026bp//97%//X96484
C-NT2RP2006238//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//0//1669bp//88%//U49055
C-NT2RP2006275//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//2.00E-59//388aa//32%//P46821
C-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.80E-274//1236bp//99%//AF035262
C-NT2RP2006436//ANTERIOR-RESTRICTED HOMEOBOX PROTEIN (RATHKE POUCH HOMEO BOX).//

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3.40E-07//50aa//50%//Q61658
C-NT2RP2006456//Homo sapiens leucine-rich glioma-inactivated protein precursor (LGI1) mRNA, complete cds.// 1.30E-37//484bp//65%//AF055636
C-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//0//2181bp//99%//AJ006266
C-NT2RP2006534//5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-1 CHAIN (EC 2.7.1.-) (AMPK ALPHA-1 CHAIN) (FRAGMENT).//3.20E-11//32aa//96%//Q13131
C-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds.//3.10E-272//1220bp//95%//AF038966
C-NT2RP2006571//CYTOCHROME P450 2G1 (EC 1.14.14.1) (CYPIIG1) (P450-NMB) (OLFACTIVE).//4.20E-134//486aa//50%//P24461
C-NT2RP2006573//2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37) (CNP).//0.0000055// 169aa//25%//P09543
C-NT2RP2006598//Homo sapiens retinoid x receptor interacting protein mRNA, complete cds.//3.10E-295// 1193bp//99%//AF113538
C-NT2RP3000031//HISTONE DEACETYLASE HDA1.//1.10E-71//350aa//42%//P53973
C-NT2RP3000046//MITOCHONDRIAL GTPASE MSS1 PRECURSOR.//4.60E-78//421aa//37%//P32559
C-NT2RP3000047//NPL4 PROTEIN.//1.10E-85//526aa//36%//P33755
C-NT2RP3000050//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.20E-150//490aa// 53%//Q05481
C-NT2RP3000068//SON OF SEVENLESS PROTEIN HOMOLOG 1 (SOS-1) (MSOS-1).//2.20E-06//165aa//27%// Q62245
C-NT2RP3000085//ACETYL-/PROPIONYL-COENZYME A CARBOXYLASE ALPHA CHAIN [CONTAINS: BIOTIN CARBOXYLASE (EC 6.3.4.14); BIOTIN CARBOXYL CARRIER PROTEIN (BCCP)].//1.90E-123//436aa//50%// P46401
C-NT2RP3000109//P54 PROTEIN PRECURSOR.//0.0000065//358aa//22%//P13692
C-NT2RP3000207//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//2.90E-11//721aa//23%//P08640
C-NT2RP3000233//RING CANAL PROTEIN (KELCH PROTEIN).//9.30E-84//453aa//42%//Q04652
C-NT2RP3000252//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2388bp//99%//AF120334
C-NT2RP3000299//Rattus norvegicus mRNA for Crk-associated substrate, pi 30, complete cds.//0//2730bp//82%// D29766
C-NT2RP3000320//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//100%//AJ242978
C-NT2RP3000333//Rattus norvegicus db83 mRNA, complete cds.//2.90E-191//1094bp//85%//AB006135
C-NT2RP3000341//Homo sapiens mitochondrial inner membrane preprotein translocase Tim17a mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.50E-246//1124bp//99%//AF106622
C-NT2RP3000350//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2392bp//99%//AF120334
C-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2.00E-111// 226aa//92%//P08760
C-NT2RP3000361//Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1/Zer1 and Prp6.//0//2072bp//98%//AB019219
C-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.10E-107//206aa//99%//P35293
C-NT2RP3000393//Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds.//5.80E-266// 1373bp//86%//AF061817
C-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)// 1.70E-139//679aa//41%//O43143
C-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//0//2364bp//99%//AF071185
C-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//2.90E-15// 319aa//26%//P37908
C-NT2RP3000441//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.//3.40E-42//645bp//67%//AF098066
C-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//0//1934bp//99%//X16667
C-NT2RP3000527//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//4.80E-28//536aa//27%//P28160
C-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//1.90E-12//192aa//30%// P15151
C-NT2RP3000562//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//2165bp//99%// AF093097
C-NT2RP3000578//HES1 PROTEIN.//1.30E-22//229aa//27%//P35843

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C-NT2RP3000590//UVS-2 PROTEIN.//1.30E-22//458aa//24%//P33288
C-NT2RP3000596//TRICHOHYALIN.//2.50E-17//304aa//28%//Q07283
C-NT2RP3000603//NEUROGENIC DIFFERENTIATION FACTOR 1.//3.70E-11//90aa//42%//Q13562
C-NT2RP3000605//Mus musculus mRNA for wizL, complete cds.//0//2232bp//82%//AB012265
C-NT2RP3000624//Rattus norvegicus mRNA for SECIS binding protein 2 (sbp2 gene).//5.80E-234//1562bp//81%//AJ251245
C-NT2RP3000632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.00E-140//499aa//46%//P51523
C-NT2RP3000739//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//1.40E-24//155aa//37%//Q10149
C-NT2RP3000742//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).//4.10E-165//371aa//49%//P10895
C-NT2RP3000753//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//2.00E-10//565aa//24%//P12036
C-NT2RP3000759//ADP-RIBOSYLATION FACTOR.//7.00E-28//176aa//34%//Q94650
C-NT2RP3000825//NEUROGENIC LOCUS NOTCH 3 PROTEIN.//2.50E-36//417aa//31%//Q61982
C-NT2RP3000826//Homo sapiens mRNA for seven transmembrane protein TM7SF3, complete cds.//0//2522bp//99%//AB032470
C-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).//8.30E-108//331aa//50%//P27448
C-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//6.90E-69//1611bp//61%//U53445
C-NT2RP3000869//Drosophila melanogaster AAA family protein Bor (bor) mRNA, complete cds.//2.60E-138//1673bp//67%//AF227209
C-NT2RP3000875//MEVALONATE KINASE (EC 2.7.1.36) (MK).//7.70E-87//175aa//98%//Q03426
C-NT2RP3000917//DHP1 PROTEIN.//1.00E-193//428aa//55%//P40848
C-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//2.70E-185//585bp//88%//AF015264
C-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A.//1.90E-46//73aa//98%//P39027
C-NT2RP3000994//MATERNAL EFFECT PROTEIN STAUFEN.//0.00000006//78aa//48%//P25159
C-NT2RP3001055//Drosophila melanogaster separation anxiety protein (san) mRNA, complete cds.//3.80E-38//462bp//70%//AF225902
C-NT2RP3001057//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//9.00E-201//584aa//54%//Q05481
C-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//7.10E-47//537bp//74%//AF060219
C-NT2RP3001096//Rattus norvegicus leprecan (lepre1) mRNA, complete cds.//1.70E-94//787bp//66%//AF087433
C-NT2RP3001107//PEREGRIN (BR140 PROTEIN).//3.00E-44//260aa//40%//P55201
C-NT2RP3001111//Homo sapiens TRF-proximal protein mRNA, complete cds.//1.50E-149//731bp//97%//AF097725
C-NT2RP3001113//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//2.90E-11//631aa//23%//P25386
C-NT2RP3001120//ZINC FINGER. PROTEIN 136.//7.80E-170//512aa//58%//P52737
C-NT2RP3001140//F-SPONDIN PRECURSOR.//9.90E-238//419aa//96%//P35446
C-NT2RP3001150//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000031//207aa//29%//P52154
C-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//0//2732bp//99%//AJ006266
C-NT2RP3001176//HYPOTHETICAL 65.3 KD PROTEIN IN MAD1-SCY1 INTERGENIC REGION.//1.70E-10//196aa//27%//P53154
C-NT2RP3001216//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT).//0.0000023//137aa//33%//P35663
C-NT2RP3001221//GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-BUTYROBETAINE HYDROXYLASE).//1.90E-31//353aa//30%//P80193
C-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CONTAINS: LIGHT CHAIN LC1].//1.20E-166//395aa//51%//P14873
C-NT2RP3001253//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//1.70E-10//540aa//23%//P32380

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C-NT2RP3001268//Homo sapiens zinc finger protein ZNF228 (ZNF228) mRNA, complete cds.//0//3606bp//99%// AF198358
C-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein.// 1.30E-99//669bp//83 %//Y18101
C-NT2RP3001307//Gallus gallus RPE65 mRNA, complete cds.//4.20E-29//530bp//63%//AB017594
C-NT2RP3001338//ZINC FINGER PROTEIN 81 (FRAGMENT).//2.40E-16//175aa//28%//P51508
C-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN).//3.60E-25//129aa//34%//P32089
C-NT2RP3001383//Mus musculus ARL-6 interacting protein-6 (Aip-6) mRNA, partial cds.//3.40E-40//355bp//79%// AF133913
C-NT2RP3001384//Homo sapiens mRNA for LA95 protein.//0//1214bp//99%//AJ243467
C-NT2RP3001398//TRANSCRIPTIONAL REPRESSOR CTCF.//1.30E-61//374aa//36%//P49711
C-NT2RP3001399//SSU72 PROTEIN.//1.30E-16//84aa//52%//P53538
C-NT2RP3001407//SCY1 PROTEIN.//0.00000033//143aa//25%//P53009
C-NT2RP3001426//DNAJ PROTEIN (FRAGMENT).//1.00E-16//77aa//46%//O33529
C-NT2RP3001427//WERNER SYNDROME HEUCASE HOMOLOG.//2.70E-10//159aa//33%//O09053
C-NT2RP3001428//NUCLEOPROTEIN TPR.//1.40E-128//152aa//99%//P 12270
C-NT2RP3001453//ANTIGEN PEPTIDE TRANSPORTER 2 (APT2) (HISTOCOMPATIBILITY ANTIGEN MODIFIER 2).//3.20E-90//157aa//59%//P36371
C-NT2RP3001457//Drosophila melanogaster Melted (melt) mRNA, partial cds.//4.60E-20//792bp//59%// AF205831
C-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A.//9.10E-13//87aa//43%//P11632
C-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//0//1475bp//99%//U13395
C-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.// 0//2295bp//99%//AF064801
C-NT2RP3001527//Human Sp140 protein (Sp140) mRNA, complete cds.//4.30E-290//793bp//93%//U63420
C-NT2RP3001529//SPO0B-ASSOCIATED GTP-BINDING PROTEIN.//1.00E-61//345aa//42%//P20964
C-NT2RP3001538//HYPOTHETICAL 39.0 KD PROTEIN T28D9.3 IN CHROMOSOME II.//9.10E-10//158aa// 31%//Q10022
C-NT2RP3001554//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//1.40E-76// 388aa//32%//P46821
C-NT2RP3001580//Mus musculus strain C57BL/J germ cell-less protein (Gcl) mRNA, complete cds.//0//1730bp// 85%//AF163665
C-NT2RP3001587//Human anthracycline-associated resistance ARX mRNA, complete cds.//0//2617bp//99%// U35832
C-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210.//6.80E-18//91aa//38%//Q92609
C-NT2RP3001646//WD-40 REPEAT PROTEIN MSI2.//8.80E-09//132aa//31%//O22468
C-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1557bp//98%//AJ012449
C-NT2RP3001672//Homo sapiens Sex comb on midleg homolog 1 isoform 2 (SCMH1) mRNA, complete cds.//0// 2836bp//99%//AF149046
C-NT2RP3001679//Homo sapiens rec mRNA, complete cds.//0//2495bp//99%//AB023584
C-NT2RP3001688//Homo sapiens DNA binding protein p96PIF mRNA, complete cds.//0//1869bp//99%// AF173868
C-NT2RP3001690//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.00000024//481aa//21%// P25386
C-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR.//3.40E-33//161aa//32%//P54356
C-NT2RP3001712//Homo sapiens HP1-BP74 protein mRNA, complete cds.//0//1788bp//99%//AF113534
C-NT2RP3001723//Homo sapiens cell recognition molecule Caspr2 (CASPR2) mRNA, complete cds.//1.40E-58// 1138bp//63%//AF193613
C-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//1.10E-240//902bp//99%//AF054177
C-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds.//6.90E-132// 774bp//88%//AF008554
C-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT).//7.10E-132//294aa//84%//Q14141
C-NT2RP3001739//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//1.40E-15//190aa//32%// Q09701
C-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.80E-117// 462aa//55%//P52272

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C-NT2RP3001799//MYOSIN HEAVY CHAIN, STRIATED MUSCLE.//1.60E-11//348aa//27%//P24733
C-NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN).//7.40E-18//249aa//30%//Q04652
C-NT2RP3001854//Homo sapiens novel retinal pigment epithelial cell protein (NORPEG) mRNA, complete cds.//0//2742bp//99%//AF155135
C-NT2RP3001855//HOMEOBOX PROTEIN PKNOX1 (HOMEOBOX PROTEIN PREP-1).//8.10E-125//302aa//60%//P55347
C-NT2RP3001857//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.20E-14//242aa//24%//Q00808
C-NT2RP3001898//Homo sapiens mRNA for UDP-N-acetylglucosamine: alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV, complete cds.//0//1587bp//100%//AB000624
C-NT2RP3001931//Rattus norvegicus clone C48 CDK5 activator-binding protein mRNA, complete cds.//4.30E-91//656bp//81%//AF177478
C-NT2RP3001938//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//1.30E-22//227aa//33%//P08458
C-NT2RP3001944//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//3.10E-92//314aa//51%//Q09251
C-NT2RP3001969//TRICHOHYALIN.//2.70E-11//442aa//23%//P37709
C-NT2RP3002004//H.sapiens mRNA for FAST kinase.//1.50E-192//475bp//94%//X86779
C-NT2RP3002007//SAP1 PROTEIN.//1.1 OE-68//474aa//32%//P39955
C-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//5.30E-25//139aa//48%//Q09232
C-NT2RP3002045//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT.//1.00E-299//397aa//94%//P18484
C-NT2RP3002056//RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1).//2.00E-48//475aa//35%//P29374
C-NT2RP3002062//Homo sapiens BAG-family molecular chaperone regulator-5 mRNA, complete cds.//0//3764bp//99%//AF095195
C-NT2RP3002081//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//4.10E-233//1896bp//69%//AF111423
C-NT2RP3002108//DEC1 PROTEIN (MDM20 PROTEIN).//7.90E-09//181aa//22%//Q12387
C-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING PROTEIN GST1-HS).//2.80E-253//474aa//93%//P15170
C-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP.//1.90E-151//223aa//91%//Q02614
C-NT2RP3002273//SCD6 PROTEIN.//1.30E-09//295aa//28%//P45978
C-NT2RP3002303//PROBABLE UNDECAPRENYL PYROPHOSPHATE SYNTHETASE (EC 2.5.1.31) (UPP SYNTHETASE) (DI-TRANS-POLY-CIS-DECAPRENYLCISTRANSFERASE).//8.60E-49//243aa//43%//Q58767
C-NT2RP3002330//Homo sapiens eRFS mRNA, complete cds.//0//2443bp//99%//U87791
C-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15).//4.20E-70//590bp//76%//X16396
C-NT2RP3002399//DNA REPLICATION LICENSING FACTOR MCM4 (CDC21 HOMOLOG) (P1-CDC21).//8.60E-79//416aa//34%//P33991
C-NT2RP3002501//THREONINE DEHYDRATASE CATABOLIC (EC 4.2.1.16) (THREONINE DEAMINASE).//3.70E-43//318aa//37%//P05792
C-NT2RP3002529//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS45.//8.90E-95//542aa//38%//P38932
C-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III.//5.80E-40//161aa//52%//Q10010
C-NT2RP3002602//PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (EC 5.3.4.1) (ERP60) (58 KD MICROSOMAL PROTEIN) (P58) (HIP-70) (Q-2).//2.90E-19//173aa//28%//P11598
C-NT2RP3002628//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//2.50E-26//90aa//42%//P38660
C-NT2RP3002631//Homo sapiens Ran binding protein 11 mRNA, complete cds.//0//1703bp//99%//AF111109
C-NT2RP3002650//Mus musculus growth suppressor 1L (Gros1) mRNA, complete cds.//0//2109bp//87%//AF165163
C-NT2RP3002663//Homo sapiens putative glycolipid transfer protein mRNA, complete cds.//8.10E-263//1243bp//97%//AF103731
C-NT2RP3002671//ELONGATION FACTOR 2 (EF-2).//2.50E-73//179aa//36%//P13060
C-NT2RP3002682//Homo sapiens CGI-145 protein mRNA, complete cds.//0//1596bp//98%//AF151903
C-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kif1b), complete cds.//1.10E-93//1205bp//69%//D17577
C-NT2RP3002770//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//1.00E-07//70aa//

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41%//P17564
C-NT2RP3002785//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//2.50E-55//187aa//39%//Q24371
C-NT2RP3002810//HISTIDINE-RICH PROTEIN KE4.//2.20E-10//260aa//26%//Q31125
C-NT2RP3002818//INSERTION ELEMENT IS2A HYPOTHETICAL 48.2 KD PROTEIN.//5.70E-226//303aa//97%//P51026
C-NT2RP3002869//Mus musculus semaphorin VIa mRNA, complete cds.//2.50E-232//1282bp//85%//AF030430
C-NT2RP3002876//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//1.30E-29//805bp//61%//AF053091
C-NT2RP3002909//P53-BINDING PROTEIN 2 (53BP2) (BCL2-BINDING PROTEIN) (BBP).//1.50E-125//512aa//47%//Q13625
C-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).//2.00E-111//551aa//42%//Q04652
C-NT2RP3002953//Homo sapiens protocadherin beta 5 (PCDH-beta5) mRNA, complete cds.//0//2388bp//99%//AF152498
C-NT2RP3002969//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2722bp//99%//D89053
C-NT2RP3002972//Halocynthia roretzi mRNA for HrPET-1, complete cds.//3.90E-52//899bp//64%//AB029333
C-NT2RP3002988//Homo sapiens IkB kinase-b (IKK-beta) mRNA, complete cds.//1.80E-292//1325bp//99%//AF080158
C-NT2RP3003032//Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds.//0//2656bp//99%//AF084555
C-NT2RP3003059//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//3.80E-152//1007bp//82%//U78090
C-NT2RP3003061//ANKYRIN.//1.40E-20//200aa//37%//Q02357
C-NT2RP3003071//NEUROGENIC PROTEIN BIG BRAIN.//1.10E-05//258aa//24%//P23645
C-NT2RP3003078//Rattus norvegicus mRNA for ischemia related factor NYW-1, complete cds.//2.60E-112//633bp//88%//AB027149
C-NT2RP3003101//Mouse mRNA for tetracycline transporter-like protein, complete cds.//3.60E-83//807bp//72%//D88315
C-NT2RP3003133//Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds.//0//1998bp//91%//AB011414
C-NT2RP3003138//Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.//0//2159bp//98%//AF071592
C-NT2RP3003145//Mus musculus metallocarboxypeptidase CPX-1 mRNA, complete cds.//0//2251bp//81%//AF077738
C-NT2RP3003185//TROPOMYOSIN1, FUSION PROTEIN 33.//2.80E-06//402aa//23%//P49455
C-NT2RP3003193//ZINC FINGER PROTEIN 135.//7.30E-98//269aa//62%//P52742
C-NT2RP3003197//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I.//5.70E-09//169aa//31%//Q09674
C-NT2RP3003203//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//2.00E-210//1851 bp//76%//AF110267
C-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//4.30E-187//1750bp//75%//U20286
C-NT2RP3003230//Homo sapiens mRNA for hCRNN4, complete cds.//0//2350bp//99%//AB030656
C-NT2RP3003242//Homo sapiens stanniocalcin-related protein mRNA, complete cds.//0//2366bp//99%//AF098462
C-NT2RP3003251//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//4.20E-86//366aa//48%//P19474
C-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//0//2596bp//98%//L36983
C-NT2RP3003290//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.//1.5e-310//1468bp//82%//AB033922
C-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//1.10E-170//585aa//54%//O64948
C-NT2RP3003313//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP80 mRNA, complete cds.//0//2476bp//99%//AF117657
C-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52).//1.30E-35//178aa//44%//Q62191
C-NT2RP3003353//HYPOTHETICAL 26.2 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.//2.80E-07//161aa//28%//P40084
C-NT2RP3003385//Mus musculus SKD3 mRNA, complete cds.//0//2133bp//85%//U09874

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C-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds.//9.20E-45//782bp//65%//U90653
C-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//6.30E-270//743bp//90%//AF071317
C-NT2RP3003490//Homo sapiens mRNA for putative phospholipase, complete cds.//4.50E-81//649bp//67%//AB019435
C-NT2RP3003491//Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.//5.60E-36//842bp//62%//AF091624
C-NT2RP3003500//SCY1 PROTEIN.//9.20E-27//601aa//23%//P53009
C-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC REGION.//4.50E-30//191aa//40%//P40529
C-NT2RP3003589//Homo sapiens ras-related GTP-binding protein mRNA, complete cds.//0//3131bp//94%//AF106681
C-NT2RP3003659//HES1 PROTEIN.//5.90E-22//229aa//27%//P35843
C-NT2RP3003665//Homo sapiens mRNA for beta-ureidopropionase, complete cds.//0//1690bp//99%//AB013885
C-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//2.20E-13//146aa//42%//P14209
C-NT2RP3003701//F-SPONDIN PRECURSOR.//1.80E-17//324aa//26%//P35446
C-NT2RP3003716//SLIT PROTEIN PRECURSOR.//6.60E-10//150aa//34%//P24014
C-NT2RP3003726//Homo sapiens spermatogenesis associated PD1 mRNA, complete cds.//0//2568bp//99%//U28164
C-NT2RP3003799//Rattus norvegicus Srg1 (Sytr1) mRNA, complete cds.//9.00E-238//1529bp//84%//U71294
C-NT2RP3003800//Rattus norvegicus tyrosine protein kinase pp60-c-src mRNA, complete cds.//1.90E-163//924bp//89%//AF130457
C-NT2RP3003809//SAV PROTEIN.//1.10E-131//576aa//41%//Q07590
C-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP).//9.60E-19//174aa//31%//P02720
C-NT2RP3003831//Homo sapiens ENDOGL-1 (alias ENGL-a) mRNA for endonuclease G-like protein-1, complete cds.//2.2e-316//1436bp//99%//AB020523
C-NT2RP3003846//Homo sapiens mRNA for putative phospholipase, complete cds.//4.80E-277//1255bp//99%//AB019435
C-NT2RP3003876//Rattus norvegicus Rabin3 mRNA, complete cds.//4.50E-147//874bp//87%//U19181
C-NT2RP3003914//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//2.20E-20//76aa//64%//Q09332
C-NT2RP3003918//Homo sapiens VAMP-associated protein B (VAP-B) mRNA, complete cds.//0//2191bp//99%//AF086628
C-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein.//6.50E-240//1215bp//94%//X84692
C-NT2RP3004016//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1).//1.50E-17//226aa//26%//Q13263
C-NT2RP3004078//H.sapiens HRFX2 mRNA.//0//1806bp//99%//X76091
C-NT2RP3004125//Mus musculus zinc finger protein splice variant FIZ1-B (Fiz1) mRNA, complete cds.//4.60E-229//1560bp//78%//AF126747
C-NT2RP3004148//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//7.90E-05//271aa//22%//P08640
C-NT2RP3004155//Homo sapiens COQ7 protein mRNA, complete cds.//1.10E-179//823bp//100%//AF098948
C-NT2RP3004189//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.30E-14//242aa//24%//Q00808
C-NT2RP3004206//CROOKED NECK PROTEIN.//1.40E-220//567aa//67%//P17886
C-NT2RP3004207//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2445bp//100%//AJ245820
C-NT2RP3004209//Homo sapiens ubiquitin processing protease (Ubp-M) mRNA, complete cds.//0//2320bp//99%//AF126736
C-NT2RP3004242//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//4.70E-13//118aa//33%//P52734
C-NT2RP3004258//Homo sapiens ZIS1 mRNA, complete cds.//0//1861bp//99%//AF065391
C-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds.//2.40E-248//1126bp//100%//AF088982
C-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds.//5.10E-24//597bp//61%//AF007871
C-NT2RP3004348//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.10E-185//1130bp//82%//

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C-NT2RP3004378//Drosophila melanogaster separation anxiety protein (san) mRNA, complete cds.//3.90E-38//462bp//70%//AF225902
C-NT2RP3004424//Homo sapiens mRNA for stromal antigen 3 (STAG3 gene).//1.00E-66//364bp//93%//AJ007798
C-NT2RP3004428//CHROMODOMAIN HELICASE-DNA-BINDING PROTEIN 4 (CHD-4) (MI-2 AUTOANTIGEN 218 KD PROTEIN) (MI2-BETA).//5.20E-09//212aa//25%//Q14839
C-NT2RP3004472//GERM CELL-LESS PROTEIN.//1.60E-61//170aa//40%//Q01820
C-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//3.30E-113//466aa//42%//P34110
C-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds./4.00E-303//1385bp//99%//AB012851
C-NT2RP3004498//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.//2.00E-249//1777bp//80%//U83176
C-NT2RP3004504//M.musculus mRNA for CPEB protein.//1.90E-295//893bp//92%//Y08260
C-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).//3.70E-37//190aa//39%//P40484
C-NT2RP3004534//Mouse oncogene (ect2) mRNA, complete cds.//0//2075bp//87%//L11316
C-NT2RP3004544//THYROID RECEPTOR INTERACTING PROTEIN 10 (TRIP10) (FRAGMENT).//1.00E-22//1.3aa//53%//Q15642
C-NT2RP3004566//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-95//434aa//43%//P51523
C-NT2RP3004569//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).//3.80E-08//150aa//28%.//Q01484
C-NT2RP3004572//Homo sapiens TATA binding protein associated factor (TAFII150) mRNA, complete cds.//0//1853bp//99%//AF040701
C-NT2RP3004578//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//5.50E-12//396aa//23%//P39922
C-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//0//1807bp//99%//AJ006266
C-NT2RP3004617//ZINC-BINDING PROTEIN A33.//7.20E-75//464aa//35%//Q02084
C-NT2RP3004618//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//3972bp//98%//AF093097
C-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN).//1.70E-72//254aa//45%//P54352
C-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acetylglucosamine-6-O-sulfotransferas e (GlcNAc6ST), complete cds.//0//2393bp//99%//AB014679
C-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64.//2.60E-98//239aa//64%//P35526
C-NT2RP4000051//SYNAPTONEMAL COMPLEX PROTEIN SC65.//4.90E-51//335aa//37%//Q64375
C-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//2160bp//99%//AJ012449
C-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//0//2161bp//99%//AB011538
C-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//728aa//99%//Q10568
C-NT2RP4000129//Xenopus laevis F-box protein 28 (Fbx28) mRNA, partial cds.//1.40E-28//296bp//75%//AF176667
C-NT2RP4000147//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//4.30E-188//1543bp//78%//U35776
C-NT2RP4000210//PAIRED AMPHIPATHIC HELIX PROTEIN.//1.00E-71//396aa//36%//P22579
C-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//5.90E-15//104aa//40%//P15287
C-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//0//1932bp//99%//AJ006470
C-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//2.70E-84//208aa//76%//Q03173
C-NT2RP4000259//GLUTATHIONE PEROXIDASE.2 (EC 1.11.1.9).//5.50E-29//153aa//43%//O23968
C-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//3.50E-297//1024aa//55%//P87115
C-NT2RP4000312//ADENYLATECYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//1.50E-26//237aa//28%//Q01631
C-NT2RP4000323//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//3.00E-07//101aa//32%//P26372
C-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//0//4782bp//99%//AF044195
C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1).//2.60E-77//262aa//54%//O75570

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C-NT2RP4000376//Homo sapiens mRNA for phospholipase A2 activating protein.//0//2412bp//99%//AJ238243
C-NT2RP4000398//ZINC FINGER PROTEIN 140.//2.90E-110//435aa//50%//P52738
C-NT2RP4000415//Drosophila melanogaster fumble (fumble) mRNA, complete cds.//6.20E-19//902bp//57%//AF221546
C-NT2RP4000417//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113)(MAN(9)-ALPHA-MANNOSIDASE)(FRAGMENT).//2.60E-51//438aa//33%//P45701
C-NT2RP4000449//Homo sapiens sirtuin type 1 (SIRT1) mRNA, complete cds.//0//3143bp//99%//AF083106
C-NT2RP4000455//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//3.00E-07//175aa//27%//P09309
C-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15)(DEUBIQUITINATING ENZYME 15).//2.50E-37//291aa//38%//P50101
C-NT2RP4000481//ATP-DEPENDENT RNA HELICASE DOB1 (MRNA TRANSPORT REGULATOR MTR4).//1.90E-67//721aa//29%//Q09475
C-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//8.80E-50//214aa//50%//P40484
C-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.50E-106//495aa//45%//P45818
C-NT2RP4000524//Mus musculus Sec8 mRNA, complete cds.//0//3131bp//87%//AF022962
C-NT2RP4000528//NPL4 PROTEIN.//9.80E-86//515aa//37%//P33755
C-NT2RP4000556//SUR4 PROTEIN (SRE1 PROTEIN).//7.40E-14//233aa//31%//P40319
C-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//2.90E-188//863bp//99%//AF067730
C-NT2RP4000648//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//3.70E-07//175aa//27%//P09309
C-NT2RP4000657//SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN SPSE.//1.10E-32//350aa//30%//P39625
C-NT2RP4000713//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//1.10E-13//295aa//27%//Q11073
C-NT2RP4000724//RETROVIRUS-RELATED ENV POLYPROTEIN.//3.20E-191//199aa//78%//P10267
C-NT2RP4000737//Mus musculus F-box protein FBL10 mRNA, partial cds.//4.60E-250//1462bp//84%//AF176524
C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.000000032//67aa//31%//P53915
C-NT2RP4000817//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.80E-11//503aa//23%//P08640
C-NT2RP4000837//Homo sapiens mRNA for zinc finger protein SALL1.//4.30E-94//810bp//65%//Y18265
C-NT2RP4000839//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.50E-21//271aa//28%//Q00808
C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE)(ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//5.70E-82//324aa//48%//O09175
C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//4.10E-85//174aa//55%//P16415
C-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//6.20E-91//173aa//87%//O35682
C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN).//9.60E-96//513aa//42%//P22314
C-NT2RP4000907//Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds.//0//2127bp//86%//D45913
C-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//2.60E-26//227aa//36%//Q06828
C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//1.50E-76//346aa//43%//Q61068
C-NT2RP4000928//Homo sapiens mRNA for CDS2 protein.//0//2487bp//99%//Y16521
C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HEUCASE MJ1505.//1.40E-07//185aa//25%//Q58900
C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//1.40E-26//90aa//42%//P38660
C-NT2RP4000979//Homo sapiens putative HIV-1 infection related protein mRNA, partial cds.//2.30E-81//389bp//100%//AF094583
C-NT2RP4000989//UNC-47 PROTEIN.//8.20E-06//173aa//25%//P34579
C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//838aa//87%//P70700
C-NT2RP4001004//VACUOLAR PROTEIN 8.//3.70E-16//401aa//26%//P39968
C-NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds.//3.50E-257//1377bp//91%//U67140
C-NT2RP4001029//Homo sapiens transcription factor LBP-1b (LBP-1) mRNA, complete cds.//0//2002bp//98%//

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C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE)//1.50E-92//443aa//44%//Q09996
C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65.//6.70E-51//335aa//37%//Q64375
C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA^{2+}-ATPASE).//1.30E-123//563aa//46%//P13586
C-NT2RP4001080//Homo sapiens mRNA for Rod1, complete cds.//0//1439bp//99%//AB023967
C-NT2RP4001086//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//2.30E-07//474aa//22%//P12036
C-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//2.60E-17//121aa//36%//P51400
C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.90E-115//224aa//100%//P38378
C-NT2RP4001122/mPD PROTEIN.//1.40E-65//253aa7/41%//O15736
C-NT2RP4001126/TRICHOHYALIN.//2.90E-18//380aa//26%//Q07283
C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE (EC 3.5.1.18) (SDAP).//2.10E-07//93aa//33%//P44514
C-NT2RP4001148//SOF1 PROTEIN.//1.30E-104//236aa//52%//P33750
C-NT2RP4001149//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//4.40E-187//731bp//100%//AF037339
C-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//3.40E-29//385aa//29%//P35331
C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//4.70E-29//227aa//35%//P52178
C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//4.40E-104//1460bp//65%//U95760
C-NT2RP4001207//Homo sapiens Ran binding protein 11 mRNA, complete cds.//0//2940bp//99%//AF111109
C-NT2RP4001213//ZINC FINGER PROTEIN 184 (FRAGMENT).//5.70E-141//511aa//43%//Q99676
C-NT2RP4001219//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.20E-27//90aa//42%//P38660
C-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//1.80E-103//508aa//43%//Q04652
C-NT2RP4001256//Homo sapiens mRNA for gamma tubulin ring complex protein (76p gene).//0//2006bp//100%//AJ249677
C-NT2RP4001260//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.//0//1866bp//100%//AF174601
C-NT2RP4001274//Human transporter protein (g17) mRNA, complete cds.//4.40E-58//1196bp//61%//U49082
C-NT2RP4001276//TRICHOHYALIN.//7.90E-09//126aa//32%//Q07283
C-NT2RP4001313//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT).//5.90E-17//296aa//29%//P24391
C-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//8.50E-213//1129bp//92%//AJ001119
C-NT2RP4001336//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN.//0.000016//186aa//29%//O24076
C-NT2RP4001339//Homo sapiens mRNA for AMMERC1 protein.//9.20E-160//736bp//99%//AJ007014
C-NT2RP4001345//Homo sapiens mRNA for LCAT-like lysophospholipase (LLPL), complete cds.//2.7e-310//1400bp//100%//AB017494
C-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//1.40E-58//2425bp//59%//U53445
C-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN).//1.60E-19//222aa//30%//Q08180
C-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PROTEIN KINASE 1).//9.20E-17//146aa//35%//P18160
C-NT2RP4001379//HYPOTHETICAL 49.1 KD PROTEIN C11D3.06 IN CHROMOSOME I.//2.00E-53//436aa//30%//Q10085
C-NT2RP4001389//KESIPROTEIN.//1.70E-31//342aa//34%//P35844
C-NT2RP4001407//TRICHOHYALIN.//1.90E-05//298aa//21%//P22793
C-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//7.70E-190//422aa//82%//Q14141
C-NT2RP4001433//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.20E-138//419aa//54%//Q99676

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C-NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cdsJ/2.70E-66//738bp//71%//AF129131
C-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE EI COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE).//0//962aa//78%//Q02218
C-NT2RP4001498//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//1.00E-27//374aa//29%//P39010
C-NT2RP4001529//Homo sapiens transcription factor LBP-1b (LBP-1) mRNA, complete cds.//0//2002bp//98%//AF198487
C-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENIC REGION.//5.70E-54//242aa//38%//P25656
C-NT2RP4001551//Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit mRNA, complete cds.//0//3202bp//99%//AF152961
C-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//4.70E-09//216aa//24%//P96902
C-NT2RP4001567//ARMADILLO SEGMENT POLARITY PROTEIN.//5.40E-07//213aa//26%//Q02453
C-NT2RP4001568//ZINC FINGER PROTEIN GCS1.//1.80E-10//109aa//36%//P35197
C-NT2RP4001574//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//0//874aa//96%//P53620
C-NT2RP4001575//Rattus norvegiqus mRNA for ARE1 protein.//0//1087bp//87%//AJ223830
C-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS).//1.70E-141//373aa7/47%//P73505
C-NT2RP4001634//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//2.80E-14//652aa//22%//Q02224
C-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19.//5.10E-46//234aa//32%//P40469
C-NT2RP4001644//MYOSIN UGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//6.40E--19//111aa//45%//P25323
C-NT2RP4001656//VACUOLAR BIOGENESIS PROTEIN END1 (PEP5 PROTEIN).//1.10E-45//310aa//27%//P12868
C-NT2RP4001696//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//4.00E-10//243aa//25%//Q10568
C-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//3.00E-10//128aa//32%//Q10282
C-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//6.40E-170//1168aa//33%//Q09332
C-NT2RP4001753//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.90E-236//665aa//58%//P51523
C-NT2RP4001760//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN).//4.10E-16//263aa//27%//P98174
C-NT2RP4001790//Homo sapiens zinc finger protein ZFP-95 (ZFP95) mRNA, alternatively spliced, complete cds.//0//3053bp//99%//AF170025
C-NT2RP4001822//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.20E-30//241aa//30%//O35566
C-NT2RP4001823//MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.//1.10E-19//77aa//54%//P55083
C-NT2RP4001838//Homo sapiens CoREST protein (COREST) mRNA, complete cds.//6.30E-99//555bp//73%//AF155595
C-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1.//1.40E-85//489aa//43%//P55194
C-NT2RP4001861/HTUCHOHYALIN.//1.00E-35//307aa//34%//P37709
C-NT2RP4001896//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.40E-08//345aa7/25%//Q00808
C-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.30E-38//258aa//32%//Q12024
C-NT2RP4001938//TRANSCRIPTIONAL REPRESSOR CTCF.//9.80E-60//303aa//38%//P49711
C-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE).//1.50E-13//211aa//28%//Q43209
C-NT2RP4001950//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//1.20E-13//356aa//27%//P13816
C-NT2RP4001966//Mus musculus ODZ3 (Odz3) mRNA, partial cds.//0//3203bp//87%//AF195418
C-NT2RP4001975//Homo sapiens golgi membrane protein GP73 mRNA, complete cds.//0//3024bp//99%//AF236056
C-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//6.90E-24//370aa//27%//Q04652
C-NT2RP4002047//GTP-BINDING PROTEIN LEPA.//1.50E-168//601aa//52%//O67618
C-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)//1.00E-137//679aa//40%//O43143

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C-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.00E-150//722aa//39%//Q05481
C-NT2RP4002081//TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA CHAINS (TFIIA P35 AND PI 9 SUBUNITS) (TFIIA-42) (TFIIAL).//6.70E-06//250aa//31%//P52655
C-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.50E-63//159aa//53%//P38938
C-NT2RP4002791//NUCLEOPROTEIN TPR.//6.50E-05//659aa//23%//P12270
C-NT2RP5003461//RLR1 PROTEIN.//9.70E-22//177aa//27%//P53552
C-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.50E-15//280aa//27%//Q00808
C-NT2RP5003500//Mus musculus mRNA for heparan sulfate 6-sulfotransferase 2, complete cds.//1.30E-237//820bp//87%//AB024565
C-NT2RP5003506//Homo sapiens putative G protein-coupled receptor (RAIG1) mRNA, complete cds.//0//2289bp//99%//AF095448
C-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//3.30E-23//219aa//40%//P37116
C-OVARC1000001//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//7.00E-217//683bp//99%//AB029290
C-OVARC1000006//HISTONE H2A.1.//1.10E-55//117aa//99%//P02262
C-OVARC1000013//APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1).//4.20E-06//102aa//32%//O14727
C-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cdsJ/2.60E-295//1393bp//97%//AF058922
C-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE).//3.20E-07//60aa//45 %//P80022
C-OVARC1000071//Homo sapiens NTF2-related export protein NXT1 (NXT1) mRNA, complete cds.//1.50E-47//727bp//67%//AF156957
C-OVARC1000085//Human mRNA for proteasome subunit HC5.//1.00E-151//699bp//100%//D00761
C-OVARC1000087//HISTONE MACRO-H2A.1.//1.60E-12//174aa//26%//Q02874
C-OVARC1000091//HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1) (VCAF) (CFF).//8.40E-14//259aa//30%//P51610
C-OVARC1000106//TROPOMYOSIN 1, FUSION PROTEIN 33.//0.000032//165aa//27%//P49455
C-OVARC1000139//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//2.70E-12//120aa//32%//Q13107
C-OVARC1000151//Homo sapiens partial mRNA for putative protein p38 interacting with transcription factor Spl.//2.50E-95//461bp//98%//AJ242975
C-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//1.80E-32//511bp//65%//AF068332
C-OVARC1000241//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//8.20E-120//351aa//54%//Q16665
C-OVARC1000288//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)(LEUCINE AMINOPEPTIDASE IV) (LAPIV) (AMINOPEPTIDASE III)(AMINOPEPTIDASE YSCI).//5.40E-53//384aa//30%//P14904
C-OVARC1000304//PROTEIN MOV-10.//1.10E-249//519aa//87%//P23249
C-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//2.70E-40//154aa//38%//P29363
C-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//9.20E-148//787bp//76%//U19614
C-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//5.90E-14//200aa//27%//P40004
C-OVARC1000437//TENSIN.//7.90E-181//340aa//84%//Q04205
C-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//1.20E-25//227aa//25%//P11075
C-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE VHR).//3.10E-10//125aa//35%//P51452
C-OVARC1000479//Rattus norvegicus mRNA for TIP120, complete cds.//0//1872bp//89%//D87671
C-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.20E-157//892bp//91%//AF051850
C-OVARC1000556//RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1.-) (S6KII-ALPHA 2) (P90-RSK 2) (RIBOSOMAL S6 KINASE 3) (RSK3) (PP90RSK3).//3.30E-67//132aa//95%//Q15349
C-OVARC1000564//Homo sapiens sorting nexin 5 (SNX5) mRNA, complete cds.//1.0e-310//1440bp//98%//AF121855
C-OVARC1000649//Human squamous cell carcinama of esophagus mRNA for GRB-7 SH2 domain protein, com-

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plete cds.//0//1812bp//98%//D43772
C-OVARC1000679//Homo sapiens myosin-IXa mRNA, complete cds.//0//808bp//99%//AF117888
C-OVARC1000682//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).// 1.10E-209//293aa//95%//P39098
C-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds.//0//759bp//98%//AF038661
C-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN.//0.000000017//78aa//48%//P25159
C-OVARC1000751//PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16) (PP2C).//5.60E-11// 74aa//37%//P49596
C-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.10E-46//121aa//79%//P08886
C-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR (75 KD GLUCOSE REGULATED PROTEIN) (GRP 75).//3.90E-46//78aa//98%//O35501
C-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//2.80E-258//1183bp//99%//Y17711
C-OVARC1000846//NUCLEOLIN (PROTEIN C23).//0.0000097//109aa//30%//P08199
C-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//0//2095bp//99%//AF045584
C-OVARC1000862//M.musculus mRNA for FT1.//5.90E-226//1498bp//81%//Z67963
C-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).//2.20E-50//206aa//52%//P40484
C-OVARC1000885//OXIDOREDUCTASE UCPA (EC 1.-.-.-).//1.30E-32//170aa//34%//P37440
C-OVARC1000915//Homo sapiens histone deacetylase 5 mRNA, complete cds.//1.60E-121//591bp//97%// AF132608
C-OVARC1000936//COAT PROTEIN GP37 (ENV PROTEIN GP37).//0.0000054//135aa//28%//P03398
C-OVARC1000937//S-PHASE ENTRY CYCLIN 6.//4.90E-10//61aabp//49%//P32943
C-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//0//1961bp// 82%//AB005549
C-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//1.20E-17//127aa//33%//Q58343
C-OVARC1000999//ANKYRIN HOMOLOG PRECURSOR.//4.10E-11//189aa//32%//Q06527
C-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//1.50E-178//1113bp//86%//AF001533
C-OVARC1001038//Homo sapiens mRNA for Ariadne-2 protein.//0//1172bp//97%//AJ130978
C-OVARC1001051//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN).//1.10E-08//216aa//23%//P42566
C-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSORS.//1.90E-35//76aa//98%//P43490
C-OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.//1.00E-215//1027bp//98%//AF132946
C-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//0//1819bp//99%// AF082657
C-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))-//2.00E-214//769bp//97%//AJ005897
C-OVARC1001107//Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds.//6.10E-276//594bp// 98%//AF167572
C-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//5.1e-310//1588bp//93%// AF051782
C-OVARC1001154//Homo sapiens clone 24720 epithelin 1 and 2 mRNA, complete cds.//2.30E-296//1561bp// 93%//AF055008
C-OVARC1001171//Homo sapiens translation initiation factor 3 47 kDa subunit mRNA, complete cds.//5.70E-151// 436bp//92%//U94855
C-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2.//1.10E-11//221aa//25%//P48510
C-OVARC1001200//Mus musculus mRNA for HS1 binding protein 3.//5.80E-88//658bp//80%//AJ132192
C-OVARC1001232//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//5.10E-22//83aa//37%//Q10568
C-OVARC1001244//H.sapiens mRNA for Drosophila female sterile homeotic (FSH) homologue.//0//1467bp//99%// X62083
C-OVARC1001271//NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1).// 0.0000014//224aa//26%//P25976
C-OVARC1001306//N-MYC PROTO-ONCOGENE PROTEIN.//0.00000073//247aa//27%//P18444
C-OVARC1001342//40S RIBOSOMAL PROTEIN S8.//1.40E-110//207aa//99%//P09058
C-OVARC1001372//Homo sapiens liprin-alpha4 mRNA, partial cds.//2.00E-252//1146bp//99%//AF034801
C-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL.//6.00E-148//683bp// 99%//AJ224819
C-OVARC1001417//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP170

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mRNA, complete cds.//0//1715bp//99%//AF135802
C-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds.//4.90E-48//586bp//69%//U52426
C-OVARC1001436//ENL PROTEIN.//0.00000009//81aa//39%//Q03111
C-OVARC1001476//Mus musculus YGR163w mRNA homologue, complete cds.//1.80E-187//510bp//89%// AB017616
C-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//0//1876bp//98%// AF016507
C-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE PROTEIN 1).//0//777aa//91%//P98161
C-OVARC1001555//NGG1-INTERACTING FACTOR 3.//4.40E-19//130aa//40%//P53081
C-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//0//1167bp//100%// AF031165
C-OVARC1001610//Homo sapiens choline/ethanolaminephosphotransferase (CEPT1) mRNA, complete cds.//0// 1870bp//99%//AF068302
C-OVARC1001703//Mus musculus ARL-6 interacting protein-2 (Aip-2) mRNA, complete cds.//3.50E-16//399bp// 61%//AF133670
C-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).//2.80E-10//106aa// 38%//Q62267
C-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).//4.40E-40//195aa//41%//P07106
C-OVARC1001726//APICAL-LIKE PROTEIN (APXL PROTEIN).//4.30E-16//116aa//43%//Q13796
C-OVARC1001731//TROPOMYOSIN ALPHA CHAIN, FIBROBLAST ISOFORM F2.//4.00E-122//282aa//85%// P08942
C-OVARC1001762//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMINO, ACETYLTRANSFERASE 1).//6.40E-85//514aa//34%//P12945
C-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.// 0//963bp//99%//U97670
C-OVARC1001809//Mus musculus sphingosine kinase (SPHKIa) mRNA, partial cds.//2.70E-190//1624bp//76%// AF068748
C-OVARC1001942//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMINO, ACETYLTRANSFERASE 1).//3.10E-81//497aa//35%//P12945
C-OVARC1001943//Mus musculus DEBT-91 mRNA, complete cds.//0//2035bp//87%//AF143859
C-OVARC1001987//Homo sapiens prolactin regulatory element-binding protein (PREB) mRNA, complete cds.// 0//1083bp//99%//AF203687
C-OVARC1002050//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//0//1019bp//99%// AB029290
C-OVARC1002112//HISTONE MACRO-H2A.1.//3.00E-174//371aa//90%//Q02874
C-OVARC1002127//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER 2 (BRAIN DIGOXIN CARRIER PROTEIN) (BRAIN-SPECIFIC ORGANIC ANION TRANSPORTER) (OATP-B1).//5.40E-52//306aa//35%// O35913
C-OVARC100213 8//SAP1 PROTEIN.//7.60E-60//128aa//59%//P39955
C-OVARC1002156//Danio rerio uridine kinase mRNA, complete cds.//6.00E-16//262bp//64%//AF195851
C-OVARC1002165//3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 2 (EC 1.3.99.5) (STEROID 5-ALPHA-REDUCTASE 2) (SR TYPE 2).//7.60E-08//114aa//37%//P31213
C-OVARC1002182//BETA-TRCP (BETA-TRANSDUCIN REPEAT-CONTAINING PROTEIN) (BTRCP).//1.70E-09//207aa//30%//Q91854
C-PLACE1000004//Homo sapiens IDN3-B mRNA, complete cds.//0//2365bp//99%//AB019602
C-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//1.60E-81//212aa//70%//P34547
C-PLACE1000040//TRANSFORMING PROTEIN P21/K-RAS 2B.//1.40E-17//185aa//32%//P08643
C-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//7.90E-54//190bp//94%//L22154
C-PLACE1000066//SSU72 PROTEIN.//1.10E-39//206aa//43%//P53538
C-PLACE1000081//Human SEC7 homolog Tic (TIC) mRNA, complete cds.//0//2077bp//99%//U63127
C-PLACE1000133/TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).// 1.80E-62//158aa//81%//P20290
C-PLACE1000142//3-HYDROXYBUTYRYL-COA DEHYDRATASE (EC 4.2.1.55) (CROTONASE).//2.80E-29// 134aa//43%//P52046

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C-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//1.30E-305//1417bp//98%//AF058291
C-PLACE1000185//Homo sapiens mRNA for N-Acetylglucosamine kinase.//4.90E-258//1183bp//99%//AJ242910
C-PLACE1000213//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//4.50E-05//197aa//26%//P08640
C-PLACE1000383//Homo sapiens mRNA for MTMR1 protein.//0//753bp//99%//AJ224979
C-PLACE1000401//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//2.70E-30//352aa//31%//P15151
C-PLACE1000406//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.20E-132//334aa//72%//P23246
C-PLACE1000420//7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE).//2.80E-06//134aa//29%//P53368
C-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//0//2041bp//87%//U35245
C-PLACE1000547//Homo sapiens GDP-mannose pyrophosphorylase B (GMPPB) mRNA, complete cds.//3.70E-241//1124bp//98%//AF135421
C-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.60E-47//207aa//46%//P51522
C-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-BINDING PROTEIN 1).//1.60E-270//437aa//86%//P32455
C-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1540bp//99%//AJ012449
C-PLACE1000610//MSN5 PROTEIN.//0.0000026//136aa//26%//P52918
C-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2.00E-55//779bp//67%//AF044201
C-PLACE1000636//MALE STERILITY PROTEIN 2.//1.20E-39//261aa//27%//Q08891
C-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//0//1992bp//99%//AF180371
C-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLC110F1857Q7 (RZPD Berlin)).//2.10E-277//1260bp//99%//AJ005896
C-PLACE1000706//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.//0//1366bp//99%//AF119043
C-PLACE1000755//Homo sapiens mRNA for Helicase-MOI, complete cds.//4.60E-250//1189bp//97%//AB028449
C-PLACE1000769//Homo sapiens CGI-18 protein mRNA, complete cds.//0//1985bp//98%//AF132952
C-PLACE1000786//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//7.10E-09//59aa//47%//P52734
C-PLACE1000793//NEUROGENIC PROTEIN BIG BRAIN.//1.70E-07//251aa//24%//P23645
C-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR148W.//2.50E-49//181aa//54%//P32899
C-PLACE1000909//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//2.60E-19//404aa//26%//P39010
C-PLACE1000977//BETA-CHIMAERIN (BETA-CHIMERIN).//4.40E-22//129aa//35%//Q03070
C-PLACE1000979//ZINC FINGER PROTEIN 135.//2.50E-153//326aa//64%//P52742
C-PLACE1000987//Rattus norvegicus late gestation lung 2 protein (Lgl2) mRNA, complete cds.//5.90E-278//1476bp//92%//AF110195
C-PLACE1001036//Homo sapiens mRNA for alpha integrin binding protein 63, partial.//0//1988bp//99%//AJ131721
C-PLACE1001054//Homo sapiens mRNA for RuvB-like DNA helicase TIP49b, complete cds.//4.00E-300//1355bp//100%//AB024301
C-PLACE1001062//Homo sapiens mRNA for lysine-ketoglutarate reductase/saccharopine dehydrogenase, partial CDS.//1.60E-207//742bp//99%//AJ007714
C-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//0//1500bp//99%//AF065485
C-PLACE1001104//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//6.80E-18//529aa//23%//Q99323
C-PLACE1001118//ZINC FINGER PROTEIN 135.//5.40E-147//443aa//57%//P52742
C-PLACE1001171//MYOTUBULARIN.//7.10E-84//198aa//73%//Q13496
C-PLACE1001238//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//2.00E-202//1333bp//80%//D14336
C-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.30E-54//257aa//46%//Q04652
C-PLACE1001294//Mus musculus XY body protein (Xybp) mRNA, complete cds.//6.20E-223//1092bp//78%//AF120207
C-PLACE1001304//Homo sapiens C2H2 (Kruppel-type) zinc finger protein mRNA, complete cds.//0//2145bp//

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99%//AF159567
C-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds.//5.90E-228//827bp//99%//AF009615
C-PLACE1001383//ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUIEM).//3.00E-33//138aa//42%//Q61103
C-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//2.30E-61//132aa//46%//Q12929
C-PLACE1001517//Homo sapiens gene for glycosylphosphatidylinositol anchor attachment 1 (GPAA1), complete cds.//4.60E-112//392bp//87%//AB002137
C-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1).//5.70E-130//244aa//99%//Q60809
C-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.40E-118//429aa//48%//P51523
C-PLACE1001672//PROBABLE AMINOTRANSFERASE T01B11.2 (EC 2.6.1.-).//4.30E-66//174aa//45%//P91408
C-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//4.00E-81//263aa//56%//P08635
C-PLACE1001739//PUTATIVE ATP-DEPENDENT RNA HEUCASE PL10.//3.50E-75//439aa//41%//P16381
C-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//2602bp//99%//AF061243
C-PLACE1001771//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//2900bp//99%//AJ006276
C-PLACE1001781//PROBABLE PHOSPHOMANNOMUTASE (EC 5.4.2.8) (PMM).//5.40E-63//427aa//35%//Q57290
C-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//0//1995bp//99%//AF058953
C-PLACE1001845//Mus musculus cyclin ania-6a mRNA, complete cds.//3.30E-31//925bp//62%//AF159159
C-PLACE1001869//L-RIBULOKINASE (EC 2.7.1.16).//2.00E-27//270aa//31%//P94524
C-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1729bp//99%//AF099935
C-PLACE1001983//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//7.50E-16//319aa//26%//P37908
C-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//1.40E-78//496aa//37%//Q49091
C-PLACE1002046//UGATIN (FRAGMENT).//1.70E-240//560aa//80%//Q61211
C-PLACE1002073//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//5.30E-07//188aa//29%//P49606
C-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).//6.50E-58//112aa//100%//O76094
C-PLACE1002140//Rattus norvegicus apelin mRNA, complete cds.//1.40E-43//425bp//74%//AF179679
C-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX COMPONENT SWI3) (TRANSCRIPTION FACTOR TYE2).//0.00005//179aa//23%//P32591
C-PLACE1002395//Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds.//7.90E-100//966bp//75%//AB030505
C-PLACE1002433//CHROMOSOME ASSEMBLY PROTEIN XCAP-E.//5.10E-05//278aa//24%//P50533
C-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1.//4.50E-76//180aa//83%//P41233
C-PLACE1002438//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//4.20E-06//133aa//29%//Q13105
C-PLACE1002450//Human zinc finger protein mRNA, complete cds.//0//2565bp//99%//U69274
C-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//0//2092bp//84%//U69262
C-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds.//1.70E-113//545bp//98%//AF042273
C-PLACE1002500//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//2.90E-58//465bp//80%//U50927
C-PLACE1002532//HOMEOBOX PROTEIN DLX-5.//1.20E-152//289aa//96%//P70396
C-PLACE1002571//ACTIN-LIKE PROTEIN 13E.//5.00E-99//386aa//48%//P45890
C-PLACE1002583//GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2 PRECURSOR (GLUTAMATE RECEPTOR 6) (GLUR-6) (GLUTAMATE RECEPTOR BETA-2) (GLUR BETA-2) (FRAGMENT).//5.60E-34//76aa//98%//P39087
C-PLACE1002591//CORONIN-UKE PROTEIN P57.//4.40E-70//208aa//66%//P31146
C-PLACE1002598//OLIGORIBONUCLEASE (EC 3.1.-.-).//5.50E-17//76aa//56%//P45340
C-PLACE1002655//ADSEVERIN (SCINDERIN) (SC).//2.50E-278//543aa//92%//Q28046
C-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//0//2462bp//89%//AF079765

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C-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//0//1750bp//99%//AF068180
C-PLACE1002714//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//9.40E-13//500aa//21%//Q99323
C-PLACE1002722//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//9.00E-45//305aa//33%//Q15391
C-PLACE1002775//PEREGRIN (BR140 PROTEIN).//3.80E-13//272aa//28%//P55201
C-PLACE1002782//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//3.80E-43//385bp//77%//U50927
C-PLACE1002816//HISTONE DEACETYLASE HDA1.//2.20E-48//217aa//46%//P53973
C-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//5.50E-203//396aa//86%//P51522
C-PLACE1002908//Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds.//0//1654bp//99%//AB028600
C-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4).//1.40E-78//496aa//37%//Q49091
C-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//8.50E-44//225bp//100%//AF032387
C-PLACE1003045//POLYCYSTIN 2 (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE TYPE II PROTEIN) (POLYCYSTWIN) (R48321).//1.70E-05//150aa//24%//Q13563
C-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//2.60E-79//253aa//60%//Q13268
C-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//3.80E-37//143aa//51%//P42743
C-PLACE1003176//Homo sapiens clone pHN1868 tyrosyl-DNA phosphodiesterase protein (TDP1) mRNA, partial cds.//1.70E-148//687bp//99%//AF182003
C-PLACE1003190//SOF1 PROTEIN.//1.90E-110//325aa//48%//P33750
C-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//4.90E-76//309aa//47%//Q15391
C-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN.//7.90E-22//70aa//47%//P21541
C-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//6.90E-206//396aa//86%//P51522
C-PLACE10033537/Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//0//2435bp//99%//U92715
C-PLACE1003366//Homo sapiens otoferlin (OTOF) mRNA, complete cds.//1.40E-78//542bp//67%//AF107403
C-PLACE1003394//Homo sapiens RAB14 protein (RAB14) mRNA, complete cds.//2.60E-139//648bp//99%//AF152463
C-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//1.30E-40//278aa//36%//P40556
C-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSOR.//1.70E-23//322aa//26%//Q13201
C-PLACE1003519//H.sapiens hnRNP-E2 mRNA.//5.10E-218//905bp//99%//X78136
C-PLACE1003521//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//0.0000011//101aa//32%//Q09475
C-PLACE1003537//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).//7.70E-68//404aa//33%//P32802
C-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.//2.60E-93//270aa//66%//P46975
C-PLACE1003602//Homo sapiens mRNA expressed in placenta.//5.90E-278//1275bp//99%//D83200
C-PLACE1003605//HAP5 TRANSCRIPTIONAL ACTIVATOR.//0.00000023//82aa//35%//Q02516
C-PLACE1003611//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.//6.20E-169//683bp//99%//AF191338
C-PLACE1003625//ARMADILLO SEGMENT POLARITY PROTEIN.//3.20E-10//380aa//25%//P18824
C-PLACE1003669//TRICHOHYALIN.//5.60E-09//219aa//30%//P22793
C-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//8.00E-19//209aa//34%//Q08170
C-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA complete cds.//6.20E-282//1316bp//98%//AF053305
C-PLACE1003738//ZINC FINGER PROTEIN 135.//9.60E-118//350aa//46%//P52742
C-PLACE1003760//Homo sapiens tetraspanin TM4-A mRNA, complete cds.//5.20E-289//1313bp//97%//AF133423

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C-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//3.70E-222//651aa//66%//P25500
C-PLACE1003888//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).//6.70E-113//501aa//46%//P10895
C-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE).//1.40E-243//584aa//74%//P17812
C-PLACE1003915//PROBABLE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19) (ARGININE--TRNA UGASE) (ARGRS).//2.40E-108//581aa//40%//Q05506
C-PLACE1003923//Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds.//0//1670bp//99%//AF033120
C-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN).//2.40E-124//326aa//73%//P80385
C-PLACE1004104//Rattus norvegicus rsec5 mRNA, complete cds.//0//2384bp//86%//AF032666
C-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA CHAIN 4).//6.10E-181//340aa//96%//P29387
C-PLACE1004149//Rattus norvegicus GERp95 mRNA, complete cds.//3.30E-41//452bp//65%//AF195534
C-PLACE1004183//Homo sapiens for TOM1-like protein.//0//1279bp//97%//AJ010071
C-PLACE1004197//BUTYROPHILIN PRECURSOR (BT).//4.50E-10//208aa//27%//Q62556
C-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.//0//1882bp//99%//AF069493
C-PLACE1004256//Mus musculus short coiled coil protein SCOCO (Scoc) mRNA, complete cds.//2.00E-93//960bp//76%//AF115778
C-PLACE1004258//Homo sapiens vanilloid receptor-like protein 1 (VRL-1) mRNA//0//1144bp//98%//AF129112
C-PLACE1004270//TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21.-).//9.70E-36//389aa//31%//O15393
C-PLACE1004277//Homo sapiens two pore domain K^+ channel (TASK-2) mRNA, complete cds.//0//1498bp//99%//AF084830
C-PLACE1004302//SOF1 PROTEIN.//1.90E-110//325aa//48%//P33750
C-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//0//1767bp//99%//Y11588
C-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//0//2512bp//99%//AF100153
C-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-).//1.20E-39//385aa//33%//Q63448
C-PLACE1004437//Human NAD^+-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//0//985bp//99%//U49283
C-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0000002//218aa//23%//P25823
C-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)7/2.90E-56//276aa//41%//P51522
C-PLACE1004506//Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds.//2.10E-16//402bp//62%//U90878
C-PLACE1004510//Homo sapiens TATA binding protein associated factor (TAFII150) mRNA, complete cds.//3.40E-227//1037bp//99%//AF040701
C-PLACE1004550//Homo sapiens CGI-20 protein mRNA, complete cds.//3.50E-274//1305bp//97%//AF132954
C-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//525aa//99%//Q10568
C-PLACE1004629//PROTEIN OS-9 PRECURSOR.//7.70E-18//264aa//32%//Q13438
C-PLACE1004646//B.taurus mRNA for retinal pigment epithelial membrane receptor p63.//4.40E-42//985bp//59%//X66277
C-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds.//1.30E-195//982bp//96%//AF035606
C-PLACE1004743//PROBABLE N-END-RECOGNIZING PROTEIN (UBIQUITIN-PROTEIN LIGASE E3 COMPONENT) (N- RECOGNIN).//4.40E-35//578aa//27%//O60152
C-PLACE1004751//Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds.//7.10E-224//790bp//98%//AB022918
C-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//1.90E-32//259aa//32%//P30337
C-PLACE1004793//RETROVIRUS-RELATED ENV POLYPROTEIN.//5.20E-47//577aa//25%//P10267
C-PLACE1004804//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//4.70E-65//695aa//29%//Q01631

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C-PLACE1004814//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//5.90E-19//196aa//36%//Q08170
C-PLACE1004868//MALE STERILITY PROTEIN 27/3.90E-39//261aa//27%//Q08891
C-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//9.30E-11//94aa//47%//O42643
C-PLACE1004918//L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDH-A).//4.90E-48//198aa//44%//P06151
C-PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds//0//1853bp//98%//AF099936
C-PLACE1004937//SEL-10 PROTEIN.//6.30E-125//357aa//58%//Q93794
C-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//2.00E-14//205aa//26%//Q11073
C-PLACE1005052//Homo sapiens CGI-16 protein mRNA, complete cds.//6.6e-313//1413bp//99%//AF132950
C-PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).//2.60E-56//565aa//30%//Q04652
C-PLACE1005176//Homo sapiens hypothalamus protein HT001 mRNA, complete cds.//3.90E-212//1040bp//96%//AF113539
C-PLACE1005187//APAG PROTEIN.//3.80E-13//122aa//36%//P05636
C-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.30E-27//349aa//32%//Q01577
C-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.30E-13//269aa//28%//P53352
C-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2.00E-111//226aa//92%//P08760
C-PLACE1005331//Homo sapiens 7h3 protein mRNA, partial cds.//1.20E-226//748bp//95%//AF209931
C-PLACE1005373//TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//8.60E-09//194aa//27%//O33335
C-PLACE1005467//PENICILLIN-BINDING PROTEIN 4* (PBP 4*) (PBP 4A).//1.10E-09//93aa//31%//P32959
C-PLACE1005494//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//1649bp//99%//AJ006276
C-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//5.60E-52//173aa//57%//Q09251
C-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A.//7.60E-97//1287bp//67%//AJ010046
C-PLACE1005557//60S RIBOSOMAL PROTEIN L27.//1.90E-11//60aa//48%//P46288
C-PLACE1005584//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPQ (P135 PROTEIN) (IER 2.9/ER2.6).//6.80E-09//267aa//30%//P29128
C-PLACE1005611//Mus musculus mRNA for mDj10, complete cds.//2.00E-33//379bp//66%//AB028860
C-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//0//2130bp//99%//AF083255
C-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE).//2.10E-148//321aa//83%//P31350
C-PLACE10057277/Homo sapiens STRIN protein (STRIN) mRNA, complete cds.//2.00E-118//378bp//98%//AF162680
C-PLACE1005739//INTERFERON-GAMMA INDUCIBLE PROTEIN MG11///1.30E-237//585aa//72%//Q60710
C-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//2.50E-79//209aa//53%//P08635
C-PLACE1005803//Homo sapiens mRNA for transcription factor (SMIF gene).//0//1985bp//99%//AJ275986
C-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.10E-217//994bp//99%//AF027156
C-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2040bp//99%//AF065482
C-PLACE1005876//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//730aa//99%//Q10568
C-PLACE1005890//BEM46 PROTEIN (FRAGMENT).//9.90E-42//224aa//43%//P54069
C-PLACE1005921//AIG1 PROTEIN.//3.00E-31//284aa//31%//P54120
C-PLACE1005951//Homo sapiens prolactin regulatory element-binding protein (PREB) mRNA, complete cds.//1.10E-264//661bp//99%//AF203687
C-PLACE1005953//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//6.70E-30//198aa//37%//P43636
C-PLACE1005955/VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)//5.40E-54//455aa//32%//P14904

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C-PLACE1005966//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAFII-90)7/1.40E-07//254aa//25%//P38129
C-PLACE1006003//Homo sapiens CGI-94 protein mRNA, complete cds.//2.40E-177//829bp//99%//AF151852
C-PLACE1006011//Homo sapiens mRNA for poly(ADP-ribose) polymerase-2.//0//1564bp//99%//AJ236876
C-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.70E-161//744bp//99%//X99906
C-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.50E-148//681bp//99%//AF039023
C-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).//2.00E-28//236aa//30%//P98110
C-PLACE1006167//PAF1 PROTEIN.//7.30E-15//437aa//24%//P38351
C-PLACE1006170//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//1.70E-169//373aa//88%//P17427
C-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//2.70E-116//496aa//48%//Q09747
C-PLACE1006239//BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).//2.00E-16//244aa//31%//P28675
C-PLACE1006288//VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 1 (VDAC1) (PLASMALEMMAL PORIN) (OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN) (PORIN 31HL) (PORIN 31HM).//4.60E-117//147aa//80%//P21796
C-PLACE1006318//Mus musculus skm-BOP2 (Bop) mRNA, complete cds.//3.00E-07//376bp//59%//U76374
C-PLACE1006335//Homo sapiens NY-REN-50 antigen mRNA, partial cds.//0//1649bp//99%//AF155112
C-PLACE1006368//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//1.30E-18//460aa//24%//Q00547
C-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//0//1168bp//99%//AF062085
C-PLACE1006438//ZINC FINGER PROTEIN 165.//2.50E-45//122aa//43%//P49910
C-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.20E-83//313aa//49%//P27550
C-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//7.70E-55//142aa//85%//Q90595
C-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.10E-229//367aa//96%//Q00004
C-PLACE1006492//Homo sapiens transmembrane protein 2 (TMEM2) mRNA, complete cds.//0//2618bp//99%//AF137030
C-PLACE1006506//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.//0//2170bp//99%//AF191338
C-PLACE1006531//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//1967bp//99%//AF093097
C-PLACE1006534//POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41)(PROTEIN-UDP ACETYLGALACTOSAMINYLTRANSFERASE)(UDP-GALNAC:POLYPEPTIDE, N-ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1).//8.30E-08//100aa//41%//Q10472
C-PLACE1006552//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//1.20E-09//426aa//21%//P39922
C-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//0//1464bp//99%//U97670
C-PLACE1006626//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%//AB028449
C-PLACE1006678//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-24//734bp//62%//AB015630
C-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//6.90E-13//177aa//33%//Q59263
C-PLACE1006754//BILIARY GLYCOPROTEIN 1 PRECURSOR (BGP-1) (ANTIGEN CD66) (CD66A ANTIGEN).//6.20E-63//191aa//43%//P13688
C-PLACE1006819//UNE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.80E-213//232aa//80%//P08547
C-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN).//2.00E-15//188aa//29%//P35123
C-PLACE1006878//TRNA-SPLICING ENDONUCLEASE SUBUNIT SEN2 (EC 3.1.27.9) (TRNA-INTRON ENDONUCLEASE).//1.90E-08//122aa//36%//P16658
C-PLACE1006917//HSH49 PROTEIN.//5.50E-12//97aa//35%//Q99181
C-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III.//6.70E-48//278aa//41%//

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Q10000
C-PLACE1006956//ATP-DEPENDENT PERMEASE MDL1.//1.30E-86//522aa//36%//P97998
C-PLACE1006958//Homo sapiens mRNA for heat shock protein apg-1, complete cds.//0//1770bp//99%//AB023421
C-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12) (DER12).//3.20E-35//180aa//33%//Q14542
C-PLACE1007105//Homo sapiens muskelin (MKLN1) mRNA, complete cds.//0//2449bp//98%//AF047489
C-PLACE1007140//TRICHOHYALIN.//1.30E-25//816aa//22%//P37709
C-PLACE1007226//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.-) (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1.00E-42//370aa//31%//P54304
C-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//6.50E-216//1068bp//96%//D50495
C-PLACE1007243//UNC-47 PROTEIN.//1.70E-07//211aa//27%//P34579
C-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//0//2052bp//99%//Y15908
C-PLACE1007317//Drosophila melanogaster Adrift (adrift) mRNA, complete cds.//4.10E-17//1037bp//56%//AF117649
C-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//0//2366bp//99%//AF096870
C-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13.//0.00000044//127aa//30%//P27715
C-PLACE1007409//WHTTE PROTEIN.//1.10E-64//428aa//32%//Q17320
C-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP).//8.80E-25//140aa//35%//P27487
C-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//5.40E-53//426aa//33%//P52734
C-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19).//1.40E-85//385aa//45%//P08728
C-PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds.//8.9e-316//1485bp//98%//AF159164
C-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1.00E-49//361aa//36%//P34537
C-PLACE1007598//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.60E-143//666aa//44%//Q99676
C-PLACE1007632//POLIOVIRUS RECEPTOR PRECURSOR.//1.00E-07//228aa//31%//P32506
C-PLACE1007649//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//4.50E-05//197aa//26%//P08640
C-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//8.70E-09//279aa//28%//Q26457
C-PLACE1007697//GCN20 PROTEIN.//7.60E-119//717aa//38%//P43535
C-PLACE1007705//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.//1.10E-184//1096bp//82%//AB033922
C-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//3431bp//99%//AF061243
C-PLACE1007729//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.50E-44//231aa//42%//P10265
C-PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds.//0//1836bp//99%//AB019602
C-PLACE1007897//Homo sapiens FLASH mRNA, complete cds.//0//2145bp//99%//AF154415
C-PLACE1007946//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//2.60E-14//370aa//25%//Q99323
C-PLACE1007954//HYPOTHETICAL 45.5 KD PROTEIN IN FIG1-GIP1 INTERGENIC REGION.//6.70E-13//168aa//31%//P38226
C-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//0//2252bp//99%//AF084530
C-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//0//2300bp//99%//AF079529
C-PLACE1007969//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.10E-36//202aa//48%//P52272
C-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSYN-110) (SYNAPTIC DENSITY PROTEIN PSD-93).//6.10E-14//128aa//39%//Q63622
C-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NUCLEOPORIN) (P105).//4.6e-318//613aa//94%//P52590

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C-PLACE1008080//Homo sapiens mRNA for HEXIM1 protein, complete cds.//0//2152bp//99%//AB021179
C-PLACE1008111//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).//3.00E-25//208aa//37%//Q03326
C-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//1.30E-24//395aa//31%//Q09531
C-PLACE1008177//TRICHOHYALIN.//2.30E-29//487aa//26%//P37709
C-PLACE1008201//Rattus rattus zinc finger protein, complete cds.//0//2265bp//83%//L23077
C-PLACE1008244//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//9.50E-21//148aa//38%//Q00808
C-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.30E-283//671aa//77%//P53620
C-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-).//2.30E-18//162aa//37%//P12689
C-PLACE1008309//Rattus norvegicus putative four repeat ion channel mRNA, complete cds.//5.20E-137//672bp//77%//AF078779
C-PLACE1008330//EOSINOPHIL LYSOPHOSPHOLIPASE (EC 3.1.1.5) (CHARCOT-LEYDEN CRYSTAL PROTEIN) (LYSOLECITHIN ACYLHYDROLASE) (CLC) (GALACTIN-10).//2.20E-23//94aa//47%//Q05315
C-PLACE1008356//Homo sapiens meningioma-expressed antigen 5 (MEA5) mRNA, partial cds.7/1.90E-170//780bp//100%//AF036144
C-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).//5.30E-26//309aa//30%//Q04652
C-PLACE1008398//GENE 33 POLYPEPTIDE.//7.30E-114//243aa//87%//P05432
C-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRAN-SCYTOSIS ASSOCIATED PROTEIN) (TAP).//0//698aa//95%//P41541
C-PLACE1008426//RESTIN (CYTOPLASMIC LINKER PROTEIN-170) (CLIP-170).//1.80E-11//365aa//25%//O42184
C-PLACE1008429//ANKYRIN HOMOLOG PRECURSOR.//3.10E-11//189aa//32%//Q06527
C-PLACE1008465//Homo sapiens mRNA for rapa-1 (rapa gene).//6.60E-243//1102bp//99%//AJ277275
C-PLACE1008533//101 KD MALARIA ANTIGEN (P101) (ACIDIC BASIC REPEAT ANTIGEN).//1.10E-09//62aa//48%//P22620
C-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//7.80E-236//453aa//96%//P37199
C-PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.//0//1850bp//99%//AJ006591
C-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (III HEAVY CHAIN H2).//5.20E-90//483aa//38%//O02668
C-PLACE1008650//PRL1/PRL2-LIKE PROTEIN.//2.00E-127//354aa//62%//O13615
C-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//0//3002bp//99%//AF03 8406
C-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds.//0//1670bp//99%//AF060543
C-PLACE1008808//Homo sapiens mRNA for cell cycle checkpoint protein radIA.//2.30E-269//1225bp//99%//AJ004974
C-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//8.80E-268//1171bp//90%//AF032668
C-PLACE1009020//NIFS PROTEIN.//3.90E-55//279aa//41%//P12623
C-PLACE1009027//Homo sapiens mRNA for doublecortin.//0//1919bp//99%//AJ003112
C-PLACE1009060//BRO1 PROTEIN.//6.70E-19//567aa//24%//P48582
C-PLACE1009094//FURIN-LIKE PROTEASE 2 PRECURSOR (EC 3.4.21.75) (FURIN 2).//1.90E-44//480aa//30%//P30432
C-PLACE1009099//ZINC FINGER PROTEIN 41 (FRAGMENT).//1.10E-179//452aa//67%//P51814
C-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//0//2529bp//99%//AF035586
C-PLACE1009130/UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.2.-) (ONCOGENIC PROTEIN-ASSOCIATED PROTEIN E6-AP).//2.00E-68//181aa//43%//Q05086
C-PLACE1009158//Mus musculus mRNA for death inducer-obliterator-1 (Dio-1).//5.40E-200//1790bp//75%//AJ238332
C-PLACE1009186//Homo sapiens small zinc finger-like protein (TIM9b) mRNA, complete cds.//9.60E-255//1179bp//98%//AF150105
C-PLACE1009246//POLLEN SPECIFIC PROTEIN SF3.//4.40E-16//82aa//43%//P29675
C-PLACE1009298//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//2.00E-78//262aa//43%//P34110
C-PLACE1009308//GLUCOSE REPRESSION MEDIATOR PROTEIN.//4.00E-06//439aa//23%//P14922
C-PLACE1009319//Rattus norvegicus outer membrane protein (OMP25) mRNA, complete cds; nuclear gene for mitochondrial product.//2.10E-132//1229bp//75%//AF107295

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C-PLACE1009368//METAL HOMEOSTASIS FACTOR ATX27/2.50E-10//151aa//29%//Q12067
C-PLACE1009398//ZINC FINGER PROTEIN 135.//6.20E-97//361aa//51%//P52742
C-PLACE1009404//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I.//4.70E-08//165aa//33%//Q09820
C-PLACE1009443//Mus musculus F-box protein FBL8 mRNA, complete cds.//1.00E-173//1367bp//77%//AF176523
C-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//7.80E-71//82aa//89%//P42356
C-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.10E-289//550aa//93%//P54319
C-PLACE1009476//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//3.90E-40//179aa//37%//P34580
C-PLACE1009477//Homo sapiens ubiquitin-fusion degradation protein 2 (UFD2) mRNA, complete cds.//6.60E-147//592bp//99%//AF043117
C-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FACTOR)7/8.10E-99//228aa//75%//Q99418
C-PLACE1009571//Homo sapiens PTD002 mRNA, complete cds.//5.90E-185//857bp//99%//AF078857
C-PLACE1009596//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.10E-54//291aa//40%//Q00808
C-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.30E-60//209aa//41%//P25159
C-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN).//1.50E-285//538aa//99%//P55161
C-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//0//1854bp//100%//AF062534
C-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN CHROMOSOME I.//7.00E-33//166aa//43%//Q09876
C-PLACE1009721//MSF1 PROTEIN.//1.70E-22//176aa//33%//P35200
C-PLACE1009731//AIG1 PROTEIN.//1.60E-22//274aa//28%//P54120
C-PLACE1009763//Homo sapiens mRNA for Nedd8-activating enzyme hUba3, complete cds.//4.30E-294//1329bp//100%//AB012190
C-PLACE1009798//RLR1 PROTEIN.//1.60E-18//270aa//23%//P53552
C-PLACE1009845//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//2.30E-59//405aa//33%//P38968
C-PLACE1009861//CATHEPSIN B-LIKE CYSTEINE PROTEINASE 6 PRECURSOR (EC 3.4.22.-).//6.50E-28//209aa//38%//P43510
C-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC REGION.//1.90E-108//277aa//43%//P53145
C-PLACE1009925//Homo sapiens RNA helicase (RIG-I) mRNA, complete cds.//0//1730bp//99%//AF038963
C-PLACE1009992//LIMULUS CLOTTING FACTOR C PRECURSOR (EC 3.4.21.84).//4.60E-59//450aa//34%//P28175
C-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds.//5.20E-70//736bp//73 %//U48288
C-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//6.00E-279//1402bp//94%//X84692
C-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2019bp//99%//AF065482
C-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.40E-268//506aa//98%//Q62671
C-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//7.30E-114//537aa//44%//Q04652
C-PLACE1010134//TRANSCRIPTION REGULATORY PROTEIN SNF2 (SWI/SNF COMPLEX COMPONENT SNF2) (REGULATORY PROTEIN SWI2) (REGULATORY PROTEIN GAM1) (TRANSCRIPTION FACTOR TYE3).//1.70E-20//156aa//42%//P22082
C-PLACE1010148//CYUCIN I (MULTIPLE-BAND POLYPEPTIDE I).//4.60E-07//431aa//23%//P35662
C-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPUCING COMPONENT, 35 KD) (PR264 PROTEIN).//9.80E-11//95aa//49%//Q01130
C-PLACE1010231//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR).//5.1 OE-27//371aa//28%//Q14246
C-PLACE1010261//SEGREGATION DISTORTER PROTEIN.//1.60E-77//214aa//62%//P25722
C-PLACE1010310//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//1.20E-18//467aa//30%//P46804
C-PLACE1010321//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//1.10E-09//350aa//22%//P52178
C-PLACE1010362//1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE PRECURSOR (EC 3.1.4.10) (PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC).//2.00E-09//126aa//29%//P34024
C-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds//0//2082bp//91%//AF003927

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C-PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induced by progesterone), complete cds.//0//1981 bp//99%//AB022718
C-PLACE1010529//Homo sapiens TANK binding kinase TBK1 (TBK1) mRNA, complete cds.//0//1750bp//99%//AF191838
C-PLACE1010547//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//1.20E-07//616aa//24%//P25386
C-PLACE1010579//Homo sapiens CED-6 protein (CED-6) mRNA, complete cds.//8.80E-300//1359bp//99%//AF191771
C-PLACE1010599//Homo sapiens Pex14 mRNA for peroxisomal membrane anchor protein, complete cds.//0//1904bp//99%//AB017546
C-PLACE1010622//TROPONIN T, CARDIAC MUSCLE ISOFORMS (TNTC).//0.00000016//120aa//28%//P02642
C-PLACE1010628//Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds.//7.50E-08//324bp//64%//AF109907
C-PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS 13.//5.70E-75//423aa//39%//Q01755
C-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//1.80E-222//808aa//52%//Q09332
C-PLACE1010702//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//5.20E-151//427aa//55%//P28160
C-PLACE1010720//Homo sapiens mRNA for chromosome-associated polypeptide-C, complete cds.//4.00E-299//1091bp//99%//AB019987
C-PLACE1010743//Homo sapiens myosin-IXb splice variant (Myo9b) mRNA, partial cds.//8.90E-91//668bp//82%//AF020267
C-PLACE1010761//Homo sapiens mRNA for cisplatin resistance-associated overexpressed protein, complete cds.//0//1448bp//99%//AB034205
C-PLACE1010771//M.musculus HCNGP mRNA.//7.40E-168//966bp//89%//X68061
C-PLACE1010811//Rattus norvegicus mRNA for protein encoded by bdeight gene, partial.//1.60E-217//858bp//87%//AJ010392
C-PLACE1010833//CALTRACTIN(CENTRIN).//0.0000001//154aa//28%//P41209
C-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.30E-143//407aa//58%//Q05481
C-PLACE1010896//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//1.50E-25//583aa//23%//P35580
C-PLACE1010926//HYPOTHETICAL 72.2 KD PROTEIN C12C2.05C IN CHROMOSOME II.//7.60E-23//103aa//53%//Q09746
C-PLACE1010942//Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds.//0//1440bp//99%//AF114487
C-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//5.30E-98//297aa//48%//P45890
C-PLACE1011041//Homo sapiens mRNA for BAP2-alpha protein, complete cds.//0//1701bp//97%//AB015019
C-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1 (EC 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PLC-154).//0//646aa//97%//P10894
C-PLACE1011056//HISTONE HI, GONADAL.//6.80E-13//154aa//37%//P02256
C-PLACE1011109//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEFG).//1.50E-22//63aa//88%//Q07803
C-PLACE1011114//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//2.90E-71//190aa//44%//Q03532
C-PLACE1011160//Homo sapiens HFB30 mRNA, complete cds.//0//1691bp//99%//AB022663
C-PLACE1011185//INSERTION ELEMENT IS1 PROTEIN INSB.//1.30E-89//167aa//100%//P03830
C-PLACE1011219//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).//3.20E-12//212aa//29%//Q03326
C-PLACE1011229//Homo sapiens ubiquitin-specific protease homolog (UPH) mRNA, complete cds.//2.30E-152//701bp//99%//AF153604
C-PLACE1011310//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE.//3.50E-20//496aa//25%//P10587
C-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//7.20E-151//697bp//99%//AF102265
C-PLACE1011340//Homo sapiens IDN3-B mRNA, complete cds.//1.20E-74//380bp//97%//AB019602
C-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2).//1.70E-78//383aa//39%//Q61703
C-PLACE1011399//Homo sapiens CGI-72 protein mRNA, complete cds.//3.20E-90//427bp//99%//AF151830
C-PLACE1011433//TRANSCRIPTION FACTOR IIIA (FACTOR A) (TFIIIA).//3.00E-10//236aa//25%//P34695
C-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2040bp//99%//AF065482
C-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//

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4.90E-11//147aa//32%//P52178
C-PLACE1011576//Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds.//0//1791bp//82%//L11672
C-PLACE1011586//Rattus norvegicus clone C53 CDK5 activator-binding protein mRNA, complete cds7/4.10E-259//1538bp//87%//AF177476
C-PLACE1011635//Homo sapiens heparan sulfate D-glucosaminyl 3-O-sulfotransferase-3B (3OST3B1) mRNA, complete cds.//0//1559bp//99%//AF105377
C-PLACE1011664//CROOKED NECK PROTEIN.//1.60E-187//505aa//64%//P17886
C-PLACE1011858//Homo sapiens BAG-family molecular chaperone regulator-2 mRNA, complete cds.//1.30E-255//1179bp//99%//AF095192
C-PLACE1011896//Mus musculus Wnt10a mRNA, complete cds.//2.60E-287//1820bp//85%//U61969
C-PLACE1011922//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//1.30E-15//409aa//27%//P35580
C-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//0//2782bp//99%//AF059617
C-PLACE101-2031//Homo sapiens sorting nexin 13 (SNX13) mRNA, partial cds.//0//1701bp//100%//AF121862
C-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//2.60E-42//104aa//49%//Q09475
C-PLACE2000015//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN).//1.10E-116//364aa//45%//P42566
C-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, complete cds.//2.70E-107//981bp//74%//AF082556
C-PLACE2000034//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//2.20E-29//212aa//35%//P10586
C-PLACE2000039//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C).//6.10E-293//388aa//99%//P38650
C-PLACE2000062//Homo sapiens mRNA for type II membrane protein similar to HIV gp120-binding C-type lectin, complete cds, clone:HP01347.//6.30E-166//656bp//94%//AB015629
C-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0//3174bp//99%//AF027219
C-PLACE2000164//TIPD PROTEIN.//2.10E-59//481aa//33%//O15736
C-PLACE2000216//SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1).//6.60E-115//226aa//99%//Q01082
C-PLACE2000246//RING CANAL PROTEIN (KELCH PROTEIN).//6.00E-57//239aa//34%//Q04652
C-PLACE2000274//DYNEIN BETA CHAIN, CILIARY.//2.20E-167//880aa//37%//P23098
C-PLACE2000341//Homo sapiens sodium-dependent multivitamin transporter (SMVT) mRNA, complete cds.//0//1554bp//99%//AF069307
C-PLACE2000371/TENSIN.//2.90E-78//561aa//37%//Q04205
C-PLACE2000373//F-SPONDIN PRECURSOR.//8.60E-16//371aa//28%//P35446
C-PLACE2000398//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//6.30E-37//90aa//98%//P10586
C-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//1.60E-14//180aa//39%//P14209
C-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//9.90E-229//821aa//54%//Q09996
C-PLACE2000411//Homo sapiens epsin 2b mRNA, complete cds.//3.80E-271//642bp//99%//AF062085
C-PLACE2000427//PROBABLE HELICASE MOT1.//1.20E-26//200aa//27%//P32333
C-PLACE2000438//POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1).//2.10E-86//348aa//41%//Q10472
C-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//2.50E-25//165aa//40%//P33450
C-PLACE2000477//Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds.//6.70E-127//671bp//94%//AF072733
C-PLACE3000009//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1)(FRAGMENT).//3.50E-30//400aa//30%//P11414
C-PLACE3000020//Homo sapiens type III adenylyl cyclase (AC-III) mRNA, complete cds.//0//2253bp//99%//AF033861
C-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//0//1979bp//90%//Y17267
C-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC157/1.90E-08//281aa//22%//P22224
C-PLACE3000145//TENSIN.//1.00E-108//277aa//75%//Q04205

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C-PLACE3000147//Homo sapiens metalloproteinase with thrombospondin type 1 motifs ADAMTS1 (ADAMTS1) mRNA, complete cds.//0//2043bp//99%//AF170084
C-PLACE3000169//ZINC FINGER PROTEIN 135.//2.50E-90//358aa//47%//P52742
C-PLACE3000218//Homo sapiens putative protein O-mannosyltransferase (POMT2) mRNA, complete cds.//0//1862bp//98%//AF105020
C-PLACE3000242//Human trophinin mRNA, complete cds.//0//2290bp//99%//U04811
C-PLACE3000244//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//0//1435aa//92%//P53995
C-PLACE3000254//Homo sapiens transcriptional activator SRCAP (SRCAP) mRNA, complete cds.//0//4583bp//83%//AF143946
C-PLACE3000339//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.60E-08//359aa//23%//P08640
C-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE SULU (EC 2.7.1.-).//1.00E-54//418aa//38%//P46549
C-PLACE3000416//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//1.80E-141//565bp//98%//AB029290
C-PLACE3000477//Homo sapiens phosphoprotein pp75 mRNA, partial cds.//0//3012bp//98%//AF153085
C-PLACE4000009//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//2.90E-54//626aa//29%//P35580
C-PLACE4000014//X-LINKED HEUCASE II (X-LINKED NUCLEAR PROTEIN) (XNP).//3.10E-111//348aa//41%//P46100
C-PLACE4000052//Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA, complete cds.//0//4661bp//99%//AF165281
C-PLACE4000063//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//1.70E-15//740aa//23%//P08640
C-PLACE4000100//Homo sapiens hydroxypyruvate reductase (GRHPR) gene, complete cds.//0//4199bp//97%//AF146689
C-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds.//1.60E-86//190aabp//88%//AF091234
C-PLACE4000156//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.40E-235//516aa//51%//Q05481
C-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//7.00E-22//369aa//25%//P52746
C-PLACE4000211//Homo sapiens BAZ2A mRNA for bromodomain adjacent to zinc finger domain 2A, complete cds.//0//5709bp//96%//AB032254
C-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds.//0//2567bp//88%//AF030430
C-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD protem.//0//5143bp//90%//Z70200
C-PLACE4000261//PEREGRIN (BR140 PROTEIN).//9.50E-10//128aa//34%//P55201
C-PLACE4000269//Rattus norvegicus rexo70 mRNA, complete cds.//0//2034bp//89%//AF032667
C-PLACE4000326//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1).//8.10E-24//319aa//31%//P30771
C-PLACE4000369//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP240 mRNA, complete cds.//1.40E-185//1135bp//67%//AF117754
C-PLACE4000401//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//7.20E-22//54aa//62%//Q01576
C-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//0//5142bp//90%//Z70200
C-PLACE4000450//Homo sapiens BAZ2A mRNA for bromodomain adjacent to zinc finger domain 2A, complete cds.//0//5709bp//96%//AB032254
C-PLACE4000489//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1)7/5.70E-60//254aa//44%//P13002
C-PLACE4000522//NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (XOTCH PROTEIN).//2.40E-191//828aa//48%//P21783
C-PLACE4000548//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.70E-13//784aa//21%//P08640
C-PLACE4000558//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE FAF) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF) (DEUBIQUITINATING ENZYME FAF) (FAT FACETS PROTEIN).//1.50E-26//252aa//35%//P55824
C-PLACE4000581//FIBROPELLIN I PRECURSOR (EPIDERMAL GROWTH FACTOR-RELATED PROTEIN 1) (UEGF-1).//9.30E-70//226aa//52%//P10079
C-PLACE4000650//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).//7.90E-17//201aa//34%//

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P49816
C-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//0//6340bp//87%//Y17267
C-SKNMC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//5.50E-35//431aa//29%//O60100
C-SKNMC1000013//Homo sapiens ATP-binding cassette protein M-ABC1 mRNA, nuclear gene encoding mitochondrial protein, complete cds7/0//2384bp//99%//AF047690
C-SKNMC1000046//Homo sapiens liprin-alpha3 mRNA, partial cds.//1.90E-162//749bp//99%//AF034800
C-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (M-TYPE).//3.20E-41//87aa//98%//P17655
C-SKNMC1000091//Homo sapiens mRNA for leucine-zipper protein, complete cds.//6.10E-190//872bp//99%//AB021663
C-THYRO1000034/TRICHOHYALIN.//9.40E-10//176aa//30%//P37709
C-THYRO1000072//MYOSIN UGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//3.40E-16//201aa//29%//P11799
C-THYRO1000085//PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B.//2.00E-72//155aa//92%//Q06710
C-THYRO1000121//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//0//1737bp//87%//U49055
C-THYRO1000132//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//1.10E-159//824bp//95%//U97018
C-THYRO1000173//Homo sapiens AP-mu chain family member mulB (HSMU1B) mRNA, complete cds.//0//1713bp//99%//AF020797
C-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//0//2362bp//99%//AJ005698
C-THYRO1000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.00E-118//239aa//66%//P51523
C-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//0//2161bp//99%//AB016068
C-THY-RO1000327//Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds.//0//1567bp//99%//AF124145
C-THYRO1000343//ATROPHIN-1 (DENTATORUBRAL-PALUDOLUYSIAN ATROPHY PROTEIN).//4.90E-06//280aa//31%//P54259
C-THYRO1000358//SELENIUM-BINDING LIVER PROTEIN.//2.30E-229//237aa//79%//P17563
C-THYRO1000394//Homo sapiens peroxisomal membrane protein PMP 24 mRNA, complete cds.//1.20E-299//1325bp//99%//AF072864
C-THYRO1000395//Homo sapiens actin-binding protein (IPP) mRNA, complete cds.//0//2092bp//99%//AF156857
C-THYRO1000401//Human TcD37 homolog (HTcD37) mRNA, partial cds.//1.10E-90//430bp//99%//U67085
C-THYRO1000488//Homo sapiens HFB30 mRNA, complete cds.//0//2254bp//100%//AB022663
C-THYRO1000501//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//4.20E-98//408aa//42%//P19474
C-THYRO1000569//Mus musculus hematopoietic zinc finger protein mRNA, complete cds.//0//1557bp//91%//AF118566
C-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds.//0//1901bp//99%//AF075587
C-THYRO1000605//Homo sapiens histone acetyltransferase (HBOa) mRNA, complete cds.//0//3080bp//99%//AF140360
C-THYRO1000662//Homo sapiens XPV mRNA for DNA polymerase eta, complete cds.//0//2341 bp//99%//AB024313
C-THYRO1000666//Mus musculus mRNA for kinesin like protein 9.//0//2001bp//86%//AJ132889
C-THYRO1000684//Homo sapiens BAG-family molecular chaperone regulator-5 mRNA, complete cds.//0//3347bp//99%//AF095195
C-THYRO1000748//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//3.30E-96//335aa//52%//P98171
C-THYRO1000756//ALPHA-N-ACETYLGALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (EC 2.4.99.-) (ST6GALNACIII)(STY).//1.80E-55//243aa//42%//Q64686
C-THYRO1000783//Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds.//2.40E-157//1656bp//70%//U37373
C-THYRO1000852//Human branched-chain amino acid aminotransferase (ECA40) mRNA, complete cds.//1.40E-137//689bp//96%//U62739
C-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//0//2387bp//99%//AF079529

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C-THYRO11000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).// 7.50E-57//315aa//43%//P32322
C-THYRO1000951//DIHYDROXYACETONE KINASE 2 (EC 2.7.1.29) (GLYCERONE KINASE).//5.00E-83// 566aa//37%//P43550
C-THYRO1000983//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//6.30E-17//143aa//39%//P35132
C-THYRO1001003//UBIQUITIN-CONJUGATING ENZYME E2-21.2 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN UGASE) (UBIQUITIN CARRIER PROTEIN).//5.90E-14//84aa//41%//P52491
C-THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//8.40E-12//167aa//29%//P31948
C-THYRO1001100//ZINC FINGER X-UNKED PROTEIN ZXDA (FRAGMENT).//1.20E-67//245aa//62%//P98168
C-THYRO1001120//Homo sapiens deltex (Dx) mRNA, complete cds.//1.30E-110//1947bp//65%//AF053700
C-THYRO1001134//Homo sapiens CGI-78 protein mRNA, complete cds.//0//1898bp//99%//AF151835
C-THYRO1001189//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-200//546aa// 62%//Q05481
C-THYRO1001204//Homo sapiens cathepsin Z precursor (CTSZ) gene, exons 4, 5, and 6 and complete cds; and TH1 gene partial sequence.//3.80E-100//478bp//99%//AF136276
C-THYRO1001287//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE) (FRAGMENT).//3.40E-51//429aa//33%//P45701
C-THYRO1001313//Homo sapiens sorting nexin 11 (SNX11) mRNA, complete cds.//0//2330bp//94%//AF121861
C-THYRO1001347//Homo sapiens RAN binding protein 16 mRNA, complete cds.//2.00E-263//3101bp//68%// AF064729
C-THYRO1001374//CYTOSOLIC ACYL COENZYME A THIOESTER HYDROLASE (EC 3.1.2.2) (LONG CHAIN ACYL-COA THIOESTER HYDROLASE) (CTE-II).//1.80E-13//361aa//22%//O00154
C-THYRO1001405//PLECTIN.//6.90E-19//450aa//27%//P30427
C-THYRO1001406//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).//1.10E-131//219aa//81%// O70503
C-THYRO1001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//2.70E-171//559aa//59%//P35580
C-THYRO1001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//0//1784bp// 99%//AJ002190
C-THYRO1001656//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.//4.10E-273//1947bp// 82%//AF175968
C-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//0//1820bp//99%// AJ225089
C-THYRO1001703//NIFR3-LIKEPROTEIN.//2.90E-32//282aa//32%//P45672
C-THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).//9.30E-34//220aa//38%//Q04652
C-THYRO1001738//TUBULIN--TYROSINE LIGASE (EC 6.3.2.25) (TTL).//2.40E-20//217aa//30%//P38584
C-THYRO1001809//MYOCYTE NUCLEAR FACTOR (MNF).//1.40E-74//158aa//89%//P42128
C-Y79AA1000013//Mus musculus RING finger protein A07 mRNA, complete cds.//8.90E-205//1435bp//81%// AF171060
C-Y79AA1000033//Homo sapiens CARD4 mRNA, complete cds.//0//2929bp//96%//AF126484
C-Y79AA1000037//DNA-BINDING PROTEIN BMI-1.//2.40E-30//80aa//60%//P25916
C-Y79AA1000059//Homo sapiens aryl-hydrocarbon interacting protein-like 1 (AIPL1) gene, complete cds.//0// 980bp//96%//AF180472
C-Y79AA1000181//Homo sapiens CGI-01 protein mRNA, complete cds.//0//1858bp//99%//AF132936
C-Y79AA1000214//Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds.//7.10E-71//345bp// 100%//AF081192
C-Y79AA1000231//Homo sapiens nucleolar protein NOP5/NOP58 mRNA, complete cds.//0//1515bp//99%// AF123534
C-Y79AA1000268//Mus musculus Nip21 mRNA, complete cds.//2.10E-50//648bp//64%//AF035207
C-Y79AA1000313//CALPHOTIN.//0.000011//336aa//23%//Q02910
C-Y79AA1000328//SEL-10 PROTEIN.//0.000000067//219aa//25%//Q93794
C-Y79AA1000342//Homo sapiens Ciz1 mRNA, complete cds.//0//2644bp//81%//AB030835
C-Y79AA1000346//Homo sapiens nonclathrin coat protein gamma2-COP mRNA, complete cds.//0//2520bp//99%// AF157833
C-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//0//2048bp//93%//X84692
C-Y79AA1000368//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//4.00E-20//261aa//27%//P25343
C-Y79AA1000469//Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete

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cds.//8.30E-252//1207bp//85%//U41736
C-Y79AA1000540//CELL POLARITY PROTEIN TEA1.//2.10E-12//211aa//33%//P87061
C-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT)7/0//652aa//98%//P17427
C-Y79AA1000589//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//2.40E-27//216aa//34%//P28320
C-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds.//2.00E-287//2031bp//82%//AF060503
C-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1.//5.80E-254//1477bp//84%//X69942
C-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds.//0//1594bp//99%//AF093670
C-Y79AA1000748//Rattus norvegicus clone C42 CDK5 activator-binding protein mRNA, complete cds.//6.60E-286//1832bp//84%//AF177477
C-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//4.90E-91//200aa//64%//Q61990
C-Y79AA1000782//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3.00E-37//469aa//27%//P49902
C-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//1.10E-236//1076bp//99%//AF098799
C-Y79AA1000794//Homo sapiens actin-associated protein 2E4/kaptin (2E4) mRNA, 2E4-1 allele, complete cds.//0//1610bp//99%//AF105369
C-Y79AA1000800//Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds.//1.60E-284//1288bp//99%//AF072733
C-Y79AA1000833//TUBULIN ALPHA-1 CHAIN.//5.00E-173//220aa//79%//P05209
C-Y79AA1000962//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II)7/4.20E-17//430aa//27%//Q99323
C-Y79AA1000966//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%//AF100757
C-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//3.90E-248//1468bp//87%//U38253
C-Y79AA1000985//Human centrosomal protein kendrin mRNA, complete cds.//4.70E-151//985bp//87%//U52962
C-Y79AA1001048//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD).//3.10E-138//583aa//47%//P45953
C-Y79AA1001211//Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds.//0//1435bp//99%//AF139658
C-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HYDROXYSTEROID DEHYDROGENASE 1).//7.70E-50//228aa//42%//P51657
C-Y79AA1001236//Homo sapiens cell division protein mRNA, complete cds.//0//1612bp//99%//AF063015
C-Y79AA1001299//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//996bp//99%//AJ011738
C-Y79AA1001312//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46).//0.000000023//193aa//30%//Q03309
C-Y79AA1001323//Mus musculus mRNA for GSG1, complete cds.//3.30E-172//1171bp//83%//D87325
C-Y79AA1001384//Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds.//0//4708bp//99%//AF055084
C-Y79AA1001391//HOMEOBOX PROTEIN HOX-A13 (HOX-1J).//1.20E-58//178aa//66%//P31271
C-Y79AA1001394//CELL DIVISION PROTEIN FTSH HOMOLOG (EC 3.4.24.-).//1.20E-13//230aa//32%//O83746
C-Y79AA1001402//Homo sapiens paraneoplastic cancer-testis-brain antigen (MA4) mRNA, partial cds.//8.50E-65//784bp//62%//AF083115
C-Y79AA1001493//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//3.80E-18//151aa//38%//P35132
C-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//4.50E-193//1333bp//80%//D14336
C-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//7.50E-76//85aa//90%//P42356
C-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.90E-40//482aa//27%//P27550
C-Y79AA1001594//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//2.50E-14//410aa//24%//Q00547
C-Y79AA1001603//POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYLGALACTOS-

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AMINYLTRANSFERASE) (GALNAC-T1).//1.70E-84//313aa//48%//Q07537
C-Y79AA1001613//ZINC FINGER PROTEIN 132.//3.80E-91//209aa//41%//P52740
C-Y79AA1001679//Homo sapiens lambda-crystallin mRNA, complete cds.//3.4e-310//1430bp//98%//AF077049
C-Y79AA1001692//Mus musculus strain C57BL/J germ cell-less protein (Gc1) mRNA, complete cds.//1.40E-78//227aa//40%//Q01820
C-Y79AA1001705//Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds.//3.40E-47//626bp//68%//AF033120
C-Y79AA1001711//Human 60-kdal ribonucleoprotein (Ro) mRNA, complete cds.//1.20E-258//1185bp//99%//J04137
C-Y79AA1001827//Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA, complete cds.//0//1689bp//98%//AF177145
C-Y79AA1001866//Homo sapiens zinc finger protein ZNF180 (ZNF180) mRNA, complete cds.//0//2927bp//97%//AF192913
C-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//4.50E-08//135aa//31%//P43489
C-Y79AA1001875//RAS-RELATED PROTEIN RAB-7.//9.40E-12//34aa//97%//P51149
C-Y79AA1001923//Homo sapiens F-box protein Fbx22 (FBX22) gene, partial cds.//7.10E-52//279bp//97%//AF174602
C-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//1.00E-10//94aa//47%//O42643
C-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.90E-39//143aa//52%//P42743
C-Y79AA1002083//H.sapiens mRNA for MUF1 protein.//5.00E-163//752bp//99%//X86018
C-Y79AA1002103//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.00E-257//549aa//76%//P16415
C-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1).//9.00E-17//120aa//45%//Q24133
C-Y79AA1002204//COMPLEXIN 2 (SYNAPHIN 1) (921-L).//7.50E-09//131aa//35%//Q13329
C-Y79AA1002208//ANKYRIN.//8.10E-34//188aa//38%//Q02357
C-Y79AA1002209/TYROSYL-TRNA SYNTHETASE (EC 6.1.1.1) (TYROSINE--TRNA LIGASE) (TYRRS).//1.60E-72//437aa//39%//P00952
C-Y79AA1002210//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//0.0000018//140aa//25%//Q13829
C-Y79AA1002211//PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN HOMOLOG F40A3.3.//1.70E-17//146aa//35%//O16264
C-Y79AA1002229//DNA CROSS-LINK REPAIR PROTEIN PSO2/SNM1.//7.10E-17//213aa//31%//P30620
C-Y79AA1002246//SYNAPTOTAGMIN V.//1.60E-28//286aa//32%//O00445
C-Y79AA1002258//Homo sapiens mRNA for HIP1R, complete cds.//0//2106bp//99%//AB013384
C-Y79AA1002307//Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds.//0//1209bp//99%//AF116574
C-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.90E-186//1130bp//82%//X67877
C-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//6.90E-140//966bp//82%//Y18208
C-Y79AA1002399//Homo sapiens mRNA for sperm protein.//0//1163bp//95%//X91879
C-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds.//3.9e-317//1902bp//86%//U49385
C-Y79AA1002431//TRANSDUCIN-LIKE ENHANCER PROTEIN 2 (ESG2).//9.80E-62//318aa//35%//Q04725
C-Y79AA1002433//Homo sapiens chromatin- specific transcription elongation factor FACT 140 kDa subunit mRNA, complete cds.//0//1545bp//96%//AF152961
C-Y79AA1002472//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.50E-136//472aa//49%//Q05481
C-Y79AA1002482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.70E-137//340aa//51%//Q05481
C-Y79AA1002487//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.//7.3e-311//1444bp//98%//AF129534

Claims

1. Use of an oligonucleotide as a primer for synthesizing the polynucleotide comprising the nucleotide sequence set

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forth in any one of SEQ ID NOs: 1-5547 and SEQ ID NOs: 16111-16164, or the complementary strand thereof, wherein said oligonucleotide is complementary to said polynucleotide or the complementary strand thereof and comprises at least 15 nucleotides.

2. A primer set for synthesizing polynucleotides, the primer set comprising an oligo-dT primer and an oligonucleotide complementary to the complementary strand of the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-5547 and SEQ ID NOs: 16111-16164, wherein said oligonucleotide comprises at least 15 nucleotides.

3. A primer set for synthesizing polynucleotides, the primer set comprising a combination of an oligonucleotide comprising a nucleotide sequence complementary to the complementary strand of the polynucleotide comprising a 5'-end nucleotide sequence and an oligonucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising a 3'-end nucleotide sequence, wherein said oligonucleotides comprise at least 15 nucleotides and wherein said combination of 5'-end nucleotide sequence 3'-end nucleotide sequence is selected from the group consisting of:

SEQ ID NO: 1 / SEQ ID NO: 5548, SEQ ID NO: 4 / SEQ ID NO: 5549, SEQ ID NO: 5 / SEQ ID NO: 5550, SEQ ID NO: 6 / SEQ ID NO: 5551, SEQ ID NO: 7 / SEQ ID NO: 5552, SEQ ID NO: 8 / SEQ ID NO: 5553, SEQ ID NO: 9 / SEQ ID NO: 5554, SEQ ID NO: 10 / SEQ ID NO: 5555, SEQ ID NO: 11 / SEQ ID NO: 5556, SEQ ID NO: 12 / SEQ ID NO: 5557, SEQ ID NO: 13 / SEQ ID NO: 5558, SEQ ID NO: 14 / SEQ ID NO: 5559, SEQ ID NO: 15 / SEQ ID NO: 5560, SEQ ID NO: 16 / SEQ ID NO: 5561, SEQ ID NO: 17 / SEQ ID NO: 5562, SEQ ID NO: 18 / SEQ ID NO: 5563, SEQ ID NO: 19 / SEQ ID NO: 5564, SEQ ID NO: 20 / SEQ ID NO: 5565, SEQ ID NO: 21 / SEQ ID NO: 5566, SEQ ID NO: 22 / SEQ ID NO: 5567, SEQ ID NO: 23 / SEQ ID NO: 5568, SEQ ID NO: 24 / SEQ ID NO: 5569, SEQ ID NO: 25 / SEQ ID NO: 5570, SEQ ID NO: 26 / SEQ ID NO: 5571, SEQ ID NO: 27 / SEQ ID NO: 5572, SEQ ID NO: 28 / SEQ ID NO: 5573, SEQ ID NO: 29 / SEQ ID NO: 5574, SEQ ID NO: 30 / SEQ ID NO: 5575, SEQ ID NO: 31 / SEQ ID NO: 5576, SEQ ID NO: 32 / SEQ ID NO: 5577, SEQ ID NO: 33 / SEQ ID NO: 5578, SEQ ID NO: 34 / SEQ ID NO: 5579, SEQ ID NO: 35 / SEQ ID NO: 5580, SEQ ID NO: 37 / SEQ ID NO: 5581, SEQ ID NO: 38 / SEQ ID NO: 5582, SEQ ID NO: 39 / SEQ ID NO: 5583, SEQ ID NO: 40 / SEQ ID NO: 5584, SEQ ID NO: 42 / SEQ ID NO: 5585, SEQ ID NO: 43 / SEQ ID NO: 5586, SEQ ID NO: 44 / SEQ ID NO: 5587, SEQ ID NO: 45 / SEQ ID NO: 5588, SEQ ID NO: 46 / SEQ ID NO: 5589, SEQ ID NO: 47 / SEQ ID NO: 5590, SEQ ID NO: 48 / SEQ ID NO: 5591, SEQ ID NO: 49 / SEQ ID NO: 5592, SEQ ID NO: 50 / SEQ ID NO: 5593, SEQ ID NO: 51 / SEQ ID NO: 5594, SEQ ID NO: 52 / SEQ ID NO: 5595, SEQ ID NO: 53 / SEQ ID NO: 5596, SEQ ID NO: 54 / SEQ ID NO: 5597, SEQ ID NO: 55 / SEQ ID NO: 5598, SEQ ID NO: 56 / SEQ ID NO: 5599, SEQ ID NO: 57 / SEQ ID NO: 5600, SEQ ID NO: 58 / SEQ ID NO: 5601, SEQ ID NO: 59 / SEQ ID NO: 5602, SEQ ID NO: 60 / SEQ ID NO: 5603, SEQ ID NO: 61 / SEQ ID NO: 5604, SEQ ID NO: 62 / SEQ ID NO: 5605, SEQ ID NO: 63 / SEQ ID NO: 5606, SEQ ID NO: 65 / SEQ ID NO: 5607, SEQ ID NO: 66 / SEQ ID NO: 5608, SEQ ID NO: 67 / SEQ ID NO: 5609, SEQ ID NO: 68 / SEQ ID NO: 5610, SEQ ID NO: 69 / SEQ ID NO: 5611, SEQ ID NO: 70 / SEQ ID NO: 5612, SEQ ID NO: 71 / SEQ ID NO: 5613, SEQ ID NO: 72 / SEQ ID NO: 5614, SEQ ID NO: 74 / SEQ ID NO: 5615, SEQ ID NO: 76 / SEQ ID NO: 5616, SEQ ID NO: 77 / SEQ ID NO: 5617, SEQ ID NO: 78 / SEQ ID NO: 5618, SEQ ID NO: 79 / SEQ ID NO: 5619, SEQ ID NO: 80 / SEQ ID NO: 5620, SEQ ID NO: 81 / SEQ ID NO: 5621, SEQ ID NO: 82 / SEQ ID NO: 5622, SEQ ID NO: 83 / SEQ ID NO: 5623, SEQ ID NO: 84 / SEQ ID NO: 5624, SEQ ID NO: 85 / SEQ ID NO: 5625, SEQ ID NO: 86 / SEQ ID NO: 5626, SEQ ID NO: 87 / SEQ ID NO: 5627, SEQ ID NO: 88 / SEQ ID NO: 5628, SEQ ID NO: 89 / SEQ ID NO: 5629, SEQ ID NO: 90 / SEQ ID NO: 5630, SEQ ID NO: 91 / SEQ ID NO: 5631, SEQ ID NO: 92 / SEQ ID NO: 5632, SEQ ID NO:

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NO: 16216, SEQ ID NO: 16163 / SEQ ID NO: 16217, and SEQ ID NO: 16164 / SEQ ID NO: 16218

4. A polynucleotide which can be synthesized with the primer set of claim 2 or 3.

5. A polynucleotide comprising a coding region in the polynucleotide of claim 4.

6. A substantially pure protein encoded by polynucleotide of claim 4.

7. A partial peptide of the protein of claim 6.

8. An isolated polynucleotide selected from the group consisting of

(a) a polynucleotide comprising a coding region of the nucleotide sequence set forth in any one of the following SEQ ID NOs:

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SEQ ID NO: 10468, SEQ ID NO: 10470, SEQ ID NO: 10471, SEQ ID NO: 10472, SEQ ID NO: 10473, SEQ ID NO: 10475, SEQ ID NO: 10477, SEQ ID NO: 10479, SEQ ID NO: 10481, SEQ ID NO: 10483, SEQ ID NO: 10485, SEQ ID NO: 10487, SEQ ID NO: 10488, SEQ ID NO: 10489, SEQ ID NO: 10491, SEQ ID NO: 10493, SEQ ID NO: 10495, SEQ ID NO: 10496, SEQ ID NO: 10497, SEQ ID NO: 10498, SEQ ID NO: 10500, SEQ ID NO: 10502, SEQ ID NO: 10503, SEQ ID NO: 10504, SEQ ID NO: 10505, SEQ ID NO: 10507, SEQ ID NO: 10508, SEQ ID NO: 10510, SEQ ID NO: 10511, SEQ ID NO: 10512, SEQ ID NO: 10514, SEQ ID NO: 10516, SEQ ID NO: 10517, SEQ ID NO: 10519, SEQ ID NO: 10521, SEQ ID NO: 10523, SEQ ID NO: 10524, SEQ ID NO: 10526, SEQ ID NO: 10528, SEQ ID NO: 10529, SEQ ID NO: 10530, SEQ ID NO: 10532, SEQ ID NO: 10534, SEQ ID NO: 10535, SEQ ID NO: 10537, SEQ ID NO: 10539, SEQ ID NO: 10540, SEQ ID NO: 10542, SEQ ID NO: 10543, SEQ ID NO: 10545, SEQ ID NO: 10546, SEQ ID NO: 10548, SEQ ID NO: 10550, SEQ ID NO: 10551, SEQ ID NO: 10553, SEQ ID NO: 10555, SEQ ID NO: 10556, SEQ ID NO: 10557, SEQ ID NO: 10558, SEQ ID NO: 10560, SEQ ID NO: 10562, SEQ ID NO: 10564, SEQ ID NO: 10566, SEQ ID NO: 10567, SEQ ID NO: 10569, SEQ ID NO: 10571, SEQ ID NO: 10573, SEQ ID NO: 10574, SEQ ID NO: 10576, SEQ ID NO: 10578, SEQ ID NO: 10580, SEQ ID NO: 10582, SEQ ID NO: 10584, SEQ ID NO: 10586, SEQ ID NO: 10588, SEQ ID NO: 10590, SEQ ID NO: 10592, SEQ ID NO: 10594, SEQ ID NO: 10596, SEQ ID NO: 10597, SEQ ID NO: 10599, SEQ ID NO: 10601, SEQ ID NO: 10603, SEQ ID NO: 10604, SEQ ID NO: 10606, SEQ ID NO: 10607, SEQ ID NO: 10609, SEQ ID NO: 10611, SEQ ID NO: 10613, SEQ ID NO: 10614, SEQ ID NO: 10615, SEQ ID NO: 10616, SEQ ID NO: 10618, SEQ ID NO: 10619, SEQ ID NO: 10620, SEQ ID NO: 10622, SEQ ID NO: 10624, SEQ ID NO: 10625, SEQ ID NO: 10627, SEQ ID NO: 10629,
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(b) a polynucleotide comprising a nucleotide sequence encoding a protein comprising the amino acid sequence set forth in any one of the following SEQ ID NOs:

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(c) a polynucleotide comprising a nucleotide sequence encoding a protein comprising an amino acid sequence selected from the amino acid sequences of (b), in which one or more amino acids are substituted, deleted, inserted, and/or added, wherein said protein is functionally equivalent to the protein comprising said amino acid sequence selected from the amino acid sequences of (b);
(d) a polynucleotide that hybridizes with a polynucleotide comprising a nucleotide sequence selected from the nucleotide sequences of (a), and that comprises a nucleotide sequence encoding a protein functionally equivalent to the protein encoded by the nucleotide sequence selected from the nucleotide sequences of (a);
(e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a protein encoded by the polynucleotide of (a) to (d);
(f) a polynucleotide comprising a nucleotide sequence with at least 70% identity to the nucleotide sequence of (a).

9. A substantially pure protein encoded by the polynucleotide of claim 8.

10. An antibody against the protein or peptide of any one of claims 6, 7, and 9.

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11. A vector comprising the polynucleotide of claim 5 or 8.

12. A transformant carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.

13. A transformant expressively carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.

14. A method for producing the protein or peptide of any one of claims 6, 7, and 9, comprising culturing the transformant of claim 13 and recovering the expression product.

15. An oligonucleotide comprising the nucleotide sequence of claim 8 (a) or the nucleotide sequence complementary to the complementary strand thereof, wherein said oligonucleotide comprises 15 nucleotides or more.

16. Use of the oligonucleotide of claim 15 as a primer for synthesizing a polynucleotide.

17. Use of the oligonucleotide of claim 15 as a probe for detecting a gene.

18. An antisense polynucleotide against the polynucleotide of claim 8, or the portion thereof.

19. A method for synthesizing a polynucleotide, the method comprising:

a) synthesizing a complementary strand using a cDNA library as a template, and using the primer set of claim 2 or 3, or the primer of claim 16; and
b) recovering the synthesized product.

20. The method of claim 19, wherein the cDNA library is obtainable by oligo-capping method.

21. The method of claim 19, wherein the complementary strand is obtainable by PCR.

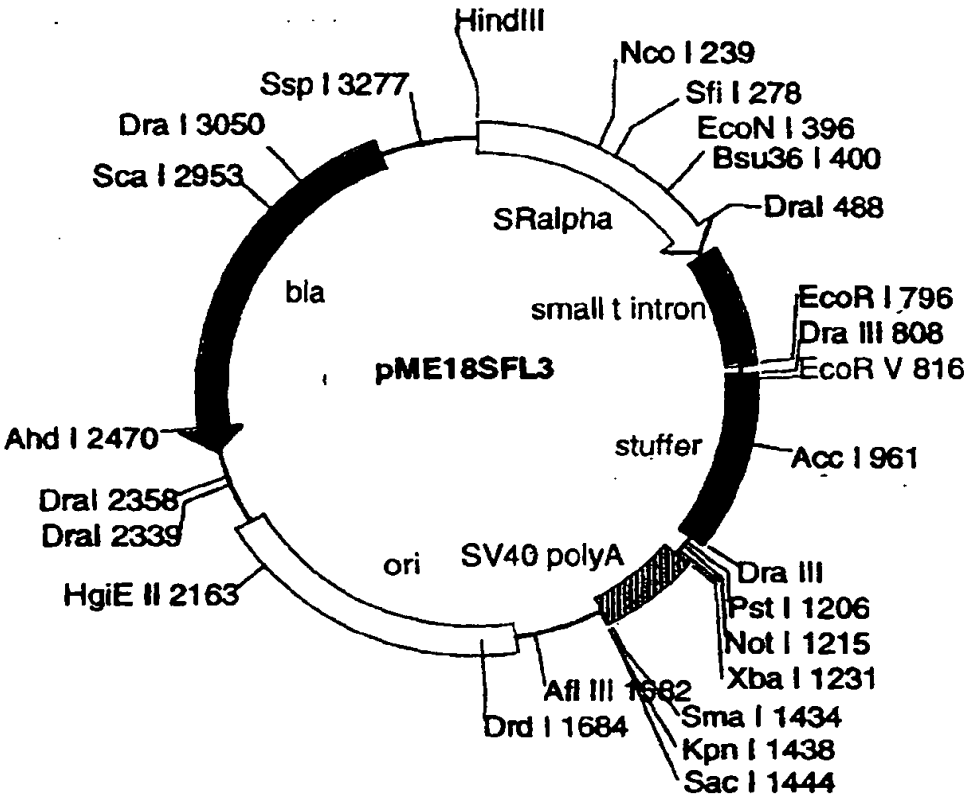
22. A method for detecting the polynucleotide of claim 8, the method comprising:

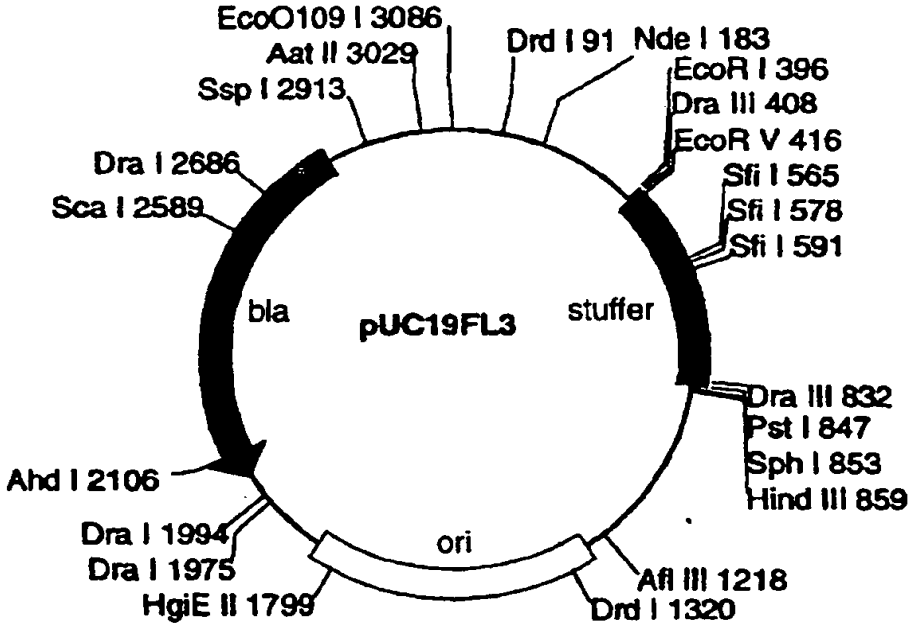
a) incubating a target polynucleotide with the oligonucleotide of claim 15 under the conditions where hybridization occurs, and
b) detecting the hybridization of the target polynucleotide with the oligonucleotide of claim 15.

23. A database of polynucleotides and/or proteins, the database comprising information on at least one sequence selected from the nucleotide sequences of claim 8 (a) and/or the amino acid sequences of claim 8 (b), or a medium on which the database is stored.

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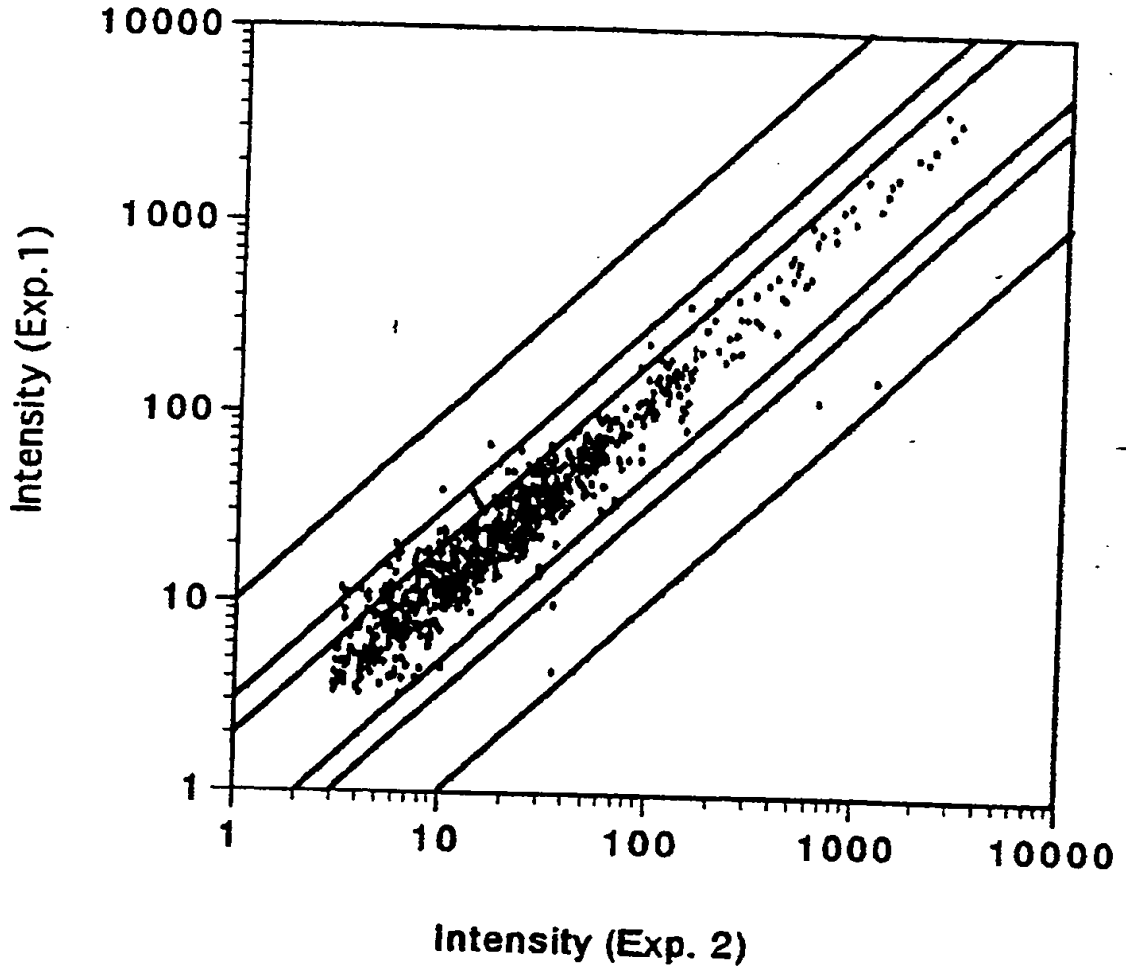
Figure 1





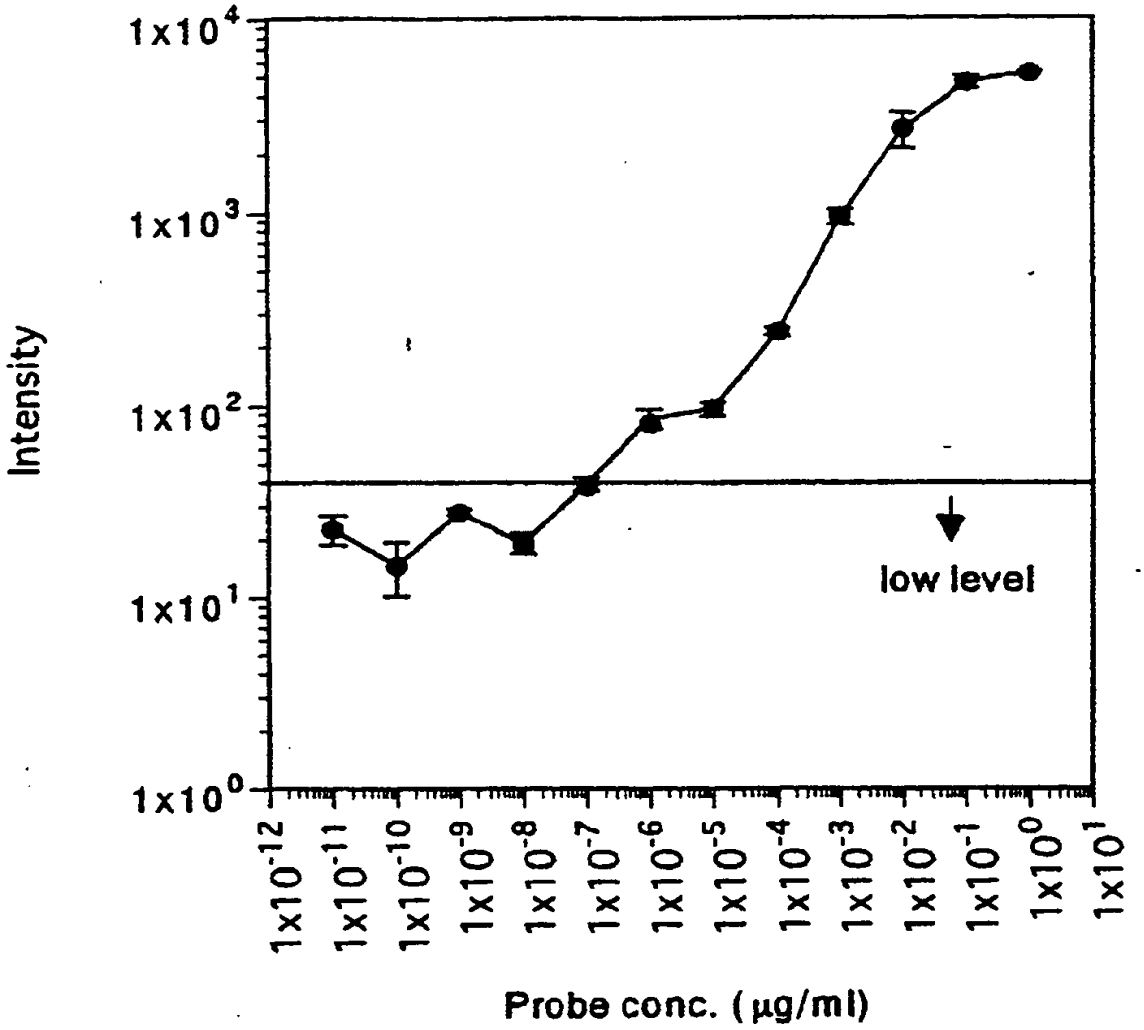
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Figure 2



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Figure 3



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